



Full wwPDB EM Validation Report ⓘ

Mar 12, 2026 – 07:40 AM UTC

PDB ID : 6QX9 / pdb_00006qx9
EMDB ID : EMD-4665
Title : Structure of a human fully-assembled precatalytic spliceosome (pre-B complex).
Authors : Charenton, C.; Wilkinson, M.E.; Nagai, K.
Deposited on : 2019-03-07
Resolution : 3.28 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

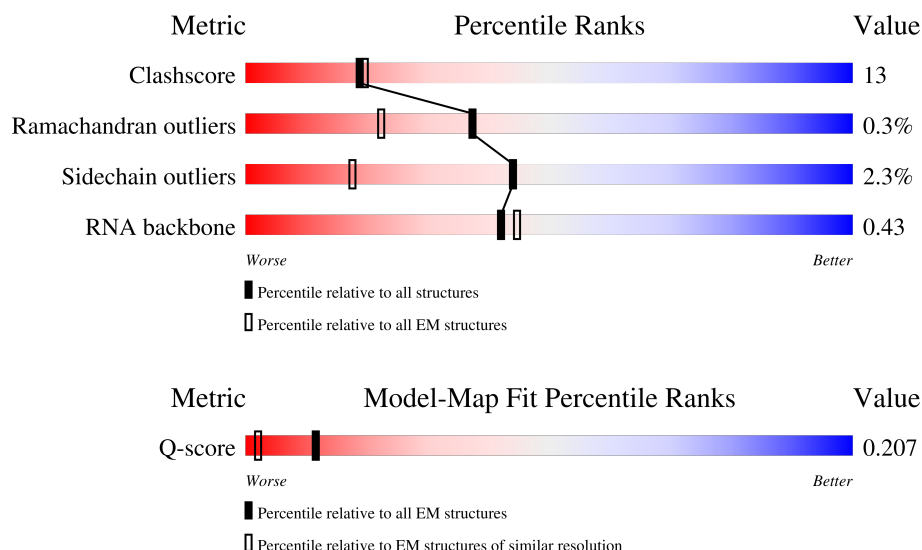
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.28 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	14492 (2.78 - 3.78)

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	1	164	
2	6	106	
3	50	357	

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Mol	Chain	Length	Quality of chain
4	B4	424	
5	13	126	
5	23	126	
5	43	126	
5	53	126	
6	4B	522	
7	1e	92	
7	2e	92	
7	4e	92	
7	5e	92	
8	I	62	
9	1K	437	
10	4C	499	
11	11	119	
11	21	119	
11	41	119	
11	51	119	
12	R	480	
13	1f	86	
13	2f	86	
13	4f	86	
13	5f	86	
14	66	80	
15	X	155	
16	12	118	

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Mol	Chain	Length	Quality of chain
16	22	118	
16	42	118	
16	52	118	
17	5	117	
18	67	103	
19	62	95	
20	2B	225	
21	A2	209	
22	B2	895	
23	5C	854	
24	5X	820	
25	1b	240	
25	2b	240	
25	4b	240	
25	5b	240	
26	B5	86	
27	1A	282	
28	S	800	
29	5J	850	
30	4D	128	
31	63	102	
32	2	188	
33	B3	1217	
34	1g	76	
34	2g	76	

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Mol	Chain	Length	Quality of chain
34	4g	76	
34	5g	76	
35	68	96	
36	5A	2311	
37	A3	501	
38	U	555	
39	5D	142	
40	64	139	
41	BP	104	
42	1C	159	
43	K	1007	
44	4A	683	
45	4	146	
46	2A	255	
47	A1	647	
48	65	91	
49	5B	2136	
50	B1	1304	

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 137494 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 U1 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	164	Total	C	N	O	P	0	0
			3485	1555	607	1159	164		

- Molecule 2 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	6	53	Total	C	N	O	P	0	0
			1133	506	203	371	53		

- Molecule 3 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5O	306	Total	C	N	O	S	0	0
			2394	1501	422	457	14		

- Molecule 4 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B4	78	Total	C	N	O	S	0	0
			618	399	101	115	3		

- Molecule 5 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	13	81	Total	C	N	O	S	0	0
			637	400	112	119	6		
5	53	84	Total	C	N	O	S	0	0
			657	412	116	123	6		
5	23	83	Total	C	N	O	S	0	0
			652	409	115	122	6		
5	43	83	Total	C	N	O	S	0	0
			652	409	115	122	6		

- Molecule 6 is a protein called U4/U6 small nuclear ribonucleoprotein Prp4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	4B	359	Total	C	N	O	S	0	0
			2842	1793	509	521	19		

- Molecule 7 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	5e	77	Total	C	N	O	S	0	0
			638	405	113	115	5		
7	4e	76	Total	C	N	O	S	0	0
			631	400	112	114	5		
7	1e	77	Total	C	N	O	S	0	0
			638	405	113	115	5		
7	2e	81	Total	C	N	O	S	0	0
			669	424	119	121	5		

- Molecule 8 is a RNA chain called AdML pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	25	Total	C	N	O	P	0	0
			530	237	92	177	24		

- Molecule 9 is a protein called U1 small nuclear ribonucleoprotein 70 kDa.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	1K	201	Total	C	N	O	S	0	0
			1649	1036	317	291	5		

- Molecule 10 is a protein called U4/U6 small nuclear ribonucleoprotein Prp31.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	4C	301	Total	C	N	O	S	0	0
			2375	1486	418	456	15		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	41	81	Total	C	N	O	S	0	0
			641	408	112	118	3		
11	11	81	Total	C	N	O	S	0	0
			641	408	112	118	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
11	51	81	Total	C	N	O	S	0	0
			641	408	112	118	3		
11	21	80	Total	C	N	O	S	0	0
			634	404	111	115	4		

- Molecule 12 is a protein called RNA-binding protein 42.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	R	106	Total	C	N	O	S	0	0
			874	553	160	157	4		

- Molecule 13 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	1f	74	Total	C	N	O	S	0	0
			576	373	95	103	5		
13	2f	72	Total	C	N	O	S	0	0
			562	364	93	100	5		
13	5f	73	Total	C	N	O	S	0	0
			567	367	94	101	5		
13	4f	72	Total	C	N	O	S	0	0
			562	364	93	100	5		

- Molecule 14 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	66	72	Total	C	N	O	S	0	0
			567	360	97	108	2		

- Molecule 15 is a protein called U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	X	49	Total	C	N	O	S	0	0
			394	247	74	69	4		

- Molecule 16 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	22	95	Total	C	N	O	S	0	0
			774	486	141	142	5		
16	42	92	Total	C	N	O	S	0	0
			737	463	138	131	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
16	52	98	Total	C	N	O	S	0	0
			796	498	144	148	6		
16	12	95	Total	C	N	O	S	0	0
			777	486	141	144	6		

- Molecule 17 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	5	104	Total	C	N	O	P	0	0
			2192	983	372	734	103		

- Molecule 18 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	67	77	Total	C	N	O	S	0	0
			604	383	102	116	3		

- Molecule 19 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	62	95	Total	C	N	O	S	0	0
			761	486	126	145	4		

- Molecule 20 is a protein called U2 small nuclear ribonucleoprotein B”.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	2B	92	Total	C	N	O	S	0	0
			745	480	130	130	5		

- Molecule 21 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	A2	144	Total	C	N	O	S	0	0
			1221	782	219	214	6		

- Molecule 22 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	B2	208	Total	C	N	O	S	0	0
			1699	1093	302	295	9		

- Molecule 23 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	5C	852	Total	C	N	O	S	0	0
			6727	4300	1127	1266	34		

- Molecule 24 is a protein called Probable ATP-dependent RNA helicase DDX23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	5X	583	Total	C	N	O	S	7	0
			4780	3014	855	893	18		

- Molecule 25 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	1b	86	Total	C	N	O	S	0	0
			692	435	126	124	7		
25	2b	82	Total	C	N	O	S	0	0
			664	419	121	117	7		
25	5b	73	Total	C	N	O	S	0	0
			594	376	108	103	7		
25	4b	82	Total	C	N	O	S	0	0
			669	423	122	117	7		

- Molecule 26 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B5	69	Total	C	N	O	S	0	0
			567	360	99	103	5		

- Molecule 27 is a protein called U1 small nuclear ribonucleoprotein A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	1A	98	Total	C	N	O	S	0	0
			787	506	134	143	4		

- Molecule 28 is a protein called U4/U6.U5 tri-snRNP-associated protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	S	120	Total	C	N	O	S	0	0
			917	576	168	168	5		

- Molecule 29 is a protein called Pre-mRNA-processing factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	5J	803	Total	C	N	O	S	0	0
			6316	3963	1155	1170	28		

- Molecule 30 is a protein called NHP2-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4D	123	Total	C	N	O	S	0	0
			955	604	170	176	5		

- Molecule 31 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	63	85	Total	C	N	O	S	0	0
			699	440	120	136	3		

- Molecule 32 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	2	94	Total	C	N	O	P	0	0
			1984	887	331	672	94		

- Molecule 33 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	B3	1186	Total	C	N	O	S	0	0
			9296	5898	1580	1773	45		

- Molecule 34 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	1g	73	Total	C	N	O	S	0	0
			568	358	102	102	6		
34	2g	73	Total	C	N	O	S	0	0
			568	358	102	102	6		
34	5g	74	Total	C	N	O	S	0	0
			577	364	104	103	6		
34	4g	74	Total	C	N	O	S	0	0
			577	364	104	103	6		

- Molecule 35 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	68	95	Total	C	N	O	S	0	0
			722	446	124	151	1		

- Molecule 36 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	5A	2212	Total	C	N	O	S	0	0
			18366	11840	3193	3253	80		

- Molecule 37 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	A3	383	Total	C	N	O	S	0	0
			3227	2029	566	618	14		

- Molecule 38 is a protein called U4/U6.U5 tri-snRNP-associated protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	U	456	Total	C	N	O	S	0	0
			3750	2427	635	674	14		

- Molecule 39 is a protein called Thioredoxin-like protein 4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	5D	141	Total	C	N	O	S	0	0
			1169	751	194	214	10		

- Molecule 40 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	64	73	Total	C	N	O	S	0	0
			596	376	105	109	6		

- Molecule 41 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BP	100	Total	C	N	O	S	0	0
			766	473	135	145	13		

- Molecule 42 is a protein called U1 small nuclear ribonucleoprotein C.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	1C	50	Total	C	N	O	S	0	0
			425	266	73	82	4		

- Molecule 43 is a protein called Serine/threonine-protein kinase PRP4 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	K	322	Total	C	N	O	S	0	0
			2626	1682	462	467	15		

- Molecule 44 is a protein called U4/U6 small nuclear ribonucleoprotein Prp3.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	4A	239	Total	C	N	O	S	0	0
			1946	1237	360	342	7		

- Molecule 45 is a RNA chain called U4 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	4	126	Total	C	N	O	P	0	0
			2690	1202	474	888	126		

- Molecule 46 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	2A	162	Total	C	N	O	S	0	0
			1282	820	219	240	3		

- Molecule 47 is a protein called Splicing factor 3A subunit 1,Splicing factor 3A subunit 1,Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	A1	168	Total	C	N	O	S	0	0
			1339	855	237	245	2		

- Molecule 48 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	65	76	Total	C	N	O	S	0	0
			587	373	96	114	4		

- Molecule 49 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	5B	2001	Total	C	N	O	S	0	0
			16077	10235	2767	2991	84		

- Molecule 50 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	B1	848	Total	C	N	O	S	0	0
			6749	4330	1160	1220	39		

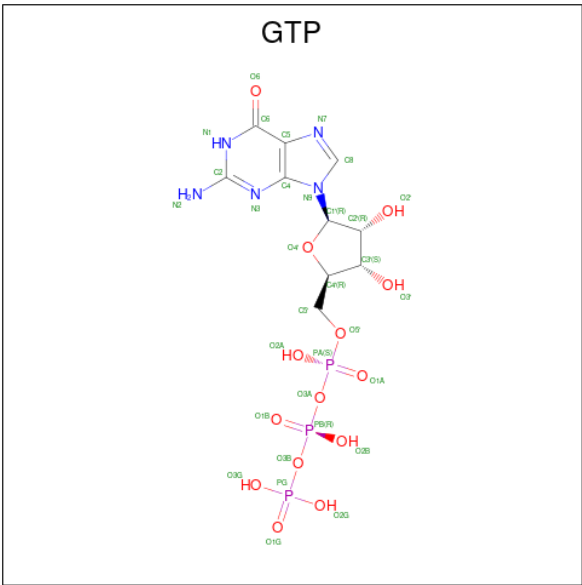
- Molecule 51 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
51	A2	1	Total	Zn	0
			1	1	
51	U	1	Total	Zn	0
			1	1	
51	BP	3	Total	Zn	0
			3	3	
51	1C	1	Total	Zn	0
			1	1	

- Molecule 52 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

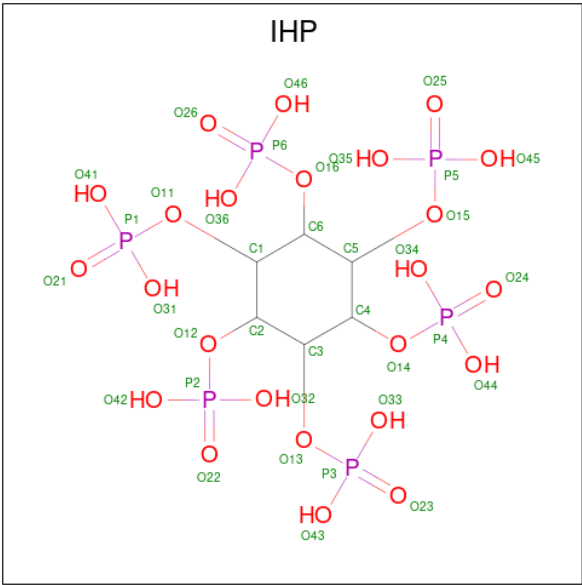
Mol	Chain	Residues	Atoms		AltConf
52	5C	1	Total	Mg	0
			1	1	

- Molecule 53 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

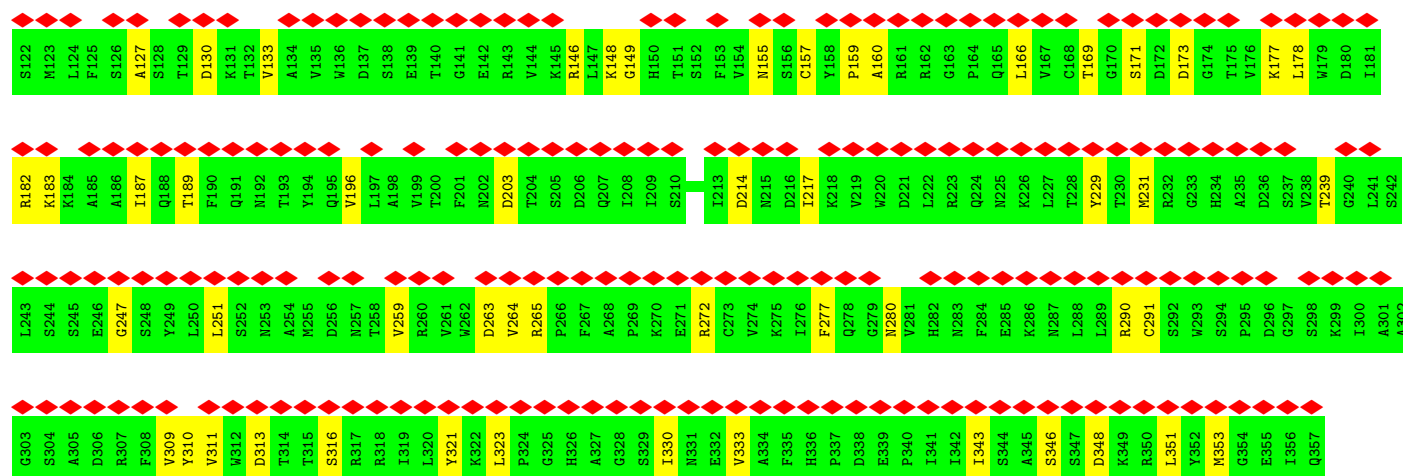


Mol	Chain	Residues	Atoms					AltConf
53	5C	1	Total	C	N	O	P	0
			32	10	5	14	3	

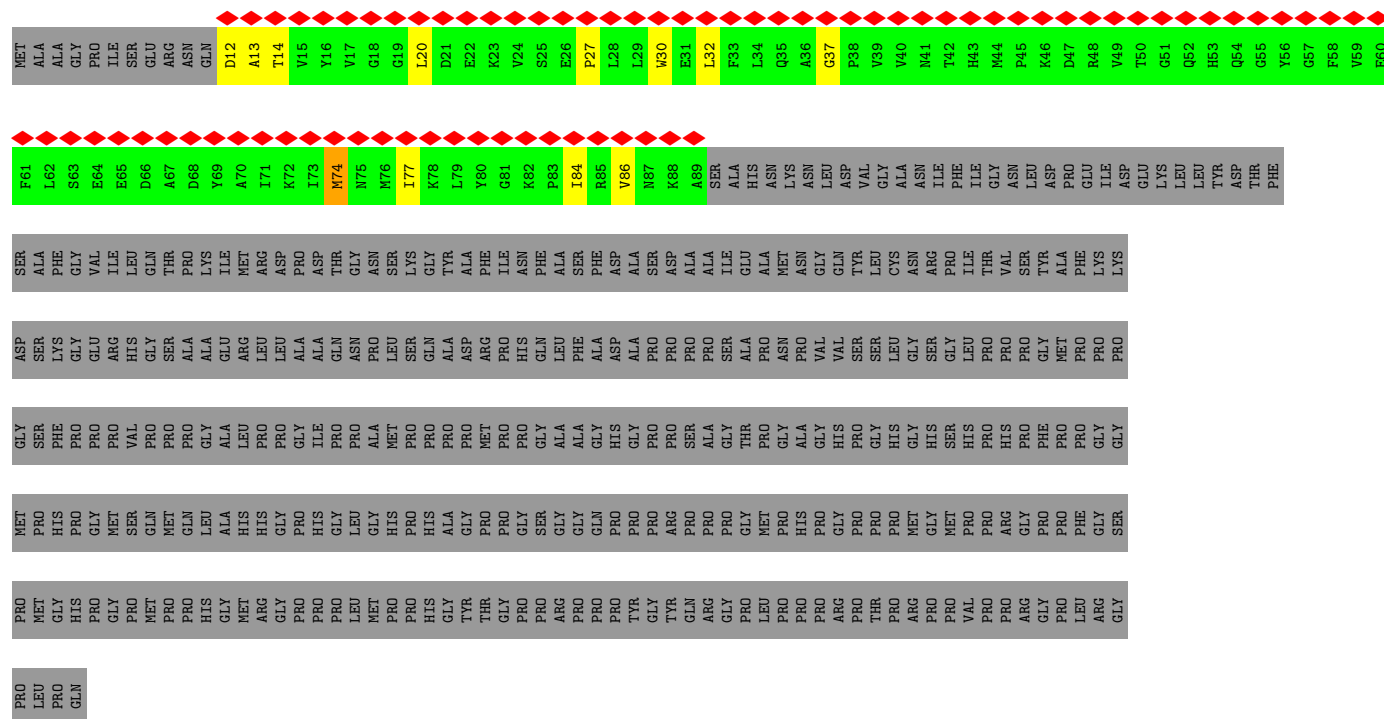
- Molecule 54 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$).



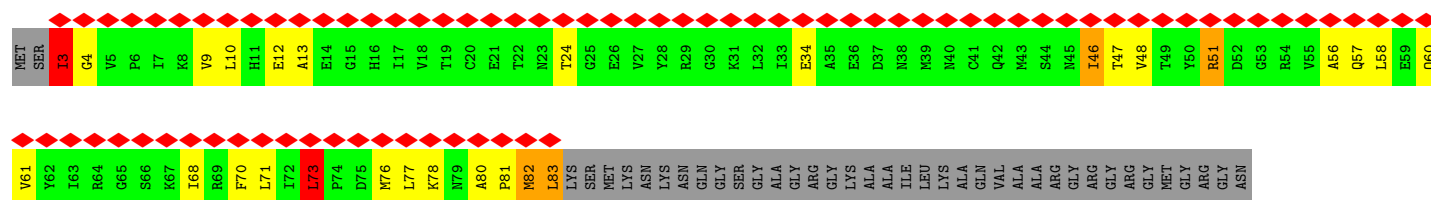
Mol	Chain	Residues	Atoms				AltConf
54	5A	1	Total	C	O	P	0
			36	6	24	6	

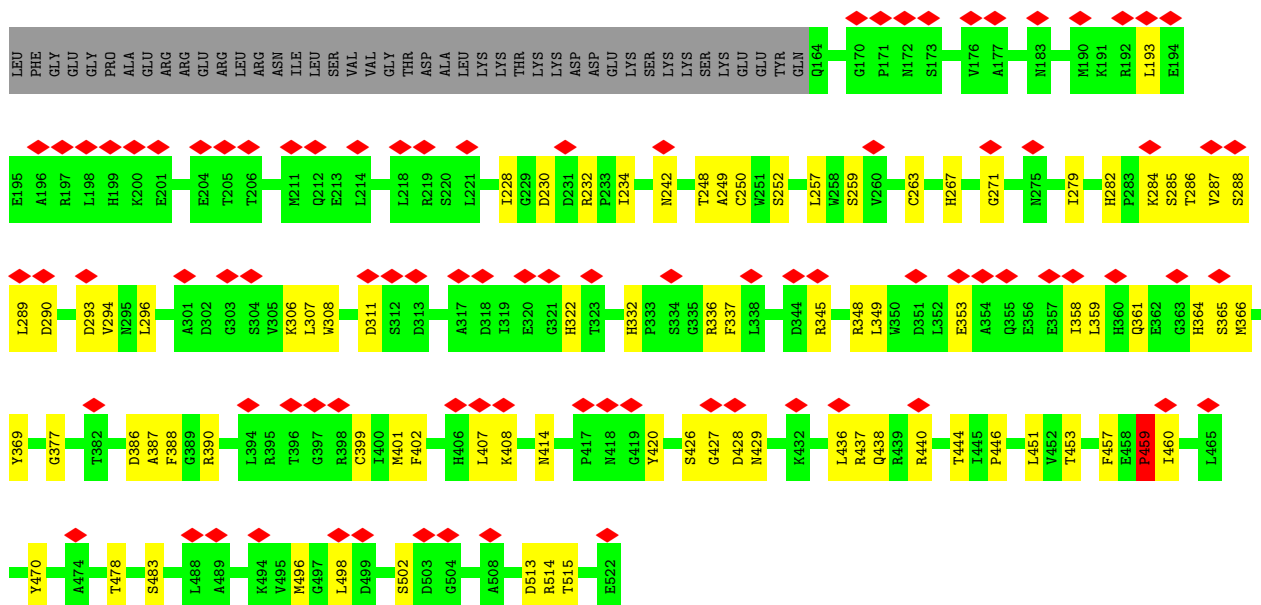


• Molecule 4: Splicing factor 3B subunit 4

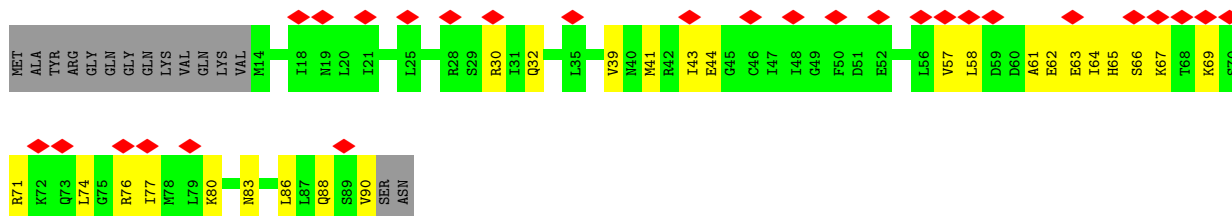


• Molecule 5: Small nuclear ribonucleoprotein Sm D3

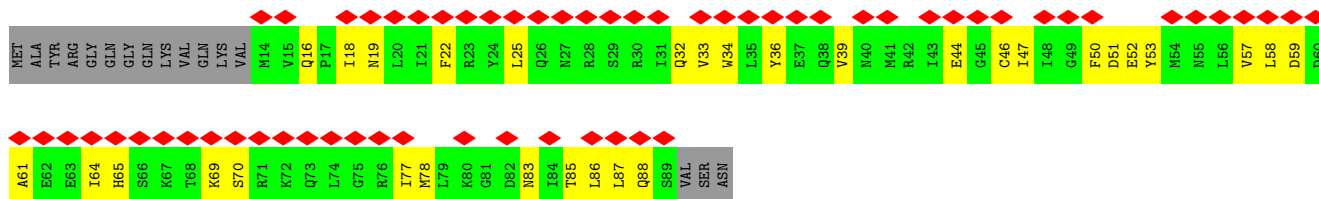




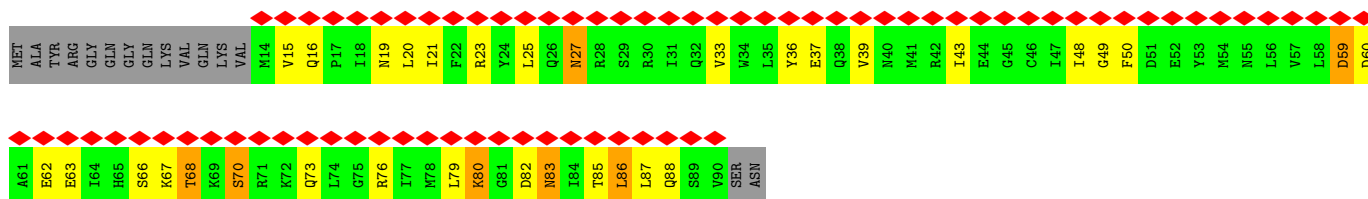
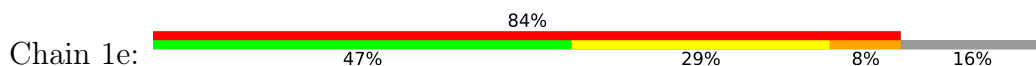
- Molecule 7: Small nuclear ribonucleoprotein E



- Molecule 7: Small nuclear ribonucleoprotein E

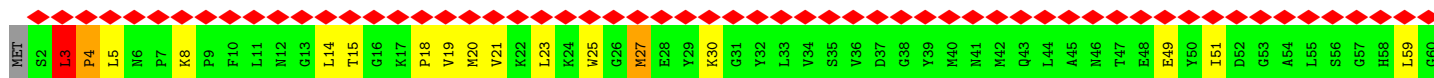


- Molecule 7: Small nuclear ribonucleoprotein E



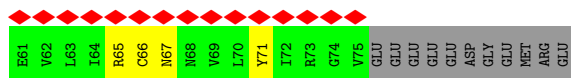
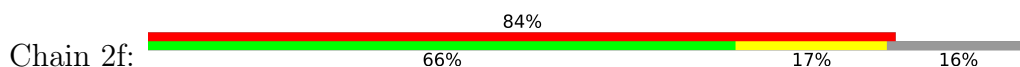
Chain 4C:



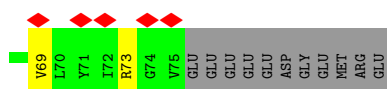




- Molecule 13: Small nuclear ribonucleoprotein F



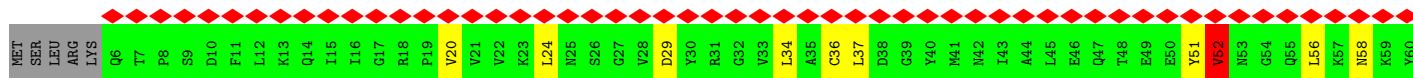
- Molecule 13: Small nuclear ribonucleoprotein F



- Molecule 13: Small nuclear ribonucleoprotein F

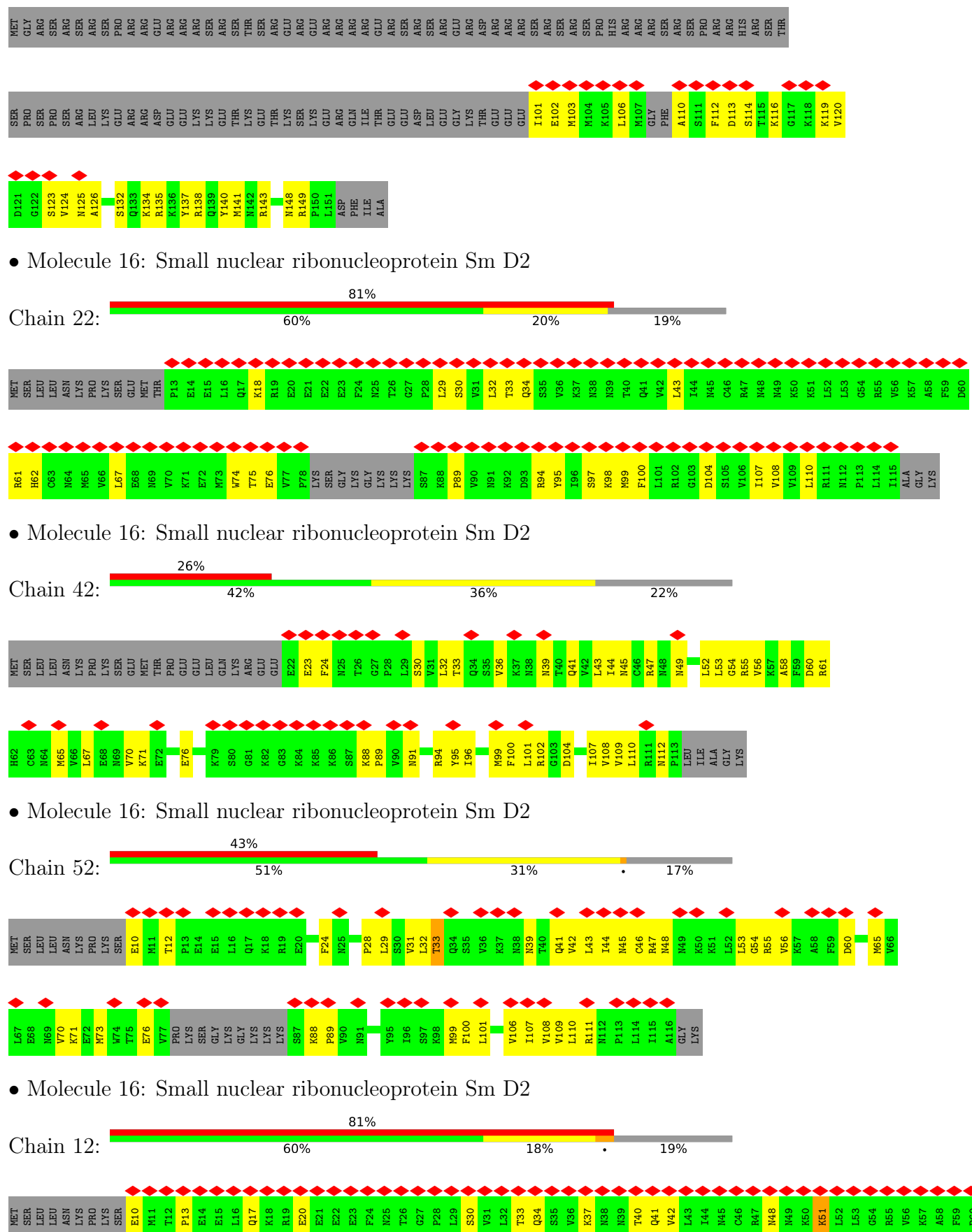


- Molecule 14: U6 snRNA-associated Sm-like protein LSm6



- Molecule 15: U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein



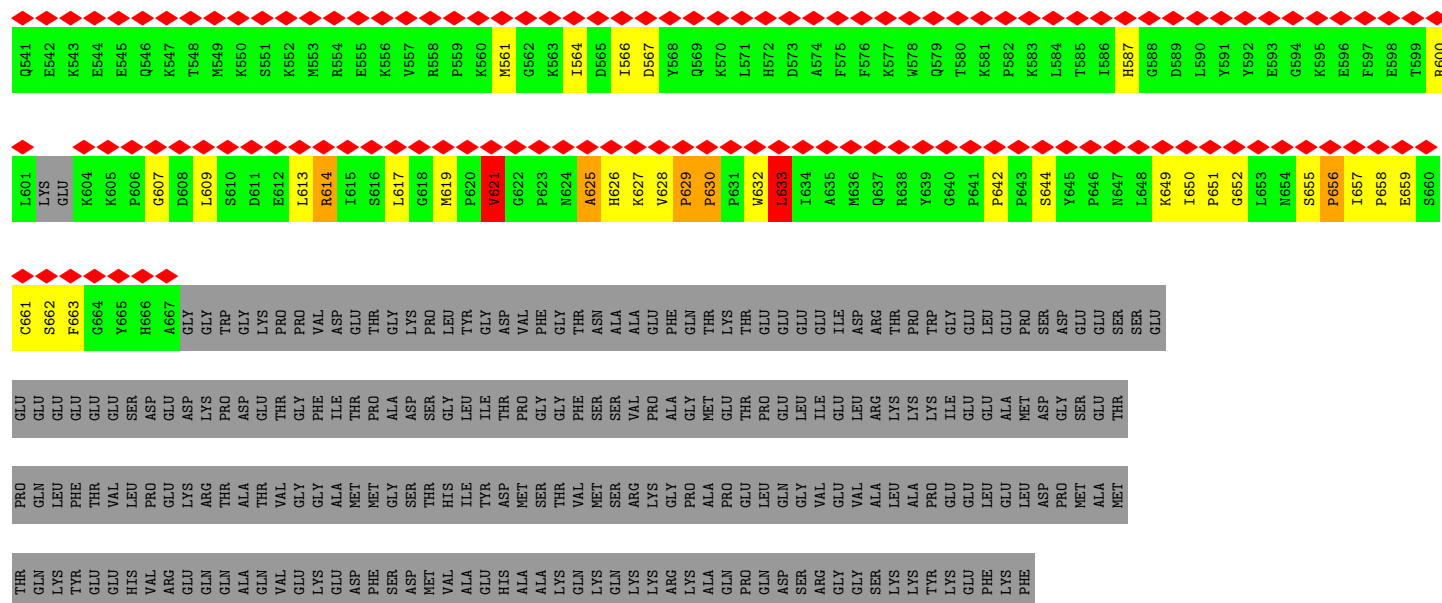


- Molecule 21: Splicing factor 3A subunit 2

F181	K182	V183	P184	S185	R186	E187	I188	D189	K190	A191	E192	G193	K194	F195	V196	T197	H198	W199	N200	R201	E202	T203	K204	Q205	F206	L207	L208	Q209																																
T61	K121	Q122	R123	D124	S125	E126	MET	G127	G128	G129	SER	LEU	L133	F134	Q135	I136	D137	Y138	P139	E140	I141	A142	E143	G144	I145	M146	P147	R148	H149	R150	F151	M152	S153	A154	Y155	E156	Q157	R158	I159	E160	P161	P162	D163	R164	R165	V166	Q167	V168	L169	L170	M171	A172	A173	E174	P175	Y176	E177	T178	I179	A180
ASP	PHE	GLN	HIS	ARG	PRO	GLY	LYS	THR	GLY	SER	GLY	VAL	ALA	SER	SER	SER	GLU	SER	ASN	ARG	ASP	ARG	GLU	ARG	LEU	ARG	GLN	LEU	ALA	LYS	GLU	THR	ILE	ASP	ASP	ILE	ASN	K42	D43	P44	Y45	F46	N47	K48	N49	H50	L51	G52	S53	T54	E55	C56	K57	L58	C59	L60				
T61	L62	H63	N64	N65	E66	G67	S68	Y69	L70	A71	H72	T73	Q74	G75	K76	K77	H78	Q79	T80	N81	L82	A83	R84	R85	ALA	ALA	LYS	GLU	ALA	LYS	GLU	VAL	LYS	PRO	ALA	GLN	PRO	ALA	PRO	GLU	LYS	VAL	LYS	V104	E105	V106	K107	K108	F109	V110	K111	I112	G113	R114	P115	G116	Y117	K118	V119	T120

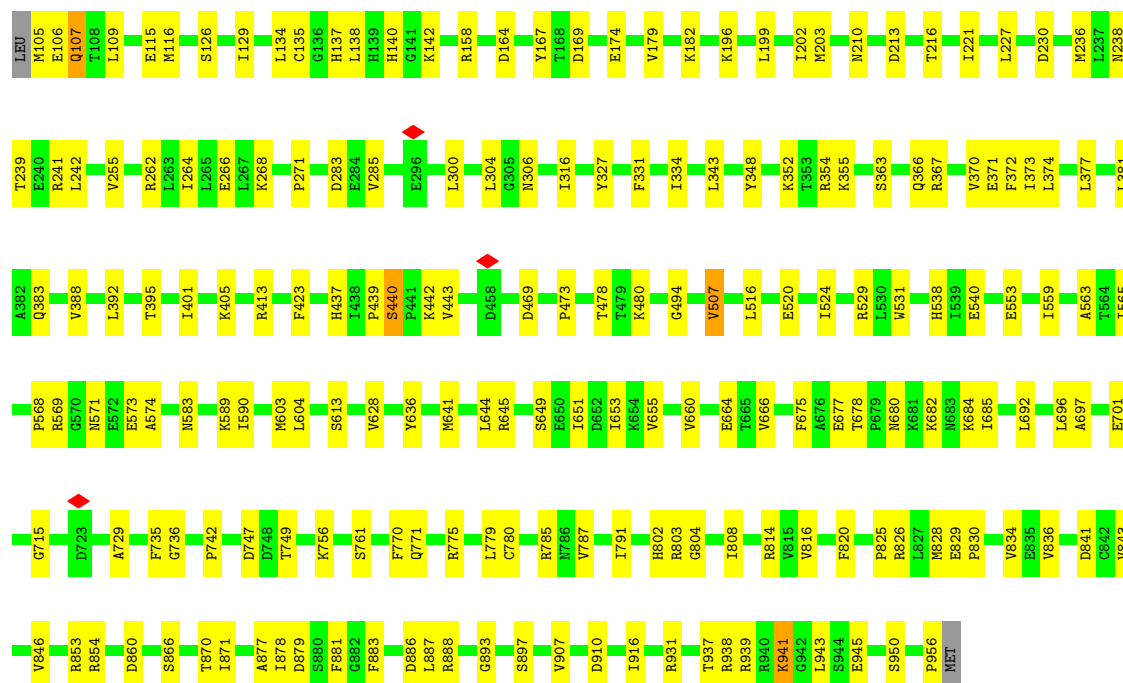
- Molecule 22: Splicing factor 3B subunit 2

T481	LYS	ASP	ARG	ALA	GLN	MET	THR	MET
A482	LYS	SER	SER	PRO	LYS	ALA	ILE	GLY
Q483	PHE	PRO	SER	VAL	ARG	HIS	THR	GLY
D484	GLU	ALA	LEU	PRO	ALA	PRO	VAL	VAL
P485	GLU	ASP	GLN	PRO	VAL	ASN	ASN	ASN
K486	GLU	VAL	SER	ARG	LEU	LEU	ARG	ARG
L487	HIS	GLU	ALA	GLY	LEU	GLY	PRO	PRO
L488	LYS	ILE	SER	PRO	GLU	PRO	VAL	VAL
V489	ASP	TYR	THR	PRO	GLN	PRO	LEU	LEU
H490	ASP	VAL	GLU	PRO	ARG	PRO	GLY	ALA
L491	ASP	THR	GLU	PRO	GLN	LEU	GLU	LEU
K492	GLU	GLU	THR	GLY	GLN	ARG	ASP	GLN
A493	SER	PRO	VAL	GLU	ILE	VAL	ASP	PRO
T494	ASP	ILE	VAL	ASN	ALA	GLU	LYS	PRO
R495	GLN	TYR	SER	ARG	LYS	PRO	ALA	PRO
N496	GLU	GLU	SER	GLU	MET	VAL	ALA	PRO
S497	LYS	PRO	LYS	MET	GLY	ALA	PRO	PRO
V498	LYS	ASN	GLU	ASP	THR	LEU	PRO	PRO
P499	PRO	PHE	LYS	PRO	VAL	GLU	MET	GLY
V500	ALA	PHE	ARG	VAL	ARG	GLU	ALA	GLY
F501	PRO	LYS	ARG	GLY	PRO	ARG	GLN	ALA
R502	LYS	ARG	LYS	LYS	GLN	LEU	LEU	TRP
H503	LEU	ILE	ASN	ILE	ASP	LYS	PRO	ALA
W504	SER	PHE	ARG	ILE	ASP	LEU	GLY	ALA
C505	LYS	GLU	LYS	GLN	GLY	GLN	PRO	GLN
F506	LYS	PHE	LYS	LEU	ILE	GLN	PRO	GLN
K507	ARG	LEU	LYS	GLU	VAL	ALA	PRO	LYS
R508	ARG	THR	PRO	ILE	ARG	LEU	PRO	ALA
K509	MET	ASP	GLN	LEU	THR	LEU	LEU	ALA
Y510	M458	VAL	ARG	GLN	PRO	MET	GLY	GLU
L511	R459	VAL	VAL	LEU	LEU	GLN	LEU	ILE
Q512	F460	LYS	ARG	LYS	GLY	GLN	PRO	GLY
G513	T461	LYS	GLY	GLU	PRO	GLU	PRO	ALA
K514	V462	LYS	VAL	SER	ARG	GLU	LEU	ILE
R515	A463	GLU	SER	GLN	VAL	ARG	GLN	GLN
G516	E464	LYS	SER	GLU	ALA	ALA	PRO	GLY
I517	L465	PRO	SER	GLU	PRO	LYS	PRO	ASN
E518	K466	GLU	GLY	MET	VAL	GLN	ARG	ARG
F519	Q467	LYS	ASP	SER	PRO	ASP	PRO	GLU
P520	L468	LEU	ARG	GLN	VAL	HIS	PRO	LEU
P521	V469	ASP	GLU	GLN	GLY	SER	PRO	VAL
F522	A470	LYS	GLU	GLN	PRO	ASN	PRO	GLU
E523	P472	SER	THR	GLU	THR	HIS	LEU	GLN
L524	L524	ALA	ARG	MET	VAL	GLU	GLY	SER
P525	D473	ALA	SER	GLU	LEU	LEU	LEU	TYR
D526	V474	PRO	ARG	THR	PRO	LEU	GLY	THR
F527	V475	PRO	GLY	GLY	MET	GLU	PHE	ASP
I528	E476	LYS	SER	ALA	GLY	GLN	PRO	GLN
K529	M477	LYS	THR	ALA	THR	GLN	THR	GLY
R530	H478	ALA	ARG	GLU	VAL	GLU	GLY	TYR
T531	D479	ALA	SER	THR	LEU	LEU	LEU	GLY
G532	V480	PRO	ARG	THR	PRO	LEU	PHE	THR
I533	F480	PRO	SER	ALA	GLY	GLN	PRO	GLN
Q534								
E535								
M536								
R537								
E538								
A539								
L540								



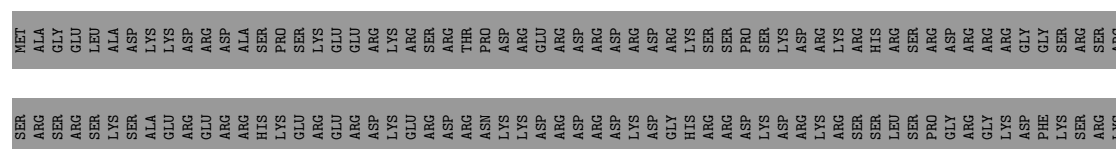
- Molecule 23: 116 kDa U5 small nuclear ribonucleoprotein component

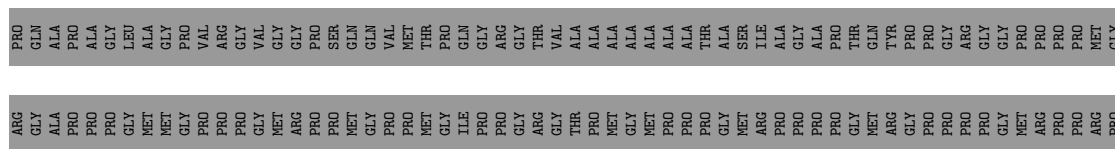
Chain 5C: 77% 22%



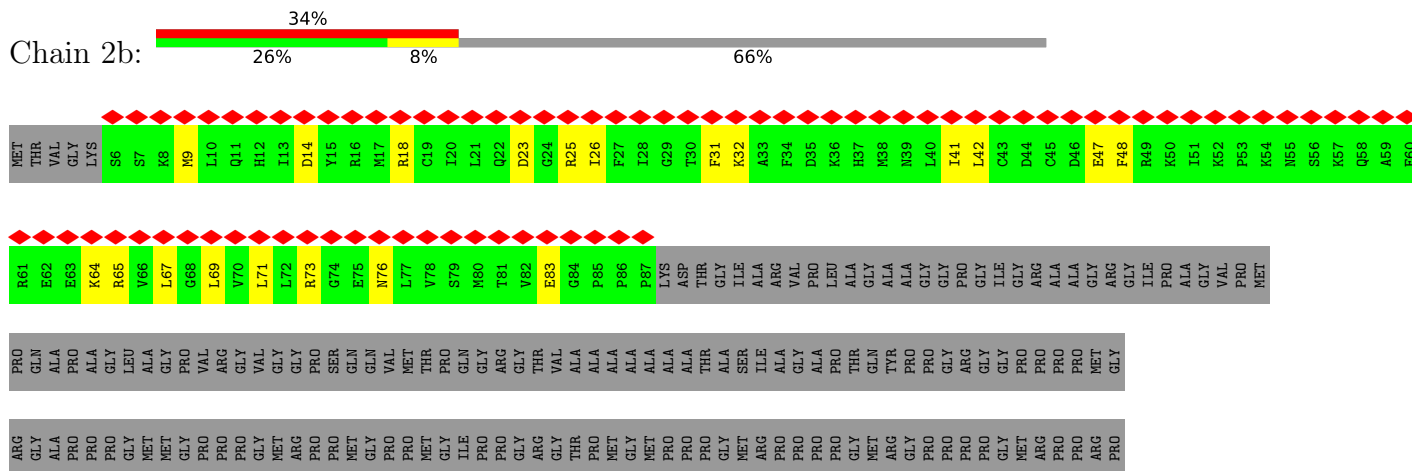
- Molecule 24: Probable ATP-dependent RNA helicase DDX23

Chain 5X: 52% 18% 29%

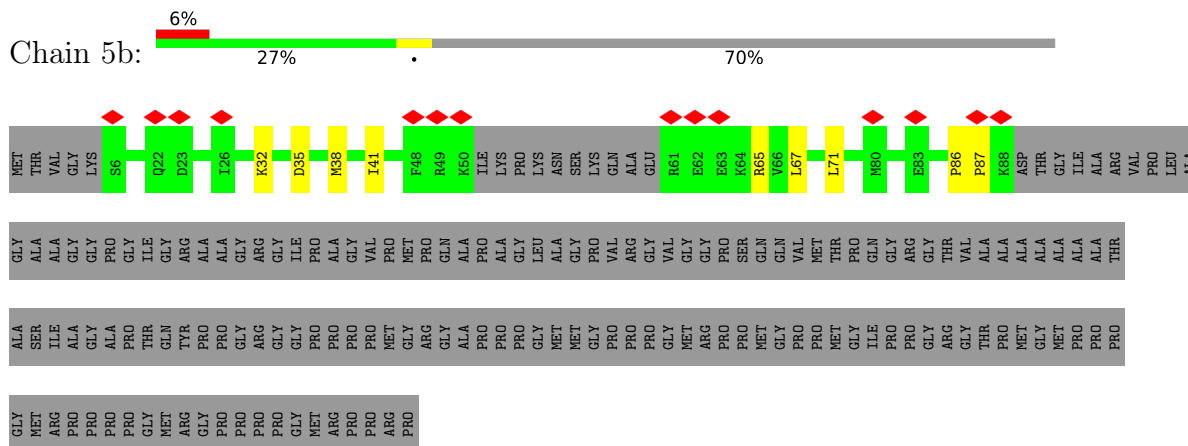




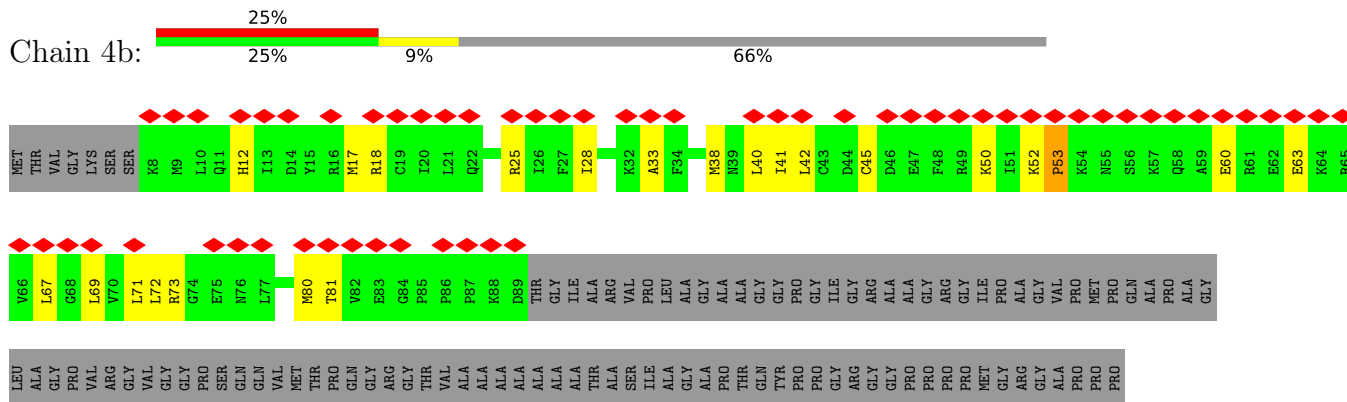
- Molecule 25: Small nuclear ribonucleoprotein-associated proteins B and B'

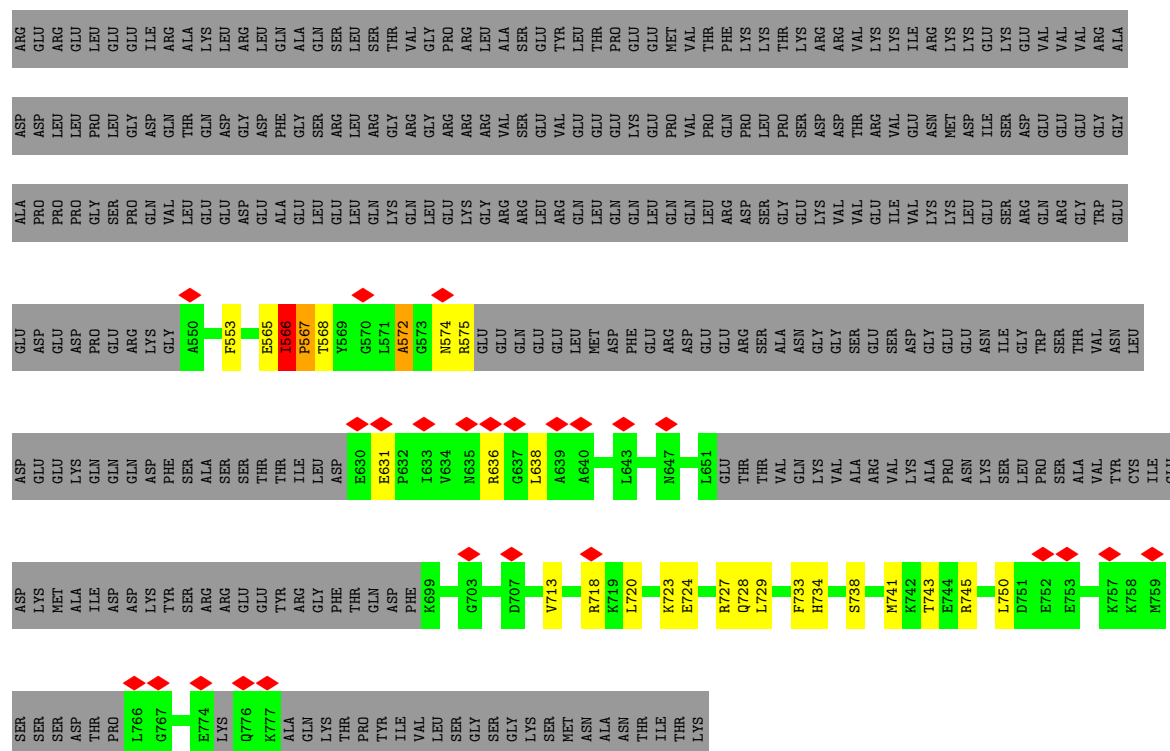


- Molecule 25: Small nuclear ribonucleoprotein-associated proteins B and B'

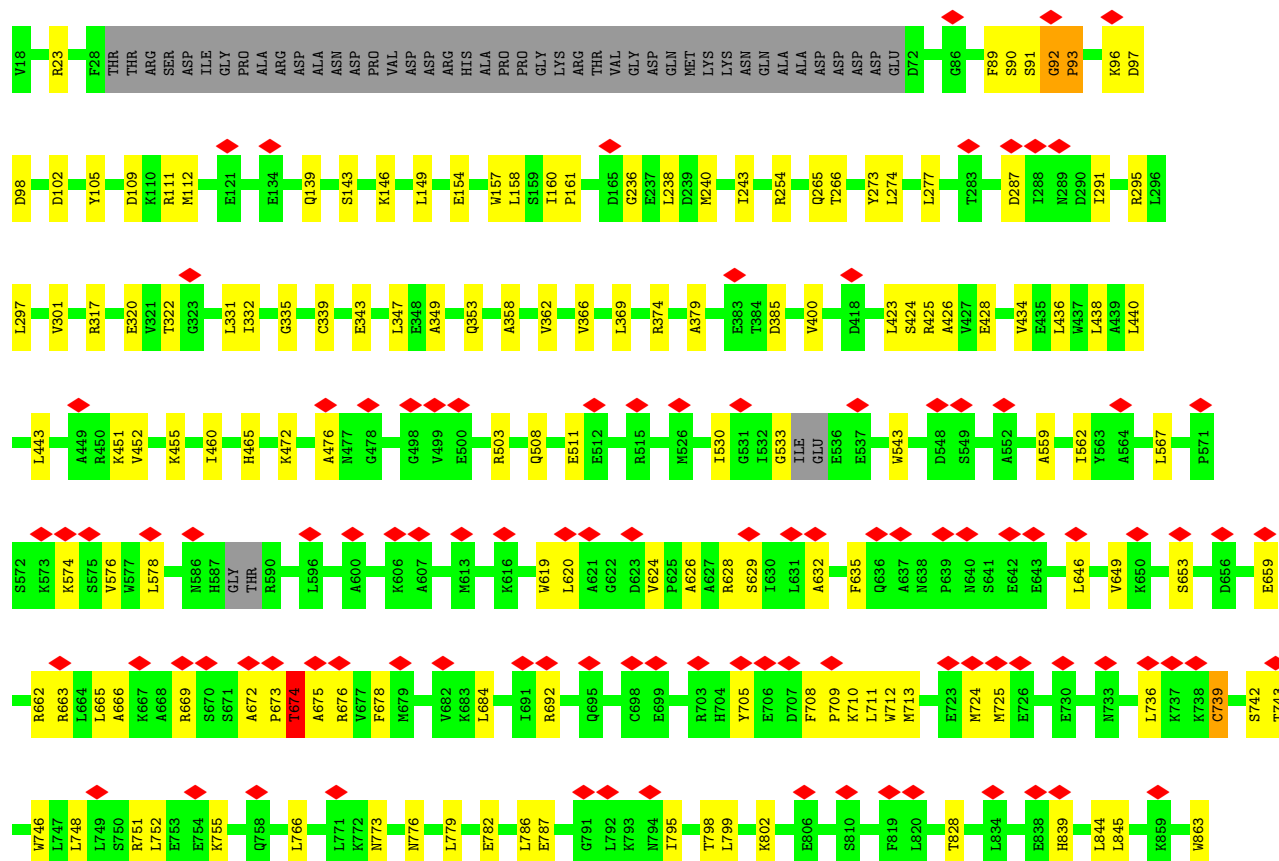
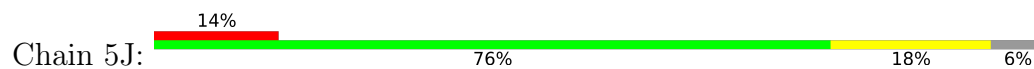


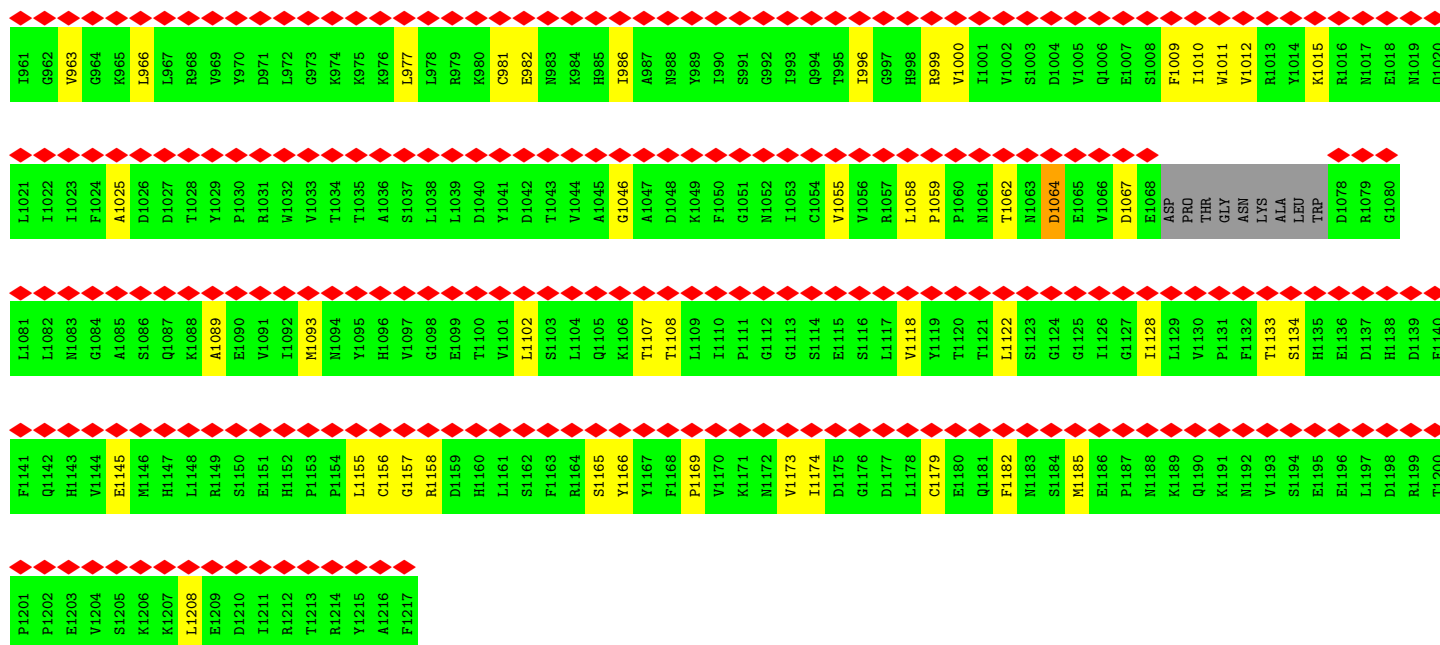
- Molecule 25: Small nuclear ribonucleoprotein-associated proteins B and B'





• Molecule 29: Pre-mRNA-processing factor 6

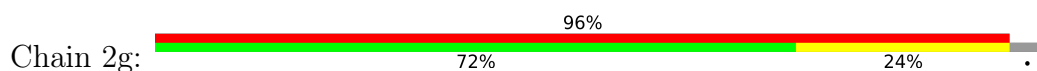




• Molecule 34: Small nuclear ribonucleoprotein G



• Molecule 34: Small nuclear ribonucleoprotein G

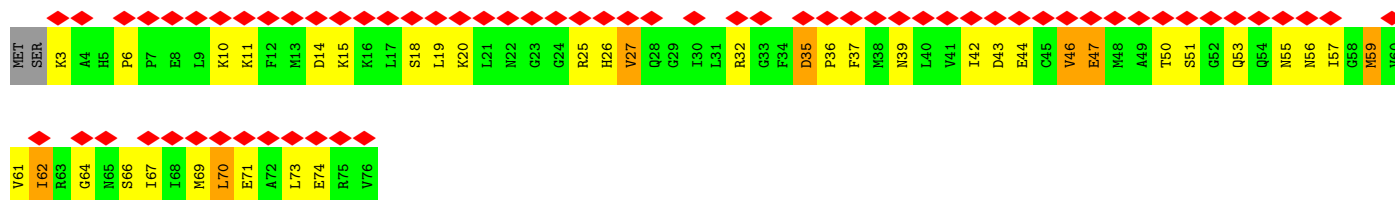
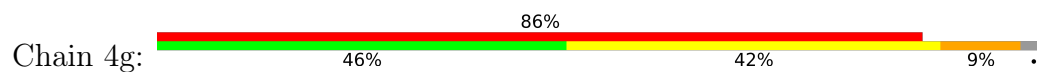


• Molecule 34: Small nuclear ribonucleoprotein G

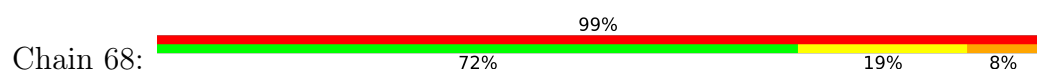




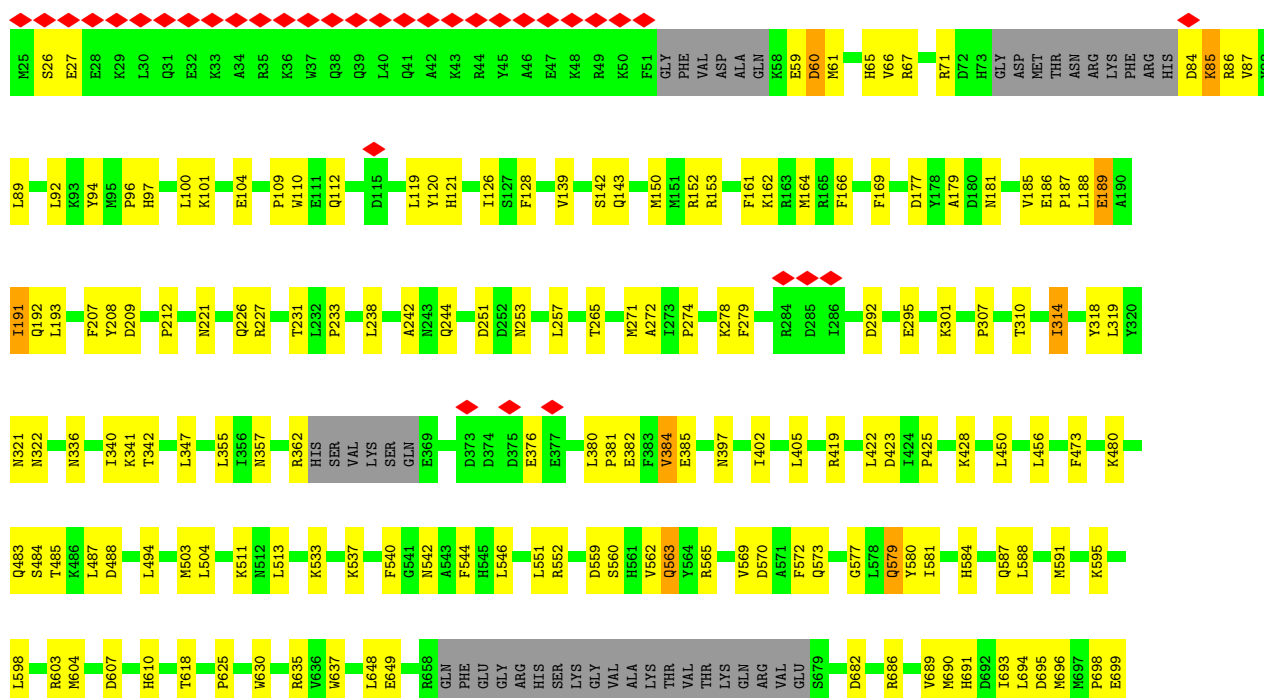
• Molecule 34: Small nuclear ribonucleoprotein G



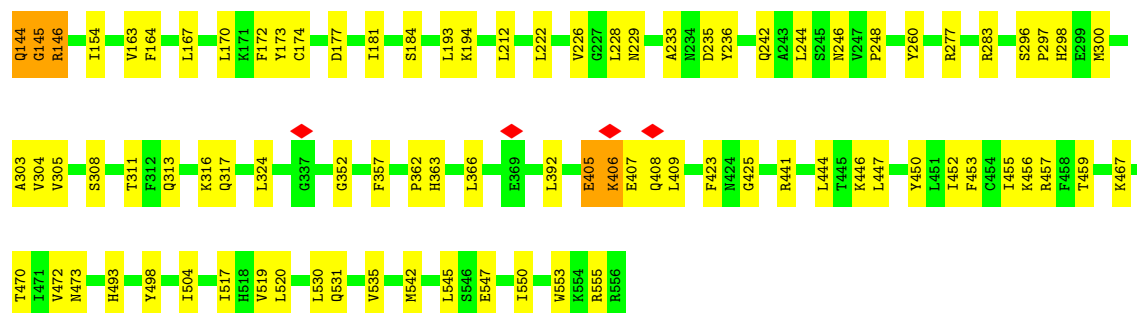
• Molecule 35: U6 snRNA-associated Sm-like protein LSm8



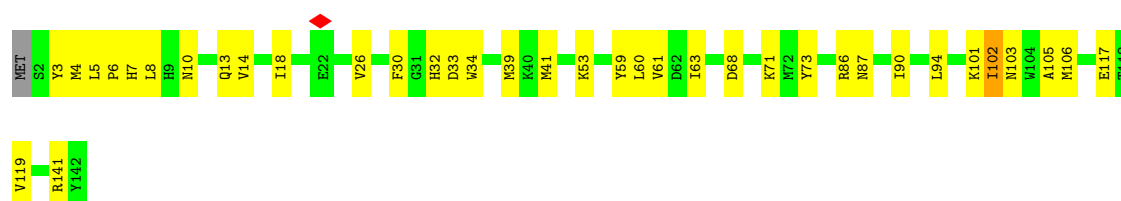
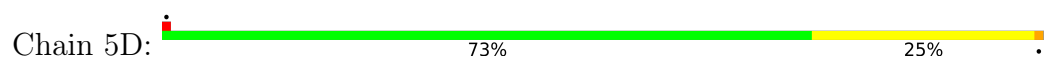
• Molecule 36: Pre-mRNA-processing-splicing factor 8



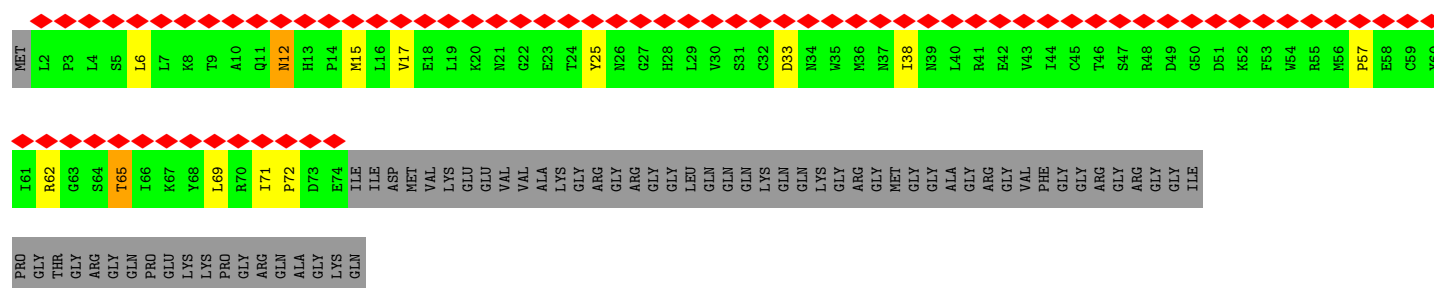
GLN	S2001	Q1860	Q1775	D1663	Q1450	V1314	C1190	R1086	I940	K796	G700
THR	L2002	I1776	I1776	Q1665	Q1451	Y1317	F1192	Q1191	K941	I801	I701
F2067	T2003	V1863	W1778	L1666	P1452	T1318	R1195	R1090	P942	T802	K702
S2068	Q2004	T1864	F1779	R1667	W1455	L1569	R1195	R1094	P947	A803	Q703
E2072	D2009	R1865	V1785	D1670	W1455	G1324	R1201	R1086	P948	E804	K705
N2073	L2010	M1868	Y1786	Y1671	R1459	L1325	T1202	F1098	P949	A706	A707
R2074	I2011	L1869	R1787	D1672	H1460	L1328	S1203	F1099	V952	V807	R707
R2076	M2014	L1872	I1790	A1579	L1478	S1329	Y1204	R1100	V909	A808	L708
R2077	E2015	H1791	D1675	K1584	E1486	M1330	E1205	D1104	D964	A810	L710
R2078	E2016	K1792	I1676	H1585	F1490	G1331	E1206	D1104	D964	T811	Q711
R2086	SER	T1793	E1681	H1586	K1491	H1332	G1212	R1107	E967	V814	H712
K2098	ALA	E1794	R1681	E1587	G1492	D1347	W1213	D1108	T968	V814	H713
T2103	PRO	E1795	L1685	D1592	K1491	W1214	G1212	L1109	S969	P824	A722
L2106	GLN	P1892	G1796	D1596	T1493	E1492	W1214	L1109	E970	P824	N723
P2107	GLN	K1998	N1797	V1596	T1493	D1347	W1214	I1110	P828	P828	I724
V2110	ARG	D1904	I1803	E1600	F1502	S1385	M1218	N1121	N974	P828	V728
I2115	GLN	L1905	N1804	L1604	W1503	GLY	E1219	V1126	V975	L838	L731
S2118	ILE	I1906	G1805	E1665	K1505	MET	T1221	N1126	M976	L839	P732
V2131	ALA	L1907	A1806	E1607	A1506	HIS	K1222	S979	S979	E844	T733
V2139	GLU	I1907	I1807	E1607	S1507	GLU	C1228	N1129	E982	R845	P733
K2140	ILE	K1908	F1808	E1607	G1508	ASP	C1228	K1132	L992	R845	E736
T2142	GLU	D1908	F1810	T1613	F1509	Q1363	V1244	K1132	L992	S851	E736
R2143	LYS	N1927	N1811	I1614	F1509	L1364	R1245	W1134	L996	V852	L739
V2146	THR	L1924	P1812	H1615	E1510	I1365	Q1246	D1137	L996	K853	L740
P2164	LYS	K1925	R1813	R1617	E1511	P1366	I247	A1138	D1002	K853	R741
T2165	GLU	T1925	T1814	G1715	S1512	N1367	M1249	R1139	H1003	S854	R741
E2167	GLN	T1926	T1814	G1716	M1513	P1374	M1249	R1139	H1003	S854	R741
T2168	GLN	T1927	T1814	G1716	K1514	P1374	M1249	R1139	H1003	S854	R741
T2168	SER	I1927	F1818	F1719	W1515	E1378	T1255	M1143	M1004	I867	K746
M2172	LEU	T1931	L1819	F1719	K1516	E1378	F1256	K1012	K1012	L878	W750
P2164	THR	I1937	I1821	L1725	L1517	D1381	T1257	L1149	L1017	L878	T751
T2165	ALA	I1937	I1821	L1725	L1518	S1382	T1257	L1149	L1017	L878	T751
E2167	GLN	R1941	W1827	A1729	L1526	Q1383	V1260	A1152	M1018	I881	R758
T2168	THR	A1942	A1828	A1729	L1529	R1384	K1262	V1153	M1018	E759	R758
T2168	ARG	A1942	G1829	I1733	I1529	Q1383	K1262	V1153	Y1019	K892	R760
M2172	THR	R1949	Q1830	N1737	R1532	V1385	L1262	M1023	M1023	M899	I761
M2172	VAL	A1950	K1831	L1740	R1533	Y1389	T1265	L1031	M1023	D900	R761
L2188	ASN	A1950	K1831	L1740	R1533	L1405	L1268	S1038	M1023	L901	R762
S2189	LYS	D1957	R1832	L1743	L1536	D1413	M1271	Q1042	Q1042	P907	D768
T2190	HIS	K1958	L1833	L1743	W1537	R1414	M1271	Q1042	Q1042	V908	N775
Q2191	GLY	Q1835	G1834	L1743	G1415	G1415	Y1273	L1046	L1046	D910	N775
Q2191	ASP	L1836	Q1835	L1743	P1540	I1416	F1274	V1047	V1047	E912	L776
H2196	ILE	L1836	L1836	L1751	P1540	I1416	F1274	V1177	V1047	R778	R778
H2196	ILE	A1837	L1836	L1751	P1540	I1416	F1274	V1177	V1047	R778	R778
M2200	THR	T1960	K1837	L1753	M1543	R1418	E1276	L1051	L1051	P913	R781
D2207	THR	D1973	K1838	L1763	R1544	D1433	M1280	R1057	R1057	K916	L782
K2210	SER	E1974	W1839	L1763	R1544	K1434	M1280	R1057	R1057	I917	L782
K2210	THR	E1974	K1840	L1763	R1544	K1434	M1280	R1057	R1057	I917	L782
S2222	THR	I1987	T1841	L1645	G1550	R1437	V1289	E1060	E1060	T918	K785
	THR	I1987	T1841	L1645	F1551	R1437	V1289	E1060	E1060	D919	K785
	ASN	E1843	L1771	D1653	Q1552	V1438	C1291	D1070	D1070	Y925	A786
	THR	E1843	L1771	D1653	Q1553	R1439	E1292	F1187	F1071	R938	E787
	TYR	Y1991	N1774	I1662	Q1554	K1443	K1293	M1189	L1072	P938	Q791
	GLU	G1992	N1774	I1662	L1555	K1443	K1294	M1189	L1072	P938	Q791
	THR	G1992	N1774	I1662	L1557	K1443	K1294	M1189	L1072	P938	Q791



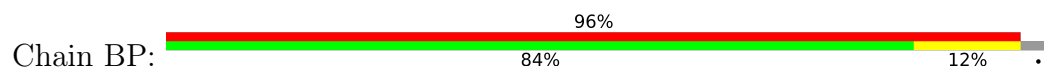
- Molecule 39: Thioredoxin-like protein 4A



- Molecule 40: U6 snRNA-associated Sm-like protein LSm4



- Molecule 41: PHD finger-like domain-containing protein 5A

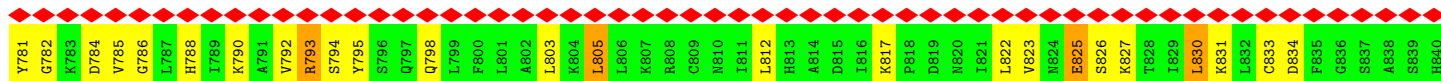


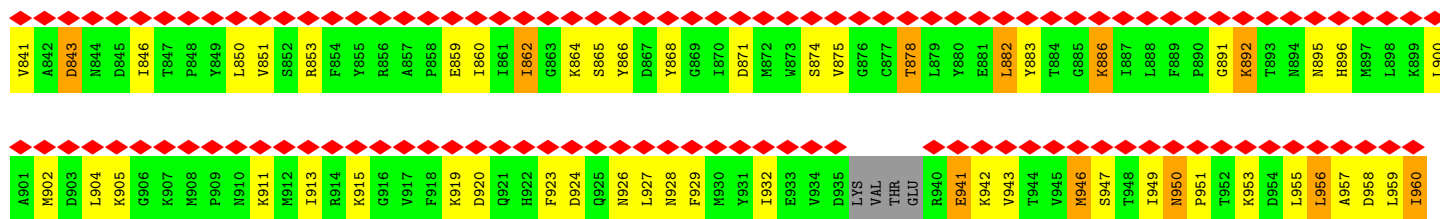
- Molecule 42: U1 small nuclear ribonucleoprotein C



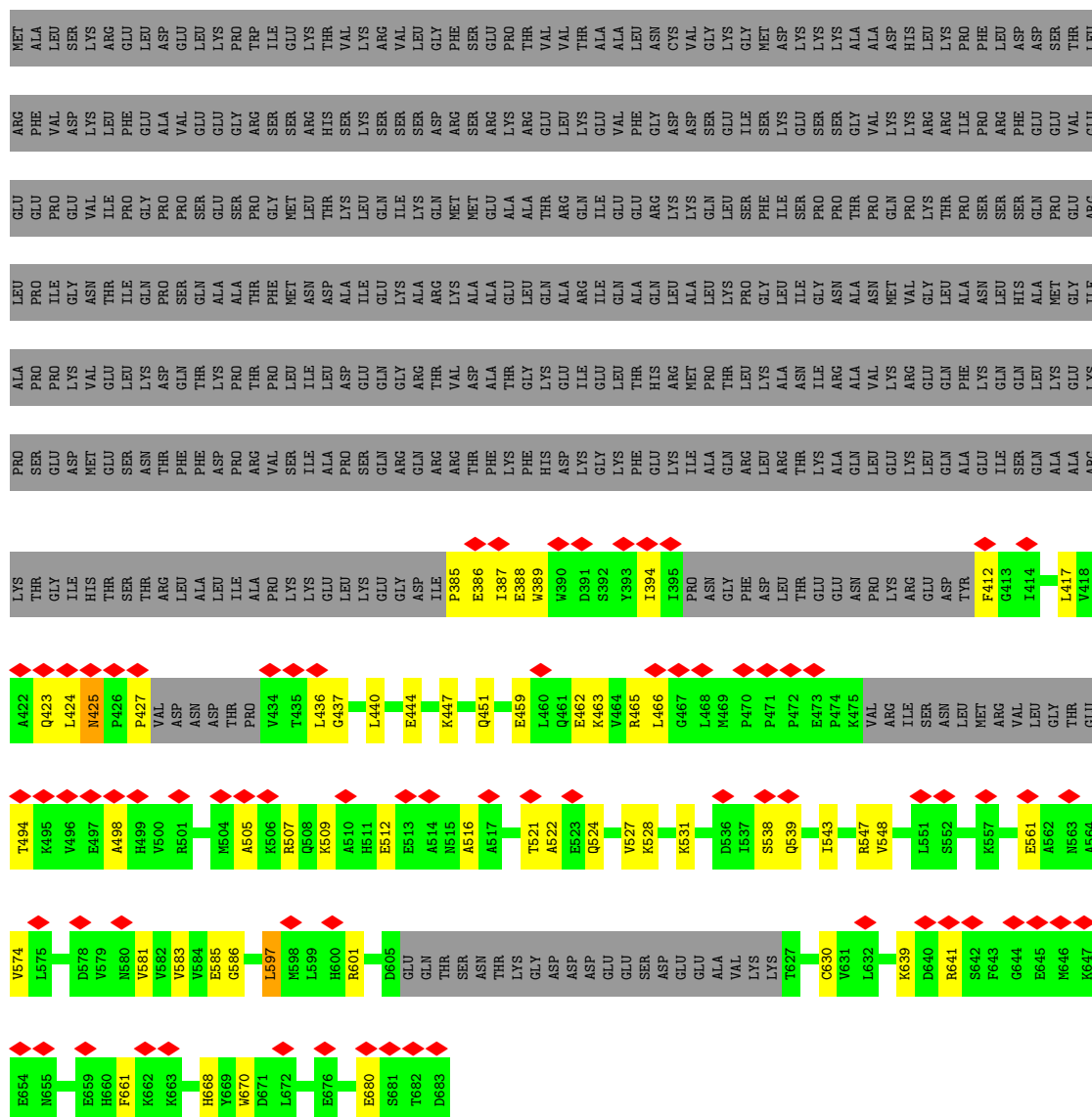
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- Molecule 43: Serine/threonine-protein kinase PRP4 homolog

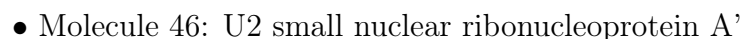


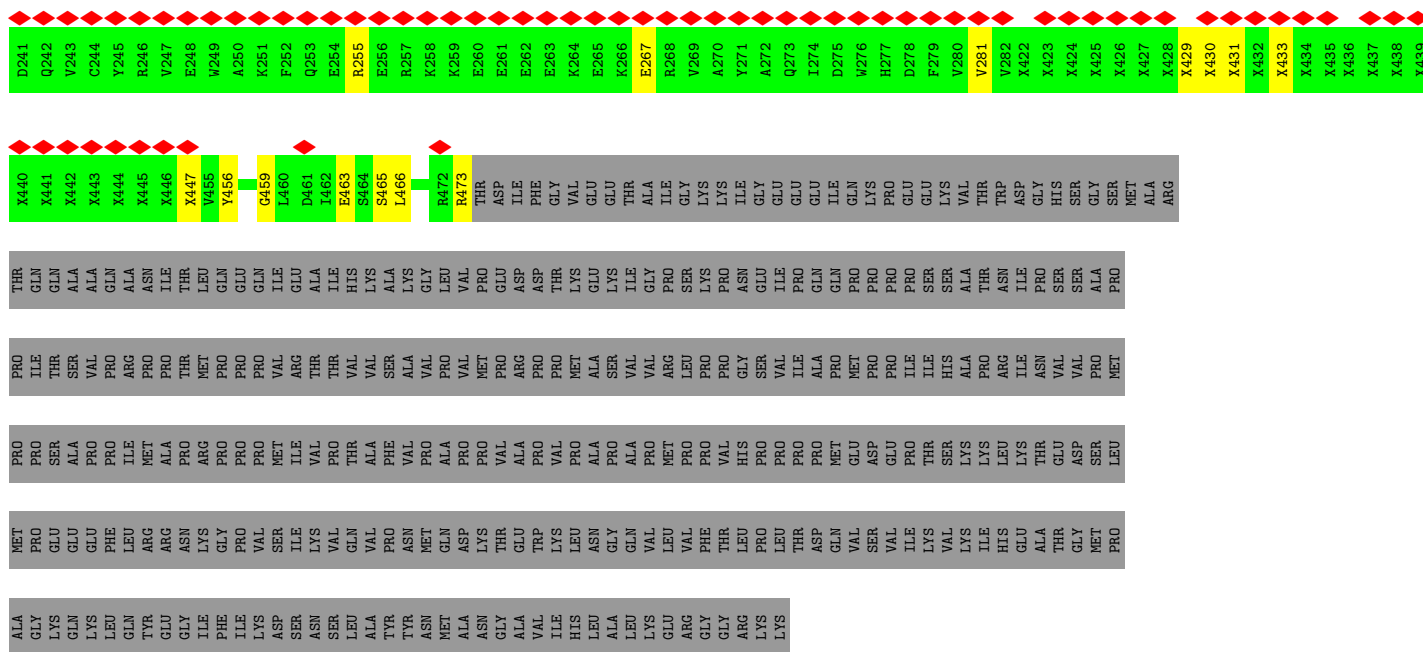


• Molecule 44: U4/U6 small nuclear ribonucleoprotein Prp3

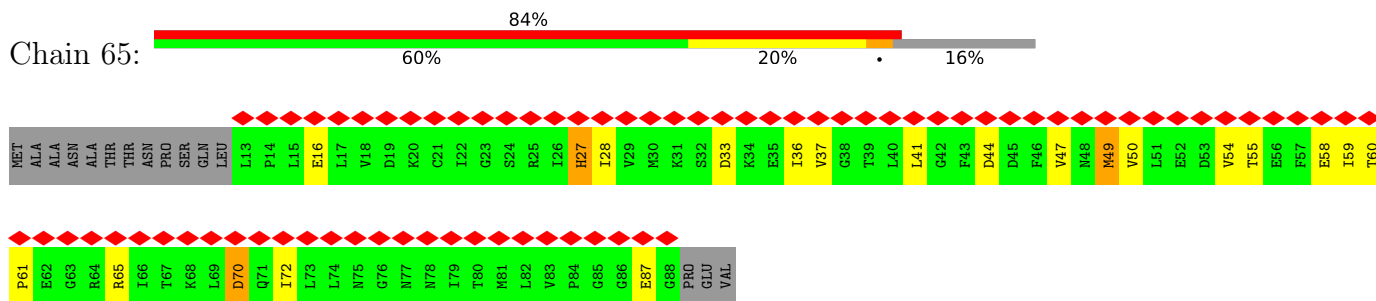


• Molecule 45: U4 snRNA

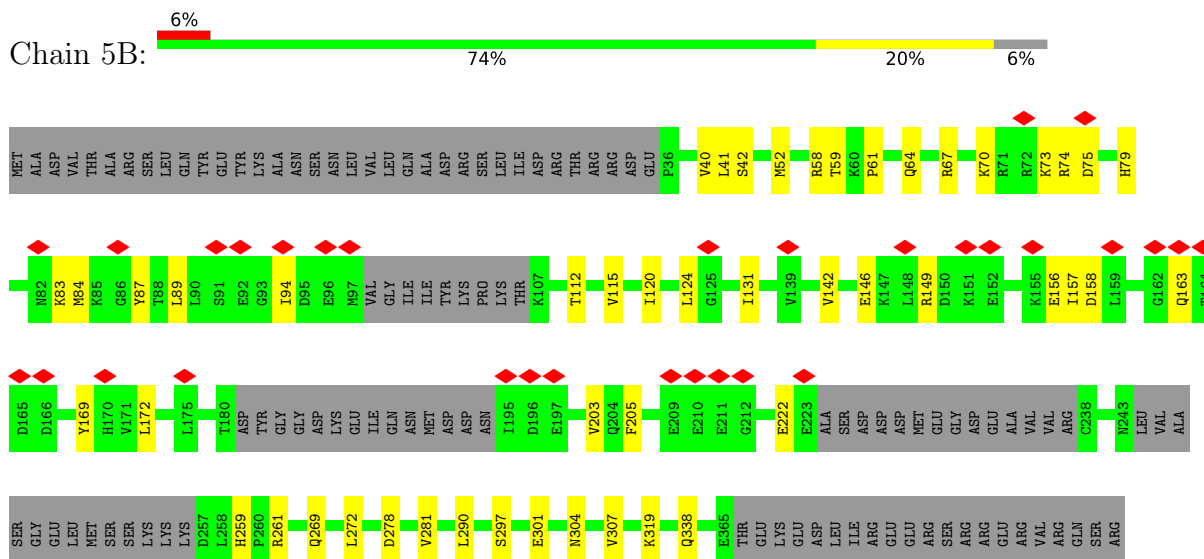




- Molecule 48: U6 snRNA-associated Sm-like protein LSm5



- Molecule 49: U5 small nuclear ribonucleoprotein 200 kDa helicase



P2054	L2055	F2056	K2059	R2060	E2061	E2062	G2063	W2064	W2065	V2066	V2067	L2068	G2069	D2070	A2071	K2072	R2081	L2082	T2083	L2084	Q2085	Q2086	K2087	A2088	K2089	V2090	D2093	F2094	V2095	A2096	P2097	A2098	T2099	G2100	A2101	H2102	N2103	L2106	Y2107	F2108	N2109	S2110	D2111	G2115	E2119	Y2120	K2121	V2124	D2125	VAL	LYS	GLU																																	
D1984	I1985	M1986	E1987	M1988	E1989	D1990	E1991	E1992	R1993	N1994	A1995	L1996	L1997	Q1998	L1999	T2000	D2001	T2004	A2005	D2006	V2007	A2008	R2009	F2010	C2011	N2012	R2013	N2016	I2017	E2018	L2019	S2020	V2024	D2025	K2026	D2027	S2028	I2029	R2030	S2031	L2038	V2039	Q2040	L2041	E2044	E2045	E2046	V2047	T2048	G2049	P2050	I2052	A2053																																
E1699	G1700	R1701	I1704	M1705	P1723	D1729	H1735	F1736	M1737	A1738	Q1749	L1755	T1756	Y1761	R1762	R1763	S1782	L1785	L1793	I1804	V1810	G1816	Y1822	Y1823	I1824	V1843	V1844	V1845	W1852	H1859	I1863	M1864	D1865	T1866	Y1876	A1891	L1896	Y1855	E1856	N1857	R1861	E1864	A1872	L1879	D1886	V1889	K1890	N1892	M1901	R1902	Q1903	D1911	S1917	T1923	L1936	L1940	Q1947	M1948	Q1951	W1954	S1955	K1956	K1961	Q1962	T1967	S1968	E1969	H1970	I1971	K1972	R1973	C1974	T1975	L1976	K1977	G1978	V1979	S1981	V1982	F1983					
T1511	F1514	H1515	P1516	N1517	V1518	R1519	V1520	V1521	T1535	R1538	L1539	M1542	K1557	R1566	K1567	Q1568	T1569	R1572	Q1585	P1598	P1599	S1605	V1617	H1621	P1626	R1629	V1643	V1644	V1645	W1652	H1659	I1663	M1664	D1665	T1666	Y1676	A1691	L1696	N1857	R1861	E1864	A1872	L1879	D1886	V1889	K1890	N1892	M1901	R1902	Q1903	D1911	S1917	T1923	L1936	L1940	Q1947	M1948	Q1951	W1954	S1955	K1956	K1961	Q1962	T1967	S1968	E1969	H1970	I1971	K1972	R1973	C1974	T1975	L1976	K1977	G1978	V1979	S1981	V1982	F1983						
A1360	E1361	M1367	L1368	C1376	V1377	I1378	T1379	T1380	P1381	M1382	W1393	K1403	K1404	V1405	D1415	L1418	K1421	I1424	P1429	D1433	I1434	S1436	R1437	R1438	Q1441	D1454	E1455	V1456	V1469	I1470	R1473	T1487	L1490	S1491	S1492	D1499	L1504	S1507	A1360	E1361	M1367	L1368	C1376	V1377	I1378	T1379	T1380	P1381	M1382	W1393	K1403	K1404	V1405	D1415	L1418	K1421	I1424	P1429	D1433	I1434	S1436	R1437	R1438	Q1441	D1454	E1455	V1456	V1469	I1470	R1473	T1487	L1490	S1491	S1492	D1499	L1504	S1507								
S1196	V1200	E1201	L1202	D1207	V1214	W1222	V1225	E1226	D1227	V1228	I1233	H1236	F1254	V1255	P1257	V1258	P1264	Q1265	I1268	R1269	D1273	R1274	R1287	H1288	L1289	P1292	P1298	L1301	R1313	Y1321	Q1322	D1323	Q1332	Y1340	P1351	G1355	S1196	V1200	E1201	L1202	D1207	V1214	W1222	V1225	E1226	D1227	V1228	I1233	H1236	F1254	V1255	P1257	V1258	P1264	Q1265	I1268	R1269	D1273	R1274	R1287	H1288	L1289	P1292	P1298	L1301	R1313	Y1321	Q1322	D1323	Q1332	Y1340	P1351	G1355												
L1059	M1060	V1061	L1062	M1063	Q1064	A1065	F1066	T1067	S1068	Q1069	L1070	A1076	M1081	T1085	Q1086	R1093	I1098	R1102	T1108	D1109	I1118	R1130	V1139	V1140	I1143	R1152	D1155	L1156	I1161	I1165	R1166	M1167	L1180	E1185	L1186	S1187	V1188	P1192	T1194	R1195	L1059	M1060	V1061	L1062	M1063	Q1064	A1065	F1066	T1067	S1068	Q1069	L1070	A1076	M1081	T1085	Q1086	R1093	I1098	R1102	T1108	D1109	I1118	R1130	V1139	V1140	I1143	R1152	D1155	L1156	I1161	I1165	R1166	M1167	L1180	E1185	L1186	S1187	V1188	P1192	T1194	R1195				
Q885	Q886	Q892	M893	V894	I905	N912	R928	S932	L949	R952	N968	L969	K971	Y972	D973	K974	Q980	L994	G985	E986	I987	T993	V998	Q999	M1002	Q1003	L1004	L1009	E1013	V1017	T1028	V1029	R1030	E1033	L1041	T1052	K1058	Q885	Q886	Q892	M893	V894	I905	N912	R928	S932	L949	R952	N968	L969	K971	Y972	D973	K974	Q980	L994	G985	E986	I987	T993	V998	Q999	M1002	Q1003	L1004	L1009	E1013	V1017	T1028	V1029	R1030	E1033	L1041	T1052	K1058										
I612	A491	A492	N498	L501	A513	L514	M515	C516	M517	E520	G522	I525	N526	M527	D528	I531	D535	F536	K537	I538	E539	Y540	M544	K557	Y562	I564	D572	I580	I585	I586	V587	T597	E602	R603	T604	Y605	T608	Q607	L608	V609	R610	L611	I612	A491	A492	N498	L501	A513	L514	M515	C516	M517	E520	G522	I525	N526	M527	D528	I531	D535	F536	K537	I538	E539	Y540	M544	K557	Y562	I564	D572	I580	I585	I586	V587	T597	E602	R603	T604	Y605	T608	Q607	L608	V609	R610	L611
MET	ASP	THR	ASP	LEU	GLU	THR	MET	ASP	LEU	GLN	GLY	GLY	ALA	P405	R406	D410	L414	G419	S420	H421	F422	M423	C428	Q429	D432	R436	R439	Y442	E443	E444	V445	H446	V447	S457	E458	L462	P463	K466	T480	Q485	L488	MET	ASP	THR	ASP	LEU	GLU	THR	MET	ASP	LEU	GLN	GLY	GLY	ALA	P405	R406	D410	L414	G419	S420	H421	F422	M423	C428	Q429	D432	R436	R439	Y442	E443	E444	V445	H446	V447	S457	E458	L462	P463	K466	T480	Q485	L488		

Response	Percentage
Yes	65%
No	54%
Don't know	11%
No answer	35%



V1261	G1201	L1141	F1081	T1021	V961	Q901	A841
R1262	F1202	M1142	G1082	P1022	H962	E902	N842
D1263	G1203	V1143	Y1083	I1023	K963	Q903	K843
V1264	G1204	Q1144	I1084	L1024	T964	T904	V844
Y1265	E1205	N1145	A1085	K1025	C965	T905	G845
W1266	D1206	G1146	K1086	N1026	Q966	E906	A846
K1267	S1207	V1147	A1087	R1027	E967	D907	A847
I1268	L1208	L1148	I1088	H1028	E968	S908	E848
Y1269	N1209	K1149	G1089	E1029	E969	V909	I849
N1270	H1210	S1150	P1090	K1030	L970	M910	I850
S1271	L1211	L1151	H1091	V1031	M971	L911	S851
I1272	L1212	S1152	D1092	Q1032	G972	N912	R852
Y1273	N1213	F1153	V1093	E1033	H973	G913	I853
I1274	Y1214	L1154	L1094	M1034	L974	F914	V854
G1275	V1215	F1155	A1095	C1035	G975	G915	D855
S1276	W1216	E1156	T1096	I1036	V976	T916	D856
D1277	P1217	Y1157	L1097	D1037	V977	V917	L857
N1218	N1218	I1158	L1098	L1038	L978	V918	K858
A1279	V1219	G1159	N1099	V1039	Y979	N919	D859
L1280	F1220	E1160	M1100	G1040	E980	A920	E860
I1281	E1221	M1161	L1101	R1041	Y981	L921	A861
A1282	T1222	G1162	K1102	I1042	L982	G922	E862
Y1283	S1223	K1163	V1103	A1043	G983	K923	Q863
I1284	P1224	D1164	Q1104	D1044	E984	R924	Y864
P1285	H1225	Y1165	E1105	R1045	E985	V925	R865
R1286	V1226	I1166	R1106	G1046	Y986	K926	K866
I1287	I1227	Y1167	Q1107	E1047	P987	P927	M867
Y1288	Q1228	A1168	N1108	E1048	E988	Y928	V868
N1289	A1229	V1169	R1109	Y1049	V989	L929	M869
D1290	V1230	T1170	V1110	V1050	L990	P930	E870
D1291	M1231	P1171	C1111	S1051	G991	Q931	T871
K1292	G1232	L1172	T1112	A1052	S992	I932	I872
N1293	A1233	L1173	T1113	R1053	L993	C933	E873
T1294	L1234	E1174	V1114	E1054	L994	G934	K874
Y1295	E1235	D1175	A1115	W1055	G995	T935	I875
I1296	G1236	A1176	I1116	M1056	A996	V936	M876
R1297	L1237	L1177	A1117	R1057	L997	L937	G877
Y1298	R1238	M1178	I1118	I1058	K998	W938	N878
E1299	V1239	D1179	V1119	C1059	A999	R939	L879
L1300	A1240	R1180	A1120	F1060	T1000	L940	G880
D1301	I1241	D1181	E1121	E1061	V1001	N941	A881
Y1302	G1242	L1182	T1122	L1062	M1002	N942	A882
I1303	P1243	V1183	C1123	L1063	V1003	K943	D883
L1304	R1244	H1184	S1124	E1064	I1004	S944	I884
	C1245	R1185	P1125	L1065	G1005	A945	D885
	M1246	Q1186	F1126	L1066	M1006	K946	H886
	L1247	T1187	T1127	K1067	H1007	V947	K887
	Q1248	A1188	V1128	A1068	R948	R949	L888
	Y1249	S1189	L1129	H1069	Q949	Q949	E889
	C1250	A1190	P1130	K1070	T1010	Q950	E890
	L1251	V1191	A1131	K1071	P1011	A951	Q891
	Q1252	V1192	L1132	A1072	P1012	A952	L892
	G1253	Q1193	M1133	I1073	I1013	D953	I893
	L1254	H1194	N1134	R1074	K1014	L954	D894
	F1255	M1195	E1135	R1075	D1015	I955	G895
	H1256	S1196	Y1136	A1076	L1016	S956	I896
	P1257	L1197	R1137	T1077	L1017	R957	L897
	A1258	G1198	V1138	V1078	P1018	T958	Y898
	R1259	V1199	P1139	N1079	R1019	A959	E899
	K1260	Y1200	F1140	T1080	L1020	V960	F900

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	86146	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.097	Depositor
Minimum map value	-0.048	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	429.24, 429.24, 429.24	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.022, 1.022, 1.022	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: IHP, GTP, MG, M7M, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.63	3/3891 (0.1%)	0.78	9/6061 (0.1%)
2	6	0.51	5/1264 (0.4%)	0.45	0/1961
3	5O	0.26	0/2448	0.60	0/3316
4	B4	0.91	0/632	1.39	4/855 (0.5%)
5	13	0.72	0/645	1.22	4/870 (0.5%)
5	23	0.47	0/660	0.71	0/889
5	43	0.32	0/660	0.71	0/889
5	53	0.36	0/665	0.55	0/896
6	4B	0.45	0/2921	0.74	1/3966 (0.0%)
7	1e	0.82	0/646	1.42	6/867 (0.7%)
7	2e	0.47	0/677	0.69	0/908
7	4e	0.34	0/639	0.87	2/857 (0.2%)
7	5e	0.34	0/646	0.75	0/867
8	I	0.54	0/590	0.84	2/916 (0.2%)
9	1K	1.47	13/1695 (0.8%)	1.33	11/2288 (0.5%)
10	4C	0.31	0/2406	0.65	2/3232 (0.1%)
11	11	0.93	0/649	1.35	6/878 (0.7%)
11	21	0.41	0/642	0.60	0/867
11	41	0.36	0/649	0.78	0/878
11	51	0.36	0/649	0.78	1/878 (0.1%)
12	R	0.34	0/891	1.01	2/1188 (0.2%)
13	1f	0.82	1/588 (0.2%)	1.34	5/795 (0.6%)
13	2f	0.43	0/574	0.65	0/775
13	4f	0.39	0/574	0.74	0/775
13	5f	0.37	0/579	0.82	0/783
14	66	1.12	1/575 (0.2%)	1.55	5/776 (0.6%)
15	X	0.38	0/398	0.84	2/524 (0.4%)
16	12	0.95	0/786	1.33	0/1055
16	22	0.40	0/784	0.65	0/1053
16	42	0.38	0/747	0.71	0/1000
16	52	0.33	0/805	0.79	0/1081
17	5	0.32	0/2444	0.56	1/3798 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
18	67	1.11	1/611 (0.2%)	1.53	6/824 (0.7%)
19	62	1.00	0/773	1.59	7/1043 (0.7%)
20	2B	0.34	0/759	0.50	0/1016
21	A2	0.72	0/1254	1.18	4/1682 (0.2%)
22	B2	0.82	5/1747 (0.3%)	1.22	24/2356 (1.0%)
23	5C	0.48	0/6879	0.63	6/9344 (0.1%)
24	5X	0.60	1/4859 (0.0%)	0.85	5/6522 (0.1%)
25	1b	0.88	1/702 (0.1%)	1.32	5/936 (0.5%)
25	2b	0.44	0/674	0.59	0/899
25	4b	0.30	0/679	0.66	0/905
25	5b	0.33	0/602	0.55	0/801
26	B5	0.53	0/584	0.62	0/789
27	1A	1.32	1/801 (0.1%)	1.22	2/1074 (0.2%)
28	S	0.40	1/925 (0.1%)	0.79	5/1229 (0.4%)
29	5J	0.30	0/6430	0.69	13/8681 (0.1%)
30	4D	0.43	0/967	0.58	0/1305
31	63	1.05	0/709	1.41	7/959 (0.7%)
32	2	0.44	5/2209 (0.2%)	0.48	1/3429 (0.0%)
33	B3	0.42	0/9485	0.64	4/12870 (0.0%)
34	1g	0.81	0/575	1.40	6/768 (0.8%)
34	2g	0.47	0/575	0.67	0/768
34	4g	0.38	0/584	0.78	0/779
34	5g	0.38	0/584	0.78	0/779
35	68	1.09	0/728	1.67	12/987 (1.2%)
36	5A	0.43	1/18874 (0.0%)	0.65	16/25606 (0.1%)
37	A3	0.83	0/3294	1.47	18/4423 (0.4%)
38	U	0.49	0/3846	0.67	4/5208 (0.1%)
39	5D	0.31	0/1198	0.58	2/1620 (0.1%)
40	64	1.05	0/609	1.53	3/824 (0.4%)
41	BP	0.50	0/779	0.61	0/1047
42	1C	0.70	0/437	1.33	2/587 (0.3%)
43	K	0.43	0/2673	0.82	2/3593 (0.1%)
44	4A	0.39	1/1983 (0.1%)	0.69	2/2657 (0.1%)
45	4	0.38	1/2967 (0.0%)	0.50	3/4610 (0.1%)
46	2A	0.28	0/1299	0.64	0/1761
47	A1	0.83	0/1234	1.45	4/1657 (0.2%)
48	65	1.12	0/593	1.66	7/800 (0.9%)
49	5B	0.39	0/16393	0.60	2/22174 (0.0%)
50	B1	0.48	0/6878	0.68	0/9315
All	All	0.54	41/141171 (0.0%)	0.81	235/193369 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
6	4B	0	3
7	4e	0	1
9	1K	0	1
10	4C	0	2
13	4f	0	1
13	5f	0	1
14	66	0	1
16	12	0	1
16	52	0	3
18	67	0	1
19	62	0	1
21	A2	0	4
23	5C	0	2
25	4b	0	1
29	5J	0	2
31	63	0	2
33	B3	0	1
35	68	0	3
36	5A	0	2
37	A3	0	6
38	U	0	3
40	64	0	1
44	4A	0	2
45	4	0	1
47	A1	0	4
49	5B	0	2
50	B1	0	4
All	All	0	56

All (41) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	78	U	O3'-P	-15.64	1.37	1.61
1	1	2	U	O3'-P	-14.60	1.39	1.61
22	B2	629	PRO	CA-C	-13.89	1.39	1.52
14	66	70	VAL	C-O	-10.01	1.13	1.24
18	67	61	GLN	C-O	-9.74	1.11	1.23
45	4	87	C	O3'-P	9.22	1.75	1.61
22	B2	629	PRO	C-N	-8.34	1.24	1.33
9	1K	176	VAL	C-O	-7.93	1.15	1.24
28	S	566	ILE	C-N	7.22	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	B2	629	PRO	N-CD	-7.16	1.37	1.47
9	1K	142	LYS	CA-C	7.04	1.60	1.53
2	6	87	C	C1'-N1	6.86	1.58	1.48
2	6	95	G	C1'-N9	-6.76	1.37	1.48
32	2	11	G	C1'-N9	-6.76	1.37	1.48
2	6	93	G	C1'-N9	-6.61	1.38	1.48
9	1K	104	THR	C-O	-6.50	1.16	1.24
32	2	12	G	C1'-N9	-6.45	1.38	1.48
9	1K	192	LEU	N-CA	-6.38	1.38	1.46
2	6	86	U	C1'-N1	6.16	1.57	1.48
9	1K	129	ILE	C-O	-6.02	1.17	1.24
2	6	89	U	C1'-N1	5.80	1.57	1.48
1	1	35	A	O3'-P	-5.80	1.52	1.61
9	1K	110	VAL	CA-C	5.66	1.59	1.52
9	1K	103	LYS	C-O	5.64	1.31	1.24
27	1A	54	GLN	CA-C	5.62	1.59	1.52
9	1K	122	GLU	C-O	-5.61	1.17	1.24
32	2	5	C	C1'-N1	5.61	1.56	1.48
22	B2	626	HIS	C-O	-5.55	1.17	1.24
9	1K	72	ARG	C-O	-5.55	1.17	1.24
22	B2	626	HIS	CA-C	5.38	1.59	1.52
9	1K	83	GLU	C-O	-5.36	1.17	1.24
9	1K	165	ASP	C-O	-5.26	1.17	1.23
9	1K	125	VAL	C-O	-5.25	1.17	1.24
25	1b	11	GLN	C-O	-5.25	1.17	1.24
32	2	13	C	C1'-N1	5.18	1.56	1.48
13	1f	4	PRO	N-CD	5.14	1.54	1.47
24	5X	447	ILE	CA-CB	5.13	1.57	1.54
36	5A	119	LEU	CA-CB	-5.13	1.46	1.53
44	4A	425	ASN	C-N	5.12	1.39	1.33
9	1K	180	ARG	CA-C	-5.10	1.46	1.52
32	2	3	C	C1'-N1	5.07	1.56	1.48

All (235) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5A	853	LYS	N-CA-C	-16.73	92.94	113.18
29	5J	674	THR	N-CA-C	-15.87	83.54	109.40
22	B2	629	PRO	CB-CA-C	-12.37	95.83	110.92
48	65	70	ASP	CA-CB-CG	12.35	124.95	112.60
36	5A	1550	GLY	N-CA-C	11.62	127.29	111.03
36	5A	1551	PHE	N-CA-C	-11.10	89.14	109.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5A	384	VAL	N-CA-C	10.90	123.64	109.58
45	4	87	C	O3'-P-O5'	10.22	119.33	104.00
1	1	78	U	P-O3'-C3'	9.56	134.54	120.20
22	B2	626	HIS	N-CA-C	9.55	123.44	111.69
6	4B	287	VAL	N-CA-C	9.46	119.42	110.53
14	66	29	ASP	CA-CB-CG	9.19	121.79	112.60
21	A2	115	PRO	CA-N-CD	-8.86	99.59	112.00
36	5A	851	SER	N-CA-C	-8.75	94.64	108.90
22	B2	629	PRO	N-CA-CB	8.70	111.51	103.08
47	A1	196	ASP	CA-CB-CG	-8.64	103.96	112.60
36	5A	705	LYS	N-CA-C	8.61	121.61	111.71
47	A1	221	PRO	N-CA-C	8.60	121.20	110.70
28	S	572	ALA	N-CA-C	8.48	123.09	112.24
29	5J	92	GLY	C-N-CD	-8.33	90.84	125.00
1	1	132	G	C2'-C3'-O3'	-8.07	101.59	113.70
36	5A	382	GLU	N-CA-C	8.07	120.07	111.28
38	U	145	GLY	N-CA-C	7.91	126.73	111.31
12	R	378	ALA	N-CA-C	-7.71	100.97	110.61
11	11	67	TYR	N-CA-C	7.70	120.78	109.07
37	A3	144	ASP	CA-CB-CG	-7.64	104.96	112.60
12	R	377	ASP	N-CA-C	7.60	121.28	109.96
22	B2	625	ALA	CA-C-N	7.56	133.50	120.58
22	B2	625	ALA	C-N-CA	7.56	133.50	120.58
29	5J	739	CYS	C-N-CD	-7.55	104.00	120.60
36	5A	1622	MET	N-CA-C	7.53	119.48	111.28
4	B4	12	ASP	CA-CB-CG	-7.49	105.11	112.60
36	5A	852	VAL	N-CA-C	7.47	119.38	107.73
19	62	3	PHE	CA-CB-CG	-7.42	106.38	113.80
25	1b	7	SER	CA-CB-OG	7.42	125.94	111.10
22	B2	630	PRO	CB-CA-C	7.41	118.13	111.17
37	A3	77	GLY	CA-C-N	7.40	129.09	119.84
37	A3	77	GLY	C-N-CA	7.40	129.09	119.84
42	1C	3	LYS	CB-CG-CD	7.28	128.03	111.30
34	1g	47	GLU	N-CA-C	7.22	119.15	111.28
23	5C	828	MET	CA-C-N	7.22	134.65	120.94
23	5C	828	MET	C-N-CA	7.22	134.65	120.94
31	63	19	ASP	CA-CB-CG	-7.11	105.49	112.60
43	K	965	LEU	CA-C-N	7.03	126.95	120.21
43	K	965	LEU	C-N-CA	7.03	126.95	120.21
37	A3	281	ARG	N-CA-C	6.96	119.46	111.11
9	1K	96	ASN	N-CA-C	6.90	119.65	111.71
42	1C	48	SER	N-CA-C	6.87	118.46	110.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	62	47	ASP	CB-CA-C	6.81	123.59	110.17
29	5J	739	CYS	CA-C-N	6.80	143.31	127.00
29	5J	739	CYS	C-N-CA	6.80	143.31	127.00
13	1f	3	LEU	CA-C-N	-6.75	111.40	119.84
13	1f	3	LEU	C-N-CA	-6.75	111.40	119.84
22	B2	628	VAL	CA-C-N	6.75	127.33	120.38
22	B2	628	VAL	C-N-CA	6.75	127.33	120.38
22	B2	642	PRO	CA-C-N	6.68	126.63	119.28
22	B2	642	PRO	C-N-CA	6.68	126.63	119.28
17	5	57	G	O4'-C1'-N9	6.67	118.20	108.20
9	1K	56	PRO	N-CA-C	6.62	118.78	110.70
37	A3	179	ASN	CA-CB-CG	-6.56	106.04	112.60
36	5A	1813	ARG	N-CA-C	6.48	118.13	111.14
25	1b	87	PRO	CB-CA-C	6.47	119.86	111.64
40	64	65	THR	CA-CB-CG2	-6.47	99.49	110.50
5	13	3	ILE	CA-CB-CG2	6.46	121.48	110.50
36	5A	706	ALA	N-CA-C	6.44	118.30	111.28
11	11	66	ARG	N-CA-C	-6.44	102.88	111.96
23	5C	440	SER	CA-C-N	6.41	142.39	127.00
23	5C	440	SER	C-N-CA	6.41	142.39	127.00
22	B2	621	VAL	CB-CA-C	-6.40	104.37	111.35
14	66	66	ARG	CB-CA-C	-6.39	100.67	110.26
33	B3	369	GLU	CA-C-N	6.37	129.25	120.39
33	B3	369	GLU	C-N-CA	6.37	129.25	120.39
28	S	567	PRO	N-CA-C	-6.36	105.69	114.98
9	1K	191	ARG	CG-CD-NE	-6.32	98.09	112.00
7	1e	83	ASN	N-CA-C	6.32	118.16	111.28
25	1b	78	VAL	O-C-N	6.30	126.64	121.85
29	5J	773	ASN	CA-C-N	6.27	142.04	127.00
29	5J	773	ASN	C-N-CA	6.27	142.04	127.00
13	1f	73	ARG	NE-CZ-NH1	-6.24	115.26	121.50
1	1	71	C	C2'-C3'-O3'	-6.21	104.38	113.70
48	65	27	HIS	ND1-CG-CD2	6.19	112.29	106.10
36	5A	1794	PHE	N-CA-C	6.19	118.03	111.28
18	67	55	MET	CG-SD-CE	-6.16	87.34	100.90
45	4	87	C	P-O3'-C3'	-6.15	110.97	120.20
44	4A	425	ASN	CA-C-N	-6.15	114.05	120.38
44	4A	425	ASN	C-N-CA	-6.15	114.05	120.38
27	1A	8	PRO	N-CA-C	6.13	120.86	111.11
22	B2	625	ALA	N-CA-C	6.11	118.74	111.71
18	67	28	GLN	N-CA-C	6.09	118.70	111.33
37	A3	351	ARG	N-CA-C	6.09	118.63	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	1g	51	SER	N-CA-C	-6.07	102.10	110.35
7	1e	59	ASP	N-CA-CB	5.99	119.12	110.20
13	1f	73	ARG	NE-CZ-NH2	5.98	124.58	119.20
9	1K	188	ARG	CA-C-N	-5.98	114.47	120.21
9	1K	188	ARG	C-N-CA	-5.98	114.47	120.21
9	1K	186	GLY	N-CA-C	5.94	123.25	115.47
35	68	66	ASN	CA-CB-CG	-5.91	106.69	112.60
5	13	73	LEU	CB-CG-CD2	5.88	128.34	110.70
35	68	18	SER	CA-C-N	5.88	128.75	120.28
35	68	18	SER	C-N-CA	5.88	128.75	120.28
23	5C	941	LYS	N-CA-C	-5.87	104.89	111.28
21	A2	140	GLU	N-CA-C	5.84	118.80	110.10
36	5A	191	ILE	N-CA-C	5.83	117.10	111.91
45	4	87	C	OP2-P-O3'	-5.83	90.50	108.00
29	5J	92	GLY	CA-C-N	-5.81	112.58	119.84
29	5J	92	GLY	C-N-CA	-5.81	112.58	119.84
29	5J	672	ALA	O-C-N	5.79	127.98	121.32
9	1K	117	SER	N-CA-C	5.77	117.24	111.07
22	B2	644	SER	N-CA-CB	-5.76	101.91	110.61
24	5X	634	LYS	CA-C-N	5.76	125.89	119.32
24	5X	634	LYS	C-N-CA	5.76	125.89	119.32
37	A3	291	LYS	CA-C-N	5.75	132.53	121.54
37	A3	291	LYS	C-N-CA	5.75	132.53	121.54
48	65	49	MET	CG-SD-CE	-5.71	88.33	100.90
8	I	1	G	C3'-C2'-O2'	5.69	119.24	110.70
36	5A	186	GLU	CA-C-N	-5.68	114.08	119.76
36	5A	186	GLU	C-N-CA	-5.68	114.08	119.76
39	5D	102	ILE	CA-C-N	5.66	133.77	124.31
39	5D	102	ILE	C-N-CA	5.66	133.77	124.31
25	1b	55	ASN	N-CA-C	5.65	117.44	111.28
40	64	33	ASP	CA-CB-CG	5.65	118.25	112.60
5	13	51	ARG	NE-CZ-NH2	5.64	124.28	119.20
22	B2	625	ALA	CA-C-O	-5.64	113.72	120.10
48	65	27	HIS	CG-CD2-NE2	-5.64	101.56	107.20
22	B2	661	CYS	N-CA-C	5.62	119.88	113.19
15	X	143	ARG	CA-C-N	5.61	132.25	121.54
15	X	143	ARG	C-N-CA	5.61	132.25	121.54
37	A3	78	PRO	N-CA-C	5.61	124.02	112.47
34	1g	75	ARG	N-CA-C	5.61	119.30	111.90
29	5J	773	ASN	C-N-CD	-5.59	108.30	120.60
35	68	96	HIS	ND1-CG-CD2	5.58	111.68	106.10
19	62	92	GLN	N-CA-C	5.56	117.42	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	66	52	VAL	CA-CB-CG1	5.55	119.83	110.40
8	I	0	G	C3'-C2'-O2'	5.52	118.98	110.70
9	1K	121	ARG	N-CA-C	5.51	117.72	111.11
35	68	19	ASP	CA-CB-CG	5.51	118.11	112.60
21	A2	177	GLU	CA-C-N	5.51	128.53	120.71
21	A2	177	GLU	C-N-CA	5.51	128.53	120.71
7	1e	59	ASP	N-CA-C	5.50	118.46	111.69
24	5X	399	PRO	O-C-N	5.50	123.84	121.31
14	66	58	ASN	CA-CB-CG	-5.49	107.11	112.60
33	B3	318	ASP	CA-C-N	5.48	129.91	121.19
33	B3	318	ASP	C-N-CA	5.48	129.91	121.19
35	68	96	HIS	CB-CA-C	-5.47	99.70	110.10
7	1e	66	SER	N-CA-C	5.46	117.23	111.28
37	A3	104	VAL	CA-C-O	-5.46	115.03	118.69
31	63	82	ILE	CA-C-N	5.46	125.11	119.05
31	63	82	ILE	C-N-CA	5.46	125.11	119.05
38	U	406	LYS	N-CA-C	5.44	118.53	110.48
34	1g	33	GLY	N-CA-C	5.43	118.66	110.18
1	1	37	G	C2'-C3'-O3'	-5.42	105.58	113.70
14	66	70	VAL	CB-CA-C	-5.40	104.76	111.08
22	B2	656	PRO	CA-C-N	5.40	124.65	120.33
22	B2	656	PRO	C-N-CA	5.40	124.65	120.33
37	A3	284	ARG	NE-CZ-NH2	5.39	124.05	119.20
18	67	78	GLY	CA-C-N	5.39	128.50	120.31
18	67	78	GLY	C-N-CA	5.39	128.50	120.31
10	4C	357	ARG	CB-CA-C	-5.38	109.91	117.23
35	68	79	SER	N-CA-CB	5.38	119.59	110.49
37	A3	351	ARG	NE-CZ-NH2	5.38	124.05	119.20
13	1f	15	THR	N-CA-CB	5.38	117.96	109.83
1	1	133	G	C1'-C2'-O2'	-5.37	103.74	111.80
37	A3	10	ARG	NE-CZ-NH2	5.36	124.02	119.20
11	11	66	ARG	CG-CD-NE	5.36	123.78	112.00
10	4C	355	GLY	N-CA-C	5.35	118.93	110.96
19	62	41	THR	CA-C-N	5.35	129.78	122.34
19	62	41	THR	C-N-CA	5.35	129.78	122.34
4	B4	37	GLY	CA-C-N	5.33	125.64	119.93
4	B4	37	GLY	C-N-CA	5.33	125.64	119.93
11	11	45	MET	CG-SD-CE	-5.33	89.17	100.90
1	1	73	C	C2'-C3'-O3'	-5.32	105.72	113.70
24	5X	461	ARG	N-CA-C	-5.31	106.75	113.18
29	5J	673	PRO	N-CA-C	5.31	119.42	111.14
31	63	90	ASP	CA-CB-CG	5.31	117.91	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	S	566	ILE	CA-C-N	-5.29	114.64	121.04
28	S	566	ILE	C-N-CA	-5.29	114.64	121.04
23	5C	440	SER	C-N-CD	-5.27	109.00	120.60
18	67	85	CYS	CA-C-N	5.27	125.25	120.03
18	67	85	CYS	C-N-CA	5.27	125.25	120.03
24	5X	381	THR	N-CA-C	5.27	117.49	108.90
38	U	405	GLU	N-CA-C	5.27	117.10	111.36
22	B2	633	LEU	CD1-CG-CD2	-5.25	99.26	110.80
35	68	61	ILE	CB-CA-C	-5.24	103.80	110.98
22	B2	621	VAL	N-CA-CB	5.24	117.07	111.46
22	B2	626	HIS	CB-CA-C	-5.22	101.14	110.70
1	1	63	C	C3'-C2'-O2'	5.22	118.53	110.70
19	62	59	ASN	OD1-CG-ND2	-5.22	117.38	122.60
19	62	89	GLU	N-CA-C	5.22	116.78	111.14
11	11	4	VAL	CB-CA-C	-5.22	104.08	112.16
38	U	144	GLN	N-CA-C	-5.21	102.58	110.24
22	B2	629	PRO	N-CD-CG	5.21	111.01	103.20
35	68	88	ALA	CA-C-N	5.21	134.51	121.80
35	68	88	ALA	C-N-CA	5.21	134.51	121.80
35	68	77	THR	N-CA-C	-5.20	100.83	108.79
7	1e	73	GLN	CA-CB-CG	5.19	124.48	114.10
32	2	46	U	P-O3'-C3'	5.19	127.99	120.20
48	65	33	ASP	CA-CB-CG	-5.19	107.41	112.60
37	A3	184	ARG	NE-CZ-NH2	5.18	123.87	119.20
9	1K	56	PRO	CA-C-N	-5.17	114.34	119.56
9	1K	56	PRO	C-N-CA	-5.17	114.34	119.56
9	1K	62	THR	N-CA-C	-5.17	101.43	109.24
34	1g	53	GLN	N-CA-C	5.17	117.58	110.35
31	63	22	ARG	N-CA-CB	5.16	119.43	110.39
22	B2	614	ARG	N-CA-C	5.16	117.81	111.82
40	64	12	ASN	CA-CB-CG	5.16	117.76	112.60
34	1g	51	SER	CA-C-O	-5.15	116.09	121.55
29	5J	92	GLY	N-CA-C	5.14	122.83	112.34
5	13	51	ARG	CA-CB-CG	5.14	124.38	114.10
35	68	35	ASN	N-CA-CB	5.13	118.01	109.60
7	4e	53	TYR	CA-C-N	5.13	129.84	122.40
7	4e	53	TYR	C-N-CA	5.13	129.84	122.40
28	S	567	PRO	CA-C-O	5.11	124.16	118.38
7	1e	39	VAL	CB-CA-C	5.11	117.23	110.84
31	63	19	ASP	N-CA-C	5.10	116.84	111.28
37	A3	312	ARG	CA-C-N	5.09	131.25	121.54
37	A3	312	ARG	C-N-CA	5.09	131.25	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	63	53	ILE	N-CA-CB	5.08	117.86	111.46
47	A1	162	PHE	CA-C-N	5.08	127.05	120.44
47	A1	162	PHE	C-N-CA	5.08	127.05	120.44
36	5A	1417	PRO	N-CA-C	-5.08	102.53	110.50
27	1A	98	LYS	N-CA-C	5.08	118.73	112.54
49	5B	2084	LEU	CA-C-N	5.07	131.23	121.54
49	5B	2084	LEU	C-N-CA	5.07	131.23	121.54
11	11	66	ARG	NE-CZ-NH2	5.07	123.76	119.20
1	1	131	U	P-O5'-C5'	-5.07	113.30	120.90
48	65	44	ASP	CA-C-N	5.06	127.06	120.28
48	65	44	ASP	C-N-CA	5.06	127.06	120.28
4	B4	74	MET	CG-SD-CE	-5.06	89.77	100.90
37	A3	35	ASP	CA-CB-CG	-5.04	107.56	112.60
22	B2	650	ILE	CA-C-N	5.04	125.33	119.93
22	B2	650	ILE	C-N-CA	5.04	125.33	119.93
25	1b	78	VAL	CB-CA-C	-5.04	107.42	111.71
37	A3	42	ARG	NE-CZ-NH2	5.04	123.73	119.20
1	1	131	U	C2'-C3'-O3'	5.01	117.02	109.50
11	51	51	GLU	CB-CG-CD	5.01	121.11	112.60

There are no chirality outliers.

All (56) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
16	12	17	GLN	Peptide
9	1K	56	PRO	Peptide
45	4	90	G	Sidechain
44	4A	421	PRO	Peptide
44	4A	538	SER	Peptide
6	4B	420	TYR	Peptide
6	4B	459	PRO	Peptide
6	4B	470	TYR	Peptide
10	4C	350	GLN	Peptide
10	4C	386	ASP	Peptide
25	4b	53	PRO	Peptide
7	4e	51	ASP	Peptide
13	4f	40	MET	Peptide
16	52	46	CYS	Peptide
16	52	60	ASP	Peptide
16	52	88	LYS	Peptide
36	5A	1416	ILE	Peptide
36	5A	1792	LYS	Peptide

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Mol	Chain	Res	Type	Group
49	5B	1265	GLN	Peptide
49	5B	526	ASN	Peptide
23	5C	167	TYR	Peptide
23	5C	439	PRO	Peptide
29	5J	624	VAL	Peptide
29	5J	724	MET	Peptide
13	5f	40	MET	Peptide
19	62	69	TYR	Sidechain
31	63	30	TYR	Sidechain
31	63	46	TYR	Sidechain
40	64	25	TYR	Sidechain
14	66	51	TYR	Sidechain
18	67	62	TYR	Sidechain
35	68	60	TYR	Sidechain
35	68	8	TYR	Sidechain
35	68	89	GLU	Peptide
47	A1	191	ARG	Sidechain
47	A1	193	TYR	Sidechain
47	A1	199	ARG	Sidechain
47	A1	255	ARG	Sidechain
21	A2	138	TYR	Sidechain
21	A2	175	PRO	Peptide
21	A2	176	TYR	Sidechain
21	A2	201	ARG	Sidechain
37	A3	163	TYR	Sidechain
37	A3	281	ARG	Sidechain
37	A3	312	ARG	Sidechain
37	A3	42	ARG	Sidechain
37	A3	58	ARG	Sidechain
37	A3	61	TYR	Sidechain
50	B1	1050	VAL	Peptide
50	B1	460	PRO	Peptide
50	B1	483	ASP	Peptide
50	B1	488	SER	Peptide
33	B3	913	LEU	Peptide
38	U	244	LEU	Peptide
38	U	423	PHE	Peptide
38	U	531	GLN	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	3485	0	1756	389	0
2	6	1133	0	573	46	0
3	5O	2394	0	2326	56	0
4	B4	618	0	613	15	0
5	13	637	0	652	32	0
5	23	652	0	670	22	0
5	43	652	0	670	27	0
5	53	657	0	675	16	0
6	4B	2842	0	2746	88	0
7	1e	638	0	657	43	0
7	2e	669	0	692	20	0
7	4e	631	0	648	29	0
7	5e	638	0	657	23	0
8	I	530	0	271	11	0
9	1K	1649	0	1607	166	0
10	4C	2375	0	2375	39	0
11	11	641	0	680	18	0
11	21	634	0	679	59	0
11	41	641	0	681	18	0
11	51	641	0	681	16	0
12	R	874	0	883	44	0
13	1f	576	0	589	19	0
13	2f	562	0	574	11	0
13	4f	562	0	574	36	0
13	5f	567	0	575	19	0
14	66	567	0	571	15	0
15	X	394	0	406	79	0
16	12	777	0	798	31	0
16	22	774	0	802	42	0
16	42	737	0	780	44	0
16	52	796	0	821	27	0
17	5	2192	0	1110	36	0
18	67	604	0	623	8	0
19	62	761	0	777	4	0
20	2B	745	0	767	11	0
21	A2	1221	0	1197	69	0
22	B2	1699	0	1736	60	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	5C	6727	0	6735	138	0
24	5X	4780	0	4845	298	0
25	1b	692	0	717	25	0
25	2b	664	0	690	19	0
25	4b	669	0	697	19	0
25	5b	594	0	615	6	0
26	B5	567	0	533	14	0
27	1A	787	0	797	10	0
28	S	917	0	921	67	0
29	5J	6316	0	6227	163	0
30	4D	955	0	1008	30	0
31	63	699	0	702	13	0
32	2	1984	0	1005	23	0
33	B3	9296	0	9216	172	0
34	1g	568	0	590	40	0
34	2g	568	0	590	12	0
34	4g	577	0	603	20	0
34	5g	577	0	603	20	0
35	68	722	0	712	19	0
36	5A	18366	0	18268	574	0
37	A3	3227	0	3117	89	0
38	U	3750	0	3766	81	0
39	5D	1169	0	1141	66	0
40	64	596	0	591	9	0
41	BP	766	0	737	9	0
42	1C	425	0	392	20	0
43	K	2626	0	2698	192	0
44	4A	1946	0	2011	105	0
45	4	2690	0	1368	63	0
46	2A	1282	0	1305	27	0
47	A1	1339	0	1234	44	0
48	65	587	0	605	12	0
49	5B	16077	0	16192	256	0
50	B1	6749	0	6948	89	0
51	1C	1	0	0	0	0
51	A2	1	0	0	0	0
51	BP	3	0	0	0	0
51	U	1	0	0	0	0
52	5C	1	0	0	0	0
53	5C	32	0	12	0	0
54	5A	36	0	6	1	0
All	All	137494	0	132089	3475	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 13.

All (3475) 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)
1:1:7:A:C5'	24:5X:478:ARG:H	1.04	1.64
38:U:134:TYR:CD1	38:U:145:GLY:HA3	1.13	1.64
24:5X:362:LEU:HD23	24:5X:391:ARG:CD	1.21	1.62
21:A2:115:PRO:CG	21:A2:176:TYR:HD1	1.00	1.59
29:5J:839:HIS:HD2	43:K:942:LYS:CE	0.95	1.59
29:5J:839:HIS:CD2	43:K:942:LYS:CE	1.80	1.57
24:5X:380:THR:CG2	24:5X:628:TYR:HB3	1.29	1.56
29:5J:839:HIS:CD2	43:K:942:LYS:HE2	1.39	1.55
24:5X:379:ILE:CG2	24:5X:629[A]:ILE:HG13	1.35	1.54
24:5X:362:LEU:CD2	24:5X:391:ARG:CG	1.89	1.50
1:1:92:C:H2'	1:1:93:G:C8	1.44	1.49
21:A2:115:PRO:HG2	21:A2:176:TYR:CD1	0.96	1.49
9:1K:61:GLU:CB	9:1K:65:GLU:HG2	1.41	1.48
1:1:32:A:N3	9:1K:135:VAL:HG22	1.22	1.48
1:1:29:A:C8	9:1K:200:ARG:NH1	1.80	1.46
36:5A:1908:LYS:CE	43:K:843:ASP:HB3	1.40	1.46
22:B2:630:PRO:HG3	22:B2:663:PHE:CZ	1.49	1.46
44:4A:447:LYS:NZ	47:A1:430:UNK:C	1.79	1.45
36:5A:710:LEU:HD22	39:5D:4:MET:CE	1.47	1.45
44:4A:447:LYS:NZ	47:A1:431:UNK:N	1.64	1.44
24:5X:362:LEU:CD2	24:5X:391:ARG:NE	1.74	1.43
6:4B:365:SER:CA	44:4A:423:GLN:OE1	1.64	1.43
1:1:50:G:H1'	1:1:91:G:N2	1.15	1.42
16:22:95:TYR:HB3	37:A3:147:LEU:CD1	1.45	1.42
1:1:137:U:O4	9:1K:34:HIS:CA	1.68	1.42
36:5A:852:VAL:CG2	36:5A:854:SER:HA	1.50	1.42
1:1:29:A:N3	9:1K:200:ARG:HD2	1.31	1.41
44:4A:447:LYS:NZ	47:A1:430:UNK:CA	1.85	1.40
12:R:432:PRO:O	44:4A:466:LEU:CD2	1.69	1.39
36:5A:710:LEU:CD2	39:5D:4:MET:CE	2.01	1.39
23:5C:520:GLU:OE2	38:U:146:ARG:CB	1.71	1.39
28:S:574:ASN:ND2	29:5J:451:LYS:HD3	1.34	1.38
38:U:134:TYR:CD1	38:U:145:GLY:CA	2.03	1.38
24:5X:362:LEU:CD2	24:5X:391:ARG:HE	1.27	1.37
12:R:456:LYS:NZ	44:4A:465:ARG:HA	1.35	1.37
1:1:33:C:C4'	9:1K:137:SER:HA	1.52	1.35
24:5X:362:LEU:HD23	24:5X:391:ARG:NE	1.08	1.35

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:105:U:O4	36:5A:1607:GLU:CB	1.73	1.35
24:5X:378:SER:OG	24:5X:630:GLY:CA	1.73	1.35
24:5X:362:LEU:HD21	24:5X:391:ARG:CB	1.55	1.34
15:X:135:ARG:NH2	36:5A:1592:ASP:OD1	1.58	1.34
1:1:7:A:H5''	24:5X:478:ARG:CA	1.58	1.33
1:1:7:A:H5''	24:5X:478:ARG:N	1.02	1.33
1:1:7:A:C4'	24:5X:478:ARG:H	1.39	1.33
29:5J:839:HIS:CD2	43:K:942:LYS:HE3	1.52	1.33
1:1:137:U:C4	9:1K:34:HIS:HA	1.51	1.32
24:5X:380:THR:CG2	24:5X:628:TYR:CB	2.09	1.29
16:22:95:TYR:O	37:A3:147:LEU:CD1	1.79	1.29
1:1:32:A:O4'	9:1K:135:VAL:CG1	1.80	1.29
1:1:32:A:C4	9:1K:135:VAL:HG22	1.66	1.28
16:22:95:TYR:O	37:A3:147:LEU:HD11	1.19	1.28
39:5D:3:TYR:OH	39:5D:39:MET:HG3	1.27	1.28
24:5X:370:TRP:CE3	24:5X:389:PRO:HD2	1.69	1.28
1:1:30:U:H3	9:1K:175:LEU:CD2	1.35	1.28
1:1:32:A:C4	9:1K:135:VAL:CG2	2.15	1.28
1:1:8:C:OP1	24:5X:503:ILE:HB	1.21	1.27
15:X:124:VAL:HG11	13:4f:39:TYR:CE2	1.70	1.25
37:A3:356:ARG:CB	11:21:75:PRO:HB3	1.66	1.25
24:5X:362:LEU:CD2	24:5X:391:ARG:CD	2.02	1.25
37:A3:360:GLU:OE1	11:21:74:LEU:HD23	1.08	1.25
1:1:30:U:C2	9:1K:175:LEU:HD22	1.71	1.24
24:5X:378:SER:OG	24:5X:630:GLY:HA2	1.23	1.24
22:B2:630:PRO:HG3	22:B2:663:PHE:CE2	1.71	1.24
25:1b:8:LYS:O	25:1b:12:HIS:NE2	1.70	1.23
36:5A:710:LEU:CD2	39:5D:4:MET:HE3	1.62	1.23
1:1:32:A:H5'	9:1K:146:TYR:OH	1.32	1.22
21:A2:115:PRO:CG	21:A2:176:TYR:CD1	1.85	1.22
23:5C:105:MET:CG	23:5C:540:GLU:O	1.87	1.21
44:4A:447:LYS:NZ	47:A1:430:UNK:HA	1.46	1.20
1:1:118:A:N6	5:13:3:ILE:C	1.99	1.20
3:5O:148:LYS:NZ	17:5:7:U:O5'	1.75	1.20
36:5A:694:LEU:HD13	47:A1:463:GLU:OE2	1.40	1.20
2:6:103:U:H1'	35:68:65:ASP:OD1	1.35	1.19
21:A2:117:TYR:OH	21:A2:176:TYR:CD2	1.90	1.19
24:5X:378:SER:OG	24:5X:630:GLY:C	1.84	1.19
36:5A:1908:LYS:CE	43:K:843:ASP:CB	2.19	1.19
24:5X:649:SER:OG	36:5A:1685:LEU:HB3	1.35	1.19
1:1:118:A:H62	5:13:3:ILE:C	1.51	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:22:95:TYR:C	37:A3:147:LEU:HD11	1.68	1.19
6:4B:284:LYS:HE2	6:4B:288:SER:CB	1.73	1.19
16:22:95:TYR:CB	37:A3:147:LEU:CD1	2.19	1.19
24:5X:380:THR:HG22	24:5X:628:TYR:CB	1.69	1.19
1:1:29:A:C4	9:1K:200:ARG:HD2	1.77	1.18
1:1:7:A:C5'	24:5X:478:ARG:N	1.72	1.17
24:5X:536:ARG:CB	34:1g:10:LYS:HE3	1.74	1.17
44:4A:447:LYS:HZ2	47:A1:430:UNK:CA	1.45	1.17
1:1:105:U:O4	36:5A:1607:GLU:HB2	0.99	1.16
30:4D:108:GLU:HB2	43:K:928:ASN:ND2	1.59	1.16
12:R:436:VAL:HG21	44:4A:462:GLU:OE1	1.42	1.16
1:1:32:A:N3	9:1K:135:VAL:CG2	2.06	1.16
1:1:164:G:O3'	11:11:50:ARG:O	1.64	1.16
1:1:28:G:C2	9:1K:112:TYR:CE2	2.34	1.15
36:5A:710:LEU:CD2	39:5D:4:MET:HE1	1.69	1.15
38:U:134:TYR:CE1	38:U:145:GLY:HA3	1.80	1.15
2:6:64:U:OP1	43:K:911:LYS:CD	1.95	1.15
24:5X:378:SER:CB	24:5X:630:GLY:HA2	1.77	1.15
1:1:50:G:C1'	1:1:91:G:N2	2.09	1.15
28:S:574:ASN:ND2	29:5J:451:LYS:CD	2.10	1.15
2:6:64:U:OP1	43:K:911:LYS:HD2	1.46	1.14
1:1:32:A:O4'	9:1K:135:VAL:HG11	0.99	1.14
23:5C:105:MET:HG2	23:5C:540:GLU:O	1.42	1.14
36:5A:192:GLN:HB3	36:5A:208:TYR:CD2	1.83	1.14
37:A3:356:ARG:HB3	11:21:75:PRO:CB	1.77	1.14
1:1:9:C:OP2	24:5X:503:ILE:O	1.65	1.14
24:5X:362:LEU:CD2	24:5X:391:ARG:HG3	1.59	1.14
1:1:28:G:N2	9:1K:112:TYR:CE2	2.17	1.13
24:5X:647:SER:HB3	36:5A:1686:ASP:OD2	1.48	1.13
3:5O:146:ARG:NH2	17:5:7:U:O2'	1.81	1.13
6:4B:365:SER:HA	44:4A:423:GLN:OE1	1.43	1.12
37:A3:356:ARG:CG	11:21:75:PRO:HB3	1.79	1.12
6:4B:402:PHE:CZ	44:4A:424:LEU:HD12	1.83	1.12
37:A3:356:ARG:HB3	11:21:75:PRO:HB3	1.12	1.12
37:A3:360:GLU:OE1	11:21:74:LEU:CD2	1.96	1.12
44:4A:427:PRO:HB2	44:4A:639:LYS:HE3	1.27	1.12
6:4B:284:LYS:HE2	6:4B:288:SER:HB2	1.24	1.12
38:U:132:ASN:O	38:U:145:GLY:N	1.82	1.12
24:5X:378:SER:HG	24:5X:630:GLY:C	1.56	1.11
24:5X:379:ILE:HA	24:5X:628:TYR:O	1.49	1.11
36:5A:1908:LYS:HE2	43:K:843:ASP:CB	1.78	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:4B:365:SER:CB	44:4A:423:GLN:OE1	1.97	1.11
36:5A:1908:LYS:HE3	43:K:843:ASP:CB	1.80	1.11
12:R:432:PRO:HB2	44:4A:466:LEU:HD22	1.23	1.11
1:1:29:A:C5'	9:1K:200:ARG:NH2	2.02	1.11
1:1:92:C:C2'	1:1:93:G:C8	2.33	1.11
1:1:92:C:O2	1:1:93:G:N7	1.83	1.10
28:S:574:ASN:HD21	29:5J:451:LYS:CD	1.63	1.10
1:1:32:A:C5	9:1K:148:PHE:CE1	2.22	1.10
1:1:29:A:N3	9:1K:200:ARG:CD	2.13	1.10
1:1:32:A:N7	9:1K:148:PHE:CE1	2.20	1.10
1:1:33:C:C2	9:1K:139:ARG:NE	2.19	1.10
2:6:103:U:C1'	35:68:65:ASP:OD1	2.00	1.09
21:A2:115:PRO:HD2	21:A2:177:GLU:H	0.94	1.09
30:4D:108:GLU:HB2	43:K:928:ASN:HD21	0.99	1.09
39:5D:8:LEU:HD13	39:5D:14:VAL:HA	1.25	1.09
24:5X:380:THR:N	24:5X:628:TYR:O	1.84	1.09
1:1:7:A:H4'	24:5X:477:THR:HA	1.34	1.09
36:5A:852:VAL:CG2	36:5A:854:SER:CA	2.31	1.09
1:1:8:C:OP1	24:5X:503:ILE:CB	2.01	1.09
6:4B:365:SER:N	44:4A:423:GLN:OE1	1.86	1.09
1:1:29:A:C4	9:1K:200:ARG:CD	2.36	1.08
12:R:432:PRO:C	44:4A:466:LEU:HD22	1.77	1.08
1:1:29:A:H5'	9:1K:200:ARG:HH21	1.16	1.08
10:4C:357:ARG:HG3	10:4C:358:ARG:H	1.08	1.08
24:5X:380:THR:HG23	24:5X:628:TYR:HB3	1.08	1.08
37:A3:356:ARG:C	11:21:75:PRO:HG3	1.76	1.08
38:U:407:GLU:O	38:U:409:LEU:N	1.85	1.08
36:5A:192:GLN:HB3	36:5A:208:TYR:CE2	1.88	1.08
36:5A:192:GLN:HG2	36:5A:208:TYR:CG	1.89	1.08
12:R:432:PRO:O	44:4A:466:LEU:HD22	1.49	1.07
16:22:95:TYR:CB	37:A3:147:LEU:HD12	1.79	1.07
36:5A:710:LEU:HD22	39:5D:4:MET:HE1	1.11	1.07
24:5X:370:TRP:CH2	24:5X:389:PRO:O	2.08	1.07
1:1:33:C:C5'	9:1K:137:SER:HA	1.85	1.07
36:5A:694:LEU:HD12	47:A1:466:LEU:CD1	1.83	1.07
6:4B:284:LYS:CE	6:4B:288:SER:CB	2.33	1.06
24:5X:536:ARG:HB3	34:1g:10:LYS:HE3	1.13	1.06
36:5A:1908:LYS:HE3	43:K:843:ASP:HB3	1.11	1.06
1:1:29:A:N9	9:1K:200:ARG:NH1	2.01	1.06
1:1:33:C:H4'	9:1K:137:SER:HA	1.13	1.06
1:1:105:U:C2	36:5A:1634:SER:HA	1.90	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B4:14:THR:OG1	37:A3:429:TRP:CH2	2.06	1.06
24:5X:380:THR:HG22	24:5X:628:TYR:HB3	1.08	1.06
1:1:30:U:N3	9:1K:175:LEU:HD22	1.54	1.06
24:5X:362:LEU:HD22	24:5X:391:ARG:HG3	1.07	1.06
36:5A:1510:GLU:O	36:5A:1513:MET:HG2	1.55	1.06
1:1:8:C:OP2	24:5X:478:ARG:HB2	1.53	1.06
36:5A:1908:LYS:HE2	43:K:843:ASP:HB3	1.21	1.06
34:1g:66:SER:OG	7:1e:85:THR:HG23	1.55	1.05
36:5A:710:LEU:HD23	39:5D:4:MET:HE3	1.32	1.05
21:A2:115:PRO:HD2	21:A2:177:GLU:N	1.69	1.05
36:5A:852:VAL:HG22	36:5A:854:SER:CA	1.85	1.05
9:1K:61:GLU:CB	9:1K:65:GLU:CG	2.36	1.04
15:X:149:ARG:NH1	36:5A:1616:PRO:HG3	1.71	1.04
36:5A:1794:PHE:CD2	36:5A:1795:GLU:HG2	1.92	1.04
24:5X:373:PHE:CZ	24:5X:419:ARG:HD3	1.93	1.04
36:5A:60:ASP:OD1	36:5A:484:SER:O	1.76	1.04
36:5A:852:VAL:HG23	36:5A:854:SER:HA	1.35	1.04
22:B2:607:GLY:O	22:B2:663:PHE:HB3	1.56	1.04
1:1:32:A:C1'	9:1K:135:VAL:CG1	2.36	1.04
1:1:17:G:O2'	1:1:18:G:H5'	1.57	1.03
1:1:9:C:OP2	24:5X:503:ILE:C	2.02	1.03
1:1:33:C:N3	9:1K:139:ARG:NH2	2.05	1.03
22:B2:630:PRO:CG	22:B2:663:PHE:CZ	2.42	1.03
9:1K:59:ARG:CZ	11:11:77:ASP:OD1	2.07	1.03
15:X:149:ARG:HH12	36:5A:1616:PRO:HG3	0.89	1.03
16:22:95:TYR:HD1	37:A3:147:LEU:HD13	1.19	1.03
21:A2:117:TYR:OH	21:A2:176:TYR:CG	2.12	1.03
29:5J:158:LEU:CD1	36:5A:701:ILE:HG23	1.88	1.02
22:B2:630:PRO:CG	22:B2:663:PHE:CE2	2.41	1.02
36:5A:60:ASP:OD1	36:5A:61:MET:N	1.92	1.02
17:5:45:C:O2	36:5A:603:ARG:NH2	1.92	1.02
24:5X:362:LEU:CG	24:5X:391:ARG:HE	1.71	1.02
12:R:432:PRO:O	44:4A:466:LEU:HD21	1.59	1.01
15:X:137:TYR:CE1	28:S:729:LEU:HD13	1.95	1.01
24:5X:380:THR:HG22	24:5X:628:TYR:CG	1.94	1.01
21:A2:136:ILE:HG22	21:A2:138:TYR:CD1	1.94	1.01
24:5X:362:LEU:HD21	24:5X:391:ARG:HB2	1.01	1.01
1:1:11:G:N7	24:5X:507:SER:HA	1.75	1.00
30:4D:108:GLU:OE1	43:K:926:ASN:ND2	1.95	1.00
12:R:432:PRO:HB2	44:4A:466:LEU:CD2	1.91	1.00
1:1:7:A:H5''	24:5X:478:ARG:CB	1.91	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:X:140:TYR:CE2	36:5A:1587:GLU:OE1	2.15	1.00
24:5X:370:TRP:CE3	24:5X:389:PRO:CD	2.44	1.00
44:4A:447:LYS:HZ2	47:A1:430:UNK:C	1.56	0.99
33:B3:929:LYS:HB3	33:B3:931:VAL:HG13	1.44	0.99
38:U:146:ARG:NH2	38:U:173:TYR:CE1	2.27	0.99
1:1:7:A:O5'	24:5X:478:ARG:HB3	1.62	0.99
12:R:432:PRO:CB	44:4A:466:LEU:HD22	1.91	0.99
36:5A:694:LEU:HD12	47:A1:466:LEU:HD12	1.39	0.99
1:1:29:A:H5'	9:1K:200:ARG:NH2	1.71	0.99
21:A2:117:TYR:HE1	21:A2:139:PRO:HD2	1.27	0.99
21:A2:115:PRO:CD	21:A2:177:GLU:H	1.75	0.99
1:1:123:A:O2'	16:12:10:GLU:HG3	1.22	0.99
9:1K:59:ARG:NH1	11:11:77:ASP:OD1	1.95	0.99
24:5X:536:ARG:HB3	34:1g:10:LYS:CE	1.93	0.99
44:4A:447:LYS:NZ	47:A1:429:UNK:O	1.95	0.99
1:1:140:G:OP1	25:1b:54:LYS:HD3	1.61	0.99
24:5X:380:THR:HG22	24:5X:628:TYR:CD2	1.97	0.99
21:A2:115:PRO:HG2	21:A2:176:TYR:CG	1.98	0.99
1:1:33:C:H4'	9:1K:137:SER:CA	1.92	0.98
24:5X:370:TRP:CD2	24:5X:389:PRO:HD2	1.96	0.98
1:1:33:C:N3	9:1K:139:ARG:CZ	2.27	0.98
16:22:95:TYR:HB3	37:A3:147:LEU:HD12	1.03	0.98
24:5X:379:ILE:HA	24:5X:629[A]:ILE:HA	1.46	0.98
21:A2:136:ILE:CG2	21:A2:138:TYR:CE1	2.47	0.98
1:1:105:U:C4	36:5A:1607:GLU:CD	2.42	0.98
30:4D:108:GLU:CB	43:K:928:ASN:ND2	2.26	0.98
36:5A:559:ASP:HA	36:5A:562:VAL:HG22	1.46	0.98
1:1:8:C:O5'	24:5X:504:GLY:N	1.96	0.98
7:5e:58:LEU:O	7:5e:76:ARG:HA	1.63	0.98
33:B3:932:ASN:ND2	33:B3:936:LYS:HE3	1.79	0.97
1:1:7:A:O3'	24:5X:525:THR:HG21	1.64	0.97
1:1:105:U:O4	36:5A:1607:GLU:CG	2.11	0.97
1:1:137:U:O4	9:1K:34:HIS:HA	0.80	0.97
24:5X:380:THR:HG23	24:5X:628:TYR:CB	1.83	0.97
23:5C:520:GLU:OE2	38:U:146:ARG:HB3	0.80	0.97
4:B4:14:THR:OG1	37:A3:429:TRP:HH2	1.41	0.97
1:1:32:A:H1'	9:1K:135:VAL:HG13	1.46	0.97
23:5C:520:GLU:CD	38:U:146:ARG:HB3	1.89	0.97
24:5X:379:ILE:CA	24:5X:628:TYR:O	2.10	0.96
24:5X:361:LYS:C	24:5X:391:ARG:NH2	2.19	0.96
36:5A:169:PHE:CE1	36:5A:563:GLN:NE2	2.33	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:4A:427:PRO:HB2	44:4A:639:LYS:CE	1.95	0.96
15:X:120:VAL:HG11	13:4f:39:TYR:CZ	1.99	0.96
1:1:32:A:C4	9:1K:135:VAL:HG21	1.98	0.96
16:22:95:TYR:CD1	37:A3:147:LEU:CD1	2.48	0.96
24:5X:379:ILE:HA	24:5X:629[B]:ILE:HA	1.48	0.96
1:1:123:A:O2'	16:12:10:GLU:CG	2.13	0.96
21:A2:136:ILE:HG21	21:A2:138:TYR:CE1	1.99	0.96
1:1:33:C:H5'	9:1K:136:TYR:O	1.66	0.96
22:B2:630:PRO:HG3	22:B2:663:PHE:HZ	1.17	0.96
44:4A:447:LYS:HZ2	47:A1:430:UNK:HA	1.03	0.96
36:5A:110:TRP:O	36:5A:192:GLN:NE2	1.96	0.96
15:X:140:TYR:OH	36:5A:1587:GLU:OE1	1.81	0.95
4:B4:14:THR:HG1	37:A3:429:TRP:HH2	0.97	0.95
28:S:575:ARG:NH2	29:5J:428:GLU:OE1	1.99	0.95
24:5X:361:LYS:HA	24:5X:391:ARG:HH22	1.29	0.95
1:1:50:G:C1'	1:1:91:G:H22	1.74	0.95
2:6:86:U:H3	32:2:12:G:H1	1.15	0.95
10:4C:357:ARG:HG3	10:4C:358:ARG:N	1.80	0.95
21:A2:115:PRO:HD3	21:A2:176:TYR:HA	1.46	0.95
36:5A:1510:GLU:N	36:5A:1510:GLU:OE1	1.98	0.95
21:A2:117:TYR:CE1	21:A2:139:PRO:HD2	2.01	0.95
36:5A:691:HIS:HB2	47:A1:466:LEU:HD22	1.48	0.95
15:X:124:VAL:HG11	13:4f:39:TYR:HE2	1.17	0.94
6:4B:284:LYS:CE	6:4B:288:SER:HB2	1.95	0.94
16:22:95:TYR:CB	37:A3:147:LEU:HD11	1.88	0.94
36:5A:1508:GLY:N	36:5A:1752:GLN:HE21	1.64	0.94
37:A3:360:GLU:OE2	11:21:74:LEU:HA	1.66	0.94
15:X:137:TYR:CG	28:S:729:LEU:HD12	2.00	0.94
36:5A:1510:GLU:O	36:5A:1513:MET:HE2	1.65	0.94
22:B2:630:PRO:HD3	22:B2:663:PHE:CE2	2.01	0.94
29:5J:158:LEU:HD12	36:5A:701:ILE:HD13	1.50	0.94
21:A2:115:PRO:CD	21:A2:177:GLU:N	2.31	0.94
6:4B:284:LYS:O	6:4B:289:LEU:HB2	1.69	0.93
36:5A:853:LYS:H	36:5A:853:LYS:HD2	1.33	0.93
37:A3:360:GLU:OE2	11:21:75:PRO:HD3	1.67	0.93
2:6:103:U:O3'	35:68:65:ASP:OD1	1.87	0.93
1:1:8:C:P	24:5X:504:GLY:H	1.91	0.93
15:X:124:VAL:HG11	13:4f:39:TYR:CD2	2.04	0.93
1:1:30:U:O2	9:1K:175:LEU:HD22	1.68	0.93
1:1:105:U:N3	36:5A:1634:SER:HA	1.43	0.93
6:4B:365:SER:HB3	44:4A:423:GLN:OE1	1.65	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5A:852:VAL:HG22	36:5A:854:SER:HA	1.40	0.93
1:1:123:A:C8	16:12:13:PRO:HA	2.04	0.92
16:22:95:TYR:CA	37:A3:147:LEU:HD11	1.98	0.92
1:1:33:C:C4'	9:1K:137:SER:CA	2.45	0.92
12:R:436:VAL:HG21	44:4A:462:GLU:CD	1.93	0.92
12:R:456:LYS:HZ3	44:4A:465:ARG:HA	1.33	0.92
24:5X:362:LEU:HD23	24:5X:391:ARG:HD3	1.51	0.92
37:A3:360:GLU:OE2	11:21:73:SER:O	1.86	0.92
12:R:456:LYS:HZ1	44:4A:465:ARG:HA	0.96	0.92
24:5X:445:PHE:CD2	24:5X:605:PHE:HE2	1.87	0.92
1:1:32:A:C1'	9:1K:135:VAL:HG13	1.98	0.92
1:1:32:A:C4'	9:1K:135:VAL:HG11	2.00	0.91
33:B3:932:ASN:HD22	33:B3:936:LYS:HE3	1.33	0.91
37:A3:360:GLU:CD	11:21:73:SER:O	2.13	0.91
1:1:123:A:N7	16:12:13:PRO:HB3	1.86	0.91
16:22:95:TYR:HB3	37:A3:147:LEU:HD11	1.37	0.91
16:22:95:TYR:CD1	37:A3:147:LEU:HD13	2.05	0.91
22:B2:630:PRO:CD	22:B2:663:PHE:CE2	2.54	0.91
1:1:92:C:C2'	1:1:93:G:H8	1.74	0.91
36:5A:1508:GLY:H	36:5A:1752:GLN:HE21	1.05	0.91
39:5D:3:TYR:OH	39:5D:39:MET:CG	2.18	0.91
1:1:7:A:H5'	24:5X:477:THR:HB	1.53	0.91
1:1:92:C:O2	1:1:93:G:C8	2.24	0.91
16:22:95:TYR:HD1	37:A3:147:LEU:CD1	1.83	0.91
12:R:456:LYS:NZ	44:4A:465:ARG:CA	2.30	0.91
36:5A:1908:LYS:CE	43:K:843:ASP:CA	2.49	0.91
1:1:7:A:C5'	24:5X:478:ARG:CB	2.49	0.90
21:A2:136:ILE:CG2	21:A2:138:TYR:CD1	2.53	0.90
15:X:125:ASN:OD1	16:42:61:ARG:HD3	1.70	0.90
24:5X:733[A]:VAL:HG12	24:5X:735:MET:H	1.35	0.90
21:A2:136:ILE:HG22	21:A2:138:TYR:HD1	1.33	0.90
1:1:10:U:H6	24:5X:508:ARG:HG2	1.35	0.90
43:K:676:ARG:HH21	43:K:677:VAL:HG22	1.34	0.90
24:5X:362:LEU:CD2	24:5X:391:ARG:HB2	1.96	0.90
1:1:50:G:H1'	1:1:91:G:H22	1.08	0.90
16:52:76:GLU:O	16:52:89:PRO:HA	1.72	0.89
28:S:574:ASN:HD21	29:5J:451:LYS:CE	1.86	0.89
1:1:33:C:N3	9:1K:139:ARG:NE	2.21	0.89
15:X:137:TYR:CD1	28:S:729:LEU:CD1	2.56	0.89
34:1g:57:ILE:HG12	7:1e:88:GLN:HG3	1.55	0.89
1:1:7:A:C5'	24:5X:478:ARG:HB3	2.02	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:5C:937:THR:O	23:5C:941:LYS:HG2	1.74	0.88
1:1:8:C:C6	24:5X:504:GLY:HA3	2.09	0.88
29:5J:93:PRO:HG3	36:5A:85:LYS:NZ	1.88	0.88
38:U:134:TYR:CE1	38:U:145:GLY:C	2.51	0.88
1:1:118:A:H61	5:13:4:GLY:HA2	1.39	0.88
9:1K:61:GLU:C	9:1K:65:GLU:HG3	1.97	0.88
24:5X:647:SER:CB	36:5A:1686:ASP:OD2	2.22	0.88
38:U:146:ARG:HH22	38:U:173:TYR:HE1	1.15	0.88
1:1:8:C:OP2	24:5X:478:ARG:CB	2.20	0.88
4:B4:27:PRO:HG3	22:B2:600:ARG:HG3	1.55	0.88
24:5X:362:LEU:HD21	24:5X:391:ARG:HE	1.39	0.88
43:K:774:LEU:HA	43:K:777:VAL:HG13	1.55	0.88
39:5D:33:ASP:OD2	47:A1:465:SER:OG	1.91	0.87
6:4B:284:LYS:HE2	6:4B:288:SER:HB3	1.56	0.87
7:4e:52:GLU:HB3	15:X:113:ASP:H	1.39	0.87
1:1:7:A:OP1	24:5X:479[A]:GLU:N	2.07	0.87
9:1K:47:GLU:HG2	16:12:112:ASN:OD1	1.74	0.87
15:X:140:TYR:CZ	36:5A:1587:GLU:OE1	2.26	0.87
1:1:29:A:C8	9:1K:200:ARG:CZ	2.54	0.87
39:5D:8:LEU:HD13	39:5D:14:VAL:CA	2.05	0.87
7:5e:44:GLU:O	7:5e:61:ALA:HA	1.75	0.87
15:X:124:VAL:CG1	13:4f:39:TYR:CE2	2.56	0.87
9:1K:61:GLU:C	9:1K:65:GLU:CG	2.48	0.86
28:S:574:ASN:HD21	29:5J:451:LYS:HD3	1.06	0.86
1:1:32:A:C5	9:1K:148:PHE:HE1	1.93	0.86
1:1:32:A:C1'	9:1K:135:VAL:HG11	2.04	0.86
36:5A:60:ASP:CG	36:5A:61:MET:H	1.83	0.86
1:1:118:A:N6	5:13:3:ILE:O	2.08	0.86
43:K:950:ASN:HD22	43:K:950:ASN:H	1.22	0.86
1:1:7:A:OP1	24:5X:479[B]:GLU:N	2.08	0.86
1:1:32:A:H5'	9:1K:146:TYR:HH	1.39	0.86
24:5X:373:PHE:HZ	24:5X:419:ARG:HD3	1.37	0.86
1:1:118:A:N7	5:13:3:ILE:N	2.24	0.86
24:5X:380:THR:CG2	24:5X:628:TYR:CG	2.54	0.86
15:X:137:TYR:CZ	28:S:729:LEU:HD13	2.11	0.86
43:K:740:ASN:HD21	43:K:753:LEU:H	1.21	0.86
1:1:7:A:H4'	24:5X:477:THR:CA	2.04	0.85
1:1:92:C:O2	1:1:93:G:C5	2.28	0.85
1:1:92:C:H4'	1:1:93:G:OP1	1.75	0.85
38:U:134:TYR:HD1	38:U:145:GLY:CA	1.58	0.85
1:1:137:U:H2'	9:1K:35:ASN:HB2	1.58	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:5J:158:LEU:CG	36:5A:701:ILE:HG23	2.06	0.85
1:1:164:G:N2	11:11:49:ASN:OD1	1.83	0.85
36:5A:192:GLN:HG2	36:5A:208:TYR:CB	2.06	0.85
10:4C:357:ARG:HG3	10:4C:358:ARG:HG3	1.59	0.85
1:1:30:U:N3	9:1K:175:LEU:CD2	2.03	0.85
1:1:33:C:H5'	9:1K:137:SER:HA	1.56	0.85
33:B3:929:LYS:HD3	33:B3:931:VAL:CG1	2.06	0.85
2:6:64:U:P	43:K:911:LYS:HD2	2.16	0.85
12:R:456:LYS:HZ1	44:4A:465:ARG:CA	1.87	0.85
21:A2:117:TYR:CE2	21:A2:176:TYR:HB3	2.12	0.85
37:A3:357:GLU:CA	11:21:75:PRO:HG2	2.07	0.85
36:5A:852:VAL:HG22	36:5A:854:SER:N	1.92	0.84
24:5X:361:LYS:CA	24:5X:391:ARG:HH22	1.91	0.84
24:5X:445:PHE:HD2	24:5X:605:PHE:CE2	1.94	0.84
2:6:64:U:OP1	43:K:911:LYS:CG	2.25	0.84
15:X:149:ARG:HH12	36:5A:1616:PRO:CG	1.83	0.84
21:A2:164:ARG:O	21:A2:165:ARG:HB3	1.75	0.84
29:5J:158:LEU:HG	36:5A:701:ILE:HG23	1.59	0.84
36:5A:1908:LYS:HE2	43:K:843:ASP:CA	2.08	0.84
29:5J:97:ASP:OD1	36:5A:84:ASP:HB3	1.77	0.84
1:1:123:A:N7	16:12:13:PRO:CB	2.41	0.84
1:1:92:C:H2'	1:1:93:G:H8	1.02	0.83
7:5e:63:GLU:O	7:5e:71:ARG:HA	1.78	0.83
36:5A:577:GLY:O	36:5A:581:ILE:HG13	1.78	0.83
36:5A:1511:GLU:N	36:5A:1511:GLU:OE1	2.11	0.83
1:1:8:C:OP2	24:5X:478:ARG:HG3	1.78	0.83
36:5A:552:ARG:HG3	36:5A:552:ARG:HH21	1.41	0.83
1:1:7:A:C4'	24:5X:478:ARG:N	2.19	0.83
28:S:575:ARG:NH2	29:5J:424:SER:HB3	1.93	0.83
36:5A:1510:GLU:O	36:5A:1513:MET:CG	2.27	0.83
36:5A:1794:PHE:HD2	36:5A:1795:GLU:HG2	1.42	0.83
1:1:50:G:H1'	1:1:91:G:H21	1.04	0.83
24:5X:370:TRP:CE3	24:5X:389:PRO:HG2	2.12	0.83
1:1:33:C:O3'	9:1K:144:ARG:HD3	1.79	0.82
1:1:91:G:OP1	1:1:91:G:H4'	1.78	0.82
9:1K:61:GLU:CA	9:1K:65:GLU:HG2	2.08	0.82
36:5A:1908:LYS:CE	43:K:843:ASP:HA	2.08	0.82
1:1:73:C:H2'	1:1:74:C:H6	1.44	0.82
7:5e:57:VAL:HA	7:5e:77:ILE:O	1.79	0.82
28:S:574:ASN:CG	29:5J:451:LYS:CD	2.45	0.82
23:5C:105:MET:HG3	23:5C:540:GLU:O	1.78	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:105:U:O4	36:5A:1607:GLU:CD	2.23	0.82
30:4D:109:GLY:HA3	43:K:947:SER:CB	2.10	0.82
37:A3:357:GLU:N	11:21:75:PRO:CG	2.42	0.82
12:R:436:VAL:CG2	44:4A:462:GLU:OE1	2.25	0.81
36:5A:86:ARG:NE	36:5A:86:ARG:HA	1.92	0.81
5:13:58:LEU:HD22	34:1g:71:GLU:OE1	1.79	0.81
28:S:575:ARG:CZ	29:5J:424:SER:HB3	2.10	0.81
36:5A:86:ARG:HH11	36:5A:89:LEU:CD1	1.93	0.81
24:5X:472:ILE:HG13	24:5X:540:LEU:HD21	1.62	0.81
24:5X:649:SER:OG	36:5A:1685:LEU:CB	2.24	0.81
43:K:823:VAL:HG22	43:K:827:LYS:HA	1.63	0.81
1:1:8:C:P	24:5X:503:ILE:HB	2.21	0.81
21:A2:115:PRO:CD	21:A2:176:TYR:HA	2.11	0.81
24:5X:370:TRP:CZ3	24:5X:389:PRO:HD2	2.14	0.81
7:2e:58:LEU:O	7:2e:76:ARG:HA	1.80	0.81
15:X:140:TYR:HE2	36:5A:1587:GLU:OE1	1.63	0.81
29:5J:675:ALA:HB2	29:5J:705:TYR:CG	2.16	0.81
36:5A:559:ASP:HA	36:5A:562:VAL:CG2	2.10	0.81
1:1:73:C:H2'	1:1:74:C:C6	2.16	0.81
37:A3:356:ARG:C	11:21:75:PRO:CG	2.53	0.80
1:1:32:A:C5'	9:1K:146:TYR:OH	2.25	0.80
16:22:95:TYR:CG	37:A3:147:LEU:HD12	2.16	0.80
24:5X:373:PHE:CE1	24:5X:419:ARG:HD3	2.16	0.80
36:5A:192:GLN:CG	36:5A:208:TYR:CG	2.63	0.80
1:1:33:C:O2	9:1K:139:ARG:NE	2.14	0.80
1:1:22:U:H6	1:1:22:U:H5''	1.46	0.80
28:S:574:ASN:CG	29:5J:451:LYS:HD3	2.05	0.80
2:6:54:G:OP2	10:4C:356:GLY:CA	2.29	0.80
15:X:137:TYR:CE1	28:S:729:LEU:CD1	2.65	0.80
21:A2:117:TYR:OH	21:A2:176:TYR:CB	2.29	0.80
21:A2:119:VAL:HG12	21:A2:136:ILE:HG12	1.64	0.80
1:1:10:U:OP2	24:5X:528:ARG:NH2	2.15	0.79
2:6:54:G:OP2	10:4C:356:GLY:N	2.13	0.79
1:1:123:A:C8	16:12:13:PRO:CA	2.65	0.79
13:5f:30:LYS:O	13:5f:47:THR:HA	1.82	0.79
1:1:73:C:C2	1:1:74:C:C5	2.70	0.79
28:S:565:GLU:C	28:S:567:PRO:HD3	2.08	0.79
36:5A:1811:ASN:CG	36:5A:1814:THR:HG22	2.07	0.79
1:1:30:U:H3	9:1K:175:LEU:HD21	1.42	0.79
12:R:436:VAL:HG11	44:4A:462:GLU:OE2	1.81	0.79
15:X:124:VAL:CG1	13:4f:39:TYR:CD2	2.66	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:6:103:U:H1'	35:68:65:ASP:CG	2.08	0.79
36:5A:579:GLN:HA	36:5A:579:GLN:HE21	1.45	0.79
1:1:17:G:N2	1:1:47:C:O2	2.16	0.79
1:1:28:G:N2	9:1K:112:TYR:CZ	2.50	0.79
1:1:37:G:OP1	9:1K:74:LYS:NZ	2.13	0.79
24:5X:675:LYS:O	24:5X:679:VAL:HG12	1.83	0.79
29:5J:102:ASP:OD2	36:5A:86:ARG:HD3	1.82	0.78
43:K:913:ILE:HG22	43:K:919:LYS:HE2	1.64	0.78
29:5J:158:LEU:HD12	36:5A:701:ILE:CG2	2.13	0.78
36:5A:86:ARG:HH11	36:5A:89:LEU:HD13	1.48	0.78
37:A3:357:GLU:N	11:21:75:PRO:HG2	1.98	0.78
1:1:15:G:H2'	1:1:16:G:C8	2.19	0.78
25:1b:53:PRO:HG3	25:1b:58:GLN:O	1.83	0.78
43:K:803:LEU:HD11	43:K:875:VAL:HG21	1.64	0.78
1:1:137:U:H2'	9:1K:35:ASN:CB	2.14	0.78
36:5A:85:LYS:HG2	36:5A:89:LEU:CD1	2.13	0.78
1:1:137:U:C2'	9:1K:36:GLN:HG3	2.12	0.78
24:5X:378:SER:HB3	24:5X:630:GLY:HA2	1.63	0.78
36:5A:694:LEU:CD1	47:A1:466:LEU:HD12	2.12	0.78
4:B4:27:PRO:HG3	22:B2:600:ARG:CG	2.13	0.78
21:A2:115:PRO:HG3	21:A2:176:TYR:CD1	2.12	0.78
7:1e:48:ILE:HD11	7:1e:59:ASP:CG	2.09	0.78
6:4B:284:LYS:HB3	6:4B:288:SER:HB2	1.63	0.78
10:4C:357:ARG:CG	10:4C:358:ARG:H	1.83	0.78
33:B3:699:VAL:HA	33:B3:715:MET:O	1.83	0.78
29:5J:158:LEU:CD1	36:5A:701:ILE:CG2	2.62	0.78
1:1:137:U:C4	9:1K:34:HIS:CA	2.33	0.77
39:5D:8:LEU:HB2	39:5D:61:VAL:HG22	1.66	0.77
1:1:118:A:H2'	42:1C:2:PRO:HD3	1.66	0.77
1:1:8:C:OP2	24:5X:478:ARG:CG	2.33	0.77
15:X:125:ASN:HA	16:42:61:ARG:CG	2.14	0.77
24:5X:540:LEU:HD22	24:5X:570:MET:SD	2.23	0.77
36:5A:192:GLN:CB	36:5A:208:TYR:CD2	2.65	0.77
36:5A:1317:TYR:CE1	36:5A:1329:SER:HB2	2.20	0.77
39:5D:8:LEU:CD1	39:5D:14:VAL:HG22	2.14	0.77
1:1:92:C:O2'	1:1:93:G:O4'	2.00	0.77
13:1f:19:VAL:HG11	13:1f:72:ILE:HD11	1.66	0.77
23:5C:107:GLN:OE1	23:5C:107:GLN:N	2.12	0.77
29:5J:839:HIS:HD2	43:K:942:LYS:HE2	0.61	0.77
1:1:105:U:C4	36:5A:1607:GLU:HB2	2.11	0.77
7:1e:48:ILE:HD11	7:1e:59:ASP:CB	2.14	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:U:134:TYR:CE1	38:U:145:GLY:CA	2.53	0.77
1:1:32:A:N9	9:1K:135:VAL:HG21	1.97	0.77
1:1:119:C:H2'	1:1:120:U:C6	2.19	0.77
22:B2:607:GLY:HA2	22:B2:663:PHE:HD1	1.47	0.77
36:5A:192:GLN:HG2	36:5A:208:TYR:HB3	1.67	0.77
3:5O:148:LYS:HZ3	17:5:7:U:H4'	1.49	0.76
37:A3:360:GLU:CD	11:21:74:LEU:HD23	2.09	0.76
1:1:7:A:H4'	24:5X:478:ARG:N	1.98	0.76
1:1:11:G:N7	24:5X:507:SER:CA	2.47	0.76
1:1:8:C:P	24:5X:478:ARG:HB2	2.25	0.76
29:5J:158:LEU:HD11	36:5A:701:ILE:HG12	1.66	0.76
39:5D:34:TRP:O	47:A1:473:ARG:NH2	2.17	0.76
1:1:32:A:N9	9:1K:135:VAL:CG2	2.48	0.76
16:22:95:TYR:CD1	37:A3:147:LEU:HD12	2.19	0.76
24:5X:370:TRP:CE3	24:5X:389:PRO:CG	2.67	0.76
9:1K:30:HIS:HB3	7:1e:37:GLU:OE2	1.85	0.76
25:1b:8:LYS:O	25:1b:12:HIS:CD2	2.38	0.76
36:5A:1908:LYS:HZ1	43:K:843:ASP:HA	1.51	0.76
7:4e:64:ILE:HA	7:4e:70:SER:O	1.86	0.76
7:1e:33:VAL:HG12	7:1e:87:LEU:CD2	2.16	0.76
36:5A:1510:GLU:O	36:5A:1513:MET:CE	2.34	0.76
25:4b:28:ILE:O	25:4b:45:CYS:HA	1.86	0.76
24:5X:711:LYS:HA	24:5X:731:GLN:HE22	1.51	0.75
36:5A:853:LYS:O	36:5A:854:SER:OG	2.02	0.75
29:5J:157:TRP:HB3	36:5A:701:ILE:HG21	1.68	0.75
1:1:28:G:C2	9:1K:112:TYR:HE2	2.03	0.75
21:A2:115:PRO:HD3	21:A2:176:TYR:CA	2.14	0.75
36:5A:1908:LYS:HE2	43:K:843:ASP:HA	1.68	0.75
37:A3:356:ARG:CG	11:21:75:PRO:CB	2.63	0.75
16:22:95:TYR:CG	37:A3:147:LEU:CD1	2.68	0.75
24:5X:379:ILE:C	24:5X:628:TYR:O	2.29	0.75
33:B3:929:LYS:HD3	33:B3:931:VAL:HG12	1.68	0.75
2:6:103:U:H3	35:68:35:ASN:HD21	1.33	0.75
12:R:432:PRO:HB2	44:4A:466:LEU:HB3	1.68	0.75
21:A2:164:ARG:O	21:A2:165:ARG:CB	2.34	0.75
24:5X:692:CYS:SG	24:5X:715:LYS:HG3	2.25	0.75
45:4:114:U:H4'	45:4:115:G:OP1	1.87	0.75
36:5A:579:GLN:HE21	36:5A:579:GLN:CA	1.99	0.75
38:U:407:GLU:C	38:U:409:LEU:H	1.93	0.75
12:R:432:PRO:CA	44:4A:466:LEU:HD22	2.17	0.75
16:22:95:TYR:O	37:A3:147:LEU:HD13	1.86	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:U:405:GLU:OE1	38:U:406:LYS:N	2.20	0.75
1:1:7:A:P	24:5X:478:ARG:HB3	2.27	0.74
1:1:33:C:C2	9:1K:139:ARG:CZ	2.68	0.74
2:6:35:A:H61	45:4:74:C:H42	1.35	0.74
1:1:33:C:H5'	9:1K:137:SER:CA	2.16	0.74
33:B3:886:GLU:HA	33:B3:910:ALA:O	1.87	0.74
1:1:7:A:H4'	24:5X:478:ARG:H	1.45	0.74
43:K:781:TYR:HB3	43:K:785:VAL:CG2	2.17	0.74
1:1:33:C:O2	9:1K:139:ARG:HD2	1.88	0.74
1:1:33:C:O2	9:1K:139:ARG:CD	2.36	0.74
36:5A:1623:ASN:OD1	36:5A:1624:SER:N	2.21	0.74
43:K:950:ASN:H	43:K:950:ASN:ND2	1.86	0.74
6:4B:414:ASN:HD22	6:4B:457:PHE:H	1.35	0.73
23:5C:331:PHE:CD2	36:5A:384:VAL:HG22	2.23	0.73
1:1:137:U:O4	9:1K:33:HIS:O	2.04	0.73
2:6:54:G:OP2	10:4C:356:GLY:HA2	1.88	0.73
24:5X:361:LYS:CA	24:5X:391:ARG:NH2	2.50	0.73
24:5X:679:VAL:O	24:5X:682:LYS:HG2	1.89	0.73
43:K:696:GLY:O	43:K:697:VAL:HG13	1.88	0.73
34:5g:42:ILE:O	34:5g:59:MET:HA	1.89	0.73
27:1A:33:ILE:HG23	27:1A:72:MET:HE2	1.70	0.73
36:5A:580:TYR:CE2	36:5A:588:LEU:HD11	2.23	0.73
36:5A:853:LYS:HD2	36:5A:853:LYS:N	2.02	0.73
34:4g:42:ILE:O	34:4g:59:MET:HA	1.89	0.73
1:1:9:C:C5	24:5X:508:ARG:NH1	2.34	0.73
24:5X:649:SER:CB	36:5A:1685:LEU:HB3	2.17	0.73
29:5J:160:ILE:HB	36:5A:705:LYS:HE2	1.71	0.73
36:5A:559:ASP:CA	36:5A:562:VAL:HG22	2.18	0.73
43:K:990:LYS:HE3	45:4:4:U:OP1	1.89	0.73
15:X:124:VAL:CG1	13:4f:39:TYR:HE2	1.97	0.73
15:X:124:VAL:O	16:42:61:ARG:HG2	1.89	0.73
24:5X:442:THR:HA	24:5X:445:PHE:CE2	2.23	0.73
28:S:565:GLU:HB2	28:S:567:PRO:CD	2.19	0.73
7:4e:52:GLU:HB3	15:X:113:ASP:N	2.03	0.72
22:B2:630:PRO:HD3	22:B2:663:PHE:HE2	1.51	0.72
24:5X:362:LEU:HG	24:5X:391:ARG:HE	1.53	0.72
5:23:48:VAL:O	5:23:55:VAL:HA	1.88	0.72
43:K:841:VAL:HG21	43:K:868:TYR:CZ	2.24	0.72
1:1:15:G:H2'	1:1:16:G:N9	2.04	0.72
1:1:28:G:N1	9:1K:112:TYR:CD2	2.57	0.72
6:4B:284:LYS:CE	6:4B:288:SER:HB3	2.12	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:5C:331:PHE:CG	36:5A:384:VAL:HG22	2.25	0.72
36:5A:1508:GLY:N	36:5A:1752:GLN:NE2	2.37	0.72
1:1:118:A:H61	5:13:4:GLY:CA	2.02	0.72
10:4C:357:ARG:CG	10:4C:358:ARG:N	2.44	0.72
15:X:134:LYS:HE3	28:S:728:GLN:NE2	2.03	0.72
39:5D:3:TYR:HH	39:5D:39:MET:HG3	1.54	0.72
6:4B:402:PHE:CZ	44:4A:424:LEU:CD1	2.68	0.72
9:1K:53:ASP:OD1	9:1K:54:ALA:N	2.22	0.72
1:1:30:U:C6	9:1K:109:ARG:NE	2.46	0.72
1:1:123:A:H2'	1:1:123:A:N3	2.05	0.72
24:5X:370:TRP:HH2	24:5X:389:PRO:O	1.69	0.72
29:5J:839:HIS:HB2	43:K:942:LYS:NZ	2.05	0.72
36:5A:1752:GLN:OE1	36:5A:1752:GLN:HA	1.89	0.72
1:1:29:A:C4	9:1K:200:ARG:HD3	2.23	0.72
1:1:118:A:N6	5:13:4:GLY:N	2.37	0.72
12:R:432:PRO:HB2	44:4A:466:LEU:CB	2.19	0.72
33:B3:932:ASN:HB3	33:B3:935:GLU:OE2	1.89	0.72
37:A3:357:GLU:HA	11:21:75:PRO:HG2	1.71	0.72
1:1:48:C:O2	1:1:49:A:N7	2.22	0.71
12:R:446:TYR:CG	39:5D:86:ARG:NH2	2.57	0.71
13:5f:43:GLN:HB2	16:52:28:PRO:HA	1.72	0.71
36:5A:112:GLN:HB3	36:5A:187:PRO:HG3	1.71	0.71
43:K:695:GLN:NE2	43:K:700:ASN:HB3	2.06	0.71
1:1:48:C:H4'	1:1:48:C:OP1	1.90	0.71
1:1:123:A:C8	16:12:13:PRO:HB3	2.23	0.71
33:B3:117:PRO:HD3	33:B3:138:GLN:HE21	1.54	0.71
1:1:137:U:H1'	9:1K:36:GLN:HB2	1.72	0.71
1:1:138:G:N1	1:1:163:U:O2	2.20	0.71
24:5X:536:ARG:CG	34:1g:10:LYS:HE3	2.19	0.71
43:K:722:ASN:ND2	43:K:724:LEU:H	1.89	0.71
1:1:123:A:OP1	1:1:124:U:H5''	1.91	0.71
29:5J:93:PRO:HG3	36:5A:85:LYS:HZ1	1.56	0.71
1:1:94:A:N1	1:1:115:U:C4	2.59	0.71
1:1:32:A:C4'	9:1K:135:VAL:CG1	2.66	0.71
36:5A:59:GLU:N	36:5A:59:GLU:OE2	2.23	0.71
36:5A:1779:PHE:O	36:5A:1809:ILE:HA	1.91	0.71
15:X:137:TYR:CD2	28:S:729:LEU:HD12	2.26	0.71
43:K:739:LEU:HD22	43:K:805:LEU:HD13	1.72	0.71
36:5A:852:VAL:HG23	36:5A:854:SER:CA	2.11	0.70
34:5g:47:GLU:HB3	34:5g:55:ASN:HB2	1.73	0.70
34:4g:47:GLU:HB3	34:4g:55:ASN:HB2	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:S:565:GLU:HB2	28:S:567:PRO:HD2	1.72	0.70
30:4D:108:GLU:CD	43:K:926:ASN:ND2	2.49	0.70
1:1:118:A:H3'	1:1:118:A:N3	2.07	0.70
24:5X:666:PRO:O	24:5X:733[A]:VAL:HG13	1.92	0.70
8:I:94:G:H1	32:2:39:U:H3	1.38	0.70
24:5X:690:ASN:HB3	24:5X:715:LYS:HD3	1.73	0.70
33:B3:932:ASN:CB	33:B3:935:GLU:OE2	2.39	0.70
36:5A:707:ARG:HE	47:A1:456:TYR:HD2	1.38	0.70
1:1:2:U:H2'	1:1:3:A:H8	1.56	0.70
24:5X:682:LYS:HG3	24:5X:683:SER:N	2.03	0.70
24:5X:362:LEU:CG	24:5X:391:ARG:NE	2.38	0.70
22:B2:651:PRO:CD	22:B2:663:PHE:O	2.39	0.70
29:5J:839:HIS:CG	43:K:942:LYS:CE	2.67	0.70
32:2:12:G:C6	32:2:13:C:C4	2.79	0.70
36:5A:1385:VAL:HG21	36:5A:1414:ARG:HD2	1.74	0.70
5:53:48:VAL:O	5:53:55:VAL:HA	1.92	0.70
24:5X:361:LYS:HA	24:5X:391:ARG:NH2	2.03	0.70
36:5A:86:ARG:NH1	36:5A:89:LEU:HD13	2.05	0.70
24:5X:560:GLU:O	24:5X:564:GLN:HG3	1.92	0.69
12:R:446:TYR:CB	39:5D:86:ARG:NH2	2.56	0.69
34:1g:57:ILE:HG12	7:1e:88:GLN:CG	2.22	0.69
1:1:6:U:H3	8:I:3:G:H1	1.38	0.69
5:13:46:ILE:HD11	5:13:61:VAL:HG21	1.74	0.69
37:A3:360:GLU:OE2	11:21:73:SER:C	2.35	0.69
1:1:9:C:C4'	24:5X:508:ARG:NH2	2.54	0.69
1:1:90:U:O2'	1:1:91:G:C4'	2.40	0.69
23:5C:440:SER:HB3	23:5C:443:VAL:H	1.57	0.69
29:5J:146:LYS:HG2	36:5A:696:MET:HE2	1.75	0.69
43:K:774:LEU:HA	43:K:777:VAL:CG1	2.22	0.69
36:5A:112:GLN:HB3	36:5A:187:PRO:CG	2.21	0.69
49:5B:2106:LEU:O	49:5B:2119:GLU:HA	1.91	0.69
1:1:12:G:OP1	42:1C:15:HIS:CD2	2.45	0.69
1:1:164:G:O3'	11:11:50:ARG:C	2.36	0.69
29:5J:675:ALA:HB2	29:5J:705:TYR:CD2	2.27	0.69
36:5A:580:TYR:HE2	36:5A:588:LEU:HD11	1.57	0.69
36:5A:1621:LYS:HE3	36:5A:1623:ASN:OD1	1.91	0.69
24:5X:380:THR:CG2	24:5X:628:TYR:CD2	2.74	0.69
36:5A:251:ASP:HB3	36:5A:253:ASN:H	1.57	0.69
1:1:29:A:O5'	9:1K:200:ARG:NH2	2.25	0.69
9:1K:47:GLU:HG2	16:12:112:ASN:CG	2.17	0.69
22:B2:630:PRO:CG	22:B2:663:PHE:HE2	2.03	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:5J:146:LYS:NZ	36:5A:695:ASP:OD2	2.23	0.69
1:1:7:A:H3'	24:5X:478:ARG:HB2	1.73	0.69
6:4B:284:LYS:HE3	6:4B:288:SER:CB	2.21	0.69
28:S:575:ARG:HH22	29:5J:424:SER:C	2.01	0.69
43:K:722:ASN:HB3	43:K:725:MET:HG3	1.74	0.69
16:22:95:TYR:C	37:A3:147:LEU:CD1	2.49	0.69
24:5X:445:PHE:CD2	24:5X:605:PHE:CE2	2.70	0.69
36:5A:694:LEU:CD1	47:A1:466:LEU:CD1	2.67	0.69
43:K:798:GLN:OE1	43:K:830:LEU:HD13	1.93	0.69
1:1:123:A:N7	16:12:13:PRO:HA	2.08	0.68
29:5J:632:ALA:O	29:5J:635:PHE:HB2	1.94	0.68
36:5A:1622:MET:O	36:5A:1687:TYR:OH	2.11	0.68
12:R:432:PRO:O	44:4A:466:LEU:HD23	1.87	0.68
23:5C:354:ARG:NH2	36:5A:384:VAL:O	2.24	0.68
24:5X:378:SER:CB	24:5X:630:GLY:CA	2.55	0.68
1:1:28:G:C2	9:1K:112:TYR:CD2	2.82	0.68
1:1:137:U:C2'	9:1K:35:ASN:HB2	2.23	0.68
3:5O:148:LYS:NZ	17:5:7:U:H4'	2.08	0.68
24:5X:463:GLU:HG3	24:5X:467:GLN:OE1	1.92	0.68
29:5J:158:LEU:CD1	36:5A:701:ILE:HD13	2.21	0.68
43:K:942:LYS:HD3	43:K:943:VAL:H	1.58	0.68
44:4A:447:LYS:NZ	47:A1:429:UNK:C	2.56	0.68
2:6:103:U:O4'	35:68:65:ASP:OD2	2.11	0.68
36:5A:1908:LYS:NZ	43:K:843:ASP:HA	2.07	0.68
34:5g:35:ASP:N	34:5g:35:ASP:OD1	2.27	0.68
29:5J:662:ARG:HG2	29:5J:684:LEU:HD21	1.73	0.68
36:5A:110:TRP:HB2	36:5A:192:GLN:HG3	1.76	0.68
6:4B:284:LYS:O	6:4B:289:LEU:CB	2.40	0.68
15:X:119:LYS:HD3	45:4:116:G:H5''	1.76	0.68
1:1:10:U:H3	8:I:-1:G:H1	1.40	0.68
13:1f:20:MET:HE3	13:1f:30:LYS:HB2	1.76	0.68
14:66:52:VAL:HB	14:66:56:LEU:HD11	1.75	0.68
37:A3:360:GLU:OE2	11:21:74:LEU:CA	2.41	0.68
9:1K:45:ILE:N	9:1K:45:ILE:HD12	2.09	0.68
34:1g:42:ILE:HD11	34:1g:45:CYS:SG	2.33	0.68
1:1:10:U:C6	24:5X:508:ARG:HG2	2.24	0.68
24:5X:536:ARG:HG2	34:1g:10:LYS:HD2	1.76	0.68
36:5A:2311:PRO:O	36:5A:2315:LEU:HB2	1.94	0.68
24:5X:370:TRP:CE2	24:5X:388:ASN:HB3	2.29	0.68
25:1b:58:GLN:HG3	25:1b:59:ALA:N	2.08	0.68
12:R:432:PRO:HB2	44:4A:466:LEU:CG	2.23	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:X:137:TYR:CD1	28:S:729:LEU:HD12	2.28	0.67
20:2B:88:SER:HG	20:2B:91:ILE:H	1.43	0.67
21:A2:115:PRO:CB	21:A2:176:TYR:CD1	2.74	0.67
22:B2:511:LEU:HD22	22:B2:514:LYS:HD2	1.76	0.67
22:B2:607:GLY:HA2	22:B2:663:PHE:CD1	2.29	0.67
24:5X:536:ARG:CG	34:1g:10:LYS:CE	2.71	0.67
36:5A:494:LEU:HD21	36:5A:562:VAL:HG11	1.75	0.67
24:5X:728:ILE:HG23	24:5X:729:ASP:H	1.58	0.67
29:5J:160:ILE:O	36:5A:705:LYS:NZ	2.26	0.67
34:4g:35:ASP:OD1	34:4g:35:ASP:N	2.27	0.67
1:1:7:A:C3'	24:5X:478:ARG:HB2	2.25	0.67
2:6:85:U:H2'	2:6:86:U:H6	1.58	0.67
36:5A:60:ASP:OD1	36:5A:485:THR:HA	1.94	0.67
37:A3:356:ARG:CD	11:21:75:PRO:HB3	2.25	0.67
7:5e:44:GLU:HG2	7:5e:64:ILE:HD11	1.76	0.67
36:5A:1179:SER:O	36:5A:1201:ARG:NH1	2.27	0.67
15:X:138:ARG:HH12	36:5A:1614:ILE:HD12	1.60	0.67
29:5J:98:ASP:HB3	36:5A:86:ARG:CG	2.25	0.67
1:1:9:C:O4'	24:5X:508:ARG:NH2	2.14	0.67
1:1:119:C:H2'	1:1:120:U:H6	1.59	0.67
36:5A:86:ARG:HA	36:5A:86:ARG:HE	1.58	0.67
36:5A:1794:PHE:CE2	36:5A:1795:GLU:HG2	2.29	0.67
29:5J:93:PRO:HG3	36:5A:85:LYS:HZ3	1.57	0.67
43:K:740:ASN:ND2	43:K:753:LEU:H	1.91	0.67
45:4:114:U:P	45:4:114:U:H6	2.18	0.67
36:5A:710:LEU:HD21	39:5D:4:MET:HE1	1.72	0.67
44:4A:447:LYS:CD	47:A1:429:UNK:O	2.43	0.67
2:6:103:U:C1'	35:68:65:ASP:CG	2.65	0.67
6:4B:294:VAL:CG2	6:4B:307:LEU:HB3	2.25	0.67
21:A2:115:PRO:CD	21:A2:176:TYR:CA	2.72	0.67
41:BP:58:CYS:SG	41:BP:61:CYS:HB2	2.34	0.67
29:5J:160:ILE:HB	36:5A:705:LYS:CE	2.25	0.66
36:5A:65:HIS:HE1	36:5A:483:GLN:OE1	1.78	0.66
1:1:11:G:OP2	24:5X:509:GLU:N	2.28	0.66
43:K:895:ASN:ND2	43:K:932:ILE:H	1.93	0.66
16:42:110:LEU:HD11	13:4f:59:LEU:HB3	1.76	0.66
36:5A:853:LYS:H	36:5A:853:LYS:CD	2.06	0.66
12:R:446:TYR:HB2	39:5D:86:ARG:NH2	2.10	0.66
7:4e:39:VAL:HG12	34:4g:25:ARG:HH11	1.59	0.66
49:5B:756:SER:O	49:5B:760:GLU:HB2	1.95	0.66
1:1:137:U:O4	9:1K:34:HIS:N	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:R:446:TYR:CG	39:5D:86:ARG:CZ	2.79	0.66
29:5J:89:PHE:O	29:5J:90:SER:HB3	1.95	0.66
29:5J:154:GLU:HG2	36:5A:698:PRO:HG3	1.77	0.66
22:B2:651:PRO:HD2	22:B2:663:PHE:O	1.95	0.66
1:1:48:C:H2'	1:1:49:A:C8	2.30	0.66
33:B3:526:HIS:HB3	33:B3:534:ASN:HB2	1.76	0.66
33:B3:932:ASN:ND2	33:B3:936:LYS:CE	2.56	0.66
37:A3:354:GLU:HG3	11:21:78:THR:HG22	1.76	0.66
37:A3:356:ARG:HG2	11:21:75:PRO:HB3	1.76	0.66
1:1:29:A:N9	9:1K:200:ARG:CD	2.58	0.66
1:1:140:G:O3'	25:1b:57:LYS:HB2	1.96	0.66
13:1f:69:VAL:CG1	7:1e:80:LYS:HD3	2.26	0.66
10:4C:357:ARG:HG3	10:4C:358:ARG:CG	2.26	0.66
23:5C:645:ARG:NH1	36:5A:318:TYR:O	2.29	0.66
43:K:722:ASN:ND2	43:K:723:GLU:N	2.44	0.66
45:4:109:G:H2'	45:4:110:G:C8	2.30	0.66
1:1:137:U:O4	9:1K:33:HIS:C	2.38	0.66
21:A2:117:TYR:CZ	21:A2:176:TYR:CG	2.84	0.66
30:4D:109:GLY:HA3	43:K:947:SER:OG	1.95	0.66
36:5A:85:LYS:HG2	36:5A:89:LEU:HD12	1.77	0.66
36:5A:852:VAL:CG2	36:5A:854:SER:N	2.57	0.66
44:4A:427:PRO:CB	44:4A:639:LYS:NZ	2.58	0.66
9:1K:61:GLU:O	9:1K:65:GLU:CD	2.39	0.65
23:5C:520:GLU:CD	38:U:146:ARG:CB	2.59	0.65
24:5X:540:LEU:HD23	24:5X:543:CYS:HB2	1.78	0.65
6:4B:364:HIS:C	44:4A:423:GLN:HE22	2.04	0.65
17:5:93:U:O2'	13:5f:65:ARG:NH2	2.30	0.65
21:A2:136:ILE:CG2	21:A2:138:TYR:HE1	2.07	0.65
36:5A:231:THR:HG22	36:5A:233:PRO:HD2	1.78	0.65
1:1:29:A:N7	9:1K:200:ARG:NH1	2.42	0.65
1:1:50:G:C1'	1:1:91:G:H21	1.92	0.65
1:1:15:G:O2'	1:1:16:G:O4'	2.13	0.65
1:1:123:A:N7	16:12:13:PRO:CA	2.59	0.65
12:R:432:PRO:CB	44:4A:466:LEU:HB3	2.25	0.65
24:5X:536:ARG:HB3	34:1g:10:LYS:HG3	1.79	0.65
29:5J:839:HIS:CG	43:K:942:LYS:HE3	2.28	0.65
7:1e:36:TYR:N	7:1e:83:ASN:O	2.30	0.65
1:1:11:G:N7	24:5X:507:SER:CB	2.59	0.65
24:5X:536:ARG:HG3	34:1g:10:LYS:NZ	2.12	0.65
12:R:456:LYS:CE	44:4A:465:ARG:HA	2.26	0.65
2:6:64:U:OP1	43:K:911:LYS:HG2	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:1b:9:MET:HE2	25:1b:38:MET:SD	2.36	0.65
28:S:575:ARG:HH21	29:5J:428:GLU:CD	2.05	0.65
33:B3:981:CYS:SG	33:B3:982:GLU:N	2.66	0.65
8:I:101:C:OP2	50:B1:1106:ARG:NH1	2.30	0.65
36:5A:1374:PRO:HG3	49:5B:52:MET:HB3	1.77	0.65
44:4A:427:PRO:CB	44:4A:639:LYS:HE3	2.17	0.65
1:1:8:C:P	24:5X:504:GLY:N	2.66	0.65
1:1:117:G:H5''	1:1:118:A:O5'	1.96	0.65
28:S:572:ALA:HA	29:5J:455:LYS:HG2	1.78	0.65
34:1g:57:ILE:CG1	7:1e:88:GLN:HG3	2.27	0.65
43:K:781:TYR:O	43:K:785:VAL:HG21	1.96	0.65
1:1:118:A:H62	5:13:3:ILE:CA	2.10	0.64
37:A3:422:PHE:O	37:A3:425:HIS:ND1	2.28	0.64
39:5D:8:LEU:HD12	39:5D:61:VAL:CG2	2.27	0.64
42:1C:47:GLN:OE1	42:1C:50:ILE:HD12	1.97	0.64
1:1:20:G:H4'	9:1K:67:MET:HE2	1.79	0.64
10:4C:346:PRO:HG3	39:5D:117:GLU:HG2	1.80	0.64
7:4e:52:GLU:HA	15:X:112:PHE:HD1	1.62	0.64
36:5A:686:ARG:HE	36:5A:710:LEU:HD11	1.62	0.64
36:5A:761:ILE:HD12	36:5A:775:ASN:HD22	1.61	0.64
43:K:874:SER:O	43:K:878:THR:HG23	1.97	0.64
49:5B:1360:ALA:HB2	49:5B:1490:LEU:HD11	1.78	0.64
1:1:2:U:H2'	1:1:3:A:C8	2.33	0.64
1:1:90:U:O2'	1:1:91:G:H4'	1.97	0.64
24:5X:379:ILE:HG21	24:5X:629[A]:ILE:HG13	1.64	0.64
1:1:29:A:C4	9:1K:200:ARG:NH1	2.65	0.64
21:A2:115:PRO:CG	21:A2:176:TYR:CE1	2.76	0.64
43:K:773:ASN:OD1	43:K:775:ARG:HB3	1.97	0.64
49:5B:1456:VAL:HG22	49:5B:1491:SER:HB2	1.79	0.64
1:1:118:A:H2'	42:1C:2:PRO:CD	2.28	0.64
9:1K:48:PHE:CD1	16:12:41:GLN:OE1	2.51	0.64
24:5X:733[A]:VAL:HG12	24:5X:735:MET:N	2.10	0.64
29:5J:426:ALA:HB1	29:5J:436:LEU:HD13	1.80	0.64
36:5A:1737:ASN:HD22	36:5A:1740:LEU:H	1.44	0.64
1:1:10:U:C3'	24:5X:508:ARG:HB2	2.28	0.64
12:R:421:THR:HG22	12:R:423:GLY:H	1.63	0.64
13:1f:66:CYS:O	13:1f:69:VAL:HG12	1.97	0.64
1:1:32:A:N7	9:1K:148:PHE:HE1	1.85	0.64
49:5B:498:ASN:HD22	49:5B:648:LEU:HB2	1.62	0.64
2:6:102:A:O2'	2:6:103:U:OP2	2.16	0.63
16:22:95:TYR:O	37:A3:147:LEU:CD2	2.46	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:A2:117:TYR:CD2	21:A2:138:TYR:CZ	2.86	0.63
36:5A:552:ARG:HH21	36:5A:552:ARG:CG	2.12	0.63
44:4A:597:LEU:HA	44:4A:601:ARG:HB2	1.81	0.63
24:5X:379:ILE:CA	24:5X:629[A]:ILE:HA	2.25	0.63
2:6:85:U:H2'	2:6:86:U:C6	2.33	0.63
36:5A:60:ASP:CG	36:5A:61:MET:N	2.47	0.63
1:1:9:C:O5'	24:5X:508:ARG:NH2	2.32	0.63
37:A3:360:GLU:CD	11:21:74:LEU:HA	2.23	0.63
29:5J:649:VAL:HG11	29:5J:665:LEU:HG	1.80	0.63
6:4B:364:HIS:C	44:4A:423:GLN:OE1	2.41	0.63
13:2f:28:GLU:HB2	13:2f:50:TYR:O	1.99	0.63
27:1A:92:ASP:O	27:1A:96:LYS:HG3	1.97	0.63
36:5A:2225:LEU:HB3	36:5A:2261:MET:HE1	1.81	0.63
4:B4:13:ALA:HB3	37:A3:436:ARG:HH12	1.64	0.63
6:4B:242:ASN:CB	6:4B:286:THR:HG21	2.29	0.63
23:5C:829:GLU:HG3	23:5C:907:VAL:HG22	1.81	0.63
13:4f:65:ARG:NH2	45:4:124:U:O2'	2.32	0.63
33:B3:456:PRO:HA	33:B3:478:PHE:HA	1.81	0.63
36:5A:1038:SER:OG	36:5A:1438:VAL:HG12	1.99	0.63
2:6:64:U:OP1	43:K:911:LYS:CE	2.47	0.63
28:S:565:GLU:CB	28:S:567:PRO:HD3	2.29	0.63
36:5A:1806:ALA:HA	36:5A:1820:LYS:O	1.98	0.63
16:22:95:TYR:CE2	37:A3:150:ILE:HD13	2.34	0.63
28:S:566:ILE:HD13	49:5B:693:THR:HG21	1.81	0.63
37:A3:356:ARG:CB	11:21:75:PRO:CB	2.49	0.63
49:5B:984:LEU:HD11	49:5B:1102:ARG:HH21	1.64	0.63
49:5B:1793:LEU:HD13	49:5B:1810:VAL:HG11	1.81	0.63
24:5X:370:TRP:CZ3	24:5X:389:PRO:CD	2.78	0.62
29:5J:663:ARG:O	29:5J:666:ALA:HB3	1.98	0.62
36:5A:1579:ALA:O	36:5A:1584:LYS:NZ	2.31	0.62
39:5D:6:PRO:HG2	39:5D:59:TYR:CD2	2.34	0.62
1:1:10:U:H3'	24:5X:508:ARG:HB2	1.80	0.62
16:22:95:TYR:CZ	37:A3:150:ILE:HD13	2.34	0.62
23:5C:105:MET:HB3	23:5C:107:GLN:OE1	1.99	0.62
16:52:42:VAL:O	16:52:53:LEU:HA	1.99	0.62
1:1:29:A:C5'	9:1K:200:ARG:HH22	2.09	0.62
49:5B:1822:TYR:HB2	49:5B:1824:ILE:HD11	1.80	0.62
1:1:90:U:O2'	1:1:91:G:O4'	2.16	0.62
3:5O:259:VAL:HB	3:5O:277:PHE:HB2	1.81	0.62
24:5X:370:TRP:HE3	24:5X:389:PRO:HG2	1.63	0.62
28:S:565:GLU:O	28:S:566:ILE:HG13	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:43:19:THR:HB	5:43:72:ILE:HB	1.80	0.62
37:A3:133:GLU:OE2	11:21:73:SER:CB	2.47	0.62
7:4e:33:VAL:HG12	7:4e:87:LEU:HG	1.82	0.62
15:X:120:VAL:HG11	13:4f:39:TYR:OH	1.98	0.62
23:5C:520:GLU:OE2	38:U:146:ARG:CG	2.45	0.62
36:5A:65:HIS:ND1	36:5A:120:TYR:OH	2.29	0.62
36:5A:1777:ILE:HG12	36:5A:1860:GLN:HB3	1.80	0.62
37:A3:356:ARG:HG2	11:21:75:PRO:CB	2.29	0.62
43:K:772:MET:HE3	43:K:827:LYS:HE3	1.80	0.62
44:4A:447:LYS:HG2	47:A1:429:UNK:O	1.99	0.62
21:A2:117:TYR:HE2	21:A2:176:TYR:HB3	1.60	0.62
36:5A:272:ALA:HB2	36:5A:278:LYS:HD3	1.82	0.62
10:4C:209:GLU:HG2	10:4C:225:ALA:HB3	1.82	0.62
13:1f:65:ARG:NH1	16:12:62:HIS:O	2.33	0.62
15:X:125:ASN:HA	16:42:61:ARG:HG3	1.81	0.62
22:B2:477:MET:HE3	37:A3:448:ASN:HD22	1.65	0.62
36:5A:191:ILE:HG23	36:5A:572:PHE:CZ	2.35	0.62
37:A3:356:ARG:O	11:21:75:PRO:HG3	1.98	0.62
9:1K:48:PHE:HE2	9:1K:53:ASP:HA	1.65	0.62
25:1b:10:LEU:O	25:1b:13:ILE:HG22	1.99	0.62
25:2b:26:ILE:HB	25:2b:48:PHE:HB2	1.81	0.62
49:5B:969:LEU:HD21	49:5B:998:VAL:HG21	1.82	0.62
1:1:73:C:O2	1:1:74:C:C5	2.53	0.62
1:1:137:U:N1	9:1K:35:ASN:HB2	2.14	0.62
7:1e:59:ASP:OD2	7:1e:76:ARG:NH1	2.32	0.62
46:2A:27:ARG:HG2	46:2A:50:SER:HB3	1.81	0.62
6:4B:249:ALA:HB2	6:4B:279:ILE:HG22	1.82	0.62
25:2b:76:ASN:ND2	5:23:69:ARG:O	2.33	0.62
36:5A:192:GLN:HG2	36:5A:208:TYR:CD2	2.33	0.62
16:52:10:GLU:HG2	16:52:12:THR:H	1.64	0.62
1:1:123:A:C8	16:12:13:PRO:CB	2.83	0.61
13:2f:30:LYS:O	13:2f:47:THR:HA	2.00	0.61
24:5X:379:ILE:CA	24:5X:629[B]:ILE:HA	2.27	0.61
1:1:73:C:C2'	1:1:74:C:C6	2.83	0.61
1:1:90:U:H4'	1:1:91:G:OP1	1.99	0.61
33:B3:426:ALA:HB1	33:B3:785:PRO:HG2	1.82	0.61
36:5A:2207:ASP:HB3	36:5A:2210:LYS:HG2	1.81	0.61
43:K:740:ASN:HD21	43:K:753:LEU:N	1.96	0.61
43:K:774:LEU:HD23	43:K:777:VAL:HG11	1.82	0.61
6:4B:364:HIS:O	44:4A:423:GLN:NE2	2.34	0.61
8:I:0:G:H2'	8:I:1:G:C8	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:X:120:VAL:HG11	13:4f:39:TYR:CE2	2.35	0.61
13:5f:20:MET:HE1	13:5f:73:ARG:HH11	1.65	0.61
49:5B:2067:VAL:HG13	49:5B:2107:TYR:HB2	1.82	0.61
1:1:105:U:N3	36:5A:1634:SER:CA	2.30	0.61
1:1:137:U:H1'	9:1K:36:GLN:CB	2.30	0.61
25:1b:12:HIS:CD2	25:1b:12:HIS:H	2.16	0.61
32:2:102:U:O2'	11:21:61:ARG:NH1	2.33	0.61
24:5X:373:PHE:CZ	24:5X:419:ARG:CD	2.76	0.61
36:5A:150:MET:SD	36:5A:153:ARG:NH1	2.74	0.61
49:5B:421:HIS:NE2	49:5B:875:GLU:OE1	2.30	0.61
1:1:72:U:H5''	1:1:73:C:OP1	2.01	0.61
23:5C:137:HIS:O	23:5C:142:LYS:NZ	2.34	0.61
24:5X:667:ILE:HA	24:5X:733[A]:VAL:HG11	1.82	0.61
36:5A:1212:GLY:HA2	36:5A:1276:GLU:HB3	1.82	0.61
12:R:456:LYS:HZ3	44:4A:465:ARG:CA	2.05	0.61
1:1:17:G:C2'	1:1:18:G:H5'	2.30	0.61
1:1:92:C:C2	1:1:93:G:N7	2.68	0.61
24:5X:536:ARG:HG3	24:5X:536:ARG:O	2.00	0.61
11:51:66:ARG:HH12	16:52:47:ARG:HB2	1.65	0.61
47:A1:431:UNK:O	47:A1:433:UNK:N	2.33	0.61
3:5O:146:ARG:HH12	17:5:7:U:H4'	1.65	0.61
17:5:36:C:O2	17:5:44:A:N6	2.33	0.61
28:S:553:PHE:HB3	49:5B:877:GLN:HG3	1.82	0.61
37:A3:357:GLU:CG	11:21:75:PRO:HG2	2.30	0.61
1:1:73:C:C2'	1:1:74:C:H6	2.13	0.61
24:5X:768:LEU:HD11	24:5X:779:LEU:HD23	1.82	0.61
49:5B:626:PRO:HG3	49:5B:893:MET:HA	1.81	0.61
1:1:29:A:C2	9:1K:200:ARG:HB2	2.36	0.60
3:5O:62:LEU:HB2	3:5O:351:LEU:HB2	1.82	0.60
9:1K:45:ILE:O	9:1K:45:ILE:HG22	2.01	0.60
9:1K:61:GLU:O	9:1K:65:GLU:HG3	2.01	0.60
27:1A:75:PHE:HB3	27:1A:82:MET:HE3	1.83	0.60
36:5A:257:LEU:HD22	36:5A:314:ILE:HG22	1.83	0.60
16:12:61:ARG:HG3	16:12:62:HIS:CD2	2.36	0.60
14:66:74:SER:CB	48:65:72:ILE:HG22	2.30	0.60
33:B3:809:GLU:OE2	33:B3:881:GLN:NE2	2.35	0.60
3:5O:91:LEU:HD22	3:5O:101:ASN:HD21	1.66	0.60
22:B2:469:VAL:HG12	22:B2:471:ARG:H	1.66	0.60
24:5X:370:TRP:CZ2	24:5X:388:ASN:HB3	2.36	0.60
25:1b:17:MET:HE3	25:1b:82:VAL:HA	1.84	0.60
36:5A:86:ARG:NH1	36:5A:89:LEU:CB	2.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:K:950:ASN:HD22	43:K:950:ASN:N	1.85	0.60
9:1K:61:GLU:O	9:1K:65:GLU:CG	2.49	0.60
29:5J:158:LEU:HD12	36:5A:701:ILE:HG23	1.68	0.60
29:5J:844:LEU:HD22	29:5J:863:TRP:HZ3	1.67	0.60
36:5A:1042:GLN:OE1	36:5A:1090:ARG:NH2	2.35	0.60
1:1:33:C:O2	9:1K:139:ARG:CZ	2.50	0.60
3:5O:177:LYS:HG2	3:5O:189:THR:HG22	1.82	0.60
11:41:61:ARG:NH1	45:4:122:U:O2'	2.32	0.60
16:42:102:ARG:NE	16:42:104:ASP:OD1	2.33	0.60
29:5J:149:LEU:CD2	36:5A:696:MET:HB2	2.31	0.60
29:5J:158:LEU:HD11	36:5A:701:ILE:CG1	2.31	0.60
36:5A:761:ILE:HD12	36:5A:775:ASN:ND2	2.16	0.60
44:4A:427:PRO:CB	44:4A:639:LYS:CE	2.77	0.60
7:4e:47:ILE:HD11	7:4e:50:PHE:HB3	1.82	0.60
36:5A:1626:CYS:SG	36:5A:1627:ALA:N	2.74	0.60
43:K:677:VAL:HG12	43:K:678:ASN:N	2.17	0.60
43:K:846:ILE:HG13	43:K:846:ILE:O	2.00	0.60
15:X:116:LYS:NZ	45:4:124:U:OP1	2.33	0.60
23:5C:846:VAL:HG22	23:5C:887:LEU:HD11	1.82	0.60
36:5A:192:GLN:CB	36:5A:208:TYR:CE2	2.75	0.60
7:2e:30:ARG:NH2	7:2e:60:ASP:O	2.35	0.60
1:1:12:G:OP1	42:1C:15:HIS:NE2	2.35	0.60
1:1:32:A:N7	9:1K:148:PHE:CZ	2.70	0.60
29:5J:574:LYS:O	29:5J:578:LEU:HB2	2.01	0.60
5:43:28:TYR:HB3	5:43:46:ILE:HD11	1.84	0.60
7:1e:68:THR:OG1	7:1e:70:SER:HB2	2.02	0.60
3:5O:182:ARG:O	17:5:78:U:OP1	2.20	0.60
13:1f:3:LEU:HD23	13:1f:4:PRO:HD2	1.83	0.60
33:B3:931:VAL:HG21	33:B3:938:GLU:HG2	1.83	0.60
5:23:67:LYS:HG3	34:2g:68:ILE:HA	1.84	0.60
11:51:76:LEU:HA	11:51:79:LEU:HB2	1.84	0.60
36:5A:188:LEU:O	36:5A:189:GLU:C	2.45	0.60
1:1:15:G:C3'	1:1:16:G:C8	2.85	0.59
22:B2:625:ALA:HB3	22:B2:657:ILE:HG23	1.85	0.59
24:5X:601[B]:GLN:HG2	24:5X:602:THR:N	2.16	0.59
36:5A:976:MET:HG2	36:5A:1187:PHE:HB3	1.83	0.59
36:5A:1790:ILE:HG22	36:5A:1798:LEU:HD11	1.84	0.59
43:K:892:LYS:HG3	43:K:896:HIS:HD2	1.67	0.59
49:5B:1861:ARG:H	49:5B:1864:GLU:HG3	1.66	0.59
5:53:59:GLU:OE1	34:5g:75:ARG:NH1	2.35	0.59
36:5A:690:MET:O	36:5A:694:LEU:HG	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5A:1509:PHE:C	36:5A:1510:GLU:OE1	2.45	0.59
43:K:722:ASN:HD22	43:K:723:GLU:H	1.50	0.59
13:1f:25:TRP:HB2	13:1f:27:MET:CE	2.32	0.59
30:4D:108:GLU:O	43:K:947:SER:HB3	2.02	0.59
33:B3:264:GLN:HE21	33:B3:321:MET:HA	1.68	0.59
38:U:363:HIS:HB3	38:U:366:LEU:HD13	1.82	0.59
7:2e:44:GLU:OE2	7:2e:71:ARG:NH2	2.35	0.59
43:K:722:ASN:HD22	43:K:723:GLU:N	2.01	0.59
46:2A:47:ILE:HG12	46:2A:66:LEU:HD21	1.84	0.59
46:2A:112:LEU:O	46:2A:141:GLN:NE2	2.35	0.59
1:1:15:G:C2'	1:1:16:G:C8	2.85	0.59
1:1:140:G:H1'	25:1b:57:LYS:HE2	1.84	0.59
9:1K:61:GLU:O	9:1K:65:GLU:OE1	2.19	0.59
23:5C:388:VAL:HA	23:5C:392:LEU:HB2	1.84	0.59
36:5A:1838:LYS:NZ	49:5B:205:PHE:O	2.35	0.59
34:4g:19:LEU:HB2	34:4g:27:VAL:HG12	1.85	0.59
1:1:46:C:H6	1:1:46:C:H5''	1.67	0.59
5:53:19:THR:HG23	5:53:72:ILE:HB	1.84	0.59
29:5J:157:TRP:O	36:5A:705:LYS:HE2	2.02	0.59
29:5J:158:LEU:HA	36:5A:705:LYS:HD3	1.84	0.59
29:5J:317:ARG:HA	29:5J:320:GLU:HG2	1.83	0.59
39:5D:8:LEU:HD12	39:5D:14:VAL:HG22	1.83	0.59
34:1g:57:ILE:HG21	7:1e:88:GLN:OE1	2.02	0.59
36:5A:191:ILE:HG22	36:5A:191:ILE:O	2.01	0.59
36:5A:694:LEU:HD12	47:A1:466:LEU:HD13	1.79	0.59
36:5A:1905:LEU:HD21	36:5A:1915:VAL:HG11	1.83	0.59
39:5D:53:LYS:HE2	47:A1:447:UNK:CB	2.33	0.59
34:5g:19:LEU:HB2	34:5g:27:VAL:HG12	1.85	0.59
43:K:956:LEU:O	43:K:960:ILE:HG13	2.02	0.59
5:53:14:GLU:HB2	23:5C:196:LYS:HE2	1.84	0.59
23:5C:137:HIS:HD2	23:5C:238:ASN:H	1.48	0.59
28:S:575:ARG:NH2	29:5J:424:SER:C	2.60	0.59
42:1C:9:CYS:HB2	42:1C:11:THR:HG22	1.83	0.59
2:6:103:U:C3'	35:68:65:ASP:OD1	2.51	0.59
21:A2:65:ASN:OD1	21:A2:65:ASN:N	2.35	0.59
21:A2:115:PRO:HD3	21:A2:176:TYR:C	2.27	0.59
33:B3:506:LEU:HD13	33:B3:521:PRO:HD3	1.83	0.59
34:1g:55:ASN:OD1	34:1g:56:ASN:N	2.35	0.59
37:A3:356:ARG:HD2	11:21:75:PRO:HA	1.85	0.59
43:K:823:VAL:CG2	43:K:827:LYS:HA	2.31	0.59
49:5B:1499:ASP:OD2	49:5B:1763:ARG:NH1	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B3:932:ASN:C	33:B3:934:GLY:H	2.11	0.59
36:5A:761:ILE:CD1	36:5A:775:ASN:HD22	2.16	0.59
37:A3:357:GLU:HG3	11:21:75:PRO:HG2	1.84	0.59
38:U:456:LYS:HE2	38:U:459:THR:HG22	1.84	0.59
1:1:33:C:C2	9:1K:139:ARG:CD	2.86	0.59
1:1:138:G:H2'	1:1:139:G:C8	2.38	0.59
28:S:565:GLU:C	28:S:566:ILE:HG13	2.28	0.59
9:1K:42:ALA:O	9:1K:45:ILE:HD13	2.03	0.58
11:41:68:PHE:HB2	16:42:100:PHE:HB3	1.85	0.58
15:X:124:VAL:HG13	45:4:118:A:N6	2.17	0.58
16:22:95:TYR:CD2	37:A3:150:ILE:HG21	2.38	0.58
36:5A:164:MET:HE1	36:5A:560:SER:HA	1.85	0.58
36:5A:707:ARG:NE	47:A1:456:TYR:HD2	2.01	0.58
36:5A:1434:LYS:O	36:5A:1439:ARG:NH2	2.35	0.58
25:4b:50:LYS:HB3	25:4b:63:GLU:HG3	1.85	0.58
49:5B:971:LYS:HB2	49:5B:980:GLN:HB2	1.83	0.58
2:6:106:U:O4	35:68:96:HIS:ND1	2.36	0.58
9:1K:58:THR:O	9:1K:59:ARG:HG2	2.04	0.58
13:4f:21:VAL:HG12	13:4f:72:ILE:HG23	1.85	0.58
33:B3:1145:GLU:HG2	33:B3:1174:ILE:HG23	1.85	0.58
36:5A:707:ARG:NH1	36:5A:711:GLN:HE22	2.02	0.58
16:52:39:ASN:O	16:52:55:ARG:NH1	2.36	0.58
43:K:788:HIS:CE1	43:K:790:LYS:HG3	2.38	0.58
3:5O:95:VAL:HG13	3:5O:353:MET:HE1	1.85	0.58
7:5e:63:GLU:HG3	7:5e:74:LEU:HD11	1.84	0.58
23:5C:343:LEU:HD13	23:5C:373:ILE:HD11	1.85	0.58
16:42:91:ASN:ND2	28:S:631:GLU:O	2.35	0.58
28:S:575:ARG:NH2	29:5J:428:GLU:CD	2.61	0.58
33:B3:528:ARG:HG2	33:B3:532:ARG:HH21	1.67	0.58
36:5A:693:ILE:HG21	36:5A:709:ILE:CD1	2.33	0.58
39:5D:30:PHE:HB3	39:5D:63:ILE:HD11	1.84	0.58
1:1:17:G:HO2'	1:1:18:G:H5'	1.65	0.58
1:1:83:U:H2'	1:1:84:G:O4'	2.03	0.58
9:1K:49:GLU:C	9:1K:51:PRO:HD2	2.29	0.58
13:1f:69:VAL:HG13	7:1e:80:LYS:HD3	1.85	0.58
24:5X:540:LEU:CD2	24:5X:543:CYS:SG	2.91	0.58
13:4f:20:MET:HA	13:4f:29:TYR:O	2.01	0.58
33:B3:175:VAL:HB	33:B3:178:GLU:HB3	1.84	0.58
36:5A:563:GLN:OE1	36:5A:563:GLN:HA	2.01	0.58
6:4B:242:ASN:HB3	6:4B:286:THR:HG21	1.84	0.58
28:S:574:ASN:HD21	29:5J:451:LYS:HE2	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:5J:766:LEU:HD11	29:5J:782:GLU:HG3	1.85	0.58
33:B3:525:ARG:HG3	33:B3:533:VAL:HG13	1.85	0.58
49:5B:120:ILE:O	49:5B:124:LEU:HB3	2.03	0.58
49:5B:1228:VAL:HG11	49:5B:1264:PRO:HD2	1.85	0.58
1:1:91:G:C2'	1:1:92:C:O5'	2.51	0.58
9:1K:61:GLU:CA	9:1K:65:GLU:CG	2.77	0.58
24:5X:301:ARG:NH1	36:5A:341:LYS:O	2.37	0.58
13:4f:33:LEU:HA	13:4f:44:LEU:HA	1.86	0.58
1:1:73:C:H3'	1:1:74:C:C5	2.39	0.58
1:1:93:G:N2	1:1:117:G:N3	2.52	0.58
9:1K:86:LEU:HD12	9:1K:192:LEU:HD13	1.85	0.58
23:5C:478:THR:HA	23:5C:494:GLY:HA3	1.85	0.58
24:5X:536:ARG:HG3	34:1g:10:LYS:CE	2.34	0.58
29:5J:626:ALA:O	29:5J:629:SER:HB3	2.04	0.58
36:5A:85:LYS:HG2	36:5A:89:LEU:HD11	1.85	0.58
43:K:999:GLN:HA	43:K:1004:GLN:OE1	2.04	0.58
1:1:8:C:H5''	24:5X:503:ILE:HA	1.86	0.58
33:B3:893:VAL:HG12	33:B3:905:VAL:HG22	1.85	0.58
36:5A:1537:TRP:CE3	36:5A:1751:LEU:HD13	2.39	0.58
16:52:107:ILE:HG22	16:52:108:VAL:HG13	1.86	0.58
10:4C:97:ASN:ND2	10:4C:226:SER:O	2.37	0.58
11:41:3:LEU:HD23	16:42:60:ASP:HB3	1.83	0.58
23:5C:105:MET:CB	23:5C:540:GLU:O	2.52	0.58
38:U:226:VAL:O	38:U:242:GLN:NE2	2.37	0.58
39:5D:101:LYS:HG3	39:5D:103:ASN:HB3	1.85	0.58
1:1:137:U:C2	9:1K:35:ASN:HB2	2.39	0.58
15:X:124:VAL:CG1	13:4f:39:TYR:HD2	2.16	0.58
34:4g:20:LYS:HD2	34:4g:69:MET:HE2	1.86	0.58
48:65:27:HIS:HD1	48:65:37:VAL:HB	1.69	0.58
1:1:138:G:H2'	1:1:139:G:H8	1.68	0.57
33:B3:454:GLY:O	33:B3:760:ASN:ND2	2.37	0.57
33:B3:633:LEU:HD22	33:B3:637:PRO:HG3	1.84	0.57
50:B1:901:GLN:O	50:B1:939:ARG:NH1	2.37	0.57
1:1:29:A:C1'	9:1K:200:ARG:CD	2.76	0.57
7:5e:39:VAL:HG12	34:5g:25:ARG:HH11	1.67	0.57
11:41:76:LEU:HA	11:41:79:LEU:HB2	1.85	0.57
30:4D:108:GLU:OE1	43:K:926:ASN:CG	2.47	0.57
34:1g:49:ALA:O	34:1g:51:SER:O	2.22	0.57
36:5A:2164:PRO:HB3	36:5A:2296:LEU:HD11	1.84	0.57
44:4A:394:ILE:O	44:4A:412:PHE:N	2.36	0.57
50:B1:495:ARG:O	50:B1:498:MET:HB3	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:5C:182:LYS:HE2	23:5C:613:SER:HB3	1.85	0.57
29:5J:423:LEU:HD12	29:5J:443:LEU:HD12	1.86	0.57
25:2b:64:LYS:NZ	46:2A:45:ASP:OD2	2.37	0.57
1:1:105:U:N3	36:5A:1607:GLU:OE1	2.38	0.57
1:1:116:C:O5'	1:1:116:C:H6	1.87	0.57
23:5C:262:ARG:NH2	36:5A:336:ASN:O	2.37	0.57
16:42:30:SER:HA	16:42:33:THR:HG22	1.86	0.57
29:5J:503:ARG:HD3	29:5J:533:GLY:HA3	1.86	0.57
33:B3:439:ARG:O	33:B3:774:PHE:HA	2.04	0.57
33:B3:1058:LEU:HD22	33:B3:1062:THR:HG21	1.85	0.57
36:5A:1510:GLU:O	36:5A:1513:MET:SD	2.62	0.57
41:BP:23:CYS:HB3	41:BP:58:CYS:HB2	1.86	0.57
43:K:966:PRO:HB2	43:K:968:ASP:OD2	2.05	0.57
49:5B:2101:ALA:HA	49:5B:2124:VAL:O	2.03	0.57
1:1:8:C:H4'	24:5X:528:ARG:H	1.68	0.57
2:6:58:G:O6	10:4C:357:ARG:NH1	2.37	0.57
39:5D:8:LEU:CB	39:5D:14:VAL:HG22	2.34	0.57
43:K:781:TYR:HB3	43:K:785:VAL:HG21	1.86	0.57
1:1:93:G:C2	1:1:117:G:C2	2.93	0.57
1:1:122:C:C2'	1:1:123:A:OP2	2.51	0.57
7:5e:74:LEU:HD23	7:5e:77:ILE:HG21	1.87	0.57
24:5X:379:ILE:HG22	24:5X:629[B]:ILE:HG23	1.85	0.57
43:K:784:ASP:CG	43:K:886:LYS:HD3	2.29	0.57
49:5B:1002:ASN:OD1	49:5B:1102:ARG:NH2	2.37	0.57
21:A2:115:PRO:HD3	21:A2:177:GLU:N	2.17	0.57
22:B2:536:MET:HE1	22:B2:566:ILE:HB	1.87	0.57
24:5X:728:ILE:HG23	24:5X:729:ASP:N	2.20	0.57
36:5A:1795:GLU:OE1	36:5A:1795:GLU:HA	2.04	0.57
50:B1:477:LYS:O	50:B1:495:ARG:NH2	2.37	0.57
1:1:29:A:N3	9:1K:200:ARG:HB2	2.20	0.57
1:1:118:A:H5'	1:1:119:C:OP2	2.05	0.57
10:4C:141:GLU:HG2	10:4C:155:LEU:HD13	1.86	0.57
16:22:95:TYR:O	37:A3:147:LEU:HD21	2.04	0.57
38:U:106:PRO:O	49:5B:269:GLN:NE2	2.33	0.57
50:B1:586:ASP:OD1	50:B1:586:ASP:N	2.35	0.57
15:X:124:VAL:HG22	13:4f:37:ASP:HB2	1.85	0.57
13:2f:10:PHE:O	13:2f:14:LEU:HB2	2.04	0.57
30:4D:109:GLY:HA3	43:K:947:SER:HB2	1.84	0.57
36:5A:2284:MET:SD	36:5A:2287:ARG:NH1	2.78	0.57
39:5D:5:LEU:CD1	39:5D:60:LEU:HD21	2.35	0.57
16:12:30:SER:HA	16:12:33:THR:OG1	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:5B:724:PHE:HB3	49:5B:852:MET:HE2	1.86	0.57
5:13:71:LEU:HD12	5:13:71:LEU:N	2.20	0.57
15:X:137:TYR:CG	28:S:729:LEU:CD1	2.75	0.57
23:5C:559:ILE:HG21	23:5C:563:ALA:HB2	1.86	0.57
13:5f:11:LEU:O	13:5f:15:THR:OG1	2.23	0.57
5:23:19:THR:HB	5:23:72:ILE:HB	1.86	0.57
28:S:574:ASN:ND2	29:5J:451:LYS:CE	2.42	0.56
28:S:575:ARG:NH2	29:5J:424:SER:CB	2.68	0.56
33:B3:794:SER:O	33:B3:796:ASN:ND2	2.38	0.56
7:1e:48:ILE:HD11	7:1e:59:ASP:OD2	2.05	0.56
37:A3:356:ARG:HG2	11:21:75:PRO:CG	2.34	0.56
43:K:798:GLN:HB2	43:K:830:LEU:HD11	1.86	0.56
43:K:982:GLN:HB3	43:K:992:ILE:HB	1.87	0.56
49:5B:1663:ILE:HD12	49:5B:1704:ILE:HG12	1.87	0.56
2:6:106:U:OP2	14:66:66:ARG:NH1	2.34	0.56
10:4C:377:ARG:O	36:5A:1505:LYS:NZ	2.38	0.56
15:X:114:SER:HB2	45:4:120:U:OP2	2.04	0.56
16:22:107:ILE:HG22	16:22:108:VAL:HG23	1.87	0.56
21:A2:114:ARG:HG2	21:A2:114:ARG:O	2.03	0.56
24:5X:477:THR:HG22	24:5X:557:MET:HE1	1.88	0.56
33:B3:930:LEU:CD1	33:B3:934:GLY:HA2	2.34	0.56
38:U:235:ASP:N	38:U:235:ASP:OD1	2.37	0.56
49:5B:1060:ASN:OD1	49:5B:1064:GLN:NE2	2.35	0.56
49:5B:2052:ILE:HG22	49:5B:2054:PRO:HD3	1.87	0.56
49:5B:2066:VAL:HG21	49:5B:2090:VAL:HG11	1.87	0.56
1:1:86:C:H2'	1:1:87:C:O4'	2.06	0.56
2:6:85:U:C2	2:6:86:U:C5	2.93	0.56
3:5O:183:LYS:HG3	3:5O:187:ILE:HD11	1.87	0.56
11:41:25:VAL:HG22	11:41:45:MET:HG3	1.86	0.56
22:B2:625:ALA:CB	22:B2:651:PRO:HB2	2.35	0.56
22:B2:662:SER:O	22:B2:663:PHE:HB3	2.05	0.56
23:5C:105:MET:O	23:5C:106:GLU:HB3	2.05	0.56
13:5f:50:TYR:HA	13:5f:54:ALA:O	2.04	0.56
25:2b:83:GLU:O	46:2A:43:GLN:NE2	2.39	0.56
33:B3:260:ASN:ND2	33:B3:264:GLN:OE1	2.38	0.56
36:5A:689:VAL:O	36:5A:693:ILE:HG13	2.05	0.56
36:5A:1042:GLN:HA	36:5A:1090:ARG:HH22	1.71	0.56
38:U:308:SER:HB2	38:U:311:THR:HB	1.87	0.56
39:5D:6:PRO:HG2	39:5D:59:TYR:HD2	1.68	0.56
43:K:676:ARG:NH2	43:K:677:VAL:HG22	2.15	0.56
50:B1:509:PRO:HA	50:B1:512:ARG:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:6:54:G:H5''	10:4C:360:ARG:HH11	1.70	0.56
6:4B:294:VAL:HG23	6:4B:307:LEU:HB3	1.87	0.56
12:R:446:TYR:CD1	39:5D:86:ARG:NH2	2.72	0.56
29:5J:149:LEU:HD22	36:5A:696:MET:HB2	1.88	0.56
5:43:14:GLU:HA	5:43:32:LEU:HD22	1.86	0.56
36:5A:733:THR:HA	36:5A:736:GLU:HB3	1.87	0.56
36:5A:1381:ASP:O	36:5A:1385:VAL:HB	2.06	0.56
36:5A:1491:LYS:O	36:5A:1710:ASN:ND2	2.38	0.56
46:2A:121:LEU:O	46:2A:123:ASN:ND2	2.38	0.56
1:1:9:C:O5'	24:5X:508:ARG:CZ	2.53	0.56
6:4B:402:PHE:CE1	44:4A:424:LEU:HD12	2.39	0.56
12:R:436:VAL:HG21	44:4A:462:GLU:OE2	2.05	0.56
29:5J:111:ARG:HG2	29:5J:112:MET:HE2	1.88	0.56
7:1e:48:ILE:HD13	7:1e:76:ARG:NH2	2.21	0.56
36:5A:221:ASN:HD22	36:5A:226:GLN:HB2	1.69	0.56
38:U:260:TYR:OH	38:U:283:ARG:NH1	2.34	0.56
1:1:8:C:OP1	24:5X:503:ILE:CG2	2.53	0.56
1:1:15:G:C2	1:1:16:G:C2	2.94	0.56
22:B2:466:LYS:NZ	37:A3:445:HIS:O	2.36	0.56
24:5X:479[B]:GLU:H	24:5X:479[B]:GLU:CD	2.12	0.56
16:42:45:ASN:HB2	28:S:638:LEU:HD13	1.88	0.56
13:5f:64:ILE:HG22	16:52:108:VAL:HG12	1.87	0.56
11:51:25:VAL:HG22	11:51:45:MET:HG3	1.87	0.56
3:5O:311:VAL:HB	3:5O:321:TYR:HB2	1.88	0.56
10:4C:235:ALA:HB2	10:4C:252:LEU:HD21	1.87	0.56
29:5J:366:VAL:HG21	49:5B:89:LEU:HD13	1.88	0.56
33:B3:550:ASN:ND2	33:B3:593:ALA:O	2.39	0.56
36:5A:892:LYS:HD2	36:5A:912:GLU:HG3	1.87	0.56
36:5A:1289:VAL:HG11	49:5B:42:SER:HA	1.88	0.56
36:5A:1621:LYS:HE3	36:5A:1624:SER:OG	2.05	0.56
16:52:53:LEU:HD11	16:52:71:LYS:HD3	1.86	0.56
43:K:793:ARG:HG3	43:K:794:SER:N	2.17	0.56
44:4A:427:PRO:HB3	44:4A:639:LYS:HZ1	1.70	0.56
49:5B:1351:PRO:HG3	49:5B:1516:PRO:HA	1.88	0.56
16:22:94:ARG:NH2	11:21:67:TYR:OH	2.39	0.56
23:5C:413:ARG:NH2	36:5A:405:LEU:O	2.39	0.56
11:11:20:LYS:HE2	11:11:63:ASN:O	2.06	0.56
37:A3:353:GLY:O	11:21:78:THR:OG1	2.22	0.56
7:2e:62:GLU:OE2	7:2e:71:ARG:NH2	2.39	0.56
43:K:1004:GLN:O	43:K:1005:GLU:HB3	2.03	0.56
49:5B:705:ASN:OD1	49:5B:829:LYS:NZ	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:B1:1247:LEU:HD22	50:B1:1280:LEU:HD22	1.88	0.56
1:1:32:A:C1'	9:1K:135:VAL:CG2	2.83	0.56
1:1:94:A:O2'	1:1:95:U:H5'	2.05	0.56
21:A2:114:ARG:HG3	21:A2:177:GLU:CD	2.31	0.56
23:5C:105:MET:N	23:5C:105:MET:SD	2.79	0.56
24:5X:370:TRP:CZ3	24:5X:389:PRO:CG	2.88	0.56
24:5X:458:LYS:O	24:5X:462:ILE:HG13	2.06	0.56
25:1b:9:MET:HE1	25:1b:80:MET:CE	2.35	0.56
33:B3:113:ARG:HB2	33:B3:116:VAL:HG22	1.87	0.56
33:B3:603:ARG:NH1	33:B3:620:ASP:OD2	2.39	0.56
36:5A:67:ARG:HD3	36:5A:179:ALA:HB2	1.88	0.56
36:5A:2141:GLU:OE2	36:5A:2143:ARG:NH2	2.39	0.56
44:4A:447:LYS:HD3	47:A1:429:UNK:O	2.06	0.56
1:1:31:C:O4'	9:1K:146:TYR:CD1	2.32	0.56
24:5X:373:PHE:HZ	24:5X:419:ARG:CD	2.15	0.56
25:1b:12:HIS:CD2	25:1b:12:HIS:N	2.74	0.56
33:B3:275:ARG:HD2	33:B3:386:PHE:HB3	1.88	0.56
36:5A:192:GLN:CG	36:5A:208:TYR:CD2	2.89	0.56
34:5g:20:LYS:HD2	34:5g:69:MET:HE2	1.86	0.56
11:21:19:LEU:HD21	11:21:60:ILE:HD13	1.88	0.56
49:5B:1130:ARG:HG2	49:5B:1140:VAL:HG11	1.88	0.56
1:1:73:C:C2	1:1:74:C:C6	2.94	0.55
3:5O:148:LYS:NZ	17:5:7:U:C5'	2.69	0.55
12:R:446:TYR:CD2	39:5D:86:ARG:NE	2.74	0.55
22:B2:630:PRO:CD	22:B2:663:PHE:HE2	2.05	0.55
23:5C:641:MET:HE2	23:5C:655:VAL:HG22	1.88	0.55
23:5C:853:ARG:NH1	23:5C:879:ASP:O	2.36	0.55
43:K:739:LEU:CD2	43:K:805:LEU:HD13	2.35	0.55
43:K:892:LYS:NZ	43:K:892:LYS:HB3	2.22	0.55
50:B1:806:ILE:HG12	50:B1:810:ILE:HD12	1.87	0.55
1:1:7:A:H4'	24:5X:477:THR:C	2.31	0.55
1:1:33:C:H4'	9:1K:137:SER:CB	2.35	0.55
24:5X:536:ARG:HB3	34:1g:10:LYS:CD	2.35	0.55
49:5B:722:LEU:HB3	49:5B:826:VAL:HG12	1.88	0.55
49:5B:1188:VAL:HG23	49:5B:1200:VAL:HG13	1.88	0.55
1:1:46:C:H5''	1:1:46:C:C6	2.41	0.55
7:5e:43:ILE:HA	7:5e:62:GLU:O	2.06	0.55
11:41:33:ASP:HB2	11:41:37:ASN:HB2	1.88	0.55
11:51:33:ASP:HB2	11:51:37:ASN:HB2	1.88	0.55
33:B3:86:ARG:NH1	33:B3:1157:GLY:O	2.39	0.55
36:5A:852:VAL:HG21	36:5A:854:SER:HA	1.73	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:K:699:SER:HB2	43:K:718:ILE:O	2.06	0.55
11:21:22:GLY:HA3	11:21:48:LYS:HD2	1.87	0.55
45:4:114:U:O2	45:4:114:U:H2'	2.06	0.55
10:4C:374:GLN:H	10:4C:377:ARG:HD2	1.71	0.55
5:53:62:TYR:HB3	34:5g:70:LEU:HB2	1.88	0.55
22:B2:625:ALA:O	22:B2:629:PRO:HG3	2.06	0.55
24:5X:362:LEU:N	24:5X:391:ARG:NH2	2.55	0.55
24:5X:652:ARG:HH22	36:5A:1641:ARG:NH2	2.05	0.55
29:5J:725:MET:SD	29:5J:755:LYS:NZ	2.75	0.55
33:B3:449:VAL:HG22	33:B3:763:ARG:HG2	1.88	0.55
33:B3:610:VAL:HG13	33:B3:636:GLN:HE22	1.71	0.55
33:B3:903:TRP:HB3	33:B3:930:LEU:HD23	1.87	0.55
49:5B:278:ASP:HB3	49:5B:281:VAL:HG12	1.88	0.55
1:1:29:A:C2	9:1K:200:ARG:CB	2.89	0.55
21:A2:121:LYS:HG3	21:A2:134:PHE:CE1	2.41	0.55
32:2:166:G:OP2	32:2:166:G:N2	2.36	0.55
36:5A:209:ASP:HB2	36:5A:212:PRO:HA	1.89	0.55
43:K:830:LEU:O	43:K:831:LYS:HD2	2.06	0.55
44:4A:586:GLY:HA2	44:4A:641:ARG:HH21	1.71	0.55
49:5B:406:ARG:NH2	49:5B:974:LYS:O	2.40	0.55
49:5B:668:ASP:OD1	49:5B:671:LYS:NZ	2.39	0.55
49:5B:1063:LEU:HD11	49:5B:1118:ILE:HG12	1.88	0.55
49:5B:1729:ASP:OD1	49:5B:1729:ASP:N	2.39	0.55
6:4B:426:SER:OG	6:4B:428:ASP:OD1	2.23	0.55
9:1K:75:ILE:O	9:1K:79:GLN:HG3	2.07	0.55
15:X:123:SER:HB2	16:42:23:GLU:O	2.06	0.55
24:5X:551:ALA:HB3	24:5X:606[A]:THR:CG2	2.37	0.55
16:42:44:ILE:HG12	16:42:65:MET:HE1	1.87	0.55
43:K:817:LYS:HA	43:K:878:THR:HG21	1.89	0.55
50:B1:689:ILE:O	50:B1:692:HIS:ND1	2.39	0.55
1:1:33:C:H5'	9:1K:136:TYR:C	2.31	0.55
1:1:137:U:C2	9:1K:35:ASN:CB	2.85	0.55
6:4B:365:SER:HA	44:4A:423:GLN:CD	2.25	0.55
30:4D:18:LEU:HD21	30:4D:123:ILE:HG22	1.88	0.55
5:43:18:VAL:HG13	5:43:43:MET:HE3	1.87	0.55
36:5A:152:ARG:NH2	36:5A:618:THR:O	2.39	0.55
36:5A:844:GLU:OE2	36:5A:1459:ARG:NH1	2.40	0.55
44:4A:528:LYS:HA	44:4A:531:LYS:HG2	1.89	0.55
49:5B:1855:TYR:HB3	49:5B:1891:THR:HG21	1.88	0.55
7:4e:16:GLN:OE1	7:4e:19:ASN:ND2	2.40	0.55
15:X:123:SER:CB	16:42:23:GLU:O	2.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:X:134:LYS:HE3	28:S:728:GLN:HE22	1.71	0.55
23:5C:107:GLN:NE2	23:5C:109:LEU:HD11	2.22	0.55
23:5C:836:VAL:HG22	23:5C:897:SER:HB3	1.89	0.55
29:5J:295:ARG:HH21	29:5J:322:THR:HG23	1.71	0.55
33:B3:1009:PHE:HZ	33:B3:1046:GLY:HA3	1.72	0.55
36:5A:1265:THR:HG22	36:5A:1452:PRO:HG3	1.88	0.55
49:5B:1538:ARG:NH1	49:5B:1665:ASP:OD2	2.40	0.55
1:1:7:A:C5'	24:5X:477:THR:C	2.70	0.55
1:1:9:C:H5	24:5X:508:ARG:HH12	1.44	0.55
1:1:48:C:O2	1:1:48:C:H2'	2.07	0.55
15:X:124:VAL:HG13	13:4f:39:TYR:HD2	1.72	0.55
22:B2:629:PRO:CG	22:B2:633:LEU:HD12	2.37	0.55
23:5C:203:MET:HE2	23:5C:221:ILE:HD11	1.89	0.55
23:5C:804:GLY:H	23:5C:808:ILE:HD12	1.72	0.55
24:5X:162:LYS:O	49:5B:1782:SER:OG	2.25	0.55
29:5J:910:GLU:O	29:5J:914:ALA:HB2	2.06	0.55
5:43:26:GLU:OE1	5:43:28:TYR:OH	2.25	0.55
16:52:41:GLN:HE21	16:52:53:LEU:HD13	1.72	0.55
43:K:965:LEU:HB3	43:K:966:PRO:HD2	1.89	0.55
49:5B:84:MET:HG2	49:5B:87:TYR:HB2	1.89	0.55
49:5B:531:ILE:HG13	49:5B:562:TYR:HB3	1.89	0.55
49:5B:1108:THR:HG21	49:5B:1233:ILE:HD11	1.89	0.55
1:1:73:C:H2'	1:1:74:C:O4'	2.07	0.55
1:1:118:A:C1'	42:1C:2:PRO:CD	2.85	0.55
22:B2:607:GLY:O	22:B2:662:SER:O	2.25	0.55
16:42:49:ASN:HD21	28:S:636:ARG:H	1.55	0.55
33:B3:109:LYS:NZ	41:BP:79:GLU:O	2.39	0.55
36:5A:191:ILE:HG23	36:5A:572:PHE:CE2	2.42	0.55
38:U:228:LEU:HG	38:U:242:GLN:HE21	1.72	0.55
43:K:955:LEU:HB3	43:K:977:LYS:HD3	1.89	0.55
44:4A:494:THR:O	44:4A:498:ALA:HB2	2.05	0.55
46:2A:132:ARG:HG3	46:2A:145:LEU:HD23	1.88	0.55
50:B1:1258:ALA:HB3	50:B1:1261:VAL:HG12	1.89	0.55
3:5O:309:VAL:HB	3:5O:323:LEU:HB2	1.88	0.54
7:4e:78:MET:HE2	13:4f:7:PRO:HB3	1.89	0.54
29:5J:98:ASP:HA	36:5A:86:ARG:HB2	1.89	0.54
30:4D:64:GLU:HA	30:4D:67:LEU:HB2	1.90	0.54
33:B3:932:ASN:ND2	33:B3:935:GLU:OE2	2.38	0.54
36:5A:193:LEU:N	36:5A:208:TYR:OH	2.32	0.54
36:5A:911:VAL:HB	36:5A:916:LYS:HG3	1.90	0.54
36:5A:1615:HIS:HE1	36:5A:1617:ARG:HE	1.53	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:U:146:ARG:NH2	38:U:173:TYR:HE1	1.78	0.54
43:K:895:ASN:HD21	43:K:932:ILE:H	1.53	0.54
49:5B:463:PRO:HA	49:5B:480:THR:HA	1.90	0.54
1:1:123:A:O2'	1:1:124:U:OP2	2.20	0.54
3:5O:81:LEU:HD21	3:5O:343:ILE:HD12	1.88	0.54
24:5X:669:ILE:HG12	24:5X:737:VAL:CG1	2.37	0.54
16:42:39:ASN:O	16:42:55:ARG:NH1	2.39	0.54
33:B3:164:ASN:ND2	33:B3:190:GLU:OE1	2.39	0.54
36:5A:2068:SER:HB2	36:5A:2072:GLU:HB2	1.90	0.54
34:2g:19:LEU:HD13	34:2g:70:LEU:HB3	1.88	0.54
44:4A:507:ARG:NH2	45:4:13:U:OP1	2.38	0.54
48:65:28:ILE:HD11	48:65:49:MET:HE1	1.89	0.54
49:5B:1041:LEU:HD22	49:5B:1052:ILE:HD13	1.90	0.54
3:5O:346:SER:OG	3:5O:348:ASP:OD1	2.24	0.54
5:13:12:GLU:HB3	5:13:77:LEU:HD22	1.88	0.54
15:X:116:LYS:HA	45:4:119:A:OP1	2.07	0.54
29:5J:675:ALA:CB	29:5J:705:TYR:CD2	2.90	0.54
36:5A:1511:GLU:O	36:5A:1512:SER:HB3	2.06	0.54
36:5A:1809:ILE:HB	36:5A:1818:PHE:HB2	1.89	0.54
36:5A:1827:TRP:HA	36:5A:1830:GLN:HB2	1.89	0.54
44:4A:543:ILE:HG12	44:4A:585:GLU:HG3	1.89	0.54
49:5B:1617:VAL:HG22	49:5B:1643:VAL:HB	1.90	0.54
49:5B:1804:ILE:HG12	49:5B:1810:VAL:HG12	1.88	0.54
3:5O:265:ARG:H	3:5O:272:ARG:HH12	1.54	0.54
7:5e:41:MET:HA	7:5e:64:ILE:O	2.07	0.54
25:2b:47:GLU:HG2	25:2b:65:ARG:HB2	1.88	0.54
25:4b:41:ILE:HD11	25:4b:71:LEU:HD12	1.89	0.54
3:5O:146:ARG:HH22	17:5:7:U:HO2'	1.42	0.54
23:5C:107:GLN:H	23:5C:107:GLN:CD	2.11	0.54
29:5J:273:TYR:OH	36:5A:828:PRO:O	2.22	0.54
33:B3:273:ARG:NH1	33:B3:285:MET:SD	2.80	0.54
33:B3:931:VAL:CG2	33:B3:938:GLU:HG2	2.37	0.54
36:5A:712:HIS:HE1	36:5A:728:VAL:HG11	1.73	0.54
36:5A:1604:LEU:HD11	36:5A:1725:LEU:HD22	1.90	0.54
49:5B:1093:ARG:NH1	49:5B:1273:ASP:O	2.38	0.54
2:6:53:A:N6	10:4C:353:LYS:O	2.41	0.54
9:1K:59:ARG:NH1	11:11:77:ASP:CG	2.66	0.54
23:5C:366:GLN:HB2	23:5C:371:GLU:HG3	1.90	0.54
23:5C:524:ILE:HD12	23:5C:568:PRO:HB3	1.89	0.54
24:5X:428:ASN:HD21	24:5X:598:LYS:NZ	2.05	0.54
24:5X:675:LYS:H	24:5X:675:LYS:HD2	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:5J:98:ASP:HB3	36:5A:86:ARG:HG3	1.89	0.54
29:5J:158:LEU:HD12	36:5A:701:ILE:CD1	2.32	0.54
33:B3:1133:THR:OG1	33:B3:1134:SER:N	2.41	0.54
49:5B:1139:VAL:HG23	49:5B:1167:MET:HG3	1.89	0.54
3:5O:239:THR:O	3:5O:290:ARG:NH1	2.40	0.54
36:5A:271:MET:HB3	36:5A:310:THR:HG23	1.89	0.54
36:5A:559:ASP:C	36:5A:562:VAL:HG22	2.33	0.54
36:5A:900:ASP:O	36:5A:1246:GLN:NE2	2.41	0.54
36:5A:1163:ARG:HE	36:5A:1167:THR:HG23	1.73	0.54
36:5A:2103:THR:HB	36:5A:2139:VAL:HG23	1.89	0.54
37:A3:360:GLU:OE2	11:21:75:PRO:CD	2.49	0.54
1:1:8:C:O2'	24:5X:528:ARG:HA	2.07	0.54
1:1:33:C:N4	9:1K:139:ARG:HH21	2.05	0.54
6:4B:193:LEU:HD11	44:4A:388:GLU:HG3	1.90	0.54
7:5e:30:ARG:HB3	7:5e:90:VAL:HA	1.88	0.54
7:4e:32:GLN:OE1	7:4e:88:GLN:NE2	2.40	0.54
29:5J:619:TRP:HD1	29:5J:620:LEU:HD23	1.72	0.54
30:4D:97:ARG:HE	30:4D:98:PRO:HD2	1.71	0.54
32:2:168:A:C8	5:23:47:THR:HG21	2.43	0.54
36:5A:1537:TRP:HE3	36:5A:1751:LEU:HD13	1.72	0.54
49:5B:660:ASP:OD1	49:5B:928:ARG:NH1	2.40	0.54
1:1:105:U:C4	36:5A:1607:GLU:OE2	2.61	0.54
7:4e:83:ASN:HD22	13:4f:70:LEU:HD12	1.71	0.54
21:A2:115:PRO:HD2	21:A2:115:PRO:O	2.07	0.54
23:5C:866:SER:O	36:5A:357:ASN:ND2	2.41	0.54
33:B3:809:GLU:HA	33:B3:812:LYS:HB2	1.89	0.54
34:1g:42:ILE:CD1	34:1g:45:CYS:SG	2.96	0.54
36:5A:1038:SER:OG	36:5A:1438:VAL:CG1	2.56	0.54
39:5D:10:ASN:OD1	39:5D:13:GLN:NE2	2.41	0.54
7:2e:64:ILE:HG12	7:2e:71:ARG:HG2	1.89	0.54
43:K:784:ASP:OD2	43:K:886:LYS:HD3	2.08	0.54
44:4A:440:LEU:HD23	44:4A:444:GLU:HB3	1.90	0.54
49:5B:1195:ARG:NH1	49:5B:1292:PRO:O	2.39	0.54
1:1:31:C:H5'	9:1K:146:TYR:CD2	2.15	0.54
1:1:33:C:O4'	9:1K:138:LYS:N	2.41	0.54
6:4B:282:HIS:HD2	6:4B:284:LYS:H	1.54	0.54
9:1K:59:ARG:O	9:1K:60:ALA:HB3	2.07	0.54
16:22:100:PHE:HB3	11:21:68:PHE:HB2	1.90	0.54
24:5X:543:CYS:HB3	24:5X:570:MET:HE1	1.90	0.54
33:B3:353:PHE:O	33:B3:432:ARG:NH1	2.40	0.54
7:1e:33:VAL:HG12	7:1e:87:LEU:HD23	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5A:801:ILE:HD12	36:5A:1165:VAL:HG22	1.90	0.54
36:5A:1017:ILE:HD11	36:5A:1031:ILE:HG12	1.90	0.54
37:A3:98:HIS:HD1	47:A1:160:SER:N	2.05	0.54
45:4:52:U:O2	45:4:52:U:H2'	2.05	0.54
49:5B:2054:PRO:HG2	49:5B:2055:LEU:HD12	1.89	0.54
1:1:1:A:H2'	1:1:2:U:C6	2.43	0.53
6:4B:388:PHE:CZ	44:4A:425:ASN:O	2.61	0.53
21:A2:50:HIS:NE2	50:B1:1179:ASP:OD1	2.41	0.53
33:B3:91:GLU:OE2	33:B3:93:GLN:NE2	2.41	0.53
36:5A:899:MET:HE2	36:5A:1450:GLN:HB2	1.89	0.53
41:BP:97:ASP:N	41:BP:97:ASP:OD1	2.41	0.53
1:1:118:A:C2'	42:1C:2:PRO:CD	2.86	0.53
6:4B:437:ARG:HH21	44:4A:385:PRO:HG2	1.72	0.53
21:A2:115:PRO:CD	21:A2:176:TYR:C	2.82	0.53
24:5X:477:THR:CG2	24:5X:557:MET:HE1	2.38	0.53
24:5X:728:ILE:HG12	24:5X:729:ASP:N	2.23	0.53
29:5J:102:ASP:OD2	36:5A:86:ARG:CD	2.55	0.53
30:4D:108:GLU:C	43:K:947:SER:HB3	2.33	0.53
49:5B:1368:LEU:HD22	49:5B:1403:LYS:HE2	1.89	0.53
50:B1:546:ASP:N	50:B1:546:ASP:OD1	2.42	0.53
1:1:123:A:H8	16:12:13:PRO:CA	2.20	0.53
12:R:393:ASN:HA	12:R:396:ILE:HB	1.88	0.53
7:4e:52:GLU:CB	15:X:113:ASP:H	2.18	0.53
24:5X:379:ILE:HG22	24:5X:629[A]:ILE:HG13	0.57	0.53
7:1e:48:ILE:CG1	7:1e:59:ASP:HB2	2.37	0.53
16:12:34:GLN:HB3	16:12:111:ARG:NH1	2.24	0.53
43:K:772:MET:O	43:K:823:VAL:HG12	2.08	0.53
49:5B:1433:ASP:OD2	49:5B:1473:ARG:NH2	2.32	0.53
1:1:132:G:H5''	16:12:104:ASP:HB2	1.90	0.53
23:5C:241:ARG:HB3	23:5C:583:ASN:HD21	1.73	0.53
29:5J:362:VAL:HG11	29:5J:379:ALA:HB2	1.90	0.53
36:5A:996:LEU:HD13	36:5A:1047:VAL:HG21	1.89	0.53
43:K:723:GLU:H	43:K:723:GLU:CD	2.17	0.53
43:K:859:GLU:OE2	43:K:991:ARG:NH2	2.41	0.53
50:B1:457:ASN:ND2	50:B1:479:LEU:O	2.41	0.53
50:B1:493:LYS:O	50:B1:496:LYS:HB3	2.09	0.53
21:A2:162:PRO:O	21:A2:163:ASP:HB2	2.08	0.53
24:5X:744:ASN:OD1	24:5X:746:GLU:HG2	2.08	0.53
26:B5:24:ALA:O	50:B1:1262:ARG:NH1	2.41	0.53
36:5A:768:ASP:OD1	36:5A:768:ASP:N	2.41	0.53
41:BP:13:LYS:NZ	41:BP:48:GLU:OE1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:5g:64:GLY:HA2	34:5g:67:ILE:HD12	1.90	0.53
44:4A:447:LYS:CE	47:A1:430:UNK:HA	2.35	0.53
1:1:17:G:H2'	1:1:18:G:H8	1.74	0.53
9:1K:2:THR:HG22	9:1K:13:PHE:CZ	2.44	0.53
21:A2:163:ASP:O	21:A2:166:TRP:CZ3	2.61	0.53
23:5C:138:LEU:HD11	23:5C:179:VAL:HG22	1.91	0.53
23:5C:210:ASN:HB3	23:5C:636:TYR:HB2	1.91	0.53
23:5C:283:ASP:OD2	36:5A:362:ARG:NH1	2.41	0.53
34:1g:48:MET:SD	34:1g:54:GLN:HG3	2.48	0.53
36:5A:1292:GLU:HG2	49:5B:40:VAL:HG21	1.91	0.53
43:K:956:LEU:HD11	43:K:974:HIS:CE1	2.43	0.53
49:5B:1849:ILE:HD13	49:5B:1923:ILE:HG12	1.90	0.53
10:4C:357:ARG:CZ	45:4:17:A:N6	2.72	0.53
13:1f:49:GLU:HB2	13:1f:59:LEU:HD11	1.91	0.53
15:X:149:ARG:HG2	36:5A:1614:ILE:O	2.09	0.53
25:2b:69:LEU:O	5:23:73:LEU:N	2.40	0.53
33:B3:355:ASN:ND2	33:B3:400:GLU:OE2	2.41	0.53
33:B3:986:ILE:HG23	33:B3:1010:ILE:HD12	1.89	0.53
36:5A:919:ASP:OD2	36:5A:1012:LYS:NZ	2.41	0.53
34:2g:35:ASP:OD2	34:2g:39:ASN:ND2	2.42	0.53
43:K:679:ILE:N	43:K:679:ILE:HD12	2.24	0.53
49:5B:1991:GLU:O	49:5B:1995:ALA:N	2.41	0.53
50:B1:508:THR:HG22	50:B1:511:MET:HE3	1.91	0.53
1:1:135:A:C2	1:1:136:G:O2'	2.59	0.53
3:5O:146:ARG:NH2	17:5:7:U:HO2'	2.04	0.53
6:4B:361:GLN:NE2	44:4A:419:GLU:O	2.42	0.53
13:1f:5:LEU:HB3	7:1e:48:ILE:CG2	2.38	0.53
7:4e:33:VAL:HA	7:4e:86:LEU:O	2.09	0.53
17:5:91:U:O2'	11:51:61:ARG:NH1	2.42	0.53
29:5J:839:HIS:HB2	43:K:942:LYS:HZ3	1.74	0.53
30:4D:108:GLU:CD	43:K:926:ASN:HD22	2.17	0.53
25:2b:25:ARG:NH2	5:23:21:GLU:OE2	2.41	0.53
33:B3:903:TRP:CB	33:B3:930:LEU:HD23	2.39	0.53
7:1e:48:ILE:HD11	7:1e:59:ASP:CA	2.39	0.53
36:5A:1771:LEU:HD22	36:5A:1812:PRO:HG3	1.91	0.53
16:52:44:ILE:HG23	16:52:106:VAL:HG23	1.90	0.53
49:5B:912:ASN:OD1	49:5B:912:ASN:N	2.39	0.53
1:1:28:G:N2	9:1K:112:TYR:CD2	2.74	0.53
24:5X:378:SER:HG	24:5X:630:GLY:CA	1.87	0.53
27:1A:33:ILE:O	27:1A:36:GLN:HG2	2.09	0.53
28:S:565:GLU:CB	28:S:567:PRO:CD	2.87	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B3:185:LEU:HG	33:B3:235:LEU:HD11	1.90	0.53
7:1e:36:TYR:HB2	7:1e:83:ASN:O	2.09	0.53
36:5A:86:ARG:NH1	36:5A:89:LEU:HB2	2.24	0.53
36:5A:691:HIS:HA	47:A1:466:LEU:HD13	1.91	0.53
37:A3:354:GLU:CG	11:21:78:THR:HG22	2.39	0.53
38:U:134:TYR:HD1	38:U:145:GLY:HA3	0.73	0.53
49:5B:485:GLN:HB3	49:5B:515:MET:HE1	1.91	0.53
4:B4:13:ALA:HB2	37:A3:436:ARG:HH22	1.74	0.53
9:1K:42:ALA:N	9:1K:43:PRO:CD	2.71	0.53
15:X:120:VAL:CG1	13:4f:39:TYR:OH	2.56	0.53
21:A2:117:TYR:OH	21:A2:176:TYR:HB2	2.06	0.53
22:B2:460:PHE:HE2	22:B2:465:LEU:HD13	1.74	0.53
23:5C:780:CYS:O	23:5C:941:LYS:HE3	2.09	0.53
24:5X:540:LEU:HD13	24:5X:570:MET:SD	2.48	0.53
29:5J:158:LEU:CD1	36:5A:701:ILE:CD1	2.87	0.53
5:23:40:ASN:HD22	5:23:65:GLY:H	1.57	0.53
7:1e:80:LYS:O	7:1e:83:ASN:ND2	2.38	0.53
39:5D:8:LEU:HD13	39:5D:14:VAL:HG22	1.89	0.53
39:5D:8:LEU:HD12	39:5D:61:VAL:HG21	1.91	0.53
43:K:795:TYR:CD2	43:K:830:LEU:HD12	2.43	0.53
43:K:983:ILE:O	43:K:991:ARG:HD2	2.09	0.53
49:5B:1756:THR:O	49:5B:1762:ARG:NH2	2.42	0.53
1:1:57:G:O2'	1:1:58:C:H5'	2.09	0.52
29:5J:662:ARG:HA	29:5J:684:LEU:HD11	1.91	0.52
35:68:36:LEU:HB3	35:68:38:LEU:CD1	2.39	0.52
37:A3:133:GLU:OE2	11:21:73:SER:OG	2.25	0.52
39:5D:41:MET:HE2	39:5D:105:ALA:HA	1.91	0.52
43:K:841:VAL:HG21	43:K:868:TYR:CE1	2.45	0.52
49:5B:1033:GLU:OE2	49:5B:1058:LYS:NZ	2.43	0.52
1:1:100:C:O2'	1:1:101:C:H5'	2.08	0.52
2:6:89:U:H2'	2:6:90:G:H8	1.73	0.52
3:5O:203:ASP:HB3	3:5O:247:GLY:HA3	1.92	0.52
13:2f:11:LEU:HD11	7:2e:78:MET:HE2	1.90	0.52
36:5A:1625:SER:OG	36:5A:1626:CYS:N	2.43	0.52
36:5A:1941:ARG:NE	36:5A:2011:ILE:O	2.38	0.52
37:A3:153:LYS:HG2	37:A3:158:LEU:HD11	1.91	0.52
37:A3:348:LYS:HE3	11:21:73:SER:HA	1.89	0.52
49:5B:488:LEU:HD21	49:5B:501:LEU:HD13	1.92	0.52
3:5O:106:LYS:HE2	17:5:63:A:OP1	2.09	0.52
10:4C:231:ILE:HB	10:4C:252:LEU:HD23	1.90	0.52
14:66:66:ARG:HB2	14:66:69:ASN:HD22	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:5X:322:ASP:HA	24:5X:325:GLU:HG2	1.91	0.52
33:B3:12:THR:O	33:B3:34:ARG:NH1	2.42	0.52
33:B3:499:PHE:O	33:B3:525:ARG:NH1	2.42	0.52
33:B3:857:ALA:O	33:B3:861:GLN:NE2	2.34	0.52
39:5D:41:MET:HE1	39:5D:106:MET:HG2	1.92	0.52
46:2A:96:THR:HG23	46:2A:121:LEU:HB2	1.91	0.52
49:5B:602:GLU:OE1	49:5B:606:THR:OG1	2.23	0.52
50:B1:862:GLU:OE1	50:B1:865:ARG:NH1	2.42	0.52
1:1:8:C:P	24:5X:525:THR:HG21	2.49	0.52
6:4B:427:GLY:O	30:4D:125:ARG:NH2	2.38	0.52
10:4C:148:LYS:O	10:4C:152:ASN:ND2	2.35	0.52
10:4C:378:MET:HB3	36:5A:1503:TRP:HB2	1.92	0.52
29:5J:23:ARG:NH2	39:5D:87:ASN:OD1	2.43	0.52
25:2b:23:ASP:OD2	5:23:69:ARG:NH1	2.43	0.52
5:23:74:PRO:HG2	5:23:77:LEU:HD13	1.91	0.52
36:5A:1018:ASN:ND2	36:5A:1019:TYR:O	2.42	0.52
34:4g:35:ASP:OD2	34:4g:39:ASN:ND2	2.42	0.52
34:4g:64:GLY:HA2	34:4g:67:ILE:HD12	1.90	0.52
49:5B:444:GLU:OE2	49:5B:446:HIS:NE2	2.39	0.52
49:5B:1030:ARG:HH21	49:5B:1076:ALA:HB1	1.73	0.52
1:1:22:U:H6	1:1:22:U:C5'	2.21	0.52
3:5O:67:GLY:N	3:5O:87:ASP:OD1	2.43	0.52
24:5X:380:THR:O	24:5X:628:TYR:N	2.41	0.52
29:5J:708:PHE:HD2	29:5J:711:LEU:HD13	1.75	0.52
31:63:54:LEU:HB3	31:63:57:VAL:CG1	2.38	0.52
36:5A:85:LYS:NZ	36:5A:85:LYS:CB	2.73	0.52
36:5A:1618:LYS:NZ	36:5A:1663:ASP:OD1	2.37	0.52
16:52:32:LEU:HD22	16:52:56:VAL:HG11	1.90	0.52
44:4A:571:GLY:HA3	44:4A:583:VAL:O	2.10	0.52
1:1:7:A:C4'	24:5X:477:THR:HA	2.24	0.52
16:22:98:LYS:NZ	11:21:74:LEU:O	2.41	0.52
21:A2:117:TYR:CZ	21:A2:176:TYR:CB	2.92	0.52
29:5J:332:ILE:HD12	29:5J:349:ALA:HA	1.90	0.52
36:5A:838:LEU:HD13	36:5A:925:TYR:HA	1.92	0.52
36:5A:845:ARG:HD2	36:5A:1443:LYS:HE3	1.91	0.52
49:5B:691:GLY:HA3	49:5B:876:LEU:HD12	1.92	0.52
1:1:8:C:H4'	24:5X:528:ARG:N	2.24	0.52
8:I:101:C:O2'	41:BP:5:HIS:NE2	2.42	0.52
13:5f:21:VAL:HG22	13:5f:29:TYR:HB2	1.91	0.52
33:B3:88:VAL:HG11	33:B3:1156:CYS:HA	1.92	0.52
33:B3:862:TRP:HB3	33:B3:887:ALA:HB2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5A:1737:ASN:HB3	36:5A:1740:LEU:HB2	1.91	0.52
49:5B:720:GLN:NE2	49:5B:806:ILE:O	2.42	0.52
49:5B:1598:ILE:HG13	49:5B:1599:PRO:HD3	1.91	0.52
1:1:92:C:H2'	1:1:93:G:N7	2.10	0.52
16:22:95:TYR:O	37:A3:147:LEU:CG	2.55	0.52
23:5C:169:ASP:HB3	23:5C:174:GLU:HB3	1.92	0.52
23:5C:749:THR:OG1	23:5C:756:LYS:NZ	2.43	0.52
29:5J:266:THR:HG22	36:5A:824:PRO:HB2	1.92	0.52
7:1e:68:THR:OG1	7:1e:70:SER:N	2.42	0.52
36:5A:26:SER:OG	36:5A:27:GLU:N	2.42	0.52
39:5D:5:LEU:HD12	39:5D:60:LEU:HD21	1.91	0.52
44:4A:427:PRO:HB2	44:4A:639:LYS:NZ	2.21	0.52
11:21:61:ARG:NH2	11:21:63:ASN:OD1	2.42	0.52
46:2A:48:ASP:HA	46:2A:70:LEU:HB2	1.91	0.52
49:5B:987:ILE:HG21	49:5B:1098:ILE:HG13	1.92	0.52
50:B1:649:LYS:HZ3	50:B1:653:LYS:HD2	1.75	0.52
5:53:42:GLN:HE22	34:5g:11:LYS:HD3	1.74	0.52
24:5X:371:ARG:O	24:5X:375:GLU:HB2	2.10	0.52
24:5X:379:ILE:CG2	24:5X:629[B]:ILE:HG23	2.40	0.52
24:5X:540:LEU:HD23	24:5X:543:CYS:CB	2.39	0.52
36:5A:570:ASP:HB3	36:5A:573:GLN:HG3	1.91	0.52
36:5A:1212:GLY:HA3	36:5A:1280:ASN:HB2	1.92	0.52
36:5A:1508:GLY:H	36:5A:1752:GLN:NE2	1.89	0.52
37:A3:356:ARG:HG2	11:21:75:PRO:HG3	1.92	0.52
46:2A:137:TYR:HB2	46:2A:158:ALA:HB1	1.90	0.52
49:5B:419:GLY:O	49:5B:892:GLN:NE2	2.43	0.52
3:5O:160:ALA:HB3	3:5O:166:LEU:H	1.74	0.52
5:13:70:PHE:C	5:13:71:LEU:HD12	2.34	0.52
23:5C:660:VAL:HG22	23:5C:878:ILE:HD13	1.91	0.52
23:5C:761:SER:OG	23:5C:803:ARG:NH1	2.43	0.52
30:4D:91:ARG:NH2	44:4A:444:GLU:OE2	2.42	0.52
33:B3:83:ASP:OD2	33:B3:1158:ARG:NE	2.43	0.52
5:43:62:TYR:HD2	34:4g:70:LEU:HD23	1.75	0.52
43:K:905:LYS:NZ	43:K:985:MET:SD	2.83	0.52
49:5B:1321:TYR:OH	49:5B:1361:GLU:OE1	2.22	0.52
49:5B:1829:ILE:HA	49:5B:1832:PHE:HB2	1.92	0.52
49:5B:1947:GLN:HE22	49:5B:2109:MET:HE2	1.74	0.52
1:1:11:G:C8	24:5X:507:SER:OG	2.61	0.51
1:1:73:C:N3	1:1:74:C:C4	2.79	0.51
23:5C:779:LEU:O	23:5C:938:ARG:NH1	2.37	0.51
16:42:47:ARG:NH2	45:4:126:A:OP2	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:B5:25:ASP:OD1	50:B1:1259:ARG:NH2	2.39	0.51
32:2:175:G:H2'	32:2:176:G:H8	1.74	0.51
36:5A:397:ASN:N	36:5A:397:ASN:OD1	2.41	0.51
25:4b:53:PRO:HB3	25:4b:60:GLU:HB2	1.91	0.51
46:2A:81:GLU:HA	46:2A:108:PRO:HB3	1.93	0.51
16:22:97:SER:OG	11:21:72:ASP:OD1	2.27	0.51
21:A2:163:ASP:O	21:A2:165:ARG:HG2	2.10	0.51
23:5C:348:TYR:OH	23:5C:367:ARG:NH1	2.43	0.51
29:5J:628:ARG:O	29:5J:632:ALA:N	2.41	0.51
11:51:29:ILE:HA	11:51:40:LEU:HD23	1.93	0.51
33:B3:170:VAL:HG23	33:B3:184:CYS:HB3	1.91	0.51
33:B3:245:PRO:O	33:B3:258:TYR:OH	2.28	0.51
33:B3:500:LEU:HB2	33:B3:525:ARG:HH12	1.74	0.51
33:B3:1011:TRP:HB2	33:B3:1025:ALA:HB3	1.92	0.51
34:5g:35:ASP:OD2	34:5g:39:ASN:ND2	2.42	0.51
45:4:91:A:H2	45:4:110:G:H22	1.58	0.51
45:4:114:U:P	45:4:114:U:C6	3.02	0.51
23:5C:106:GLU:O	23:5C:106:GLU:HG2	2.11	0.51
23:5C:383:GLN:HG3	23:5C:395:THR:HG21	1.93	0.51
24:5X:745:ILE:O	24:5X:749:ILE:HG12	2.10	0.51
36:5A:710:LEU:HD22	39:5D:4:MET:HE3	1.36	0.51
38:U:407:GLU:O	38:U:407:GLU:HG2	2.10	0.51
40:64:71:ILE:HB	40:64:72:PRO:HD2	1.93	0.51
3:5O:231:MET:HE1	3:5O:264:VAL:HG22	1.91	0.51
15:X:132:SER:O	28:S:713:VAL:HG21	2.11	0.51
22:B2:533:ILE:HG21	50:B1:1130:PRO:HB2	1.92	0.51
23:5C:137:HIS:HA	23:5C:238:ASN:HB3	1.93	0.51
23:5C:645:ARG:NH2	36:5A:321:ASN:O	2.42	0.51
24:5X:536:ARG:HB3	34:1g:10:LYS:CG	2.41	0.51
13:4f:28:GLU:HB2	13:4f:50:TYR:HB2	1.92	0.51
33:B3:736:TYR:OH	33:B3:763:ARG:NH1	2.44	0.51
7:1e:23:ARG:HD3	7:1e:27:ASN:OD1	2.11	0.51
36:5A:97:HIS:ND1	36:5A:649:GLU:OE2	2.33	0.51
36:5A:221:ASN:HB2	36:5A:227:ARG:H	1.75	0.51
36:5A:1606:ILE:HG12	36:5A:1637:TRP:HZ2	1.75	0.51
50:B1:923:LYS:NZ	50:B1:966:GLN:OE1	2.44	0.51
1:1:30:U:C2	9:1K:108:ALA:HB3	2.46	0.51
6:4B:364:HIS:C	44:4A:423:GLN:NE2	2.68	0.51
11:41:29:ILE:HA	11:41:40:LEU:HD23	1.92	0.51
26:B5:55:ILE:HG21	33:B3:408:LEU:HD21	1.91	0.51
28:S:738:SER:HB2	28:S:743:THR:HG23	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:4D:12:PRO:HB2	30:4D:126:LEU:HB3	1.93	0.51
13:4f:41:ASN:ND2	45:4:118:A:N1	2.48	0.51
36:5A:1219:GLU:O	36:5A:1222:LYS:NZ	2.44	0.51
36:5A:1413:ASP:OD2	49:5B:59:THR:OG1	2.27	0.51
36:5A:1543:ASN:HD21	36:5A:1562:MET:HA	1.75	0.51
38:U:246:ASN:ND2	38:U:520:LEU:O	2.33	0.51
43:K:957:ALA:C	43:K:958:ASP:O	2.50	0.51
49:5B:522:GLY:HA2	49:5B:525:ILE:HD11	1.93	0.51
1:1:29:A:C1'	9:1K:200:ARG:HD2	2.39	0.51
18:67:26:LYS:HB2	18:67:83:LEU:HG	1.92	0.51
24:5X:667:ILE:HA	24:5X:733[A]:VAL:CG1	2.40	0.51
24:5X:768:LEU:HD22	24:5X:776:PHE:CE1	2.46	0.51
36:5A:1002:ASP:OD2	36:5A:1004:ASN:ND2	2.39	0.51
36:5A:1057:ARG:NH1	36:5A:1060:GLU:OE1	2.44	0.51
36:5A:1551:PHE:O	36:5A:1553:VAL:HG23	2.11	0.51
36:5A:2188:LEU:O	36:5A:2251:TYR:OH	2.29	0.51
44:4A:447:LYS:CG	47:A1:429:UNK:O	2.59	0.51
49:5B:2060:ARG:NH2	49:5B:2111:ASP:O	2.44	0.51
1:1:101:C:H2'	1:1:102:A:O4'	2.10	0.51
7:5e:44:GLU:HB2	7:5e:62:GLU:HG2	1.93	0.51
15:X:141:MET:HB2	28:S:734:HIS:HA	1.92	0.51
23:5C:300:LEU:HG	23:5C:306:ASN:HB3	1.92	0.51
24:5X:432:ILE:HG21	24:5X:609:MET:CE	2.41	0.51
29:5J:154:GLU:HA	29:5J:157:TRP:HD1	1.75	0.51
33:B3:80:VAL:HB	33:B3:88:VAL:HG13	1.92	0.51
36:5A:1927:ILE:HD12	36:5A:1931:THR:HG23	1.92	0.51
38:U:324:LEU:HD21	38:U:452:ILE:HG21	1.93	0.51
1:1:32:A:H1'	9:1K:135:VAL:CG1	2.14	0.51
3:5O:263:ASP:OD1	3:5O:263:ASP:N	2.39	0.51
6:4B:332:HIS:NE2	6:4B:377:GLY:O	2.41	0.51
29:5J:885:GLU:HG3	29:5J:897:VAL:HG11	1.93	0.51
13:4f:14:LEU:HD13	13:4f:19:VAL:HG11	1.93	0.51
33:B3:635:ALA:HB3	33:B3:669:LEU:HD23	1.92	0.51
36:5A:139:VAL:HG11	36:5A:212:PRO:HG2	1.92	0.51
36:5A:694:LEU:HD13	47:A1:463:GLU:CD	2.26	0.51
36:5A:1129:ASN:ND2	36:5A:1170:TRP:O	2.42	0.51
43:K:772:MET:HE3	43:K:827:LYS:CE	2.41	0.51
49:5B:1068:SER:HB2	49:5B:1070:LEU:HG	1.92	0.51
21:A2:161:PRO:O	21:A2:164:ARG:HG3	2.11	0.51
23:5C:304:LEU:O	23:5C:437:HIS:NE2	2.40	0.51
23:5C:473:PRO:HB2	23:5C:571:ASN:HD21	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:5X:485:GLU:HA	24:5X:523:ILE:HD13	1.93	0.51
16:42:53:LEU:O	16:42:70:VAL:HA	2.11	0.51
7:1e:86:LEU:HD12	7:1e:87:LEU:N	2.26	0.51
36:5A:852:VAL:C	36:5A:854:SER:N	2.57	0.51
36:5A:913:PRO:HA	36:5A:916:LYS:HB2	1.93	0.51
36:5A:1184:ASN:OD1	36:5A:1195:ARG:NH1	2.39	0.51
34:2g:15:LYS:HE2	34:2g:76:VAL:HA	1.91	0.51
49:5B:131:ILE:HG12	49:5B:697:ALA:HB1	1.92	0.51
3:5O:127:ALA:HB2	3:5O:157:CYS:HB3	1.91	0.51
6:4B:369:TYR:OH	30:4D:128:VAL:O	2.29	0.51
9:1K:85:GLU:HA	9:1K:88:MET:CE	2.41	0.51
15:X:119:LYS:HD3	45:4:116:G:C5'	2.41	0.51
21:A2:117:TYR:CZ	21:A2:176:TYR:HB3	2.45	0.51
23:5C:571:ASN:HB3	23:5C:574:ALA:HB2	1.93	0.51
24:5X:604:MET:HE3	24:5X:621:LEU:HD11	1.93	0.51
29:5J:89:PHE:O	29:5J:90:SER:CB	2.58	0.51
36:5A:419:ARG:NH1	36:5A:423:ASP:O	2.44	0.51
36:5A:488:ASP:OD2	36:5A:565:ARG:NH1	2.33	0.51
36:5A:881:ILE:HG23	36:5A:918:THR:HG23	1.91	0.51
36:5A:1586:HIS:NE2	36:5A:1628:ASP:OD2	2.44	0.51
49:5B:259:HIS:HD2	49:5B:261:ARG:H	1.58	0.51
1:1:118:A:H8	42:1C:3:LYS:N	2.01	0.50
2:6:74:U:H2'	2:6:75:G:H8	1.76	0.50
6:4B:332:HIS:HB2	6:4B:337:PHE:HB2	1.94	0.50
9:1K:45:ILE:N	9:1K:45:ILE:CD1	2.73	0.50
13:1f:25:TRP:HB2	13:1f:27:MET:HE1	1.93	0.50
17:5:72:U:O2	23:5C:405:LYS:NZ	2.39	0.50
46:2A:21:ASP:HB3	46:2A:45:ASP:HB2	1.92	0.50
49:5B:1901:ARG:HD2	49:5B:1961:LYS:HE3	1.92	0.50
1:1:118:A:N3	1:1:118:A:C3'	2.73	0.50
7:5e:32:GLN:OE1	7:5e:88:GLN:NE2	2.43	0.50
12:R:446:TYR:CG	39:5D:86:ARG:NE	2.79	0.50
19:62:48:PRO:HG2	19:62:50:LYS:HB3	1.92	0.50
19:62:66:VAL:HG11	35:68:68:ALA:HA	1.93	0.50
23:5C:137:HIS:HB2	23:5C:239:THR:HG23	1.92	0.50
24:5X:352:TRP:O	24:5X:355:ARG:NE	2.38	0.50
24:5X:530:ILE:HD11	24:5X:565:LYS:HB3	1.94	0.50
33:B3:291:ALA:HB2	33:B3:339:MET:HB2	1.93	0.50
33:B3:528:ARG:HH12	33:B3:572:GLY:HA3	1.75	0.50
5:43:19:THR:HA	5:43:28:TYR:O	2.11	0.50
36:5A:65:HIS:CE1	36:5A:483:GLN:OE1	2.62	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:U:457:ARG:NH1	38:U:470:THR:O	2.37	0.50
43:K:956:LEU:O	43:K:958:ASP:O	2.30	0.50
44:4A:505:ALA:O	44:4A:509:LYS:HB2	2.11	0.50
49:5B:517:MET:HE3	49:5B:613:ILE:HD12	1.93	0.50
50:B1:758:ASP:OD1	50:B1:758:ASP:N	2.44	0.50
1:1:123:A:N3	1:1:123:A:C2'	2.73	0.50
13:2f:11:LEU:HD13	13:2f:36:VAL:HG11	1.93	0.50
24:5X:380:THR:HG22	24:5X:628:TYR:HD2	1.66	0.50
5:43:32:LEU:HD11	5:43:35:ALA:HB2	1.93	0.50
36:5A:1255:THR:HG22	36:5A:1257:THR:H	1.77	0.50
36:5A:1318:THR:HB	36:5A:1324:GLY:HA3	1.94	0.50
37:A3:356:ARG:HD2	11:21:75:PRO:HB3	1.92	0.50
44:4A:447:LYS:CE	47:A1:431:UNK:N	2.68	0.50
17:5:30:A:OP1	36:5A:595:LYS:NZ	2.44	0.50
23:5C:950:SER:HB2	23:5C:956:PRO:HG2	1.94	0.50
36:5A:839:LEU:HD22	36:5A:878:LEU:HG	1.94	0.50
38:U:134:TYR:CD1	38:U:145:GLY:HA2	2.29	0.50
1:1:92:C:H2'	1:1:92:C:O2	2.09	0.50
8:I:7:A:C6	8:I:8:C:C4	2.99	0.50
19:62:69:TYR:HB3	31:63:85:LEU:HD11	1.92	0.50
32:2:12:G:C5	32:2:13:C:C5	2.99	0.50
36:5A:1622:MET:HE1	36:5A:1666:LEU:O	2.12	0.50
36:5A:2074:ARG:O	36:5A:2078:ILE:HG13	2.11	0.50
16:52:54:GLY:HA3	16:52:70:VAL:HG12	1.92	0.50
43:K:788:HIS:O	43:K:792:VAL:HG23	2.12	0.50
43:K:841:VAL:HG21	43:K:868:TYR:OH	2.11	0.50
43:K:853:ARG:HD2	43:K:891:GLY:O	2.12	0.50
50:B1:1213:ASN:OD1	50:B1:1249:TYR:OH	2.27	0.50
1:1:20:G:O3'	9:1K:67:MET:HG3	2.12	0.50
1:1:122:C:O2'	1:1:123:A:OP2	2.28	0.50
2:6:54:G:P	10:4C:356:GLY:HA2	2.52	0.50
6:4B:232:ARG:NH2	30:4D:74:GLU:OE1	2.44	0.50
9:1K:44:TYR:CE2	16:12:51:LYS:HG3	2.45	0.50
23:5C:692:LEU:HD22	23:5C:696:LEU:HD23	1.92	0.50
29:5J:158:LEU:CD1	36:5A:701:ILE:CG1	2.90	0.50
29:5J:472:LYS:O	29:5J:476:ALA:HB2	2.12	0.50
45:4:59:U:H2'	45:4:60:A:H8	1.76	0.50
49:5B:610:ARG:NH2	49:5B:645:ASP:O	2.45	0.50
49:5B:2013:ARG:HB3	49:5B:2052:ILE:HD11	1.94	0.50
1:1:124:U:OP1	1:1:124:U:H6	1.95	0.50
13:1f:18:PRO:HG2	13:1f:75:VAL:HG22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:X:126:ALA:HA	16:42:24:PHE:CD1	2.46	0.50
27:1A:33:ILE:CG2	27:1A:72:MET:HE2	2.38	0.50
33:B3:1093:MET:HE2	33:B3:1173:VAL:HG21	1.93	0.50
7:1e:20:LEU:HD12	7:1e:20:LEU:O	2.11	0.50
36:5A:161:PHE:HB3	36:5A:625:PRO:HG2	1.92	0.50
36:5A:292:ASP:OD1	36:5A:1139:ARG:NE	2.44	0.50
36:5A:759:GLU:OE2	36:5A:762:ARG:NH2	2.45	0.50
36:5A:1544:ARG:NH1	36:5A:1672:ASP:OD2	2.42	0.50
34:4g:42:ILE:HD13	34:4g:62:ILE:HG13	1.94	0.50
49:5B:617:ILE:HG22	49:5B:652:SER:HB2	1.93	0.50
1:1:15:G:N2	1:1:16:G:N2	2.60	0.50
24:5X:591:ASN:O	24:5X:594[B]:SER:HB3	2.12	0.50
29:5J:438:LEU:HD11	29:5J:465:HIS:HB3	1.93	0.50
33:B3:552:ARG:NH2	33:B3:568:MET:O	2.44	0.50
34:1g:33:GLY:HA3	7:1e:15:VAL:O	2.12	0.50
36:5A:221:ASN:N	36:5A:227:ARG:O	2.45	0.50
36:5A:265:THR:HG22	36:5A:314:ILE:HG13	1.92	0.50
37:A3:140:LEU:H	37:A3:341:THR:CG2	2.24	0.50
37:A3:357:GLU:CA	11:21:75:PRO:CG	2.84	0.50
38:U:233:ALA:HB1	38:U:317:GLN:HB3	1.94	0.50
44:4A:569:LEU:HD23	44:4A:586:GLY:HA3	1.92	0.50
49:5B:1156:LEU:HB2	49:5B:1161:ILE:HG13	1.93	0.50
49:5B:1227:ASP:OD1	49:5B:1227:ASP:N	2.40	0.50
49:5B:1626:PRO:HA	49:5B:1629:ARG:HB2	1.94	0.50
10:4C:236:GLY:O	10:4C:240:ASN:ND2	2.44	0.50
15:X:138:ARG:HH12	36:5A:1614:ILE:CD1	2.25	0.50
20:2B:39:ASP:HB3	20:2B:55:ILE:HD12	1.93	0.50
22:B2:587:HIS:O	50:B1:1249:TYR:OH	2.29	0.50
23:5C:843:VAL:HG22	23:5C:871:ILE:HD11	1.94	0.50
36:5A:843:LEU:HB3	36:5A:867:ILE:HG23	1.92	0.50
36:5A:1804:ASN:HD22	36:5A:1907:LEU:HA	1.77	0.50
1:1:92:C:O2'	1:1:93:G:C8	2.65	0.49
2:6:103:U:O4'	35:68:65:ASP:CG	2.55	0.49
9:1K:46:ARG:CG	9:1K:47:GLU:N	2.75	0.49
11:41:24:GLN:HE22	16:42:94:ARG:HH12	1.59	0.49
11:41:61:ARG:NH2	45:4:123:U:OP1	2.38	0.49
15:X:114:SER:HA	45:4:119:A:O2'	2.11	0.49
16:22:62:HIS:O	13:2f:65:ARG:NH1	2.45	0.49
18:67:82:VAL:HG12	40:64:65:THR:HG21	1.93	0.49
13:2f:65:ARG:NH2	32:2:104:U:O2'	2.38	0.49
23:5C:164:ASP:N	23:5C:164:ASP:OD1	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:5J:158:LEU:HD12	36:5A:701:ILE:HG21	1.92	0.49
25:2b:14:ASP:OD2	25:2b:32:LYS:NZ	2.44	0.49
33:B3:140:LEU:HD22	33:B3:157:PRO:HB2	1.94	0.49
33:B3:707:GLN:N	33:B3:752:GLU:OE2	2.45	0.49
33:B3:932:ASN:C	33:B3:934:GLY:N	2.70	0.49
36:5A:504:LEU:HD11	36:5A:551:LEU:HD12	1.93	0.49
38:U:143:PHE:O	38:U:144:GLN:C	2.53	0.49
39:5D:7:HIS:HA	39:5D:60:LEU:O	2.11	0.49
1:1:32:A:C2	9:1K:135:VAL:CG2	2.88	0.49
2:6:105:U:C2	31:63:49:HIS:HB3	2.47	0.49
5:13:83:LEU:HD12	5:13:83:LEU:N	2.27	0.49
23:5C:886:ASP:OD1	24:5X:290:TYR:OH	2.28	0.49
24:5X:362:LEU:HG	24:5X:391:ARG:NE	2.19	0.49
27:1A:66:THR:O	27:1A:70:ARG:HG2	2.12	0.49
28:S:738:SER:HA	45:4:66:A:H5'	1.94	0.49
33:B3:931:VAL:O	33:B3:932:ASN:HB2	2.11	0.49
33:B3:943:THR:HG21	33:B3:977:LEU:HB2	1.94	0.49
36:5A:1070:ASP:OD1	36:5A:1070:ASP:N	2.36	0.49
49:5B:1222:TRP:NE1	49:5B:1273:ASP:OD2	2.38	0.49
7:5e:88:GLN:HB2	34:5g:57:ILE:HG21	1.95	0.49
21:A2:155:TYR:O	21:A2:164:ARG:NH2	2.45	0.49
23:5C:401:ILE:HD11	23:5C:423:PHE:HB2	1.95	0.49
23:5C:666:VAL:HG22	23:5C:787:VAL:HG22	1.95	0.49
24:5X:163:PHE:H	49:5B:1749:GLN:HE22	1.59	0.49
36:5A:701:ILE:O	36:5A:705:LYS:HG2	2.12	0.49
36:5A:1104:ASP:OD1	36:5A:1107:ARG:NH2	2.44	0.49
37:A3:357:GLU:HA	11:21:75:PRO:CG	2.40	0.49
49:5B:604:THR:O	49:5B:607:GLN:NE2	2.43	0.49
1:1:29:A:H1'	9:1K:200:ARG:HD2	1.93	0.49
1:1:90:U:O2'	1:1:91:G:OP1	2.24	0.49
1:1:91:G:O2'	1:1:92:C:O5'	2.30	0.49
1:1:137:U:H2'	9:1K:35:ASN:HB3	1.93	0.49
7:4e:65:HIS:O	7:4e:69:LYS:N	2.45	0.49
14:66:52:VAL:CB	14:66:56:LEU:HD11	2.42	0.49
5:23:23:ASN:N	5:23:67:LYS:O	2.46	0.49
5:43:23:ASN:OD1	5:43:69:ARG:NH2	2.45	0.49
36:5A:85:LYS:NZ	36:5A:85:LYS:HB2	2.28	0.49
36:5A:2131:VAL:HG13	36:5A:2172:MET:HG2	1.94	0.49
38:U:277:ARG:HD2	38:U:303:ALA:HB2	1.94	0.49
43:K:924:ASP:OD1	43:K:928:ASN:HB2	2.11	0.49
1:1:8:C:P	24:5X:478:ARG:CB	2.97	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:33:C:H42	9:1K:139:ARG:HH21	1.59	0.49
6:4B:294:VAL:HG21	6:4B:307:LEU:HB3	1.93	0.49
15:X:119:LYS:HB2	45:4:116:G:H4'	1.94	0.49
24:5X:768:LEU:HD22	24:5X:776:PHE:HE1	1.77	0.49
26:B5:58:ASN:O	33:B3:856:LYS:NZ	2.45	0.49
36:5A:707:ARG:CZ	36:5A:711:GLN:HE22	2.25	0.49
38:U:455:ILE:HD13	38:U:472:VAL:HG21	1.94	0.49
49:5B:517:MET:HG2	49:5B:538:ILE:HG21	1.94	0.49
50:B1:1174:GLU:HB2	50:B1:1214:TYR:HE2	1.78	0.49
3:5O:69:VAL:HG11	3:5O:351:LEU:HD21	1.94	0.49
7:4e:36:TYR:N	7:4e:83:ASN:O	2.41	0.49
21:A2:113:GLY:O	21:A2:114:ARG:HB3	2.12	0.49
21:A2:149:HIS:CD2	21:A2:208:LEU:HD22	2.47	0.49
23:5C:126:SER:HA	23:5C:129:ILE:HD12	1.94	0.49
25:1b:58:GLN:HG3	25:1b:59:ALA:H	1.77	0.49
31:63:18:LEU:HA	31:63:21:ILE:HG22	1.95	0.49
35:68:59:LEU:HD22	40:64:71:ILE:HD11	1.93	0.49
7:1e:59:ASP:OD2	7:1e:76:ARG:CZ	2.59	0.49
44:4A:465:ARG:HH22	45:4:56:U:H4'	1.77	0.49
49:5B:79:HIS:O	49:5B:83:LYS:HB2	2.13	0.49
49:5B:1666:THR:O	49:5B:1666:THR:OG1	2.30	0.49
50:B1:1185:ARG:NH2	50:B1:1221:GLU:OE1	2.35	0.49
1:1:132:G:O6	11:11:66:ARG:NH1	2.46	0.49
1:1:137:U:H1'	9:1K:36:GLN:CG	2.43	0.49
3:5O:90:ILE:HB	3:5O:105:LEU:HB2	1.95	0.49
5:53:23:ASN:O	5:53:69:ARG:NH2	2.46	0.49
23:5C:531:TRP:HB3	23:5C:538:HIS:HB3	1.94	0.49
29:5J:567:LEU:HD11	29:5J:576:VAL:HG12	1.95	0.49
29:5J:751:ARG:NH1	29:5J:782:GLU:OE2	2.45	0.49
36:5A:86:ARG:NH1	36:5A:89:LEU:CD1	2.65	0.49
36:5A:693:ILE:HG21	36:5A:709:ILE:HD13	1.95	0.49
36:5A:1872:LEU:HB3	36:5A:1884:ILE:HD13	1.95	0.49
47:A1:220:ILE:HG22	47:A1:222:PRO:HD2	1.95	0.49
49:5B:491:ALA:O	49:5B:647:ARG:NH2	2.45	0.49
49:5B:597:THR:OG1	49:5B:634:ARG:NH1	2.45	0.49
50:B1:1166:ILE:O	50:B1:1170:THR:OG1	2.28	0.49
1:1:32:A:N1	9:1K:133:HIS:HB3	2.28	0.49
3:5O:166:LEU:HD23	3:5O:178:LEU:HD11	1.94	0.49
18:67:82:VAL:CG1	40:64:65:THR:HG21	2.43	0.49
21:A2:114:ARG:C	21:A2:177:GLU:HB2	2.37	0.49
22:B2:503:HIS:CD2	22:B2:510:TYR:HB2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B3:1107:THR:OG1	33:B3:1108:THR:N	2.46	0.49
5:23:23:ASN:OD1	5:23:69:ARG:NH2	2.42	0.49
36:5A:1490:PHE:O	36:5A:1493:THR:OG1	2.30	0.49
38:U:352:GLY:HA2	38:U:446:LYS:HD3	1.94	0.49
43:K:698:PHE:HB2	43:K:725:MET:HE1	1.95	0.49
43:K:862:ILE:HD11	43:K:923:PHE:HE2	1.77	0.49
25:4b:17:MET:O	25:4b:28:ILE:HA	2.12	0.49
45:4:109:G:H2'	45:4:110:G:H8	1.77	0.49
49:5B:1143:ILE:HG12	49:5B:1165:ILE:HD12	1.94	0.49
6:4B:290:ASP:OD1	6:4B:293:ASP:CB	2.61	0.49
6:4B:290:ASP:OD1	6:4B:293:ASP:HB2	2.13	0.49
6:4B:388:PHE:CZ	44:4A:427:PRO:HD3	2.48	0.49
6:4B:390:ARG:NH2	6:4B:399:CYS:SG	2.85	0.49
13:1f:3:LEU:CG	13:1f:4:PRO:HD2	2.43	0.49
7:4e:52:GLU:HB3	15:X:112:PHE:HA	1.95	0.49
14:66:66:ARG:CG	31:63:50:LEU:HD22	2.43	0.49
24:5X:536:ARG:O	34:1g:10:LYS:NZ	2.40	0.49
24:5X:551:ALA:HB3	24:5X:606[A]:THR:HG22	1.95	0.49
29:5J:530:ILE:O	29:5J:543:TRP:NE1	2.43	0.49
33:B3:930:LEU:HG	33:B3:930:LEU:O	2.13	0.49
38:U:177:ASP:OD1	38:U:177:ASP:N	2.43	0.49
38:U:530:LEU:HG	38:U:535:VAL:HG22	1.93	0.49
43:K:773:ASN:O	43:K:777:VAL:HG12	2.13	0.49
46:2A:17:ASN:HD21	46:2A:21:ASP:HB2	1.77	0.49
46:2A:34:ILE:HD11	46:2A:54:ILE:HD13	1.95	0.49
49:5B:537:LYS:N	49:5B:608:LEU:O	2.46	0.49
49:5B:1418:LEU:HD23	49:5B:1421:LYS:HD3	1.95	0.49
1:1:10:U:H5	24:5X:506:ILE:O	1.95	0.49
6:4B:322:HIS:CE1	6:4B:348:ARG:HD2	2.48	0.49
6:4B:446:PRO:HD3	44:4A:668:HIS:HB2	1.95	0.49
9:1K:50:ASP:N	9:1K:51:PRO:HD2	2.28	0.49
24:5X:485:GLU:O	24:5X:489:ILE:HG12	2.13	0.49
29:5J:161:PRO:O	36:5A:712:HIS:NE2	2.45	0.49
29:5J:347:LEU:HD11	29:5J:374:ARG:HB3	1.94	0.49
33:B3:330:PHE:O	33:B3:394:ASN:ND2	2.46	0.49
36:5A:713:LEU:HD12	36:5A:739:ILE:HG12	1.94	0.49
36:5A:2086:ARG:NH1	36:5A:2222:SER:O	2.45	0.49
38:U:122:LYS:HE3	38:U:193:LEU:HD11	1.95	0.49
42:1C:13:LEU:HD23	42:1C:20:VAL:HG12	1.95	0.49
50:B1:652:CYS:O	50:B1:692:HIS:NE2	2.46	0.49
4:B4:27:PRO:HG3	22:B2:600:ARG:HG2	1.93	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:4B:284:LYS:O	6:4B:289:LEU:N	2.45	0.48
16:22:29:LEU:HD23	16:22:32:LEU:HD12	1.95	0.48
23:5C:213:ASP:O	23:5C:216:THR:OG1	2.29	0.48
28:S:565:GLU:HB2	28:S:567:PRO:HD3	1.91	0.48
29:5J:646:LEU:HA	29:5J:649:VAL:HG22	1.95	0.48
30:4D:34:GLN:O	30:4D:105:THR:OG1	2.31	0.48
33:B3:996:ILE:HG22	33:B3:999:ARG:HB2	1.95	0.48
5:23:2:SER:OG	5:23:3:ILE:N	2.43	0.48
5:23:40:ASN:ND2	5:23:65:GLY:H	2.11	0.48
45:4:94:A:O2'	45:4:95:C:H5'	2.13	0.48
14:66:74:SER:HB2	48:65:72:ILE:HG22	1.95	0.48
23:5C:129:ILE:HG12	23:5C:199:LEU:HD23	1.95	0.48
23:5C:262:ARG:HA	23:5C:266:GLU:HG3	1.95	0.48
24:5X:304:ILE:O	24:5X:312:GLN:NE2	2.39	0.48
24:5X:370:TRP:CZ3	24:5X:389:PRO:HG2	2.48	0.48
26:B5:51:ASN:HD22	33:B3:353:PHE:HE1	1.61	0.48
36:5A:60:ASP:OD1	36:5A:484:SER:C	2.53	0.48
36:5A:279:PHE:HE2	36:5A:456:LEU:HG	1.78	0.48
36:5A:1776:ILE:HG13	36:5A:1811:ASN:HD21	1.78	0.48
16:52:43:LEU:HB3	16:52:110:LEU:HD23	1.95	0.48
40:64:15:MET:HE2	40:64:71:ILE:HG22	1.95	0.48
5:13:68:ILE:HG21	5:13:71:LEU:HD11	1.94	0.48
6:4B:366:MET:H	6:4B:386:ASP:HB3	1.76	0.48
15:X:101:ILE:HD13	15:X:103:MET:HE2	1.95	0.48
13:4f:47:THR:HG23	13:4f:59:LEU:HB2	1.94	0.48
33:B3:339:MET:HG2	33:B3:349:VAL:HG12	1.95	0.48
33:B3:800:ILE:HG22	33:B3:866:ILE:HG12	1.94	0.48
38:U:132:ASN:O	38:U:145:GLY:CA	2.60	0.48
43:K:871:ASP:O	43:K:875:VAL:HG23	2.12	0.48
44:4A:547:ARG:NH1	44:4A:680:GLU:OE1	2.46	0.48
49:5B:633:ALA:O	49:5B:637:ARG:HB2	2.13	0.48
49:5B:1186:LEU:HB3	49:5B:1202:LEU:HD11	1.96	0.48
1:1:12:G:O6	1:1:122:C:N3	2.47	0.48
3:5O:116:HIS:HB3	3:5O:159:PRO:HD3	1.96	0.48
25:2b:18:ARG:HG3	25:2b:26:ILE:HG23	1.94	0.48
36:5A:96:PRO:HG3	36:5A:648:LEU:HB2	1.96	0.48
36:5A:1532:ARG:HG2	36:5A:1568:THR:HG23	1.95	0.48
36:5A:1625:SER:OG	36:5A:1663:ASP:OD2	2.31	0.48
38:U:357:PHE:HB2	38:U:441:ARG:HB2	1.96	0.48
1:1:73:C:O2'	1:1:74:C:H5'	2.14	0.48
2:6:71:G:H21	30:4D:111:GLN:HE22	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B4:30:TRP:CB	22:B2:600:ARG:HH22	2.27	0.48
6:4B:284:LYS:HE3	6:4B:288:SER:OG	2.12	0.48
5:53:79:ASN:ND2	23:5C:115:GLU:OE2	2.45	0.48
21:A2:73:THR:O	21:A2:79:GLN:NE2	2.47	0.48
24:5X:282:THR:HG22	36:5A:274:PRO:HA	1.95	0.48
24:5X:375:GLU:OE2	36:5A:162:LYS:N	2.45	0.48
29:5J:795:ILE:HA	29:5J:798:THR:HG22	1.94	0.48
34:1g:66:SER:OG	7:1e:85:THR:CG2	2.45	0.48
36:5A:1510:GLU:HB3	36:5A:1513:MET:CG	2.43	0.48
46:2A:73:ASN:HA	46:2A:97:ASN:HB3	1.96	0.48
49:5B:928:ARG:NH2	49:5B:932:SER:OG	2.45	0.48
49:5B:969:LEU:HD22	49:5B:985:GLY:HA2	1.95	0.48
49:5B:1836:LEU:HD22	49:5B:1840:THR:HG21	1.94	0.48
1:1:8:C:C5	24:5X:504:GLY:HA3	2.47	0.48
6:4B:514:ARG:NH2	30:4D:75:ASP:OD2	2.47	0.48
15:X:112:PHE:O	34:4g:37:PHE:HE2	1.96	0.48
5:53:73:LEU:HD11	25:5b:71:LEU:HB2	1.94	0.48
23:5C:135:CYS:O	23:5C:227:LEU:HA	2.13	0.48
23:5C:644:LEU:O	23:5C:649:SER:OG	2.30	0.48
25:1b:11:GLN:HG2	25:1b:12:HIS:CD2	2.48	0.48
29:5J:508:GLN:NE2	29:5J:511:GLU:OE1	2.46	0.48
36:5A:104:GLU:HB2	36:5A:422:LEU:HD11	1.96	0.48
36:5A:109:PRO:HB2	36:5A:191:ILE:HD12	1.95	0.48
36:5A:1244:VAL:HG11	36:5A:1291:CYS:HB3	1.95	0.48
36:5A:1892:PRO:HD2	36:5A:1937:ILE:HD11	1.96	0.48
36:5A:2261:MET:HE3	36:5A:2261:MET:HB3	1.78	0.48
45:4:51:A:H3'	45:4:52:U:H6	1.78	0.48
1:1:97:U:O5'	1:1:97:U:H6	1.96	0.48
3:5O:148:LYS:NZ	17:5:7:U:C4'	2.76	0.48
11:11:5:ARG:HA	11:11:8:MET:CE	2.43	0.48
33:B3:932:ASN:O	33:B3:934:GLY:N	2.46	0.48
36:5A:974:ASN:OD1	36:5A:1100:ARG:NH1	2.42	0.48
43:K:892:LYS:H	43:K:896:HIS:HD2	1.62	0.48
49:5B:1180:LEU:HD13	49:5B:1214:VAL:HG21	1.96	0.48
6:4B:290:ASP:OD1	6:4B:293:ASP:CG	2.57	0.48
13:1f:3:LEU:CD2	13:1f:4:PRO:HD2	2.44	0.48
23:5C:603:MET:HB2	23:5C:651:ILE:HD11	1.95	0.48
36:5A:559:ASP:O	36:5A:562:VAL:HG22	2.14	0.48
36:5A:1329:SER:O	36:5A:1367:ASN:HA	2.14	0.48
16:52:53:LEU:HD23	16:52:73:MET:HE2	1.96	0.48
7:2e:32:GLN:N	7:2e:88:GLN:O	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:5B:949:LEU:HG	49:5B:952:ARG:HB3	1.96	0.48
49:5B:1367:MET:HE2	49:5B:1376:CYS:HB2	1.94	0.48
49:5B:1378:TYR:OH	49:5B:1454:ASP:OD2	2.30	0.48
49:5B:2064:TRP:O	49:5B:2081:ARG:HA	2.14	0.48
50:B1:529:GLY:O	50:B1:533:ASN:ND2	2.47	0.48
3:5O:263:ASP:O	3:5O:272:ARG:NH1	2.44	0.48
6:4B:436:LEU:O	44:4A:389:TRP:NE1	2.37	0.48
11:41:66:ARG:NH2	45:4:125:G:O6	2.44	0.48
23:5C:826:ARG:NH1	23:5C:910:ASP:OD1	2.47	0.48
16:42:54:GLY:HA3	16:42:70:VAL:HG12	1.96	0.48
11:51:68:PHE:HB2	16:52:100:PHE:HB3	1.96	0.48
30:4D:15:ASP:OD1	30:4D:15:ASP:N	2.47	0.48
33:B3:383:ASP:OD1	33:B3:383:ASP:N	2.46	0.48
33:B3:542:LYS:HD2	33:B3:559:THR:HB	1.95	0.48
7:2e:63:GLU:O	7:2e:71:ARG:HA	2.14	0.48
34:5g:42:ILE:HD13	34:5g:62:ILE:HG13	1.94	0.48
43:K:680:GLY:O	43:K:681:GLU:C	2.56	0.48
46:2A:115:LEU:HD22	46:2A:142:VAL:HG22	1.95	0.48
49:5B:1332:GLN:NE2	49:5B:1355:GLY:O	2.43	0.48
49:5B:1361:GLU:OE2	49:5B:1393:TRP:NE1	2.41	0.48
50:B1:850:ILE:O	50:B1:854:VAL:HB	2.13	0.48
50:B1:1015:ASP:N	50:B1:1015:ASP:OD1	2.46	0.48
1:1:10:U:P	24:5X:528:ARG:NH2	2.87	0.48
3:5O:171:SER:OG	3:5O:173:ASP:OD1	2.32	0.48
3:5O:182:ARG:O	17:5:78:U:P	2.72	0.48
3:5O:251:LEU:HD23	3:5O:291:CYS:HB3	1.95	0.48
3:5O:330:ILE:HG12	3:5O:346:SER:HB3	1.96	0.48
9:1K:47:GLU:OE2	16:12:112:ASN:HA	2.13	0.48
7:4e:22:PHE:HE1	15:X:102:GLU:HB3	1.79	0.48
23:5C:604:LEU:HD22	38:U:128:LEU:HD11	1.95	0.48
24:5X:485:GLU:HA	24:5X:523:ILE:CD1	2.44	0.48
28:S:553:PHE:HB2	49:5B:428:CYS:HB3	1.96	0.48
29:5J:23:ARG:NH1	39:5D:73:TYR:OH	2.47	0.48
29:5J:158:LEU:HD11	36:5A:701:ILE:HG23	1.88	0.48
30:4D:108:GLU:HB3	43:K:928:ASN:ND2	2.23	0.48
33:B3:931:VAL:HG21	33:B3:938:GLU:CG	2.44	0.48
36:5A:1378:GLU:HB3	36:5A:1416:ILE:HD11	1.96	0.48
36:5A:1540:PRO:O	36:5A:1671:TYR:N	2.47	0.48
38:U:305:VAL:HG22	38:U:313:GLN:HA	1.96	0.48
34:5g:6:PRO:HA	34:5g:36:PRO:HA	1.96	0.48
44:4A:451:GLN:NE2	47:A1:430:UNK:O	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:5B:74:ARG:NH2	49:5B:75:ASP:OD1	2.47	0.48
50:B1:670:GLN:HA	50:B1:673:ILE:HG12	1.96	0.48
1:1:33:C:O4'	9:1K:137:SER:HA	2.10	0.47
8:I:-1:G:H2'	8:I:0:G:H8	1.79	0.47
23:5C:645:ARG:NH2	23:5C:653:ILE:O	2.47	0.47
23:5C:680:ASN:ND2	23:5C:802:HIS:O	2.47	0.47
24:5X:283:SER:HA	36:5A:274:PRO:HB3	1.96	0.47
36:5A:425:PRO:HB2	36:5A:428:LYS:HB2	1.96	0.47
49:5B:1981:SER:OG	49:5B:1982:VAL:N	2.47	0.47
1:1:116:C:H2'	1:1:117:G:O4'	2.15	0.47
1:1:143:A:C6	1:1:144:C:C2	3.02	0.47
5:13:76:MET:HG3	9:1K:13:PHE:CE1	2.49	0.47
15:X:140:TYR:CG	28:S:733:PHE:CE1	3.02	0.47
13:2f:66:CYS:SG	13:2f:67:ASN:N	2.86	0.47
24:5X:362:LEU:CD2	24:5X:391:ARG:CB	2.32	0.47
24:5X:581[A]:GLU:CD	24:5X:587:LYS:HD3	2.38	0.47
26:B5:14:LEU:O	26:B5:18:TYR:N	2.46	0.47
29:5J:787:GLU:HG3	29:5J:799:LEU:HD12	1.96	0.47
36:5A:699:GLU:HA	36:5A:702:LYS:HG2	1.95	0.47
36:5A:2306:HIS:HD2	36:5A:2308:VAL:HG22	1.77	0.47
34:4g:6:PRO:HA	34:4g:36:PRO:HA	1.96	0.47
45:4:108:C:H2'	45:4:109:G:C8	2.49	0.47
49:5B:1699:GLU:OE2	49:5B:1701:ARG:NH2	2.46	0.47
1:1:72:U:C5'	1:1:73:C:OP1	2.62	0.47
1:1:164:G:H4'	11:11:50:ARG:CA	2.44	0.47
17:5:7:U:H3'	17:5:8:G:H8	1.78	0.47
23:5C:836:VAL:O	23:5C:870:THR:HA	2.14	0.47
36:5A:701:ILE:HG22	36:5A:705:LYS:CG	2.44	0.47
36:5A:1214:TRP:NE1	36:5A:1276:GLU:OE1	2.42	0.47
43:K:859:GLU:CD	43:K:991:ARG:HH22	2.23	0.47
45:4:92:C:O2'	45:4:93:G:H5'	2.14	0.47
49:5B:447:VAL:HB	49:5B:687:GLN:HG3	1.96	0.47
49:5B:1265:GLN:HE21	49:5B:1287:ARG:HH12	1.61	0.47
3:5O:133:VAL:HG21	3:5O:169:THR:HG21	1.96	0.47
6:4B:438:GLN:OE1	6:4B:440:ARG:NH2	2.48	0.47
12:R:387:ASP:N	45:4:68:A:N1	2.61	0.47
15:X:137:TYR:CD2	28:S:729:LEU:HA	2.50	0.47
22:B2:627:LYS:C	22:B2:629:PRO:HD2	2.40	0.47
38:U:425:GLY:O	38:U:441:ARG:NH2	2.42	0.47
46:2A:134:TYR:O	46:2A:138:LYS:HB2	2.15	0.47
49:5B:756:SER:HA	49:5B:759:THR:HG22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:B1:911:LEU:HG	50:B1:957:ARG:HG3	1.96	0.47
16:22:74:TRP:NE1	16:22:76:GLU:OE2	2.42	0.47
22:B2:497:SER:OG	50:B1:1252:GLN:NE2	2.47	0.47
23:5C:135:CYS:HB2	23:5C:242:LEU:HD13	1.95	0.47
23:5C:916:ILE:HB	23:5C:931:ARG:HG2	1.96	0.47
24:5X:246:GLU:HG3	36:5A:307:PRO:HG3	1.96	0.47
24:5X:530:ILE:HD11	24:5X:565:LYS:CG	2.44	0.47
16:42:41:GLN:O	16:42:112:ASN:ND2	2.48	0.47
36:5A:2115:ILE:O	36:5A:2118:SER:OG	2.31	0.47
38:U:172:PHE:HB2	38:U:181:ILE:HB	1.96	0.47
34:2g:39:ASN:HB2	7:2e:17:PRO:HG2	1.96	0.47
16:52:32:LEU:HD11	16:52:109:VAL:HG11	1.95	0.47
49:5B:756:SER:O	49:5B:760:GLU:CB	2.63	0.47
3:5O:148:LYS:HZ2	17:5:7:U:P	2.34	0.47
24:5X:540:LEU:HD23	24:5X:543:CYS:SG	2.54	0.47
11:11:82:ASP:N	11:11:82:ASP:OD1	2.47	0.47
36:5A:1811:ASN:CG	36:5A:1814:THR:CG2	2.85	0.47
38:U:135:ALA:HB2	38:U:167:LEU:HD21	1.96	0.47
43:K:950:ASN:ND2	43:K:950:ASN:N	2.51	0.47
49:5B:156:GLU:HG3	49:5B:157:ILE:HG12	1.97	0.47
49:5B:1298:PRO:HG3	49:5B:1515:HIS:HD2	1.78	0.47
50:B1:480:VAL:O	50:B1:495:ARG:NH2	2.35	0.47
5:13:13:ALA:HB2	5:13:77:LEU:HD11	1.96	0.47
15:X:101:ILE:HG12	15:X:103:MET:HG2	1.95	0.47
15:X:138:ARG:HH22	36:5A:1614:ILE:HD12	1.79	0.47
21:A2:124:ASP:CG	21:A2:125:SER:N	2.72	0.47
23:5C:264:ILE:HD12	23:5C:381:LEU:HD22	1.96	0.47
23:5C:878:ILE:HD12	23:5C:881:PHE:HE2	1.79	0.47
24:5X:675:LYS:HG2	24:5X:676:GLY:N	2.30	0.47
27:1A:93:ILE:O	27:1A:97:MET:HG3	2.14	0.47
33:B3:120:PHE:HB3	33:B3:170:VAL:HG12	1.95	0.47
33:B3:236:ILE:HB	33:B3:249:LEU:HB2	1.95	0.47
33:B3:407:ILE:HG23	33:B3:425:VAL:HG13	1.96	0.47
33:B3:470:PHE:HB3	33:B3:747:SER:HA	1.95	0.47
34:1g:16:LYS:HG2	34:1g:73:LEU:HD12	1.96	0.47
5:43:31:LYS:O	5:43:44:SER:N	2.47	0.47
5:43:39:MET:SD	25:4b:73:ARG:NH1	2.87	0.47
5:43:62:TYR:HB3	34:4g:70:LEU:HB2	1.97	0.47
36:5A:552:ARG:HG3	36:5A:552:ARG:NH2	2.20	0.47
36:5A:693:ILE:HG21	36:5A:709:ILE:HD12	1.97	0.47
36:5A:1510:GLU:HB3	36:5A:1513:MET:HG3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5A:1640:SER:HA	36:5A:1653:ASP:H	1.79	0.47
36:5A:1787:ARG:HG3	36:5A:1803:ILE:HG13	1.96	0.47
39:5D:34:TRP:HB2	47:A1:473:ARG:HD2	1.95	0.47
39:5D:53:LYS:NZ	47:A1:447:UNK:CB	2.77	0.47
39:5D:68:ASP:OD1	39:5D:68:ASP:N	2.48	0.47
42:1C:24:HIS:CD2	42:1C:24:HIS:C	2.92	0.47
45:4:140:G:H2'	45:4:141:A:H8	1.79	0.47
49:5B:1438:ARG:HB3	49:5B:1441:GLN:HE21	1.80	0.47
6:4B:349:LEU:HB3	6:4B:359:LEU:HB3	1.96	0.47
24:5X:457:PRO:HG2	24:5X:460:ASP:OD2	2.14	0.47
24:5X:682:LYS:CG	24:5X:683:SER:N	2.75	0.47
24:5X:693:THR:O	24:5X:694:LEU:HG	2.14	0.47
26:B5:44:MET:HE2	26:B5:44:MET:HB3	1.79	0.47
13:5f:35:SER:OG	13:5f:43:GLN:OE1	2.25	0.47
36:5A:579:GLN:CA	36:5A:579:GLN:NE2	2.73	0.47
36:5A:604:MET:O	36:5A:607:ASP:HB2	2.15	0.47
36:5A:1143:MET:HG3	36:5A:1181:ASP:HB3	1.97	0.47
36:5A:1267:LEU:O	36:5A:1271:MET:HB2	2.15	0.47
36:5A:1413:ASP:HB2	49:5B:58:ARG:HB3	1.97	0.47
16:52:31:VAL:HG13	16:52:111:ARG:HE	1.79	0.47
42:1C:41:TRP:O	42:1C:44:GLU:HB3	2.15	0.47
49:5B:61:PRO:HD2	49:5B:64:GLN:HE21	1.79	0.47
49:5B:993:ILE:HD11	49:5B:998:VAL:HG13	1.96	0.47
49:5B:1948:MET:HE3	49:5B:1954:TRP:HA	1.96	0.47
1:1:106:G:C6	1:1:107:U:C2	3.02	0.47
1:1:119:C:O2'	1:1:120:U:H5'	2.14	0.47
2:6:105:U:O2'	14:66:66:ARG:NH2	2.48	0.47
4:B4:74:MET:HB3	4:B4:86:VAL:HG21	1.96	0.47
23:5C:742:PRO:HG2	23:5C:785:ARG:HG3	1.97	0.47
24:5X:540:LEU:CD2	24:5X:543:CYS:CB	2.92	0.47
29:5J:236:GLY:O	38:U:473:ASN:ND2	2.48	0.47
29:5J:385:ASP:N	29:5J:385:ASP:OD1	2.48	0.47
33:B3:727:SER:O	33:B3:727:SER:OG	2.31	0.47
33:B3:1064:ASP:OD1	33:B3:1064:ASP:N	2.45	0.47
36:5A:226:GLN:OE1	36:5A:227:ARG:NH1	2.48	0.47
36:5A:1433:ASP:OD2	36:5A:1460:HIS:NE2	2.46	0.47
43:K:698:PHE:HB2	43:K:725:MET:CE	2.45	0.47
43:K:774:LEU:HD23	43:K:777:VAL:CG1	2.45	0.47
43:K:988:PRO:HA	43:K:991:ARG:HB2	1.96	0.47
45:4:110:G:O2'	45:4:111:C:H5'	2.13	0.47
49:5B:297:SER:N	49:5B:301:GLU:OE2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:5:89:U:O2'	5:53:64:ARG:NH2	2.48	0.47
5:53:16:HIS:HB3	5:53:74:PRO:HG2	1.97	0.47
24:5X:307:ILE:HG23	36:5A:618:THR:HG21	1.97	0.47
24:5X:606[B]:THR:HG21	24:5X:609:MET:HE2	1.96	0.47
32:2:161:U:O2	32:2:163:G:N2	2.48	0.47
7:1e:48:ILE:HD11	7:1e:59:ASP:HA	1.97	0.47
36:5A:1190:CYS:O	36:5A:1273:TYR:OH	2.28	0.47
36:5A:1206:GLU:HG3	36:5A:2098:LYS:HA	1.96	0.47
36:5A:1260:VAL:HG21	36:5A:1325:LEU:HD13	1.97	0.47
37:A3:348:LYS:CE	11:21:73:SER:HA	2.44	0.47
46:2A:110:ALA:HA	46:2A:139:VAL:HG13	1.97	0.47
49:5B:825:THR:HA	49:5B:866:GLU:O	2.15	0.47
49:5B:1831:LEU:O	49:5B:1835:SER:HB3	2.15	0.47
7:4e:18:ILE:O	7:4e:22:PHE:HB3	2.14	0.46
20:2B:40:ILE:HG12	46:2A:18:ALA:HB1	1.97	0.46
23:5C:678:THR:OG1	23:5C:682:LYS:O	2.30	0.46
23:5C:860:ASP:OD2	23:5C:860:ASP:N	2.48	0.46
11:51:19:LEU:HD21	11:51:60:ILE:HD13	1.98	0.46
34:1g:57:ILE:CG1	34:1g:57:ILE:O	2.63	0.46
36:5A:947:PRO:HB2	36:5A:949:PRO:HD2	1.97	0.46
36:5A:1137:ASP:OD1	36:5A:1137:ASP:N	2.41	0.46
38:U:467:LYS:NZ	38:U:547:GLU:OE1	2.44	0.46
7:2e:44:GLU:O	7:2e:61:ALA:HA	2.15	0.46
43:K:695:GLN:O	43:K:696:GLY:C	2.55	0.46
43:K:892:LYS:HB3	43:K:892:LYS:HZ2	1.80	0.46
49:5B:1737:ASN:HD21	49:5B:1816:GLY:HA2	1.78	0.46
49:5B:2053:ALA:HB1	49:5B:2056:PHE:HB3	1.97	0.46
16:42:43:LEU:HD13	16:42:53:LEU:HD12	1.97	0.46
36:5A:1072:LEU:HD13	36:5A:1087:LEU:HD13	1.96	0.46
36:5A:1701:VAL:HA	36:5A:1716:GLY:HA3	1.97	0.46
36:5A:1729:ALA:O	36:5A:1733:ILE:HB	2.14	0.46
36:5A:2103:THR:O	36:5A:2140:LYS:N	2.46	0.46
37:A3:195:ASP:OD2	37:A3:199:ARG:NH1	2.49	0.46
16:12:34:GLN:HB3	16:12:111:ARG:HH12	1.80	0.46
43:K:822:LEU:HG	43:K:833:CYS:SG	2.55	0.46
43:K:902:MET:HE1	43:K:929:PHE:CG	2.50	0.46
49:5B:447:VAL:HG11	49:5B:884:ASN:HD21	1.79	0.46
49:5B:1487:ILE:HG21	49:5B:1504:LEU:HD22	1.96	0.46
1:1:15:G:H4'	1:1:16:G:OP1	2.14	0.46
5:13:10:LEU:HD13	5:13:71:LEU:HD22	1.97	0.46
6:4B:336:ARG:HE	6:4B:353:GLU:HB2	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:A2:120:THR:HB	21:A2:135:GLN:HB2	1.96	0.46
24:5X:673:GLN:HB3	24:5X:675:LYS:CD	2.45	0.46
29:5J:109:ASP:OD1	36:5A:94:TYR:OH	2.32	0.46
33:B3:279:ASP:HB2	33:B3:856:LYS:H	1.80	0.46
36:5A:295:GLU:O	36:5A:301:LYS:NZ	2.43	0.46
41:BP:57:ARG:NH1	41:BP:62:GLY:O	2.46	0.46
49:5B:544:MET:HG3	49:5B:817:TRP:CE2	2.51	0.46
1:1:8:C:O2'	24:5X:528:ARG:CA	2.62	0.46
1:1:29:A:N3	9:1K:200:ARG:CB	2.78	0.46
2:6:89:U:H2'	2:6:90:G:C8	2.51	0.46
6:4B:282:HIS:CD2	6:4B:284:LYS:H	2.32	0.46
6:4B:513:ASP:OD1	29:5J:802:LYS:NZ	2.42	0.46
11:41:20:LYS:HD3	45:4:125:G:C2	2.51	0.46
24:5X:728:ILE:HG12	24:5X:729:ASP:H	1.80	0.46
24:5X:798:HIS:HE1	24:5X:800:ASP:OD2	1.98	0.46
33:B3:83:ASP:O	33:B3:111:GLY:N	2.48	0.46
33:B3:1118:VAL:HG22	33:B3:1128:ILE:HG22	1.97	0.46
35:68:37:ILE:HD12	40:64:6:LEU:HD23	1.96	0.46
36:5A:85:LYS:HB2	36:5A:85:LYS:HZ2	1.80	0.46
36:5A:852:VAL:HG13	36:5A:852:VAL:O	2.15	0.46
36:5A:1218:ASN:HB3	36:5A:1221:THR:HG22	1.97	0.46
36:5A:1600:GLU:HG2	36:5A:1725:LEU:HD13	1.98	0.46
49:5B:1009:LEU:HD22	49:5B:1013:GLU:HG2	1.98	0.46
50:B1:1272:ILE:HG22	50:B1:1280:LEU:HD11	1.97	0.46
1:1:28:G:N1	9:1K:112:TYR:CE2	2.78	0.46
8:I:-1:G:H2'	8:I:0:G:C8	2.50	0.46
9:1K:41:ILE:HG22	16:12:51:LYS:HD2	1.98	0.46
25:1b:17:MET:HE3	25:1b:82:VAL:CA	2.46	0.46
29:5J:343:GLU:HG2	29:5J:369:LEU:HD13	1.97	0.46
36:5A:71:ARG:NH1	36:5A:177:ASP:OD2	2.48	0.46
36:5A:340:ILE:HG23	36:5A:355:LEU:HD12	1.97	0.46
34:5g:59:MET:HE2	34:5g:59:MET:HB2	1.88	0.46
43:K:862:ILE:HD11	43:K:923:PHE:CE2	2.50	0.46
43:K:942:LYS:HD3	43:K:943:VAL:N	2.29	0.46
50:B1:497:ILE:HA	50:B1:500:LEU:HD12	1.97	0.46
50:B1:578:ILE:HG13	50:B1:596:ILE:HD11	1.97	0.46
50:B1:661:ARG:NH1	50:B1:696:ASP:OD1	2.49	0.46
13:1f:19:VAL:HG11	13:1f:72:ILE:CD1	2.42	0.46
7:4e:32:GLN:OE1	7:4e:34:TRP:NE1	2.41	0.46
15:X:140:TYR:CD2	28:S:733:PHE:CE1	3.04	0.46
17:5:109:G:O3'	11:51:49:ASN:ND2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:5C:701:GLU:OE2	23:5C:785:ARG:NH1	2.43	0.46
24:5X:536:ARG:CG	34:1g:10:LYS:HD2	2.45	0.46
29:5J:92:GLY:O	29:5J:93:PRO:HB3	2.16	0.46
38:U:405:GLU:CD	38:U:406:LYS:N	2.73	0.46
43:K:677:VAL:CG1	43:K:678:ASN:N	2.78	0.46
44:4A:427:PRO:HB3	44:4A:639:LYS:NZ	2.29	0.46
50:B1:773:LEU:HD21	50:B1:791:VAL:HG12	1.98	0.46
1:1:29:A:N9	9:1K:200:ARG:HD2	2.19	0.46
1:1:47:C:H2'	1:1:48:C:O4'	2.16	0.46
1:1:48:C:H2'	1:1:49:A:H8	1.77	0.46
1:1:93:G:N2	1:1:117:G:C4	2.84	0.46
1:1:118:A:H61	5:13:4:GLY:N	2.09	0.46
20:2B:16:ASP:OD1	20:2B:16:ASP:N	2.46	0.46
11:11:66:ARG:NH2	16:12:48:ASN:HB3	2.30	0.46
16:42:70:VAL:HG23	16:42:96:ILE:HB	1.98	0.46
28:S:745:ARG:HH21	45:4:60:A:H3'	1.80	0.46
29:5J:659:GLU:O	29:5J:662:ARG:HB2	2.15	0.46
33:B3:932:ASN:HB3	33:B3:935:GLU:CD	2.41	0.46
36:5A:1526:LEU:HD13	36:5A:1529:ILE:HD12	1.96	0.46
36:5A:1555:LEU:HD11	36:5A:1570:LYS:HG3	1.96	0.46
36:5A:1832:ARG:HG3	36:5A:1836:LEU:HD13	1.98	0.46
37:A3:356:ARG:HB3	11:21:75:PRO:HB2	1.83	0.46
38:U:392:LEU:HD12	38:U:453:PHE:HE1	1.81	0.46
38:U:504:ILE:HB	38:U:550:ILE:HB	1.98	0.46
46:2A:104:GLY:O	46:2A:107:ASP:HB2	2.16	0.46
50:B1:1133:MET:HE3	50:B1:1172:LEU:HB2	1.98	0.46
6:4B:271:GLY:O	6:4B:306:LYS:NZ	2.44	0.46
7:4e:34:TRP:HB2	7:4e:86:LEU:HG	1.97	0.46
17:5:56:C:H4'	36:5A:100:LEU:HD21	1.97	0.46
21:A2:119:VAL:HG11	21:A2:181:PHE:CZ	2.51	0.46
22:B2:478:HIS:O	22:B2:481:THR:OG1	2.29	0.46
23:5C:675:PHE:HA	23:5C:685:ILE:O	2.16	0.46
11:11:68:PHE:HB2	16:12:100:PHE:HB3	1.98	0.46
28:S:565:GLU:C	28:S:566:ILE:CG1	2.88	0.46
28:S:566:ILE:N	28:S:567:PRO:CD	2.79	0.46
13:5f:33:LEU:HD11	13:5f:42:MET:HB3	1.98	0.46
30:4D:11:TYR:OH	30:4D:128:VAL:OXT	2.34	0.46
30:4D:108:GLU:O	43:K:947:SER:CB	2.64	0.46
33:B3:745:PHE:HB2	33:B3:755:VAL:HG23	1.98	0.46
7:1e:16:GLN:HG2	7:1e:19:ASN:OD1	2.16	0.46
36:5A:710:LEU:HD21	39:5D:4:MET:CE	2.26	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5A:1645:LEU:HB2	36:5A:1714:ALA:H	1.81	0.46
38:U:498:TYR:CZ	38:U:555:ARG:HG3	2.51	0.46
43:K:722:ASN:OD1	43:K:725:MET:HG3	2.16	0.46
3:5O:130:ASP:OD1	3:5O:130:ASP:N	2.49	0.46
7:5e:86:LEU:HD13	34:5g:62:ILE:HG12	1.98	0.46
13:1f:21:VAL:HG23	13:1f:21:VAL:O	2.15	0.46
20:2B:8:THR:HG22	20:2B:55:ILE:HG23	1.98	0.46
21:A2:147:PRO:HB2	21:A2:171:MET:HE2	1.98	0.46
24:5X:545:TYR:CE1	24:5X:601[B]:GLN:OE1	2.69	0.46
24:5X:770:LYS:HZ3	36:5A:1690:ASP:HA	1.80	0.46
36:5A:811:THR:HA	36:5A:814:VAL:HG22	1.98	0.46
36:5A:1248:LEU:HD11	36:5A:1294:LYS:HB3	1.97	0.46
36:5A:1381:ASP:HA	36:5A:1384:ARG:HG2	1.98	0.46
36:5A:1585:ILE:HD11	36:5A:1743:LEU:HB2	1.98	0.46
36:5A:1600:GLU:HG3	36:5A:1604:LEU:HG	1.98	0.46
36:5A:1973:ASP:N	36:5A:1973:ASP:OD1	2.49	0.46
16:12:113:PRO:O	16:12:114:LEU:HD12	2.16	0.46
49:5B:1951:GLN:HG3	49:5B:1962:GLN:HG3	1.98	0.46
50:B1:811:LEU:HA	50:B1:814:PHE:HB3	1.97	0.46
5:53:28:TYR:OH	34:5g:69:MET:SD	2.59	0.46
21:A2:148:ARG:NH2	47:A1:267:GLU:OE1	2.49	0.46
28:S:568:THR:HG23	29:5J:425:ARG:HH12	1.79	0.46
13:5f:61:GLU:OE2	16:52:111:ARG:NE	2.48	0.46
33:B3:1015:LYS:NZ	33:B3:1067:ASP:OD2	2.39	0.46
36:5A:552:ARG:CG	36:5A:552:ARG:NH2	2.73	0.46
36:5A:1443:LYS:HD3	36:5A:1443:LYS:HA	1.78	0.46
36:5A:1676:ILE:HD13	36:5A:1706:ASP:HB2	1.97	0.46
34:2g:13:MET:HE3	34:2g:13:MET:HB3	1.76	0.46
43:K:830:LEU:O	43:K:830:LEU:HD22	2.16	0.46
46:2A:65:ARG:O	46:2A:67:LYS:NZ	2.49	0.46
50:B1:1036:ILE:HD11	50:B1:1073:ILE:HA	1.98	0.46
1:1:118:A:N3	1:1:118:A:H5''	2.31	0.45
6:4B:427:GLY:HA2	6:4B:451:LEU:HB2	1.97	0.45
10:4C:298:LYS:HD2	10:4C:320:LEU:HD22	1.97	0.45
12:R:393:ASN:H	12:R:396:ILE:HD12	1.82	0.45
32:2:101:U:O2	5:23:40:ASN:ND2	2.49	0.45
33:B3:317:THR:OG1	33:B3:321:MET:O	2.26	0.45
5:43:10:LEU:HD23	25:4b:71:LEU:HD13	1.98	0.45
36:5A:166:PHE:CE1	36:5A:581:ILE:HD11	2.51	0.45
36:5A:181:ASN:O	36:5A:185:VAL:HG21	2.16	0.45
36:5A:533:LYS:HD2	39:5D:71:LYS:HG3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:K:679:ILE:CD1	43:K:679:ILE:H	2.30	0.45
49:5B:439:ARG:NH1	49:5B:442:TYR:OH	2.49	0.45
49:5B:462:LEU:HD12	49:5B:466:LYS:HB2	1.97	0.45
6:4B:408:LYS:HB2	6:4B:428:ASP:HB3	1.98	0.45
9:1K:76:GLU:HA	9:1K:79:GLN:CD	2.42	0.45
12:R:458:MET:HG2	45:4:69:C:C4	2.51	0.45
15:X:103:MET:HB2	15:X:110:ALA:HB2	1.99	0.45
22:B2:630:PRO:CG	22:B2:663:PHE:HZ	2.04	0.45
24:5X:703:ARG:HE	24:5X:703:ARG:HB2	1.43	0.45
28:S:566:ILE:HD13	49:5B:693:THR:CG2	2.46	0.45
29:5J:649:VAL:O	29:5J:653:SER:OG	2.34	0.45
29:5J:665:LEU:HD12	29:5J:684:LEU:HD12	1.98	0.45
34:1g:57:ILE:O	34:1g:57:ILE:HD12	2.16	0.45
5:43:21:GLU:OE2	25:4b:25:ARG:NH1	2.49	0.45
7:1e:27:ASN:OD1	7:1e:27:ASN:N	2.48	0.45
7:1e:48:ILE:CD1	7:1e:59:ASP:OD2	2.64	0.45
36:5A:750:TRP:HH2	36:5A:781:ARG:HB2	1.81	0.45
43:K:679:ILE:N	43:K:679:ILE:CD1	2.79	0.45
49:5B:1886:ASP:HB3	49:5B:1889:VAL:HG22	1.97	0.45
50:B1:1140:GLU:HB2	50:B1:1143:VAL:HG22	1.99	0.45
50:B1:1223:SER:HB3	50:B1:1226:VAL:HG12	1.97	0.45
6:4B:282:HIS:CD2	6:4B:289:LEU:HD12	2.51	0.45
6:4B:388:PHE:HZ	44:4A:425:ASN:O	2.00	0.45
7:5e:77:ILE:HG22	13:5f:73:ARG:HB3	1.98	0.45
11:41:19:LEU:HD21	11:41:60:ILE:HD13	1.98	0.45
12:R:394:ASP:OD1	12:R:394:ASP:N	2.49	0.45
14:66:75:THR:HB	48:65:70:ASP:HB3	1.98	0.45
24:5X:427:GLN:O	24:5X:588:MET:HB3	2.17	0.45
16:42:33:THR:HA	16:42:36:VAL:HG12	1.96	0.45
26:B5:62:ALA:HB3	33:B3:288:VAL:HG12	1.98	0.45
33:B3:79:VAL:HG12	33:B3:121:LEU:HD21	1.98	0.45
36:5A:1987:ILE:HG21	36:5A:2011:ILE:HG13	1.98	0.45
38:U:498:TYR:HB3	38:U:553:TRP:HB3	1.99	0.45
34:2g:32:ARG:HB3	34:2g:41:VAL:HG12	1.98	0.45
43:K:700:ASN:OD1	43:K:700:ASN:N	2.41	0.45
49:5B:432:ASP:OD1	49:5B:432:ASP:N	2.49	0.45
1:1:105:U:C6	36:5A:1634:SER:O	2.70	0.45
3:5O:173:ASP:OD1	3:5O:173:ASP:N	2.50	0.45
10:4C:357:ARG:CZ	45:4:17:A:H61	2.28	0.45
12:R:414:ARG:HA	12:R:421:THR:HA	1.98	0.45
16:22:43:LEU:HD23	16:22:110:LEU:HD21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:A2:124:ASP:CG	21:A2:125:SER:H	2.24	0.45
13:2f:71:TYR:OH	7:2e:63:GLU:OE2	2.33	0.45
23:5C:109:LEU:HD13	23:5C:116:MET:HG3	1.98	0.45
23:5C:589:LYS:HG3	23:5C:628:VAL:HG13	1.98	0.45
23:5C:834:VAL:HG11	23:5C:883:PHE:HE2	1.81	0.45
24:5X:511:GLN:OE1	24:5X:528:ARG:NE	2.49	0.45
24:5X:606[B]:THR:CG2	24:5X:609:MET:HE2	2.46	0.45
24:5X:730:ILE:HD12	24:5X:731:GLN:O	2.16	0.45
13:4f:38:GLY:O	45:4:119:A:N6	2.43	0.45
5:43:10:LEU:HD21	5:43:39:MET:HG2	1.99	0.45
7:1e:21:ILE:HG22	7:1e:50:PHE:CE2	2.52	0.45
36:5A:542:ASN:O	36:5A:546:LEU:HB2	2.16	0.45
38:U:228:LEU:HD22	38:U:297:PRO:HB3	1.97	0.45
34:2g:57:ILE:HB	7:2e:88:GLN:HG3	1.99	0.45
43:K:724:LEU:O	43:K:727:LYS:HB3	2.16	0.45
49:5B:1535:THR:O	49:5B:1539:LEU:HB2	2.15	0.45
49:5B:1824:ILE:HD13	49:5B:1829:ILE:HD11	1.98	0.45
1:1:36:A:H2'	1:1:37:G:O4'	2.17	0.45
1:1:137:U:O5'	1:1:137:U:H6	2.00	0.45
23:5C:677:GLU:O	23:5C:814:ARG:NH1	2.50	0.45
16:42:32:LEU:HD21	16:42:109:VAL:HG11	1.99	0.45
33:B3:583:MET:HB3	33:B3:609:LEU:HD21	1.99	0.45
33:B3:589:CYS:SG	33:B3:590:MET:N	2.89	0.45
7:1e:36:TYR:CB	7:1e:83:ASN:O	2.65	0.45
36:5A:701:ILE:HG22	36:5A:705:LYS:HG3	1.97	0.45
36:5A:975:VAL:HG22	36:5A:1177:VAL:HG22	1.97	0.45
44:4A:447:LYS:CE	47:A1:429:UNK:O	2.62	0.45
49:5B:1066:PHE:CG	49:5B:1085:THR:HG21	2.52	0.45
2:6:103:U:C2'	35:68:65:ASP:OD1	2.61	0.45
3:5O:155:ASN:ND2	3:5O:196:VAL:O	2.48	0.45
10:4C:103:ILE:HG21	10:4C:201:LYS:HB2	1.98	0.45
25:1b:12:HIS:H	25:1b:12:HIS:HD2	1.65	0.45
26:B5:60:SER:HA	33:B3:429:ARG:HH22	1.82	0.45
32:2:151:C:H2'	32:2:152:G:H8	1.82	0.45
33:B3:428:GLY:HA3	33:B3:433:SER:HA	1.98	0.45
5:43:28:TYR:OH	34:4g:69:MET:SD	2.61	0.45
7:1e:23:ARG:O	7:1e:27:ASN:OD1	2.33	0.45
36:5A:164:MET:HE2	36:5A:164:MET:HB3	1.75	0.45
36:5A:513:LEU:HD21	36:5A:537:LYS:HE2	1.97	0.45
36:5A:1317:TYR:HE1	36:5A:1329:SER:HB2	1.74	0.45
36:5A:1389:TYR:OH	49:5B:222:GLU:OE2	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5A:1847:ALA:O	36:5A:1851:SER:OG	2.28	0.45
43:K:679:ILE:HD11	43:K:692:TYR:CZ	2.52	0.45
50:B1:1103:VAL:HG12	50:B1:1109:ARG:HG3	1.99	0.45
1:1:105:U:N3	36:5A:1607:GLU:CD	2.70	0.45
2:6:49:G:N2	12:R:387:ASP:HA	2.31	0.45
3:5O:148:LYS:NZ	17:5:7:U:P	2.86	0.45
7:5e:65:HIS:HB2	7:5e:69:LYS:H	1.81	0.45
11:41:5:ARG:HD3	11:41:8:MET:HE2	1.99	0.45
14:66:34:LEU:HD21	14:66:37:LEU:HD23	1.99	0.45
14:66:66:ARG:HG2	31:63:50:LEU:HD22	1.98	0.45
20:2B:15:ASN:HD22	20:2B:18:ILE:HG23	1.81	0.45
20:2B:86:THR:OG1	32:2:165:A:N6	2.40	0.45
23:5C:644:LEU:HG	23:5C:653:ILE:HD13	1.99	0.45
28:S:565:GLU:C	28:S:567:PRO:CD	2.86	0.45
25:2b:47:GLU:OE2	25:2b:65:ARG:NH1	2.49	0.45
5:43:73:LEU:HB2	25:4b:69:LEU:HG	1.98	0.45
36:5A:66:VAL:HG11	36:5A:487:LEU:HD11	1.99	0.45
36:5A:1267:LEU:HD11	36:5A:1330:MET:CG	2.47	0.45
36:5A:1604:LEU:HB3	36:5A:1719:PHE:HE1	1.81	0.45
7:2e:63:GLU:HG3	7:2e:74:LEU:HD11	1.98	0.45
43:K:990:LYS:CE	45:4:4:U:OP1	2.62	0.45
45:4:18:G:H4'	45:4:19:U:H5'	1.98	0.45
46:2A:37:LEU:HD23	46:2A:61:PRO:HD2	1.99	0.45
3:5O:58:PRO:O	3:5O:60:MET:N	2.45	0.45
8:I:90:U:H2'	8:I:91:U:C2	2.51	0.45
22:B2:649:LYS:HB3	22:B2:655:SER:OG	2.17	0.45
22:B2:657:ILE:HB	22:B2:658:PRO:CD	2.47	0.45
28:S:723:LYS:HZ3	28:S:727:ARG:HH12	1.64	0.45
29:5J:238:LEU:HD21	38:U:545:LEU:HD23	1.99	0.45
11:51:67:TYR:HB3	16:52:101:LEU:HD12	1.98	0.45
32:2:12:G:C6	32:2:13:C:N4	2.84	0.45
33:B3:136:GLU:OE2	33:B3:189:TYR:OH	2.30	0.45
34:1g:35:ASP:OD1	34:1g:36:PRO:HD2	2.17	0.45
36:5A:598:LEU:HD11	36:5A:637:TRP:HZ3	1.81	0.45
36:5A:761:ILE:HG12	36:5A:767:VAL:HG21	1.99	0.45
36:5A:1134:TRP:O	36:5A:1139:ARG:NH1	2.50	0.45
36:5A:2189:SER:OG	36:5A:2191:GLN:OE1	2.34	0.45
39:5D:5:LEU:HB2	39:5D:60:LEU:HG	1.99	0.45
43:K:747:LYS:HB2	43:K:747:LYS:HE3	1.71	0.45
49:5B:730:GLU:HA	49:5B:733:LYS:HB2	1.99	0.45
49:5B:2020:SER:HB2	49:5B:2040:GLN:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:31:C:O2	9:1K:148:PHE:CZ	2.70	0.45
1:1:74:C:H6	1:1:74:C:O5'	1.99	0.45
10:4C:222:ILE:HA	10:4C:321:LYS:HD3	1.98	0.45
17:5:26:A:O3'	36:5A:635:ARG:NH2	2.50	0.45
21:A2:180:ALA:HB3	47:A1:281:VAL:HG22	1.99	0.45
16:42:88:LYS:HD2	16:42:89:PRO:HD2	1.98	0.45
29:5J:105:TYR:OH	36:5A:121:HIS:NE2	2.50	0.45
33:B3:757:ILE:HG22	33:B3:762:LEU:HA	1.99	0.45
7:1e:36:TYR:CD1	7:1e:36:TYR:C	2.95	0.45
36:5A:1703:ILE:HG12	36:5A:1714:ALA:HB2	1.99	0.45
48:65:58:GLU:HG3	48:65:65:ARG:HH21	1.82	0.45
49:5B:112:THR:HA	49:5B:115:VAL:HG12	1.98	0.45
49:5B:414:LEU:HB2	49:5B:894:VAL:HG11	1.99	0.45
1:1:7:A:O5'	24:5X:478:ARG:CB	2.46	0.45
1:1:127:U:C6	34:1g:63:ARG:NH2	2.85	0.45
15:X:125:ASN:HA	16:42:61:ARG:HD3	1.99	0.45
15:X:137:TYR:CZ	28:S:729:LEU:CD1	2.91	0.45
18:67:44:LEU:HD11	18:67:84:ILE:HD11	1.98	0.45
23:5C:529:ARG:H	23:5C:553:GLU:HB3	1.82	0.45
23:5C:590:ILE:HG21	36:5A:319:LEU:HD11	1.99	0.45
11:11:33:ASP:C	11:11:33:ASP:OD1	2.60	0.45
29:5J:97:ASP:OD2	29:5J:97:ASP:N	2.49	0.45
33:B3:735:SER:O	33:B3:735:SER:OG	2.32	0.45
36:5A:1214:TRP:HB2	36:5A:1228:CYS:HB3	1.99	0.45
36:5A:2330:ARG:HH11	49:5B:1086:GLN:HE21	1.65	0.45
39:5D:94:LEU:HD11	39:5D:102:ILE:HD13	1.98	0.45
49:5B:540:TYR:HD1	49:5B:587:VAL:HG13	1.82	0.45
50:B1:1224:PRO:HA	50:B1:1227:ILE:HG22	1.99	0.45
4:B4:32:LEU:HD11	4:B4:77:ILE:HD13	1.99	0.44
23:5C:374:LEU:HD23	23:5C:374:LEU:HA	1.82	0.44
24:5X:404:GLU:O	24:5X:408:LYS:HG2	2.17	0.44
11:11:53:VAL:HG12	11:11:55:LEU:CD1	2.46	0.44
36:5A:1110:ILE:HD11	36:5A:1149:LEU:HB2	1.98	0.44
38:U:212:LEU:HD13	38:U:222:LEU:HG	1.99	0.44
45:4:114:U:C6	45:4:114:U:O5'	2.70	0.44
46:2A:70:LEU:HA	46:2A:94:ILE:HB	1.98	0.44
46:2A:90:LEU:HD23	46:2A:90:LEU:HA	1.86	0.44
49:5B:1568:GLN:NE2	49:5B:1572:THR:OG1	2.44	0.44
50:B1:918:VAL:HG23	50:B1:961:VAL:HG11	1.99	0.44
50:B1:1193:GLN:HB2	50:B1:1233:ALA:HA	1.98	0.44
1:1:22:U:H5''	1:1:22:U:C6	2.37	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:118:A:N3	1:1:118:A:C5'	2.80	0.44
7:4e:52:GLU:HA	15:X:112:PHE:CD1	2.48	0.44
17:5:29:A:H2'	17:5:30:A:H8	1.82	0.44
23:5C:316:ILE:HD13	23:5C:377:LEU:HD11	1.98	0.44
24:5X:673:GLN:HB3	24:5X:675:LYS:HD2	1.98	0.44
16:42:108:VAL:HG12	13:4f:64:ILE:HA	2.00	0.44
11:51:5:ARG:HD3	11:51:8:MET:HE2	1.99	0.44
33:B3:240:GLY:HA3	33:B3:246:SER:HB2	1.99	0.44
33:B3:837:GLU:HB3	33:B3:838:MET:HE2	1.99	0.44
35:68:59:LEU:HB3	40:64:71:ILE:CG1	2.47	0.44
36:5A:610:HIS:NE2	54:5A:2401:IHP:O31	2.39	0.44
36:5A:1486:GLU:OE1	36:5A:1674:HIS:NE2	2.50	0.44
36:5A:1629:ILE:HB	36:5A:1662:ILE:HB	1.98	0.44
38:U:170:LEU:HD11	38:U:194:LYS:HD3	1.98	0.44
1:1:92:C:HO2'	1:1:93:G:C1'	2.24	0.44
3:5O:155:ASN:O	3:5O:290:ARG:NH2	2.51	0.44
5:13:82:MET:HB2	5:13:83:LEU:HD12	1.98	0.44
11:41:67:TYR:OH	16:42:94:ARG:NH2	2.49	0.44
21:A2:119:VAL:HG11	21:A2:181:PHE:CE1	2.52	0.44
22:B2:630:PRO:HB2	22:B2:632:TRP:CE2	2.52	0.44
24:5X:301:ARG:NH1	36:5A:340:ILE:HG22	2.32	0.44
27:1A:75:PHE:HD2	27:1A:82:MET:HE2	1.82	0.44
30:4D:79:PRO:HG2	30:4D:120:GLN:HG2	2.00	0.44
32:2:9:U:H2'	32:2:10:C:H6	1.82	0.44
36:5A:142:SER:HA	36:5A:242:ALA:HB2	1.98	0.44
36:5A:801:ILE:HD13	36:5A:992:LEU:HD22	2.00	0.44
36:5A:853:LYS:O	36:5A:854:SER:CB	2.65	0.44
36:5A:2107:PRO:HG2	36:5A:2110:VAL:HG22	1.98	0.44
43:K:785:VAL:CG2	43:K:786:GLY:N	2.80	0.44
49:5B:681:ARG:HG2	49:5B:682:PRO:HD2	1.99	0.44
49:5B:1569:THR:OG1	49:5B:1645:VAL:O	2.34	0.44
50:B1:785:LYS:O	50:B1:789:LEU:HB2	2.17	0.44
50:B1:971:MET:HE3	50:B1:1003:VAL:HG11	1.98	0.44
1:1:91:G:H2'	1:1:92:C:O5'	2.17	0.44
3:5O:217:ILE:HB	3:5O:231:MET:HB2	1.98	0.44
13:1f:5:LEU:HB3	7:1e:48:ILE:HG22	1.98	0.44
23:5C:366:GLN:HB3	23:5C:370:VAL:HB	1.99	0.44
24:5X:297:GLN:HE22	24:5X:319:PHE:HB3	1.80	0.44
33:B3:317:THR:OG1	33:B3:318:ASP:O	2.35	0.44
33:B3:1000:VAL:HB	33:B3:1012:VAL:HB	1.98	0.44
36:5A:580:TYR:CD2	36:5A:588:LEU:HD11	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5A:591:MET:HE2	36:5A:591:MET:HB3	1.75	0.44
36:5A:1121:ASN:HD21	38:U:298:HIS:HE1	1.65	0.44
36:5A:1807:ILE:O	36:5A:1819:LEU:HA	2.17	0.44
39:5D:18:ILE:HA	39:5D:26:VAL:HG21	2.00	0.44
2:6:53:A:H2'	2:6:54:G:C8	2.52	0.44
4:B4:13:ALA:HB2	37:A3:436:ARG:NH2	2.31	0.44
11:41:57:THR:HG21	25:4b:12:HIS:NE2	2.33	0.44
16:22:95:TYR:CZ	37:A3:150:ILE:CD1	3.01	0.44
21:A2:115:PRO:CG	21:A2:176:TYR:HA	2.46	0.44
21:A2:117:TYR:CD1	21:A2:139:PRO:HD2	2.48	0.44
22:B2:498:VAL:HG22	50:B1:1249:TYR:HA	2.00	0.44
11:11:5:ARG:HA	11:11:8:MET:HE3	1.99	0.44
26:B5:79:PRO:HD2	33:B3:196:PRO:HA	1.99	0.44
7:1e:33:VAL:HG22	7:1e:43:ILE:O	2.16	0.44
36:5A:691:HIS:CB	47:A1:466:LEU:HD22	2.35	0.44
36:5A:746:LYS:O	36:5A:750:TRP:HB2	2.17	0.44
37:A3:149:TYR:CE2	37:A3:158:LEU:HD13	2.52	0.44
38:U:450:TYR:HA	38:U:553:TRP:O	2.17	0.44
43:K:749:HIS:HA	43:K:831:LYS:HE2	1.99	0.44
43:K:825:GLU:CG	43:K:826:SER:N	2.81	0.44
11:21:25:VAL:HG22	11:21:45:MET:HG3	1.99	0.44
49:5B:1659:HIS:HE1	49:5B:1701:ARG:HE	1.66	0.44
2:6:53:A:H2'	2:6:54:G:H8	1.83	0.44
3:5O:182:ARG:O	17:5:77:G:O3'	2.35	0.44
4:B4:30:TRP:CG	22:B2:600:ARG:HH22	2.35	0.44
15:X:125:ASN:HA	16:42:61:ARG:CD	2.47	0.44
22:B2:657:ILE:HB	22:B2:658:PRO:HD3	1.99	0.44
23:5C:268:LYS:HD3	36:5A:402:ILE:HG21	1.99	0.44
23:5C:775:ARG:HH21	38:U:154:ILE:HD11	1.83	0.44
24:5X:711:LYS:HA	24:5X:731:GLN:NE2	2.26	0.44
32:2:151:C:H2'	32:2:152:G:C8	2.51	0.44
33:B3:896:PHE:HE1	33:B3:959:VAL:HG13	1.82	0.44
36:5A:86:ARG:HH11	36:5A:89:LEU:HD12	1.78	0.44
36:5A:384:VAL:HG12	36:5A:385:GLU:N	2.31	0.44
36:5A:1502:PHE:O	36:5A:1753:LEU:HD12	2.18	0.44
38:U:229:ASN:HB2	38:U:296:SER:HA	1.99	0.44
16:52:48:ASN:OD1	16:52:48:ASN:N	2.42	0.44
6:4B:401:MET:HE3	6:4B:401:MET:HB3	1.90	0.44
23:5C:469:ASP:OD1	23:5C:469:ASP:N	2.49	0.44
29:5J:709:PRO:HA	29:5J:712:TRP:HD1	1.83	0.44
29:5J:725:MET:HG2	29:5J:752:LEU:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B3:3:LEU:HD12	33:B3:1093:MET:HE3	2.00	0.44
36:5A:380:LEU:HA	36:5A:381:PRO:HD3	1.72	0.44
36:5A:422:LEU:O	36:5A:635:ARG:NE	2.44	0.44
36:5A:1863:VAL:HG21	36:5A:1869:LEU:HB3	1.99	0.44
38:U:174:CYS:HB2	38:U:181:ILE:HD11	1.99	0.44
43:K:862:ILE:HD12	43:K:862:ILE:HA	1.75	0.44
43:K:902:MET:HE1	43:K:929:PHE:CD1	2.53	0.44
25:4b:42:LEU:O	25:4b:69:LEU:HA	2.18	0.44
44:4A:521:THR:OG1	44:4A:522:ALA:N	2.45	0.44
49:5B:968:ASN:ND2	49:5B:999:GLN:OE1	2.51	0.44
49:5B:1225:VAL:HG11	49:5B:1256:VAL:HG11	1.99	0.44
50:B1:475:PHE:HB3	50:B1:478:LEU:HD12	1.99	0.44
1:1:8:C:H3'	24:5X:504:GLY:N	2.33	0.44
7:5e:74:LEU:HA	13:5f:73:ARG:HH21	1.82	0.44
22:B2:461:THR:N	22:B2:464:GLU:OE1	2.50	0.44
25:2b:41:ILE:HD11	25:2b:71:LEU:HD12	2.00	0.44
33:B3:231:HIS:O	33:B3:252:SER:OG	2.35	0.44
5:43:73:LEU:HD11	25:4b:71:LEU:HB2	1.99	0.44
36:5A:92:LEU:HD13	36:5A:503:MET:HG3	2.00	0.44
36:5A:750:TRP:CE2	36:5A:778:ARG:HG2	2.53	0.44
39:5D:3:TYR:CE1	39:5D:33:ASP:HB3	2.52	0.44
43:K:950:ASN:HA	43:K:951:PRO:HD3	1.82	0.44
45:4:113:U:O3'	45:4:114:U:C6	2.71	0.44
49:5B:690:VAL:HG11	49:5B:707:ILE:HG21	2.00	0.44
49:5B:815:LEU:HD21	49:5B:821:LEU:HD11	1.99	0.44
49:5B:876:LEU:HD23	49:5B:880:LEU:HD23	2.00	0.44
50:B1:494:GLU:OE1	50:B1:534:GLN:NE2	2.51	0.44
50:B1:621:ASP:HB3	50:B1:624:VAL:HG12	1.99	0.44
1:1:73:C:C2	1:1:74:C:C4	3.06	0.44
1:1:118:A:N6	5:13:4:GLY:CA	2.71	0.44
7:4e:34:TRP:O	7:4e:85:THR:N	2.41	0.44
17:5:111:A:H2'	17:5:112:A:C8	2.52	0.44
23:5C:568:PRO:HB2	23:5C:569:ARG:HD2	1.99	0.44
24:5X:679:VAL:HG23	24:5X:682:LYS:HE2	1.99	0.44
16:42:56:VAL:HA	16:42:67:LEU:HD23	1.99	0.44
28:S:566:ILE:CD1	49:5B:693:THR:CG2	2.96	0.44
32:2:4:G:H2'	32:2:5:C:H6	1.83	0.44
33:B3:374:SER:H	33:B3:377:MET:HE2	1.82	0.44
36:5A:694:LEU:HB3	47:A1:463:GLU:OE1	2.18	0.44
36:5A:723:ASN:OD1	36:5A:785:LYS:NZ	2.50	0.44
36:5A:852:VAL:C	36:5A:854:SER:H	2.13	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5A:1838:LYS:HE3	36:5A:1865:ARG:HH22	1.83	0.44
36:5A:2280:ASN:HB3	36:5A:2309:HIS:CG	2.52	0.44
45:4:113:U:O3'	45:4:114:U:C5	2.71	0.44
49:5B:304:ASN:HA	49:5B:307:VAL:HG22	1.98	0.44
49:5B:466:LYS:HB3	49:5B:466:LYS:HE3	1.84	0.44
49:5B:1437:ARG:HG2	49:5B:1738:ALA:HB1	1.99	0.44
49:5B:1557:LYS:HD3	49:5B:1659:HIS:CD2	2.53	0.44
50:B1:604:ALA:O	50:B1:608:THR:OG1	2.31	0.44
50:B1:1044:ASP:HB3	50:B1:1083:TYR:CG	2.52	0.44
1:1:94:A:N1	1:1:115:U:C5	2.86	0.43
2:6:64:U:OP1	43:K:911:LYS:HE3	2.18	0.43
9:1K:85:GLU:HA	9:1K:88:MET:HE3	1.99	0.43
10:4C:163:THR:HA	10:4C:166:VAL:HG12	1.99	0.43
17:5:29:A:H2'	17:5:30:A:C8	2.53	0.43
24:5X:683:SER:O	24:5X:686:LYS:HB2	2.18	0.43
16:42:71:LYS:HZ3	16:42:95:TYR:HB2	1.82	0.43
13:5f:33:LEU:HD12	13:5f:44:LEU:HB3	2.00	0.43
34:1g:48:MET:HB3	34:1g:48:MET:HE3	1.75	0.43
25:5b:65:ARG:HE	25:5b:67:LEU:HD21	1.83	0.43
36:5A:970:GLU:HG3	36:5A:970:GLU:O	2.18	0.43
38:U:184:SER:HB2	49:5B:338:GLN:HA	2.00	0.43
39:5D:5:LEU:HB2	39:5D:60:LEU:CD1	2.48	0.43
16:52:65:MET:HE3	16:52:101:LEU:HD23	1.99	0.43
43:K:698:PHE:N	43:K:698:PHE:CD2	2.74	0.43
43:K:798:GLN:CD	43:K:830:LEU:HD13	2.43	0.43
43:K:970:ARG:NH1	43:K:974:HIS:NE2	2.66	0.43
1:1:7:A:H5'	24:5X:477:THR:CB	2.34	0.43
1:1:124:U:OP1	1:1:124:U:C6	2.70	0.43
6:4B:336:ARG:HH21	6:4B:353:GLU:HB3	1.83	0.43
6:4B:459:PRO:HG2	6:4B:502:SER:HA	2.00	0.43
11:41:51:GLU:OE1	11:41:51:GLU:N	2.52	0.43
16:22:30:SER:O	16:22:33:THR:HB	2.18	0.43
22:B2:614:ARG:HD3	22:B2:621:VAL:HG22	1.99	0.43
24:5X:530:ILE:CD1	24:5X:565:LYS:HB3	2.48	0.43
24:5X:670:PHE:CG	24:5X:751:ARG:HD3	2.53	0.43
29:5J:845:LEU:HD13	29:5J:877:ALA:HA	1.98	0.43
29:5J:905:GLU:HA	29:5J:906:PRO:HD3	1.80	0.43
30:4D:44:LYS:NZ	45:4:43:G:N7	2.60	0.43
13:4f:25:TRP:NE1	45:4:127:C:O2	2.51	0.43
33:B3:174:ASP:O	33:B3:246:SER:OG	2.22	0.43
33:B3:706:MET:HE3	33:B3:770:LEU:HD21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B3:1102:LEU:HD12	33:B3:1122:LEU:HD13	2.01	0.43
33:B3:1182:PHE:HA	33:B3:1185:MET:HE2	1.99	0.43
5:23:20:CYS:HB2	5:23:43:MET:HE1	2.00	0.43
36:5A:731:LEU:HD21	36:5A:739:ILE:HD12	2.00	0.43
36:5A:751:THR:HA	36:5A:782:LEU:HD11	2.00	0.43
36:5A:942:PRO:HB2	36:5A:1437:ARG:HD2	2.00	0.43
36:5A:952:VAL:HA	36:5A:1189:MET:HE3	1.99	0.43
36:5A:1267:LEU:HD23	36:5A:1328:LEU:HB2	2.00	0.43
34:2g:60:VAL:HG12	7:2e:88:GLN:HA	2.00	0.43
39:5D:5:LEU:HD13	39:5D:60:LEU:HD21	2.01	0.43
16:12:62:HIS:CD2	16:12:62:HIS:N	2.86	0.43
42:1C:46:ALA:O	42:1C:50:ILE:HG13	2.17	0.43
43:K:697:VAL:HG23	43:K:698:PHE:H	1.83	0.43
49:5B:1989:GLU:O	49:5B:1993:ARG:N	2.43	0.43
1:1:46:C:N4	1:1:47:C:N4	2.66	0.43
3:5O:149:GLY:O	3:5O:177:LYS:NZ	2.43	0.43
7:5e:66:SER:HB3	7:5e:67:LYS:HZ2	1.83	0.43
15:X:148:ASN:HB3	36:5A:1613:THR:HB	1.99	0.43
23:5C:480:LYS:NZ	23:5C:613:SER:O	2.50	0.43
23:5C:770:PHE:HA	23:5C:816:VAL:HG21	1.99	0.43
24:5X:299:LEU:HB3	36:5A:355:LEU:HD13	2.00	0.43
24:5X:530:ILE:O	24:5X:534:GLU:HG2	2.17	0.43
25:1b:18:ARG:HD2	25:1b:83:GLU:OE1	2.19	0.43
29:5J:157:TRP:CB	36:5A:701:ILE:HG21	2.43	0.43
34:1g:43:ASP:CG	34:1g:59:MET:CE	2.91	0.43
5:43:72:ILE:HD12	25:4b:67:LEU:HB2	1.99	0.43
36:5A:292:ASP:OD2	36:5A:1132:LYS:NZ	2.40	0.43
36:5A:1516:LYS:HB3	36:5A:1518:LEU:HD22	1.99	0.43
38:U:108:LEU:HD11	38:U:181:ILE:HG21	2.00	0.43
34:5g:46:VAL:HA	34:5g:56:ASN:HA	2.01	0.43
34:4g:59:MET:HE2	34:4g:59:MET:HB2	1.88	0.43
49:5B:146:GLU:OE2	49:5B:149:ARG:NH1	2.51	0.43
49:5B:769:CYS:O	49:5B:775:LYS:NZ	2.49	0.43
49:5B:1109:ASP:OD2	49:5B:1269:ARG:NH2	2.51	0.43
49:5B:1415:ASP:HB3	49:5B:1435:LEU:HD11	2.00	0.43
1:1:15:G:N2	1:1:16:G:C2	2.86	0.43
10:4C:357:ARG:CG	10:4C:358:ARG:HG3	2.41	0.43
5:53:23:ASN:N	5:53:67:LYS:O	2.52	0.43
24:5X:362:LEU:HG	24:5X:391:ARG:HH21	1.84	0.43
24:5X:373:PHE:CE1	24:5X:419:ARG:CD	2.96	0.43
24:5X:730:ILE:O	24:5X:730:ILE:HG13	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:1b:53:PRO:CG	25:1b:58:GLN:O	2.60	0.43
28:S:567:PRO:CD	28:S:568:THR:N	2.79	0.43
28:S:720:LEU:HG	28:S:724:GLU:HG3	2.00	0.43
13:4f:36:VAL:HG13	13:4f:40:MET:HA	1.99	0.43
34:1g:57:ILE:O	34:1g:57:ILE:HG13	2.19	0.43
36:5A:766:THR:O	39:5D:141:ARG:NH1	2.51	0.43
38:U:105:CYS:HB3	38:U:108:LEU:HD13	1.99	0.43
38:U:517:ILE:HG12	38:U:519:VAL:HG13	2.01	0.43
45:4:93:G:H2'	45:4:94:A:H8	1.82	0.43
49:5B:694:GLU:O	49:5B:700:ARG:NH1	2.45	0.43
49:5B:1469:VAL:HG21	49:5B:1735:HIS:CG	2.54	0.43
49:5B:1763:ARG:HA	49:5B:1763:ARG:HD2	1.71	0.43
6:4B:230:ASP:OD2	6:4B:252:SER:OG	2.35	0.43
10:4C:128:LEU:HD13	10:4C:166:VAL:HG13	1.99	0.43
7:4e:58:LEU:HB2	7:4e:77:ILE:HG22	2.00	0.43
22:B2:528:ILE:O	22:B2:531:THR:OG1	2.32	0.43
16:42:41:GLN:HG2	16:42:55:ARG:HG2	2.00	0.43
16:42:104:ASP:HB3	45:4:124:U:H1'	2.01	0.43
16:42:107:ILE:HA	13:4f:68:ASN:HD22	1.83	0.43
29:5J:92:GLY:O	29:5J:93:PRO:CB	2.65	0.43
29:5J:828:THR:HG21	45:4:41:C:H5'	2.00	0.43
33:B3:70:LEU:HD21	33:B3:146:ARG:HB2	2.01	0.43
33:B3:565:TYR:HE2	33:B3:567:GLU:HB2	1.84	0.43
33:B3:932:ASN:CB	33:B3:935:GLU:CD	2.91	0.43
36:5A:143:GLN:NE2	36:5A:207:PHE:O	2.35	0.43
36:5A:682:ASP:N	36:5A:682:ASP:OD1	2.47	0.43
36:5A:979:SER:O	36:5A:1094:ARG:HA	2.18	0.43
7:2e:57:VAL:HA	7:2e:77:ILE:O	2.18	0.43
43:K:698:PHE:CB	43:K:725:MET:HE1	2.48	0.43
11:21:7:LEU:HD12	11:21:10:LEU:HD12	2.01	0.43
45:4:22:C:H2'	45:4:23:G:H8	1.82	0.43
49:5B:905:ILE:HD13	49:5B:970:VAL:HG21	2.00	0.43
49:5B:1004:LEU:HB3	49:5B:1017:VAL:HG22	2.01	0.43
49:5B:1313:ARG:HG2	49:5B:1340:TYR:HE1	1.84	0.43
49:5B:2050:PRO:HB3	49:5B:2059:LYS:HE2	1.99	0.43
50:B1:732:TRP:NE1	50:B1:736:ARG:HE	2.16	0.43
6:4B:259:SER:O	6:4B:263:CYS:N	2.51	0.43
7:5e:80:LYS:HG3	13:5f:69:VAL:HG23	1.99	0.43
12:R:394:ASP:HB3	12:R:414:ARG:HH21	1.84	0.43
14:66:36:CYS:SG	31:63:17:PRO:HA	2.59	0.43
21:A2:117:TYR:OH	21:A2:176:TYR:HD2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:2b:31:PHE:HA	25:2b:42:LEU:HD23	1.99	0.43
35:68:36:LEU:HD11	35:68:70:ILE:HD11	2.00	0.43
36:5A:188:LEU:O	36:5A:189:GLU:O	2.37	0.43
39:5D:3:TYR:HD1	39:5D:33:ASP:OD2	2.01	0.43
43:K:882:LEU:HD12	43:K:882:LEU:HA	1.80	0.43
43:K:926:ASN:O	43:K:927:LEU:HB2	2.18	0.43
43:K:985:MET:O	43:K:991:ARG:HD3	2.19	0.43
44:4A:451:GLN:OE1	47:A1:430:UNK:O	2.32	0.43
11:21:17:ILE:HD12	11:21:40:LEU:HD11	2.00	0.43
45:4:105:A:H2'	45:4:106:G:H8	1.83	0.43
48:65:60:THR:HB	48:65:61:PRO:HD3	2.01	0.43
49:5B:1152:ARG:HH21	49:5B:1156:LEU:HD21	1.83	0.43
49:5B:1847:GLU:HG2	49:5B:1892:ASN:HD21	1.83	0.43
1:1:132:G:C5'	16:12:104:ASP:HB2	2.47	0.43
23:5C:442:LYS:HB2	23:5C:442:LYS:HE3	1.83	0.43
24:5X:379:ILE:HG22	24:5X:629[B]:ILE:HA	2.00	0.43
33:B3:639:SER:OG	33:B3:699:VAL:O	2.33	0.43
25:5b:86:PRO:HA	25:5b:87:PRO:HD3	1.84	0.43
7:1e:48:ILE:HD11	7:1e:59:ASP:HB2	1.99	0.43
36:5A:450:LEU:HG	36:5A:607:ASP:HB3	2.01	0.43
36:5A:511:LYS:HB2	36:5A:513:LEU:HG	2.00	0.43
36:5A:559:ASP:O	36:5A:562:VAL:CG2	2.67	0.43
36:5A:1544:ARG:HD3	36:5A:1671:TYR:HB3	2.00	0.43
38:U:236:TYR:OH	38:U:313:GLN:O	2.34	0.43
43:K:759:HIS:O	43:K:760:LYS:C	2.61	0.43
49:5B:1379:ILE:HG21	49:5B:1470:ILE:HD11	1.99	0.43
49:5B:1973:ARG:HB3	49:5B:1997:LEU:HD11	2.00	0.43
50:B1:503:LYS:HB3	50:B1:511:MET:HG2	2.01	0.43
50:B1:1009:MET:HE3	50:B1:1009:MET:HB2	1.83	0.43
1:1:58:C:O2'	1:1:59:U:H5'	2.19	0.43
1:1:118:A:N6	5:13:4:GLY:HA2	2.20	0.43
3:5O:75:HIS:ND1	3:5O:77:ASN:OD1	2.52	0.43
6:4B:257:LEU:HD22	6:4B:267:HIS:HE1	1.84	0.43
7:4e:46:CYS:HB2	7:4e:59:ASP:HB3	2.00	0.43
7:4e:77:ILE:HD11	13:4f:71:TYR:CG	2.54	0.43
15:X:124:VAL:HG13	13:4f:39:TYR:CD2	2.46	0.43
17:5:93:U:H4'	17:5:94:U:H5''	2.00	0.43
24:5X:362:LEU:N	24:5X:391:ARG:CZ	2.67	0.43
25:2b:71:LEU:HB2	5:23:73:LEU:HD11	2.01	0.43
33:B3:238:VAL:HG21	33:B3:258:TYR:HE1	1.84	0.43
33:B3:507:SER:OG	33:B3:508:CYS:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B3:875:ASN:OD1	33:B3:875:ASN:N	2.48	0.43
36:5A:540:PHE:HB3	36:5A:544:PHE:HB3	1.99	0.43
36:5A:569:VAL:HB	36:5A:573:GLN:HB2	2.00	0.43
36:5A:776:LEU:HD22	36:5A:900:ASP:HB2	2.00	0.43
36:5A:2106:LEU:HD12	36:5A:2107:PRO:HD2	2.01	0.43
37:A3:356:ARG:HD2	11:21:75:PRO:CA	2.48	0.43
43:K:773:ASN:HB3	43:K:822:LEU:CD2	2.49	0.43
43:K:817:LYS:HA	43:K:878:THR:CG2	2.49	0.43
46:2A:103:LEU:HD23	46:2A:128:LYS:HE3	2.01	0.43
47:A1:167:VAL:HG12	47:A1:211:LEU:HD12	2.01	0.43
48:65:37:VAL:HG12	48:65:55:THR:HB	2.00	0.43
49:5B:142:VAL:HG11	49:5B:157:ILE:HD11	2.01	0.43
49:5B:520:GLU:HG3	49:5B:611:LEU:HB2	2.00	0.43
49:5B:834:TYR:OH	49:5B:1030:ARG:NH2	2.51	0.43
2:6:105:U:C6	31:63:88:ARG:NH2	2.86	0.43
6:4B:311:ASP:N	6:4B:311:ASP:OD1	2.50	0.43
22:B2:561:MET:HG2	50:B1:1056:MET:HG2	2.01	0.43
16:42:107:ILE:HG22	16:42:108:VAL:HG13	2.01	0.43
29:5J:434:VAL:HG12	29:5J:460:ILE:HD13	2.00	0.43
25:2b:67:LEU:HB3	5:23:72:ILE:HG12	2.00	0.43
33:B3:278:LEU:H	33:B3:278:LEU:HG	1.48	0.43
33:B3:640:LEU:HD22	33:B3:667:ILE:HG12	2.01	0.43
33:B3:1055:VAL:HB	33:B3:1093:MET:HG3	2.01	0.43
33:B3:1165:SER:HB3	33:B3:1169:PRO:HA	2.00	0.43
36:5A:584:HIS:HB3	36:5A:587:GLN:HB2	2.00	0.43
36:5A:1536:LEU:HD21	36:5A:1576:ILE:HD11	2.01	0.43
38:U:308:SER:OG	38:U:311:THR:O	2.37	0.43
16:12:40:THR:HG21	16:12:111:ARG:HH21	1.83	0.43
43:K:830:LEU:HD22	43:K:830:LEU:C	2.43	0.43
43:K:941:GLU:H	43:K:941:GLU:CD	2.27	0.43
34:4g:46:VAL:HA	34:4g:56:ASN:HA	2.01	0.43
49:5B:423:MET:HE2	49:5B:423:MET:HB3	1.87	0.43
1:1:11:G:N7	24:5X:507:SER:HB2	2.32	0.43
2:6:88:G:H2'	2:6:89:U:C6	2.54	0.43
2:6:105:U:O2	31:63:49:HIS:HB3	2.18	0.43
6:4B:387:ALA:HB3	44:4A:427:PRO:HD2	2.01	0.43
7:5e:30:ARG:HD2	7:5e:30:ARG:HA	1.77	0.43
7:4e:88:GLN:HB2	34:4g:57:ILE:HG21	2.00	0.43
14:66:77:LYS:HE3	48:65:70:ASP:HB2	2.00	0.43
5:53:19:THR:HB	5:53:29:ARG:HG3	2.01	0.43
23:5C:697:ALA:HB1	23:5C:742:PRO:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:5X:593:GLU:C	24:5X:595:GLY:N	2.77	0.43
25:1b:43:CYS:O	25:1b:44:ASP:C	2.61	0.43
27:1A:75:PHE:HB3	27:1A:82:MET:CE	2.46	0.43
29:5J:710:LYS:HA	29:5J:713:MET:HE3	2.01	0.43
13:4f:11:LEU:HD21	13:4f:72:ILE:HD13	2.01	0.43
33:B3:546:LYS:HD3	33:B3:546:LYS:HA	1.78	0.43
5:23:46:ILE:HA	5:23:46:ILE:HD13	1.84	0.43
5:43:32:LEU:HA	5:43:43:MET:HA	2.00	0.43
7:1e:67:LYS:HG3	7:1e:68:THR:N	2.34	0.43
38:U:111:ILE:HG23	38:U:137:LEU:HB3	2.01	0.43
44:4A:459:GLU:HA	44:4A:462:GLU:HB3	2.01	0.43
46:2A:107:ASP:OD1	46:2A:134:TYR:OH	2.27	0.43
49:5B:1491:SER:OG	49:5B:1492:SER:N	2.52	0.43
49:5B:1514:PHE:HB3	49:5B:1518:VAL:HG11	2.00	0.43
49:5B:2009:ARG:HA	49:5B:2012:ASN:HB2	2.00	0.43
50:B1:520:THR:O	50:B1:562:LYS:NZ	2.52	0.43
50:B1:1171:PRO:HA	50:B1:1174:GLU:HG2	2.00	0.43
1:1:47:C:O5'	1:1:47:C:H6	2.01	0.42
3:5O:214:ASP:N	3:5O:214:ASP:OD1	2.46	0.42
6:4B:230:ASP:HB3	6:4B:232:ARG:H	1.84	0.42
6:4B:496:MET:HE2	6:4B:496:MET:HB3	1.92	0.42
9:1K:57:PRO:O	9:1K:58:THR:C	2.62	0.42
10:4C:297:ALA:O	10:4C:300:THR:HB	2.18	0.42
24:5X:733[A]:VAL:CG1	24:5X:735:MET:H	2.20	0.42
25:1b:17:MET:HE3	25:1b:82:VAL:CG2	2.49	0.42
36:5A:1510:GLU:C	36:5A:1513:MET:HE2	2.38	0.42
40:64:17:VAL:HG22	40:64:69:LEU:CD2	2.49	0.42
43:K:958:ASP:O	43:K:959:LEU:HB3	2.19	0.42
49:5B:755:GLY:O	49:5B:758:SER:N	2.44	0.42
49:5B:811:SER:OG	49:5B:812:THR:N	2.52	0.42
49:5B:814:THR:O	49:5B:818:GLY:N	2.50	0.42
49:5B:1382:MET:HG3	49:5B:1652:TRP:CD2	2.54	0.42
49:5B:2110:SER:OG	49:5B:2111:ASP:N	2.52	0.42
50:B1:1276:SER:O	50:B1:1276:SER:OG	2.34	0.42
5:13:80:ALA:HB1	5:13:81:PRO:HD2	2.01	0.42
16:22:30:SER:O	16:22:34:GLN:N	2.45	0.42
17:5:92:U:OP1	11:51:63:ASN:ND2	2.52	0.42
5:53:64:ARG:NE	5:53:66:SER:OG	2.49	0.42
23:5C:134:LEU:HG	23:5C:202:ILE:HG23	2.01	0.42
24:5X:411:TYR:CZ	24:5X:491:PHE:HE2	2.37	0.42
29:5J:287:ASP:O	29:5J:291:ILE:N	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B3:126:LYS:HA	33:B3:126:LYS:HD3	1.88	0.42
33:B3:471:ASP:OD2	33:B3:746:ALA:N	2.49	0.42
36:5A:142:SER:OG	36:5A:238:LEU:O	2.34	0.42
36:5A:1332:HIS:CE1	36:5A:1364:LEU:HD22	2.54	0.42
36:5A:2009:ASP:HB2	36:5A:2014:MET:HB3	2.01	0.42
37:A3:408:CYS:HB2	37:A3:422:PHE:HE1	1.84	0.42
39:5D:53:LYS:CE	47:A1:447:UNK:CB	2.96	0.42
7:2e:36:TYR:N	7:2e:83:ASN:O	2.45	0.42
43:K:792:VAL:HG21	43:K:883:TYR:HD2	1.84	0.42
43:K:825:GLU:HG2	43:K:826:SER:N	2.32	0.42
43:K:953:LYS:HE3	43:K:958:ASP:OD2	2.18	0.42
49:5B:319:LYS:HB2	49:5B:319:LYS:HE3	1.79	0.42
49:5B:429:GLN:N	49:5B:886:GLN:OE1	2.45	0.42
49:5B:1062:LEU:HD22	49:5B:1081:MET:HB2	2.01	0.42
49:5B:1962:GLN:HG2	49:5B:2010:PHE:HZ	1.84	0.42
6:4B:257:LEU:HD21	6:4B:296:LEU:HD11	2.00	0.42
10:4C:311:SER:O	10:4C:311:SER:OG	2.35	0.42
18:67:55:MET:HE1	48:65:59:ILE:HD13	2.01	0.42
23:5C:327:TYR:OH	23:5C:372:PHE:O	2.30	0.42
23:5C:841:ASP:OD2	24:5X:320:TYR:OH	2.31	0.42
28:S:636:ARG:HH12	45:4:128:A:H1'	1.84	0.42
25:2b:71:LEU:HD13	5:23:10:LEU:HB2	2.01	0.42
33:B3:591:SER:OG	33:B3:640:LEU:O	2.32	0.42
5:43:75:ASP:HB2	5:43:78:LYS:HD2	2.00	0.42
36:5A:758:ARG:NH2	36:5A:901:LEU:O	2.52	0.42
43:K:740:ASN:HD21	43:K:752:ARG:HA	1.84	0.42
44:4A:561:GLU:HB2	44:4A:648:PHE:HE1	1.85	0.42
1:1:7:A:H5''	24:5X:478:ARG:HB3	1.72	0.42
5:13:48:VAL:CG1	5:13:56:ALA:HB3	2.49	0.42
14:66:20:VAL:HG12	14:66:75:THR:HA	2.01	0.42
20:2B:16:ASP:HB2	20:2B:49:ARG:HH21	1.84	0.42
5:53:30:GLY:HA3	5:53:46:ILE:HD13	2.01	0.42
23:5C:507:VAL:HA	23:5C:568:PRO:HD3	2.01	0.42
23:5C:516:LEU:HD21	23:5C:573:GLU:HG3	2.00	0.42
16:42:58:ALA:O	16:42:65:MET:HA	2.19	0.42
29:5J:559:ALA:HA	29:5J:562:ILE:HG22	2.00	0.42
33:B3:512:GLY:N	33:B3:515:ALA:O	2.45	0.42
36:5A:1268:ILE:O	36:5A:1272:THR:OG1	2.30	0.42
41:BP:74:GLU:HB3	50:B1:1197:LEU:HD13	2.01	0.42
43:K:782:GLY:C	43:K:785:VAL:HG13	2.44	0.42
45:4:127:C:H2'	45:4:128:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:5B:537:LYS:NZ	49:5B:580:ILE:O	2.51	0.42
49:5B:1566:ARG:HG2	49:5B:1621:HIS:HB2	2.02	0.42
29:5J:240:MET:HB3	36:5A:796:LYS:HG3	2.01	0.42
29:5J:736:LEU:HD22	29:5J:746:TRP:CE2	2.54	0.42
29:5J:739:CYS:HG	29:5J:742:SER:HG	1.61	0.42
33:B3:706:MET:HE2	33:B3:767:LEU:HD12	2.00	0.42
36:5A:912:GLU:HA	36:5A:913:PRO:HD3	1.91	0.42
36:5A:1382:SER:HA	36:5A:1415:GLY:HA2	2.01	0.42
44:4A:661:PHE:CD2	44:4A:670:TRP:HB2	2.55	0.42
45:4:6:U:H2'	45:4:7:G:C8	2.55	0.42
1:1:49:A:C2	1:1:50:G:C5	3.07	0.42
9:1K:109:ARG:O	9:1K:172:ARG:HD3	2.20	0.42
16:22:18:LYS:HE2	16:22:18:LYS:HB3	1.89	0.42
23:5C:370:VAL:HA	23:5C:374:LEU:HB2	2.02	0.42
24:5X:432:ILE:HG21	24:5X:609:MET:HE1	2.01	0.42
24:5X:565:LYS:HB2	24:5X:565:LYS:HE3	1.88	0.42
25:1b:60:GLU:O	25:1b:60:GLU:HG2	2.19	0.42
13:5f:20:MET:HA	13:5f:29:TYR:O	2.19	0.42
29:5J:674:THR:C	29:5J:676:ARG:N	2.76	0.42
11:51:51:GLU:OE1	11:51:51:GLU:N	2.52	0.42
5:43:80:ALA:HA	5:43:81:PRO:HA	1.83	0.42
36:5A:87:VAL:HG12	36:5A:121:HIS:CE1	2.55	0.42
36:5A:2252:LEU:H	36:5A:2255:HIS:CD2	2.37	0.42
38:U:164:PHE:O	38:U:173:TYR:N	2.43	0.42
48:65:36:ILE:HG23	48:65:54:VAL:CG1	2.50	0.42
49:5B:1192:PRO:HG3	49:5B:1289:LEU:HD11	2.00	0.42
50:B1:578:ILE:HD13	50:B1:578:ILE:HA	1.89	0.42
1:1:94:A:C2	1:1:115:U:C5	3.07	0.42
1:1:102:A:O2'	1:1:103:A:C8	2.73	0.42
1:1:118:A:C2'	42:1C:2:PRO:HD2	2.50	0.42
5:13:46:ILE:HG12	5:13:58:LEU:HB2	2.01	0.42
18:67:44:LEU:HD12	18:67:46:LEU:HD21	2.01	0.42
22:B2:652:GLY:HA2	22:B2:657:ILE:CG1	2.49	0.42
23:5C:939:ARG:NH1	23:5C:945:GLU:OE2	2.53	0.42
16:42:76:GLU:O	16:42:89:PRO:HA	2.20	0.42
29:5J:839:HIS:HB2	43:K:942:LYS:HZ1	1.82	0.42
13:4f:11:LEU:O	13:4f:15:THR:HG23	2.19	0.42
33:B3:122:ALA:HB2	33:B3:170:VAL:HG13	2.00	0.42
33:B3:144:LEU:HD22	33:B3:152:LEU:HD11	2.02	0.42
33:B3:720:TRP:HA	33:B3:733:PRO:HA	2.02	0.42
33:B3:929:LYS:O	33:B3:930:LEU:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5A:193:LEU:N	36:5A:208:TYR:CZ	2.88	0.42
36:5A:1562:MET:HE2	36:5A:1562:MET:HB3	1.96	0.42
36:5A:1667:ARG:NH1	36:5A:1673:SER:O	2.53	0.42
34:2g:59:MET:HG2	7:2e:20:LEU:HD11	2.01	0.42
34:2g:61:VAL:HG23	7:2e:20:LEU:HD22	2.01	0.42
7:2e:55:ASN:OD1	7:2e:81:GLY:N	2.42	0.42
44:4A:386:GLU:HG3	44:4A:387:ILE:H	1.85	0.42
44:4A:436:LEU:HD12	44:4A:437:GLY:N	2.35	0.42
44:4A:494:THR:O	44:4A:498:ALA:CB	2.68	0.42
45:4:59:U:H2'	45:4:60:A:C8	2.54	0.42
45:4:108:C:H2'	45:4:109:G:H8	1.85	0.42
49:5B:1367:MET:HB3	49:5B:1367:MET:HE3	1.71	0.42
49:5B:1936:LEU:HD13	49:5B:2069:GLY:HA3	2.02	0.42
50:B1:1126:PHE:O	50:B1:1130:PRO:HD2	2.20	0.42
1:1:140:G:C1'	25:1b:57:LYS:HE2	2.49	0.42
3:5O:229:TYR:HE1	3:5O:231:MET:HE3	1.85	0.42
4:B4:20:LEU:HD23	4:B4:84:ILE:HD12	2.01	0.42
6:4B:234:ILE:HG21	6:4B:248:THR:HB	2.01	0.42
10:4C:59:MET:HE3	10:4C:59:MET:HB3	1.92	0.42
23:5C:747:ASP:HA	23:5C:791:ILE:HB	2.02	0.42
24:5X:380:THR:H	24:5X:628:TYR:C	2.13	0.42
33:B3:801:GLU:O	33:B3:864:SER:HA	2.20	0.42
39:5D:8:LEU:HD13	39:5D:14:VAL:CB	2.47	0.42
16:12:62:HIS:CD2	16:12:62:HIS:H	2.37	0.42
42:1C:46:ALA:O	42:1C:49:LEU:HG	2.20	0.42
43:K:864:LYS:HE3	43:K:915:LYS:HE2	2.01	0.42
25:4b:18:ARG:N	25:4b:81:THR:O	2.44	0.42
25:4b:40:LEU:HD11	25:4b:80:MET:HE1	2.02	0.42
44:4A:524:GLN:HA	44:4A:527:VAL:HG12	2.00	0.42
48:65:41:LEU:HD12	48:65:50:VAL:HG12	2.01	0.42
49:5B:443:GLU:OE1	49:5B:873:HIS:NE2	2.42	0.42
49:5B:1761:TYR:HD2	49:5B:1785:LEU:HD11	1.84	0.42
50:B1:1174:GLU:HB2	50:B1:1214:TYR:CE2	2.55	0.42
1:1:8:C:H3'	24:5X:504:GLY:CA	2.50	0.42
1:1:51:G:C2	1:1:52:G:C8	3.07	0.42
6:4B:296:LEU:HB2	6:4B:308:TRP:HB2	2.00	0.42
6:4B:388:PHE:CE1	44:4A:425:ASN:O	2.73	0.42
20:2B:19:LYS:HD3	20:2B:19:LYS:HA	1.94	0.42
23:5C:677:GLU:HG3	23:5C:684:LYS:HB2	2.01	0.42
23:5C:701:GLU:OE1	23:5C:785:ARG:NH2	2.41	0.42
23:5C:830:PRO:HG2	23:5C:877:ALA:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:5X:293:ARG:HH22	36:5A:274:PRO:HB2	1.85	0.42
29:5J:98:ASP:HB3	36:5A:86:ARG:HG2	1.99	0.42
29:5J:274:LEU:HD23	29:5J:277:LEU:HD12	2.01	0.42
29:5J:776:ASN:HD21	29:5J:779:LEU:HG	1.84	0.42
34:1g:59:MET:O	34:1g:60:VAL:HG13	2.20	0.42
5:43:64:ARG:NH2	45:4:120:U:O2'	2.53	0.42
36:5A:1416:ILE:HA	36:5A:1416:ILE:HD13	1.81	0.42
36:5A:2196:HIS:HD2	36:5A:2230:LEU:HD22	1.83	0.42
34:2g:7:PRO:HB2	34:2g:9:LEU:HG	2.01	0.42
41:BP:27:ASP:OD1	41:BP:67:SER:OG	2.33	0.42
42:1C:45:GLN:O	42:1C:48:SER:HB3	2.19	0.42
45:4:128:A:H2'	45:4:129:G:H8	1.85	0.42
49:5B:1225:VAL:HG22	49:5B:1268:ILE:HG12	2.01	0.42
1:1:17:G:H2'	1:1:18:G:C8	2.55	0.42
1:1:164:G:C4'	11:11:49:ASN:C	2.93	0.42
6:4B:228:ILE:HD13	6:4B:515:THR:HG22	2.02	0.42
6:4B:284:LYS:HE2	6:4B:284:LYS:HB3	1.82	0.42
6:4B:289:LEU:HD23	6:4B:289:LEU:HA	1.86	0.42
13:2f:38:GLY:O	32:2:99:A:N6	2.50	0.42
24:5X:432:ILE:HG21	24:5X:609:MET:HE3	2.02	0.42
24:5X:536:ARG:HG3	34:1g:10:LYS:HE3	1.99	0.42
11:11:53:VAL:HG12	11:11:55:LEU:HD11	2.02	0.42
13:5f:63:LEU:HD21	16:52:29:LEU:HD23	2.01	0.42
13:4f:11:LEU:HD13	13:4f:36:VAL:HG21	2.01	0.42
33:B3:319:GLU:HG2	33:B3:320:ASP:H	1.85	0.42
34:1g:76:VAL:O	34:1g:76:VAL:HG12	2.20	0.42
36:5A:940:ILE:HD11	36:5A:1046:LEU:HB2	2.01	0.42
39:5D:90:ILE:HG21	39:5D:119:VAL:HG13	2.02	0.42
39:5D:106:MET:HE2	39:5D:106:MET:HB3	1.90	0.42
16:52:32:LEU:HA	16:52:32:LEU:HD23	1.82	0.42
16:52:45:ASN:HB3	16:52:108:VAL:HG22	2.02	0.42
49:5B:1542:MET:HE2	49:5B:1705:MET:HB3	2.01	0.42
1:1:10:U:H5''	24:5X:508:ARG:HB2	1.47	0.41
1:1:29:A:H1'	9:1K:200:ARG:CD	2.49	0.41
1:1:54:G:H22	1:1:84:G:H2'	1.85	0.41
8:I:99:G:OP2	50:B1:1106:ARG:NE	2.52	0.41
9:1K:50:ASP:N	9:1K:51:PRO:CD	2.83	0.41
11:41:16:THR:HA	11:41:25:VAL:O	2.20	0.41
12:R:404:PHE:HA	12:R:405:PRO:HA	1.85	0.41
7:4e:44:GLU:O	7:4e:61:ALA:HA	2.20	0.41
15:X:123:SER:HB3	16:42:23:GLU:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:B2:617:LEU:HB3	22:B2:619:MET:HG2	2.01	0.41
23:5C:779:LEU:HD11	23:5C:825:PRO:HB2	2.02	0.41
23:5C:888:ARG:O	23:5C:893:GLY:N	2.47	0.41
16:42:107:ILE:HA	13:4f:68:ASN:ND2	2.35	0.41
26:B5:51:ASN:O	26:B5:55:ILE:HG12	2.20	0.41
29:5J:674:THR:C	29:5J:676:ARG:H	2.28	0.41
29:5J:675:ALA:O	29:5J:678:PHE:HB2	2.20	0.41
11:51:61:ARG:HG3	25:5b:38:MET:HG2	2.02	0.41
32:2:4:G:H2'	32:2:5:C:C6	2.55	0.41
33:B3:11:ALA:HB3	33:B3:37:ILE:HD13	2.02	0.41
33:B3:321:MET:HE3	33:B3:321:MET:HB3	1.71	0.41
33:B3:329:TYR:N	33:B3:370:GLU:OE2	2.52	0.41
33:B3:1166:TYR:OH	50:B1:1278:ASP:OD2	2.31	0.41
25:5b:32:LYS:HB2	25:5b:41:ILE:HG22	2.02	0.41
36:5A:736:GLU:O	36:5A:740:LEU:HG	2.19	0.41
36:5A:1513:MET:O	36:5A:1514:LYS:C	2.61	0.41
36:5A:1596:VAL:HG11	36:5A:1729:ALA:HB2	2.02	0.41
36:5A:1833:LEU:HD22	36:5A:1835:GLN:HG2	2.02	0.41
36:5A:1841:THR:HG23	36:5A:1868:MET:HE3	2.02	0.41
36:5A:2327:SER:OG	36:5A:2328:ALA:N	2.52	0.41
38:U:447:LEU:H	38:U:493:HIS:CE1	2.38	0.41
39:5D:5:LEU:HB2	39:5D:60:LEU:HD11	2.02	0.41
42:1C:25:CYS:HA	42:1C:30:HIS:CD2	2.54	0.41
43:K:864:LYS:CG	43:K:865:SER:N	2.82	0.41
43:K:1004:GLN:O	43:K:1005:GLU:CB	2.67	0.41
25:4b:52:LYS:HE2	25:4b:52:LYS:HB3	1.81	0.41
49:5B:70:LYS:HA	49:5B:73:LYS:HE2	2.01	0.41
49:5B:94:ILE:HD11	49:5B:840:ARG:HB2	2.01	0.41
49:5B:492:ALA:HA	49:5B:647:ARG:HH22	1.85	0.41
50:B1:866:LYS:HG3	50:B1:909:VAL:HG11	2.02	0.41
50:B1:947:VAL:HA	50:B1:950:GLN:HG2	2.02	0.41
1:1:32:A:N9	9:1K:135:VAL:HG22	2.19	0.41
6:4B:478:THR:HG22	6:4B:483:SER:H	1.84	0.41
9:1K:89:TRP:CZ2	9:1K:91:PRO:HG3	2.55	0.41
13:1f:3:LEU:HG	13:1f:4:PRO:HD2	2.02	0.41
13:2f:6:ASN:HB2	13:2f:9:PRO:HD2	2.02	0.41
11:51:16:THR:HA	11:51:25:VAL:O	2.20	0.41
33:B3:930:LEU:HD11	33:B3:934:GLY:HA2	2.01	0.41
35:68:28:LYS:HB2	35:68:39:ASP:OD2	2.20	0.41
5:43:7:ILE:HA	5:43:10:LEU:HG	2.00	0.41
5:43:26:GLU:HG2	5:43:50:TYR:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5A:169:PHE:CD1	36:5A:563:GLN:NE2	2.81	0.41
36:5A:804:GLU:HA	36:5A:807:VAL:HG22	2.01	0.41
36:5A:1405:LEU:HD11	49:5B:67:ARG:HH11	1.84	0.41
36:5A:1557:LEU:HA	36:5A:1620:TYR:CZ	2.55	0.41
36:5A:1681:ARG:HG3	36:5A:1715:TYR:CZ	2.55	0.41
36:5A:1763:LEU:HD11	36:5A:1768:TYR:HA	2.02	0.41
39:5D:73:TYR:O	39:5D:101:LYS:NZ	2.39	0.41
16:12:40:THR:HG21	16:12:111:ARG:NH2	2.35	0.41
42:1C:40:LYS:HA	42:1C:40:LYS:HE3	2.02	0.41
43:K:695:GLN:HA	43:K:700:ASN:HA	2.02	0.41
43:K:896:HIS:O	43:K:900:LEU:HG	2.20	0.41
44:4A:548:VAL:HG22	44:4A:630:CYS:HB2	2.01	0.41
11:21:14:THR:HA	11:21:28:THR:HA	2.02	0.41
49:5B:557:LYS:HD2	49:5B:557:LYS:HA	1.85	0.41
49:5B:789:MET:O	49:5B:794:ARG:NH1	2.53	0.41
49:5B:973:ASP:OD1	49:5B:973:ASP:N	2.50	0.41
49:5B:1301:LEU:HD23	49:5B:1301:LEU:HA	1.85	0.41
49:5B:2029:ILE:HG21	49:5B:2124:VAL:HG12	2.02	0.41
50:B1:488:SER:HB3	50:B1:492:GLN:HG2	2.02	0.41
1:1:32:A:C2	9:1K:133:HIS:O	2.73	0.41
6:4B:349:LEU:HD23	6:4B:358:ILE:HD11	2.01	0.41
9:1K:48:PHE:CE2	9:1K:53:ASP:HA	2.50	0.41
22:B2:477:MET:SD	37:A3:423:GLN:NE2	2.93	0.41
23:5C:158:ARG:HA	23:5C:158:ARG:HD3	1.79	0.41
23:5C:271:PRO:HB2	23:5C:370:VAL:HG13	2.03	0.41
24:5X:306:GLY:N	36:5A:244:GLN:O	2.45	0.41
16:42:52:LEU:HD12	16:42:101:LEU:HD22	2.02	0.41
13:5f:37:ASP:OD1	13:5f:37:ASP:N	2.54	0.41
29:5J:265:GLN:HB3	36:5A:1003:HIS:HE1	1.85	0.41
29:5J:692:ARG:HD2	29:5J:692:ARG:HA	1.80	0.41
32:2:150:U:H2'	32:2:151:C:C6	2.55	0.41
33:B3:459:VAL:HA	33:B3:475:ILE:O	2.19	0.41
33:B3:685:ASP:OD1	33:B3:685:ASP:N	2.48	0.41
36:5A:480:LYS:HB3	36:5A:480:LYS:HE2	1.89	0.41
36:5A:1314:VAL:HA	36:5A:1478:LEU:HD22	2.03	0.41
38:U:248:PRO:HD2	38:U:450:TYR:CE2	2.56	0.41
38:U:542:MET:HE2	38:U:542:MET:HB3	1.87	0.41
39:5D:8:LEU:HD13	39:5D:14:VAL:CG2	2.50	0.41
16:52:24:PHE:O	16:52:33:THR:OG1	2.35	0.41
7:2e:34:TRP:CE2	7:2e:86:LEU:HD22	2.55	0.41
42:1C:17:SER:O	42:1C:21:ARG:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:K:752:ARG:HA	43:K:752:ARG:HD2	1.76	0.41
49:5B:436:ARG:NE	49:5B:443:GLU:OE2	2.43	0.41
49:5B:823:ALA:O	49:5B:857:GLY:N	2.44	0.41
49:5B:1973:ARG:HA	49:5B:1973:ARG:HD2	1.72	0.41
49:5B:2064:TRP:HB2	49:5B:2082:LEU:HB3	2.02	0.41
1:1:7:A:C3'	24:5X:478:ARG:N	2.82	0.41
1:1:8:C:OP2	24:5X:504:GLY:O	2.39	0.41
1:1:20:G:C2'	1:1:21:A:H5'	2.50	0.41
1:1:73:C:O2	1:1:73:C:H5'	2.20	0.41
1:1:139:G:H2'	1:1:140:G:O4'	2.20	0.41
6:4B:234:ILE:HA	6:4B:250:CYS:HA	2.03	0.41
11:41:13:GLU:HG2	11:41:74:LEU:HD11	2.02	0.41
15:X:123:SER:HB3	16:42:23:GLU:O	2.20	0.41
20:2B:15:ASN:HD21	20:2B:17:LYS:HB2	1.86	0.41
23:5C:352:LYS:HE3	23:5C:352:LYS:HB2	1.87	0.41
23:5C:692:LEU:HD23	23:5C:692:LEU:HA	1.87	0.41
23:5C:715:GLY:HA2	23:5C:729:ALA:HB1	2.02	0.41
23:5C:749:THR:O	23:5C:756:LYS:NZ	2.41	0.41
24:5X:536:ARG:CG	34:1g:10:LYS:CD	2.98	0.41
24:5X:703:ARG:N	24:5X:705:PHE:HD2	2.19	0.41
28:S:718:ARG:HH12	28:S:750:LEU:HD13	1.85	0.41
33:B3:704:VAL:HG11	33:B3:754:ILE:HG22	2.02	0.41
36:5A:938:PRO:HB2	36:5A:1071:PHE:HA	2.02	0.41
36:5A:967:GLU:OE2	36:5A:969:SER:OG	2.32	0.41
36:5A:1332:HIS:HB3	49:5B:41:LEU:HB2	2.01	0.41
36:5A:1455:TRP:CD1	36:5A:1455:TRP:H	2.38	0.41
39:5D:32:HIS:CE1	39:5D:63:ILE:HB	2.55	0.41
43:K:676:ARG:HE	43:K:677:VAL:HG23	1.85	0.41
43:K:688:ASN:O	43:K:704:ALA:HA	2.20	0.41
43:K:774:LEU:HA	43:K:774:LEU:HD23	1.87	0.41
49:5B:831:THR:HA	49:5B:844:LEU:HD12	2.02	0.41
49:5B:1028:THR:O	49:5B:1030:ARG:NH1	2.53	0.41
50:B1:1245:ARG:HD3	50:B1:1245:ARG:HA	1.80	0.41
7:5e:83:ASN:OD1	17:5:95:G:N1	2.53	0.41
15:X:138:ARG:NH1	36:5A:1614:ILE:HD12	2.30	0.41
16:22:61:ARG:NH1	32:2:98:G:OP2	2.44	0.41
17:5:17:U:H2'	17:5:18:C:C6	2.56	0.41
24:5X:363:ASP:OD1	24:5X:363:ASP:N	2.51	0.41
29:5J:865:HIS:HD2	29:5J:900:ARG:HH22	1.67	0.41
25:2b:9:MET:HE3	25:2b:9:MET:HB3	1.76	0.41
25:2b:26:ILE:O	25:2b:47:GLU:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:23:28:TYR:HB3	5:23:46:ILE:HD12	2.02	0.41
7:1e:80:LYS:HB3	7:1e:80:LYS:HE2	1.66	0.41
36:5A:101:LYS:HG3	36:5A:473:PHE:CE1	2.55	0.41
36:5A:580:TYR:CD2	36:5A:580:TYR:C	2.98	0.41
36:5A:1331:GLY:HA3	49:5B:40:VAL:HG12	2.03	0.41
37:A3:353:GLY:HA3	11:21:78:THR:N	2.35	0.41
38:U:316:LYS:HE3	38:U:316:LYS:HB2	1.88	0.41
38:U:405:GLU:CD	38:U:406:LYS:H	2.28	0.41
43:K:698:PHE:CZ	43:K:834:ASP:OD1	2.73	0.41
34:4g:18:SER:HB2	34:4g:26:HIS:CE1	2.56	0.41
49:5B:513:ALA:HB2	49:5B:651:LEU:HD11	2.02	0.41
50:B1:1245:ARG:NH2	50:B1:1248:GLN:OE1	2.53	0.41
1:1:73:C:H3'	1:1:74:C:C6	2.55	0.41
5:13:9:VAL:HG12	5:13:73:LEU:HD23	2.01	0.41
6:4B:285:SER:O	6:4B:289:LEU:O	2.39	0.41
6:4B:364:HIS:C	44:4A:423:GLN:CD	2.89	0.41
16:22:104:ASP:OD1	16:22:104:ASP:N	2.54	0.41
22:B2:652:GLY:HA2	22:B2:657:ILE:HG13	2.02	0.41
22:B2:656:PRO:HB2	22:B2:659:GLU:HB3	2.02	0.41
23:5C:355:LYS:NZ	36:5A:376:GLU:O	2.53	0.41
23:5C:664:GLU:HB3	23:5C:820:PHE:CZ	2.56	0.41
24:5X:327:ARG:NH2	36:5A:357:ASN:OD1	2.53	0.41
24:5X:669:ILE:HG12	24:5X:737:VAL:HG13	2.02	0.41
29:5J:254:ARG:HD3	36:5A:803:ALA:HB1	2.02	0.41
30:4D:35:LEU:HD11	30:4D:102:CYS:HB3	2.03	0.41
33:B3:166:LEU:O	33:B3:186:GLU:HA	2.21	0.41
33:B3:442:LEU:H	33:B3:734:LEU:HA	1.85	0.41
33:B3:963:VAL:HB	33:B3:966:LEU:HB2	2.03	0.41
36:5A:787:GLU:OE2	36:5A:791:GLN:NE2	2.44	0.41
36:5A:1245:ARG:O	36:5A:1249:MET:HB2	2.21	0.41
36:5A:1260:VAL:HG11	36:5A:1325:LEU:HB3	2.03	0.41
36:5A:1433:ASP:HB3	36:5A:1460:HIS:CE1	2.56	0.41
36:5A:2072:GLU:HG3	36:5A:2076:ARG:HD3	2.03	0.41
38:U:300:MET:HE3	38:U:304:VAL:HG23	2.02	0.41
43:K:722:ASN:ND2	43:K:722:ASN:C	2.78	0.41
44:4A:512:GLU:O	44:4A:516:ALA:HB2	2.20	0.41
49:5B:1062:LEU:HD23	49:5B:1062:LEU:HA	1.91	0.41
49:5B:1225:VAL:HG21	49:5B:1254:PHE:CE1	2.56	0.41
49:5B:1994:ASN:HB3	49:5B:1999:LEU:HD13	2.02	0.41
50:B1:656:LYS:HA	50:B1:656:LYS:HD2	1.88	0.41
1:1:21:A:H2'	1:1:22:U:H5''	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:47:C:C5	1:1:48:C:C6	3.09	0.41
3:5O:280:ASN:HA	3:5O:310:TYR:HE2	1.86	0.41
5:13:57:GLN:O	5:13:58:LEU:HD23	2.20	0.41
5:13:73:LEU:N	5:13:73:LEU:CD1	2.84	0.41
15:X:120:VAL:H	15:X:120:VAL:HG22	1.63	0.41
24:5X:647:SER:OG	24:5X:650:GLU:HG3	2.21	0.41
24:5X:675:LYS:HE3	24:5X:675:LYS:HB3	1.77	0.41
27:1A:50:LYS:HG2	27:1A:51:MET:SD	2.60	0.41
29:5J:139:GLN:O	29:5J:143:SER:OG	2.28	0.41
33:B3:452:LEU:HD13	33:B3:476:VAL:HG21	2.03	0.41
33:B3:1059:PRO:HD3	33:B3:1089:ALA:HA	2.02	0.41
36:5A:87:VAL:HG12	36:5A:121:HIS:HE1	1.85	0.41
36:5A:982:GLU:N	36:5A:1167:THR:O	2.52	0.41
36:5A:1086:ARG:HB2	36:5A:1098:PHE:HD2	1.85	0.41
36:5A:1109:LEU:HG	36:5A:1152:ALA:HB1	2.03	0.41
37:A3:360:GLU:CD	11:21:75:PRO:HD3	2.44	0.41
39:5D:8:LEU:HB2	39:5D:14:VAL:HG22	2.01	0.41
43:K:860:ILE:HD13	43:K:866:TYR:CD2	2.56	0.41
45:4:113:U:O2'	45:4:114:U:P	2.79	0.41
49:5B:158:ASP:O	49:5B:163:GLN:N	2.40	0.41
49:5B:1185:GLU:HG3	49:5B:1207:ASP:HB2	2.03	0.41
49:5B:1454:ASP:HA	49:5B:1490:LEU:HB2	2.03	0.41
49:5B:1519:ARG:NH2	49:5B:1691:ALA:O	2.54	0.41
49:5B:1755:LEU:HD12	49:5B:1755:LEU:HA	1.90	0.41
50:B1:490:GLU:O	50:B1:493:LYS:HB2	2.21	0.41
1:1:33:C:C5'	9:1K:138:LYS:H	2.34	0.41
1:1:91:G:O2'	1:1:92:C:C5'	2.69	0.41
5:13:46:ILE:CD1	5:13:61:VAL:HG21	2.46	0.41
6:4B:345:ARG:HH11	6:4B:365:SER:HA	1.86	0.41
10:4C:357:ARG:O	10:4C:360:ARG:HG2	2.21	0.41
10:4C:380:PHE:H	36:5A:1502:PHE:HA	1.85	0.41
15:X:114:SER:HB3	34:4g:37:PHE:CZ	2.56	0.41
16:22:67:LEU:HB2	16:22:99:MET:HG2	2.02	0.41
16:22:75:THR:HG22	16:22:89:PRO:HB2	2.01	0.41
20:2B:25:ARG:HG2	46:2A:19:VAL:HG21	2.02	0.41
23:5C:829:GLU:OE2	23:5C:854:ARG:NH2	2.46	0.41
13:5f:29:TYR:HD2	13:5f:47:THR:HG21	1.84	0.41
29:5J:331:LEU:HD12	29:5J:331:LEU:HA	1.94	0.41
29:5J:423:LEU:HD23	29:5J:423:LEU:HA	1.92	0.41
29:5J:665:LEU:O	29:5J:669:ARG:N	2.50	0.41
25:2b:73:ARG:HB2	5:23:39:MET:HE1	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B3:1155:LEU:HD23	33:B3:1155:LEU:HA	1.91	0.41
36:5A:852:VAL:CG2	36:5A:854:SER:H	2.33	0.41
36:5A:975:VAL:HG11	36:5A:1153:VAL:HG21	2.02	0.41
36:5A:1072:LEU:HD22	36:5A:1087:LEU:HD22	2.02	0.41
36:5A:1415:GLY:O	36:5A:1418:ARG:NH1	2.42	0.41
36:5A:1785:VAL:HG13	36:5A:1822:ILE:HD13	2.02	0.41
25:4b:40:LEU:HB2	25:4b:72:LEU:HB3	2.02	0.41
34:4g:14:ASP:OD1	34:4g:32:ARG:NH2	2.52	0.41
49:5B:688:THR:HB	49:5B:868:ILE:HG13	2.03	0.41
49:5B:1196:SER:O	49:5B:1258:VAL:N	2.43	0.41
49:5B:1507:SER:O	49:5B:1511:THR:OG1	2.31	0.41
49:5B:1585:GLN:H	49:5B:1585:GLN:HG2	1.66	0.41
50:B1:893:ILE:HD13	50:B1:893:ILE:HA	1.85	0.41
1:1:149:U:O2'	1:1:150:U:H2'	2.21	0.41
2:6:105:U:C5	31:63:88:ARG:NH2	2.89	0.41
5:13:60:GLN:C	5:13:61:VAL:HG23	2.45	0.41
9:1K:134:MET:HG2	9:1K:147:ALA:HB2	2.03	0.41
7:4e:57:VAL:HG12	7:4e:78:MET:HB2	2.03	0.41
15:X:137:TYR:CD2	28:S:729:LEU:CD1	3.00	0.41
15:X:149:ARG:NH2	36:5A:1614:ILE:O	2.54	0.41
17:5:76:A:H2'	17:5:77:G:H8	1.86	0.41
18:67:44:LEU:HD23	40:64:62:ARG:HH22	1.86	0.41
22:B2:561:MET:HE3	22:B2:561:MET:HB2	1.77	0.41
22:B2:566:ILE:HG23	22:B2:567:ASP:H	1.84	0.41
23:5C:236:MET:N	23:5C:239:THR:OG1	2.49	0.41
24:5X:382:LYS:HB2	24:5X:626:VAL:HB	2.02	0.41
24:5X:536:ARG:CA	34:1g:10:LYS:HE3	2.45	0.41
26:B5:32:LEU:HD11	50:B1:1287:ILE:HG21	2.01	0.41
26:B5:59:GLU:OE1	33:B3:283:ARG:NH2	2.54	0.41
28:S:636:ARG:HH22	45:4:128:A:H1'	1.86	0.41
29:5J:297:LEU:O	29:5J:301:VAL:HG23	2.21	0.41
31:63:44:HIS:CE1	31:63:84:MET:HE1	2.55	0.41
13:4f:30:LYS:O	13:4f:47:THR:HA	2.20	0.41
33:B3:505:THR:HB	33:B3:518:GLN:HE21	1.86	0.41
25:5b:35:ASP:N	25:5b:35:ASP:OD1	2.54	0.41
35:68:37:ILE:CD1	35:68:61:ILE:HG12	2.51	0.41
5:43:7:ILE:O	5:43:11:HIS:ND1	2.47	0.41
5:43:10:LEU:HD13	5:43:35:ALA:HB1	2.03	0.41
36:5A:126:ILE:HD12	36:5A:128:PHE:CE1	2.56	0.41
36:5A:907:PRO:HB2	36:5A:909:TYR:CE1	2.56	0.41
36:5A:1275:ARG:HB3	49:5B:52:MET:HE1	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5A:1872:LEU:HD23	36:5A:1872:LEU:HA	1.85	0.41
38:U:304:VAL:O	38:U:308:SER:OG	2.31	0.41
39:5D:3:TYR:HE1	39:5D:33:ASP:O	2.04	0.41
43:K:679:ILE:HG23	43:K:690:TYR:HA	2.03	0.41
43:K:684:ASP:O	43:K:685:LYS:HB2	2.21	0.41
43:K:719:ILE:HG22	43:K:720:ARG:N	2.36	0.41
43:K:760:LYS:O	43:K:761:GLN:HB2	2.21	0.41
25:4b:33:ALA:HB3	25:4b:41:ILE:HB	2.02	0.41
44:4A:463:LYS:HD3	44:4A:463:LYS:HA	1.87	0.41
49:5B:572:ASP:OD1	49:5B:1274:ARG:NH2	2.53	0.41
49:5B:1194:THR:HG22	49:5B:1723:PRO:HG3	2.03	0.41
49:5B:1233:ILE:HG21	49:5B:1236:HIS:HB3	2.02	0.41
1:1:104:A:H4'	1:1:106:G:C6	2.55	0.41
1:1:120:U:O2'	1:1:121:G:H5'	2.20	0.41
1:1:140:G:O2'	25:1b:57:LYS:CE	2.69	0.41
6:4B:228:ILE:HG21	29:5J:795:ILE:HG13	2.03	0.41
10:4C:325:GLU:HA	10:4C:328:PHE:HB2	2.03	0.41
21:A2:152:MET:HG3	21:A2:170:LEU:HD12	2.02	0.41
22:B2:522:PHE:HB3	50:B1:1137:ARG:HG2	2.03	0.41
23:5C:736:GLY:O	23:5C:771:GLN:HG2	2.21	0.41
24:5X:540:LEU:CD2	24:5X:543:CYS:HB2	2.48	0.41
29:5J:243:ILE:HD11	38:U:542:MET:HG2	2.03	0.41
29:5J:335:GLY:O	29:5J:339:CYS:N	2.44	0.41
31:63:54:LEU:HB3	31:63:57:VAL:HG12	2.03	0.41
32:2:175:G:H2'	32:2:176:G:C8	2.54	0.41
36:5A:1023:ASN:OD1	36:5A:1023:ASN:N	2.52	0.41
36:5A:1544:ARG:HB3	36:5A:1670:ASP:HB2	2.03	0.41
38:U:111:ILE:HD11	38:U:163:VAL:HG21	2.01	0.41
38:U:444:LEU:HD13	38:U:447:LEU:HD21	2.02	0.41
43:K:785:VAL:HG23	43:K:786:GLY:N	2.35	0.41
43:K:830:LEU:C	43:K:830:LEU:CD2	2.94	0.41
44:4A:389:TRP:H	44:4A:389:TRP:CD1	2.38	0.41
49:5B:698:ILE:HG13	49:5B:702:GLN:HE21	1.86	0.41
49:5B:1831:LEU:O	49:5B:1835:SER:CB	2.69	0.41
50:B1:887:LYS:HE3	50:B1:887:LYS:HB3	1.81	0.41
50:B1:901:GLN:HE21	50:B1:935:THR:HG23	1.86	0.41
1:1:118:A:C1'	42:1C:2:PRO:HD2	2.51	0.40
3:5O:313:ASP:HB3	3:5O:316:SER:HB3	2.03	0.40
5:13:60:GLN:HB2	34:1g:72:ALA:HB3	2.03	0.40
18:67:55:MET:HB2	18:67:67:ASP:OD2	2.20	0.40
19:62:29:LEU:CD1	19:62:38:ILE:HG23	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:A2:117:TYR:CZ	21:A2:176:TYR:CD2	2.97	0.40
23:5C:140:HIS:CD2	23:5C:230:ASP:HB2	2.56	0.40
23:5C:255:VAL:HG21	23:5C:285:VAL:HG11	2.03	0.40
23:5C:363:SER:O	23:5C:363:SER:OG	2.36	0.40
24:5X:370:TRP:CZ3	24:5X:389:PRO:O	2.68	0.40
25:1b:17:MET:HE3	25:1b:82:VAL:HG22	2.04	0.40
28:S:741:MET:HE3	28:S:745:ARG:HH11	1.87	0.40
33:B3:1145:GLU:HB3	33:B3:1179:CYS:SG	2.60	0.40
36:5A:456:LEU:HD23	36:5A:456:LEU:HA	1.87	0.40
36:5A:2146:VAL:HG13	36:5A:2272:MET:HB2	2.04	0.40
44:4A:417:LEU:HD23	44:4A:417:LEU:HA	1.95	0.40
49:5B:120:ILE:O	49:5B:124:LEU:CB	2.66	0.40
49:5B:259:HIS:CD2	49:5B:261:ARG:H	2.37	0.40
49:5B:538:ILE:HB	49:5B:585:ILE:HD13	2.03	0.40
50:B1:897:LEU:HD23	50:B1:897:LEU:HA	1.93	0.40
1:1:15:G:H2'	1:1:16:G:C4	2.55	0.40
1:1:30:U:O2	9:1K:108:ALA:HB3	2.21	0.40
5:13:83:LEU:N	5:13:83:LEU:CD1	2.84	0.40
6:4B:359:LEU:HD21	6:4B:361:GLN:HB2	2.03	0.40
12:R:432:PRO:CB	44:4A:466:LEU:CB	2.93	0.40
13:1f:5:LEU:O	7:1e:49:GLY:HA3	2.21	0.40
7:4e:25:LEU:HB3	7:4e:47:ILE:HG23	2.02	0.40
14:66:24:LEU:HD21	14:66:65:ILE:HG21	2.03	0.40
15:X:106:LEU:HD23	15:X:106:LEU:HA	1.91	0.40
17:5:45:C:N4	24:5X:271:LYS:O	2.42	0.40
21:A2:162:PRO:O	21:A2:163:ASP:CB	2.70	0.40
24:5X:596:LYS:HD2	24:5X:597:HIS:CE1	2.56	0.40
29:5J:149:LEU:HD23	36:5A:696:MET:HB2	2.03	0.40
29:5J:713:MET:HG2	29:5J:748:LEU:HD22	2.03	0.40
29:5J:892:GLU:O	29:5J:896:GLU:HG3	2.21	0.40
36:5A:67:ARG:O	36:5A:71:ARG:HB2	2.21	0.40
36:5A:809:VAL:HG22	36:5A:1051:LEU:HD11	2.03	0.40
36:5A:976:MET:HE2	36:5A:1098:PHE:HD1	1.87	0.40
34:5g:13:MET:HE3	34:5g:13:MET:HB3	1.90	0.40
34:5g:18:SER:HB2	34:5g:26:HIS:CE1	2.56	0.40
43:K:695:GLN:HE21	43:K:700:ASN:HB3	1.84	0.40
11:21:9:LYS:HE3	11:21:9:LYS:HB3	1.85	0.40
45:4:127:C:H2'	45:4:128:A:H8	1.87	0.40
50:B1:601:ALA:HB1	50:B1:639:LEU:HD13	2.02	0.40
50:B1:665:ILE:HG23	50:B1:690:ILE:HD12	2.03	0.40
2:6:86:U:O2	32:2:12:G:N2	2.45	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:5O:84:ALA:HB2	3:5O:90:ILE:HG23	2.03	0.40
3:5O:127:ALA:HA	3:5O:133:VAL:HG22	2.03	0.40
7:5e:58:LEU:HD12	7:5e:77:ILE:HD11	2.03	0.40
12:R:432:PRO:C	44:4A:466:LEU:CD2	2.48	0.40
17:5:19:A:N3	17:5:21:A:N6	2.70	0.40
22:B2:614:ARG:CD	22:B2:621:VAL:HG22	2.51	0.40
24:5X:733[A]:VAL:CG1	24:5X:734:SER:N	2.84	0.40
29:5J:96:LYS:HE3	29:5J:96:LYS:HB2	1.89	0.40
29:5J:146:LYS:HE3	36:5A:695:ASP:HB2	2.02	0.40
29:5J:766:LEU:HD12	29:5J:786:LEU:HD13	2.04	0.40
33:B3:168:TYR:HB2	33:B3:185:LEU:HB2	2.03	0.40
33:B3:442:LEU:HD23	33:B3:442:LEU:HA	1.89	0.40
33:B3:462:VAL:HG23	33:B3:473:TYR:HB2	2.04	0.40
33:B3:530:ASP:O	33:B3:532:ARG:N	2.54	0.40
36:5A:546:LEU:HD12	36:5A:546:LEU:HA	1.89	0.40
36:5A:703:GLN:HA	47:A1:459:GLY:HA3	2.02	0.40
36:5A:722:ALA:HB3	36:5A:724:ILE:HG12	2.03	0.40
36:5A:1188:ASN:ND2	36:5A:1192:PHE:O	2.53	0.40
36:5A:1506:ALA:HA	36:5A:1533:ARG:HH12	1.87	0.40
36:5A:1607:GLU:N	36:5A:1632:PHE:O	2.48	0.40
36:5A:2200:MET:HE2	36:5A:2200:MET:HB3	1.74	0.40
37:A3:281:ARG:NH2	37:A3:294:GLU:OE2	2.54	0.40
16:52:70:VAL:HG21	16:52:99:MET:SD	2.62	0.40
43:K:676:ARG:HE	43:K:677:VAL:CG2	2.35	0.40
43:K:904:LEU:HA	43:K:953:LYS:HB3	2.03	0.40
43:K:1003:ILE:C	43:K:1005:GLU:H	2.30	0.40
49:5B:290:LEU:HD23	49:5B:290:LEU:HA	1.96	0.40
49:5B:1405:VAL:HG22	49:5B:1424:ILE:HD12	2.03	0.40
49:5B:2041:LEU:HD13	49:5B:2041:LEU:HA	1.93	0.40
50:B1:956:SER:HB3	50:B1:996:ALA:HA	2.03	0.40
50:B1:1196:SER:OG	50:B1:1236:GLY:O	2.38	0.40
50:B1:1223:SER:HA	50:B1:1224:PRO:HD3	1.97	0.40
1:1:73:C:C3'	1:1:74:C:C6	3.05	0.40
1:1:140:G:O2'	1:1:141:G:H5'	2.22	0.40
23:5C:649:SER:HB2	23:5C:651:ILE:HG12	2.03	0.40
24:5X:196:LYS:HE2	24:5X:196:LYS:HB3	1.93	0.40
26:B5:17:LYS:HD3	26:B5:17:LYS:HA	1.82	0.40
28:S:567:PRO:CD	28:S:568:THR:H	2.30	0.40
29:5J:353:GLN:HB2	29:5J:358:ALA:HB2	2.02	0.40
29:5J:674:THR:O	29:5J:674:THR:HG23	2.21	0.40
11:51:13:GLU:HG2	11:51:74:LEU:HD11	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B3:754:ILE:HD11	33:B3:765:LEU:HD12	2.02	0.40
33:B3:1179:CYS:HB3	33:B3:1208:LEU:HD11	2.04	0.40
36:5A:1129:ASN:ND2	36:5A:1173:SER:O	2.53	0.40
36:5A:1247:ILE:HG12	36:5A:1262:LYS:HB3	2.03	0.40
36:5A:1665:GLN:O	36:5A:1704:ALA:HA	2.22	0.40
36:5A:2166:HIS:HD2	36:5A:2168:TYR:H	1.69	0.40
43:K:738:LYS:HD2	43:K:738:LYS:O	2.21	0.40
43:K:774:LEU:O	43:K:778:LEU:HB2	2.21	0.40
43:K:929:PHE:HB3	43:K:949:ILE:HD11	2.03	0.40
25:4b:38:MET:HE3	25:4b:80:MET:HE2	2.03	0.40
44:4A:574:VAL:HG22	44:4A:581:VAL:HB	2.04	0.40
49:5B:1429:PRO:O	49:5B:1433:ASP:HB2	2.22	0.40
49:5B:1535:THR:HG21	49:5B:1676:TYR:CE1	2.56	0.40
4:B4:30:TRP:HB2	22:B2:600:ARG:NH2	2.37	0.40
10:4C:279:ILE:HG12	10:4C:321:LYS:NZ	2.36	0.40
21:A2:117:TYR:CG	21:A2:138:TYR:CE1	3.10	0.40
22:B2:609:LEU:HD22	22:B2:613:LEU:HD23	2.04	0.40
22:B2:662:SER:O	22:B2:663:PHE:CB	2.70	0.40
24:5X:428:ASN:HD21	24:5X:598:LYS:HZ2	1.70	0.40
24:5X:446:LEU:O	24:5X:450:LEU:HG	2.22	0.40
24:5X:798:HIS:CG	24:5X:799:PRO:HD2	2.57	0.40
16:42:70:VAL:HG21	16:42:99:MET:SD	2.62	0.40
28:S:723:LYS:HZ3	28:S:727:ARG:HH22	1.67	0.40
29:5J:440:LEU:HD22	29:5J:452:VAL:HG21	2.02	0.40
29:5J:913:CYS:HA	29:5J:916:SER:HB2	2.03	0.40
31:63:33:MET:SD	31:63:39:LEU:HD12	2.61	0.40
33:B3:36:LYS:HB3	33:B3:37:ILE:HD12	2.03	0.40
33:B3:313:ILE:HG23	33:B3:325:ILE:HD11	2.04	0.40
36:5A:109:PRO:HD3	36:5A:630:TRP:CZ2	2.56	0.40
43:K:946:MET:H	43:K:946:MET:HG2	1.81	0.40
49:5B:169:TYR:HA	49:5B:172:LEU:HG	2.02	0.40
49:5B:531:ILE:HG21	49:5B:564:ILE:HD11	2.03	0.40
50:B1:1234:LEU:HD22	50:B1:1246:MET:HE1	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	5O	304/357 (85%)	283 (93%)	19 (6%)	2 (1%)	18	48
4	B4	76/424 (18%)	76 (100%)	0	0	100	100
5	13	79/126 (63%)	75 (95%)	4 (5%)	0	100	100
5	23	81/126 (64%)	76 (94%)	5 (6%)	0	100	100
5	43	81/126 (64%)	76 (94%)	5 (6%)	0	100	100
5	53	82/126 (65%)	77 (94%)	5 (6%)	0	100	100
6	4B	357/522 (68%)	330 (92%)	25 (7%)	2 (1%)	21	51
7	1e	75/92 (82%)	70 (93%)	5 (7%)	0	100	100
7	2e	79/92 (86%)	77 (98%)	2 (2%)	0	100	100
7	4e	74/92 (80%)	71 (96%)	3 (4%)	0	100	100
7	5e	75/92 (82%)	72 (96%)	3 (4%)	0	100	100
9	1K	199/437 (46%)	184 (92%)	12 (6%)	3 (2%)	8	33
10	4C	293/499 (59%)	275 (94%)	18 (6%)	0	100	100
11	11	79/119 (66%)	77 (98%)	2 (2%)	0	100	100
11	21	78/119 (66%)	75 (96%)	3 (4%)	0	100	100
11	41	79/119 (66%)	75 (95%)	4 (5%)	0	100	100
11	51	79/119 (66%)	75 (95%)	4 (5%)	0	100	100
12	R	104/480 (22%)	91 (88%)	13 (12%)	0	100	100
13	1f	72/86 (84%)	69 (96%)	3 (4%)	0	100	100
13	2f	70/86 (81%)	69 (99%)	1 (1%)	0	100	100
13	4f	70/86 (81%)	69 (99%)	1 (1%)	0	100	100
13	5f	71/86 (83%)	64 (90%)	7 (10%)	0	100	100
14	66	70/80 (88%)	69 (99%)	0	1 (1%)	9	34
15	X	45/155 (29%)	39 (87%)	6 (13%)	0	100	100
16	12	91/118 (77%)	85 (93%)	6 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	22	91/118 (77%)	86 (94%)	5 (6%)	0	100	100
16	42	90/118 (76%)	84 (93%)	6 (7%)	0	100	100
16	52	94/118 (80%)	87 (93%)	7 (7%)	0	100	100
18	67	75/103 (73%)	72 (96%)	2 (3%)	1 (1%)	9	35
19	62	93/95 (98%)	84 (90%)	6 (6%)	3 (3%)	3	19
20	2B	90/225 (40%)	88 (98%)	2 (2%)	0	100	100
21	A2	138/209 (66%)	123 (89%)	11 (8%)	4 (3%)	3	20
22	B2	204/895 (23%)	181 (89%)	22 (11%)	1 (0%)	24	55
23	5C	850/854 (100%)	817 (96%)	31 (4%)	2 (0%)	43	71
24	5X	574/820 (70%)	561 (98%)	13 (2%)	0	100	100
25	1b	84/240 (35%)	82 (98%)	2 (2%)	0	100	100
25	2b	80/240 (33%)	74 (92%)	6 (8%)	0	100	100
25	4b	80/240 (33%)	71 (89%)	9 (11%)	0	100	100
25	5b	69/240 (29%)	67 (97%)	2 (3%)	0	100	100
26	B5	67/86 (78%)	61 (91%)	6 (9%)	0	100	100
27	1A	96/282 (34%)	94 (98%)	2 (2%)	0	100	100
28	S	110/800 (14%)	101 (92%)	8 (7%)	1 (1%)	14	43
29	5J	793/850 (93%)	748 (94%)	44 (6%)	1 (0%)	48	76
30	4D	121/128 (94%)	119 (98%)	2 (2%)	0	100	100
31	63	83/102 (81%)	79 (95%)	3 (4%)	1 (1%)	10	37
33	B3	1176/1217 (97%)	1082 (92%)	92 (8%)	2 (0%)	43	71
34	1g	71/76 (93%)	69 (97%)	2 (3%)	0	100	100
34	2g	71/76 (93%)	69 (97%)	2 (3%)	0	100	100
34	4g	72/76 (95%)	66 (92%)	6 (8%)	0	100	100
34	5g	72/76 (95%)	66 (92%)	6 (8%)	0	100	100
35	68	93/96 (97%)	81 (87%)	6 (6%)	6 (6%)	1	7
36	5A	2198/2311 (95%)	2094 (95%)	102 (5%)	2 (0%)	48	76
37	A3	377/501 (75%)	346 (92%)	26 (7%)	5 (1%)	9	35
38	U	454/555 (82%)	424 (93%)	27 (6%)	3 (1%)	18	48
39	5D	139/142 (98%)	131 (94%)	8 (6%)	0	100	100
40	64	71/139 (51%)	66 (93%)	3 (4%)	2 (3%)	4	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	BP	98/104 (94%)	92 (94%)	6 (6%)	0	100	100
42	1C	48/159 (30%)	47 (98%)	1 (2%)	0	100	100
43	K	316/1007 (31%)	294 (93%)	18 (6%)	4 (1%)	9	35
44	4A	229/683 (34%)	210 (92%)	18 (8%)	1 (0%)	30	60
46	2A	160/255 (63%)	147 (92%)	13 (8%)	0	100	100
47	A1	138/647 (21%)	129 (94%)	7 (5%)	2 (1%)	9	34
48	65	74/91 (81%)	70 (95%)	2 (3%)	2 (3%)	4	21
49	5B	1989/2136 (93%)	1885 (95%)	103 (5%)	1 (0%)	48	76
50	B1	846/1304 (65%)	792 (94%)	53 (6%)	1 (0%)	48	76
All	All	15337/23178 (66%)	14438 (94%)	846 (6%)	53 (0%)	37	66

All (53) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	5O	59	ILE
9	1K	59	ARG
9	1K	63	ARG
19	62	47	ASP
19	62	53	HIS
21	A2	165	ARG
28	S	566	ILE
29	5J	93	PRO
35	68	89	GLU
37	A3	78	PRO
38	U	408	GLN
43	K	697	VAL
47	A1	192	ASN
6	4B	460	ILE
9	1K	60	ALA
14	66	52	VAL
35	68	86	ILE
35	68	90	PRO
37	A3	227	PRO
37	A3	292	SER
43	K	851	VAL
48	65	87	GLU
33	B3	932	ASN
33	B3	933	ASN
35	68	79	SER

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Mol	Chain	Res	Type
36	5A	189	GLU
37	A3	308	LYS
47	A1	218	ILE
3	5O	58	PRO
19	62	55	LEU
23	5C	943	LEU
31	63	35	ASN
35	68	43	GLU
40	64	12	ASN
43	K	699	SER
21	A2	115	PRO
21	A2	208	LEU
23	5C	107	GLN
35	68	59	LEU
36	5A	60	ASP
37	A3	99	PRO
38	U	146	ARG
40	64	57	PRO
43	K	722	ASN
44	4A	539	GLN
18	67	19	ILE
49	5B	756	SER
6	4B	459	PRO
21	A2	188	ILE
50	B1	489	PRO
22	B2	521	PRO
38	U	362	PRO
48	65	47	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	5O	263/300 (88%)	262 (100%)	1 (0%)	84	85
4	B4	66/336 (20%)	66 (100%)	0	100	100
5	13	71/101 (70%)	61 (86%)	10 (14%)	3	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	23	73/101 (72%)	73 (100%)	0	100	100
5	43	73/101 (72%)	73 (100%)	0	100	100
5	53	73/101 (72%)	73 (100%)	0	100	100
6	4B	306/442 (69%)	301 (98%)	5 (2%)	55	72
7	1e	72/84 (86%)	61 (85%)	11 (15%)	3	13
7	2e	76/84 (90%)	76 (100%)	0	100	100
7	4e	71/84 (84%)	71 (100%)	0	100	100
7	5e	72/84 (86%)	72 (100%)	0	100	100
9	1K	170/373 (46%)	154 (91%)	16 (9%)	8	30
10	4C	255/424 (60%)	253 (99%)	2 (1%)	73	79
11	11	76/101 (75%)	72 (95%)	4 (5%)	20	49
11	21	75/101 (74%)	75 (100%)	0	100	100
11	41	76/101 (75%)	53 (70%)	23 (30%)	0	1
11	51	76/101 (75%)	53 (70%)	23 (30%)	0	1
12	R	94/369 (26%)	93 (99%)	1 (1%)	65	76
13	1f	63/74 (85%)	56 (89%)	7 (11%)	6	23
13	2f	61/74 (82%)	61 (100%)	0	100	100
13	4f	61/74 (82%)	61 (100%)	0	100	100
13	5f	61/74 (82%)	60 (98%)	1 (2%)	55	72
14	66	62/70 (89%)	62 (100%)	0	100	100
15	X	42/144 (29%)	42 (100%)	0	100	100
16	12	91/110 (83%)	82 (90%)	9 (10%)	7	27
16	22	91/110 (83%)	91 (100%)	0	100	100
16	42	86/110 (78%)	86 (100%)	0	100	100
16	52	93/110 (84%)	92 (99%)	1 (1%)	65	76
18	67	69/91 (76%)	67 (97%)	2 (3%)	37	62
19	62	88/88 (100%)	86 (98%)	2 (2%)	44	66
20	2B	81/195 (42%)	81 (100%)	0	100	100
21	A2	129/180 (72%)	127 (98%)	2 (2%)	55	72
22	B2	187/776 (24%)	183 (98%)	4 (2%)	47	67
23	5C	754/756 (100%)	750 (100%)	4 (0%)	81	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	5X	517/721 (72%)	500 (97%)	17 (3%)	33	59
25	1b	78/177 (44%)	69 (88%)	9 (12%)	5	22
25	2b	75/177 (42%)	75 (100%)	0	100	100
25	4b	75/177 (42%)	75 (100%)	0	100	100
25	5b	67/177 (38%)	67 (100%)	0	100	100
26	B5	60/77 (78%)	60 (100%)	0	100	100
27	1A	85/240 (35%)	81 (95%)	4 (5%)	23	52
28	S	91/681 (13%)	90 (99%)	1 (1%)	65	76
29	5J	636/715 (89%)	632 (99%)	4 (1%)	78	82
30	4D	107/111 (96%)	107 (100%)	0	100	100
31	63	79/94 (84%)	76 (96%)	3 (4%)	29	56
33	B3	1027/1051 (98%)	1018 (99%)	9 (1%)	70	78
34	1g	63/66 (96%)	54 (86%)	9 (14%)	3	15
34	2g	63/66 (96%)	61 (97%)	2 (3%)	34	60
34	4g	64/66 (97%)	43 (67%)	21 (33%)	0	1
34	5g	64/66 (97%)	43 (67%)	21 (33%)	0	1
35	68	81/82 (99%)	77 (95%)	4 (5%)	22	51
36	5A	2002/2090 (96%)	1989 (99%)	13 (1%)	78	82
37	A3	345/446 (77%)	337 (98%)	8 (2%)	44	66
38	U	418/503 (83%)	418 (100%)	0	100	100
39	5D	129/130 (99%)	129 (100%)	0	100	100
40	64	68/111 (61%)	67 (98%)	1 (2%)	57	73
41	BP	86/90 (96%)	86 (100%)	0	100	100
42	1C	48/135 (36%)	41 (85%)	7 (15%)	3	15
43	K	291/919 (32%)	257 (88%)	34 (12%)	5	21
44	4A	210/599 (35%)	209 (100%)	1 (0%)	81	83
46	2A	139/218 (64%)	138 (99%)	1 (1%)	76	80
47	A1	130/550 (24%)	126 (97%)	4 (3%)	35	61
48	65	68/80 (85%)	67 (98%)	1 (2%)	57	73
49	5B	1779/1908 (93%)	1769 (99%)	10 (1%)	78	82
50	B1	733/1104 (66%)	731 (100%)	2 (0%)	86	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	13735/20051 (68%)	13421 (98%)	314 (2%)	44 66

All (314) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	5O	333	VAL
5	13	3	ILE
5	13	24	THR
5	13	34	GLU
5	13	46	ILE
5	13	47	THR
5	13	51	ARG
5	13	73	LEU
5	13	78	LYS
5	13	82	MET
5	13	83	LEU
6	4B	407	LEU
6	4B	429	ASN
6	4B	444	THR
6	4B	453	THR
6	4B	498	LEU
9	1K	3	GLN
9	1K	19	ILE
9	1K	28	LEU
9	1K	45	ILE
9	1K	47	GLU
9	1K	48	PHE
9	1K	50	ASP
9	1K	70	LYS
9	1K	82	VAL
9	1K	86	LEU
9	1K	124	GLU
9	1K	140	SER
9	1K	167	LYS
9	1K	168	LYS
9	1K	172	ARG
9	1K	188	ARG
10	4C	267	VAL
10	4C	325	GLU
11	41	2	LYS
11	41	4	VAL
11	41	8	MET

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Mol	Chain	Res	Type
11	41	10	LEU
11	41	11	SER
11	41	15	VAL
11	41	16	THR
11	41	28	THR
11	41	33	ASP
11	41	35	SER
11	41	44	LYS
11	41	47	LEU
11	41	48	LYS
11	41	51	GLU
11	41	53	VAL
11	41	54	GLN
11	41	55	LEU
11	41	56	GLU
11	41	57	THR
11	41	58	LEU
11	41	74	LEU
11	41	76	LEU
11	41	81	VAL
12	R	379	ASP
13	1f	3	LEU
13	1f	8	LYS
13	1f	14	LEU
13	1f	23	LEU
13	1f	27	MET
13	1f	51	ILE
13	1f	65	ARG
18	67	17	LYS
18	67	26	LYS
19	62	44	SER
19	62	72	LEU
21	A2	65	ASN
21	A2	189	ASP
22	B2	475	VAL
22	B2	564	ILE
22	B2	621	VAL
22	B2	633	LEU
23	5C	334	ILE
23	5C	507	VAL
23	5C	565	ILE
23	5C	735	PHE

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Mol	Chain	Res	Type
24	5X	395	ASP
24	5X	461	ARG
24	5X	472	ILE
24	5X	516	ARG
24	5X	532	VAL
24	5X	540	LEU
24	5X	589	LEU
24	5X	664	ASP
24	5X	675	LYS
24	5X	679	VAL
24	5X	685	GLU
24	5X	703	ARG
24	5X	729	ASP
24	5X	730	ILE
24	5X	737	VAL
24	5X	746	GLU
24	5X	784	LEU
11	11	4	VAL
11	11	11	SER
11	11	19	LEU
11	11	82	ASP
25	1b	7	SER
25	1b	12	HIS
25	1b	13	ILE
25	1b	54	LYS
25	1b	56	SER
25	1b	57	LYS
25	1b	58	GLN
25	1b	67	LEU
25	1b	71	LEU
27	1A	8	PRO
27	1A	39	GLN
27	1A	61	GLU
27	1A	103	GLU
28	S	566	ILE
13	5f	11	LEU
29	5J	91	SER
29	5J	400	VAL
29	5J	674	THR
29	5J	743	THR
11	51	2	LYS
11	51	4	VAL

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Mol	Chain	Res	Type
11	51	8	MET
11	51	10	LEU
11	51	11	SER
11	51	15	VAL
11	51	16	THR
11	51	28	THR
11	51	33	ASP
11	51	35	SER
11	51	44	LYS
11	51	47	LEU
11	51	48	LYS
11	51	51	GLU
11	51	53	VAL
11	51	54	GLN
11	51	55	LEU
11	51	56	GLU
11	51	57	THR
11	51	58	LEU
11	51	74	LEU
11	51	76	LEU
11	51	81	VAL
31	63	34	ARG
31	63	39	LEU
31	63	94	LEU
33	B3	88	VAL
33	B3	175	VAL
33	B3	248	VAL
33	B3	278	LEU
33	B3	484	VAL
33	B3	607	VAL
33	B3	770	LEU
33	B3	912	ASP
33	B3	1064	ASP
34	1g	21	LEU
34	1g	27	VAL
34	1g	28	GLN
34	1g	46	VAL
34	1g	50	THR
34	1g	51	SER
34	1g	57	ILE
34	1g	59	MET
34	1g	69	MET

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Mol	Chain	Res	Type
35	68	13	VAL
35	68	19	ASP
35	68	90	PRO
35	68	91	LEU
7	1e	25	LEU
7	1e	27	ASN
7	1e	60	ASP
7	1e	62	GLU
7	1e	63	GLU
7	1e	68	THR
7	1e	70	SER
7	1e	79	LEU
7	1e	80	LYS
7	1e	82	ASP
7	1e	86	LEU
36	5A	85	LYS
36	5A	314	ILE
36	5A	322	ASN
36	5A	342	THR
36	5A	347	LEU
36	5A	563	GLN
36	5A	579	GLN
36	5A	741	ARG
36	5A	1126	VAL
36	5A	1365	ILE
36	5A	1511	GLU
36	5A	2011	ILE
36	5A	2273	VAL
37	A3	78	PRO
37	A3	81	PHE
37	A3	111	GLU
37	A3	122	GLU
37	A3	195	ASP
37	A3	225	THR
37	A3	281	ARG
37	A3	402	LEU
34	2g	43	ASP
34	2g	46	VAL
16	52	33	THR
16	12	20	GLU
16	12	37	LYS
16	12	42	VAL

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Mol	Chain	Res	Type
16	12	51	LYS
16	12	61	ARG
16	12	75	THR
16	12	94	ARG
16	12	108	VAL
16	12	114	LEU
40	64	38	ILE
42	1C	3	LYS
42	1C	26	SER
42	1C	29	LYS
42	1C	39	GLN
42	1C	44	GLU
42	1C	45	GLN
42	1C	48	SER
34	5g	3	LYS
34	5g	10	LYS
34	5g	11	LYS
34	5g	15	LYS
34	5g	27	VAL
34	5g	35	ASP
34	5g	43	ASP
34	5g	44	GLU
34	5g	46	VAL
34	5g	47	GLU
34	5g	50	THR
34	5g	51	SER
34	5g	53	GLN
34	5g	59	MET
34	5g	61	VAL
34	5g	62	ILE
34	5g	66	SER
34	5g	70	LEU
34	5g	71	GLU
34	5g	73	LEU
34	5g	74	GLU
43	K	676	ARG
43	K	678	ASN
43	K	688	ASN
43	K	697	VAL
43	K	698	PHE
43	K	700	ASN
43	K	721	ASN

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Mol	Chain	Res	Type
43	K	724	LEU
43	K	726	GLN
43	K	733	LEU
43	K	763	LEU
43	K	777	VAL
43	K	778	LEU
43	K	793	ARG
43	K	805	LEU
43	K	812	LEU
43	K	825	GLU
43	K	830	LEU
43	K	843	ASP
43	K	850	LEU
43	K	862	ILE
43	K	878	THR
43	K	882	LEU
43	K	886	LYS
43	K	892	LYS
43	K	920	ASP
43	K	941	GLU
43	K	946	MET
43	K	950	ASN
43	K	956	LEU
43	K	960	ILE
43	K	991	ARG
43	K	1004	GLN
43	K	1005	GLU
44	4A	597	LEU
34	4g	3	LYS
34	4g	10	LYS
34	4g	11	LYS
34	4g	15	LYS
34	4g	27	VAL
34	4g	35	ASP
34	4g	43	ASP
34	4g	44	GLU
34	4g	46	VAL
34	4g	47	GLU
34	4g	50	THR
34	4g	51	SER
34	4g	53	GLN
34	4g	59	MET

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Mol	Chain	Res	Type
34	4g	61	VAL
34	4g	62	ILE
34	4g	66	SER
34	4g	70	LEU
34	4g	71	GLU
34	4g	73	LEU
34	4g	74	GLU
46	2A	120	ILE
47	A1	160	SER
47	A1	223	LYS
47	A1	237	ARG
47	A1	238	GLU
48	65	16	GLU
49	5B	203	VAL
49	5B	272	LEU
49	5B	998	VAL
49	5B	1029	VAL
49	5B	1228	VAL
49	5B	1380	THR
49	5B	1518	VAL
49	5B	1521	VAL
49	5B	1985	ILE
49	5B	2067	VAL
50	B1	695	VAL
50	B1	970	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (266) such sidechains are listed below:

Mol	Chain	Res	Type
3	5O	101	ASN
3	5O	165	GLN
4	B4	41	ASN
4	B4	43	HIS
5	13	45	ASN
6	4B	215	HIS
6	4B	242	ASN
6	4B	295	ASN
6	4B	361	GLN
6	4B	414	ASN
6	4B	421	HIS
6	4B	472	ASN
7	5e	26	GLN

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Mol	Chain	Res	Type
7	5e	38	GLN
7	5e	88	GLN
9	1K	35	ASN
9	1K	36	GLN
9	1K	80	GLN
9	1K	133	HIS
9	1K	158	HIS
10	4C	131	ASN
10	4C	389	GLN
11	41	12	HIS
11	41	24	GLN
11	41	64	ASN
12	R	393	ASN
12	R	471	GLN
13	1f	46	ASN
7	4e	27	ASN
7	4e	40	ASN
14	66	69	ASN
16	22	25	ASN
18	67	28	GLN
19	62	71	GLN
20	2B	15	ASN
5	53	42	GLN
5	53	57	GLN
21	A2	78	HIS
21	A2	79	GLN
21	A2	149	HIS
22	B2	496	ASN
22	B2	569	GLN
13	2f	68	ASN
23	5C	137	HIS
23	5C	505	GLN
23	5C	513	ASN
23	5C	542	ASN
23	5C	571	ASN
23	5C	583	ASN
23	5C	702	ASN
23	5C	719	GLN
23	5C	798	GLN
23	5C	903	HIS
24	5X	185	GLN
24	5X	297	GLN

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Mol	Chain	Res	Type
24	5X	359	GLN
24	5X	420	GLN
24	5X	428	ASN
24	5X	535	ASN
24	5X	597	HIS
24	5X	731	GLN
24	5X	781	GLN
11	11	64	ASN
16	42	39	ASN
16	42	49	ASN
16	42	69	ASN
16	42	112	ASN
25	1b	22	GLN
26	B5	34	ASN
26	B5	51	ASN
26	B5	58	ASN
27	1A	67	ASN
13	5f	6	ASN
13	5f	12	ASN
29	5J	140	GLN
29	5J	141	GLN
29	5J	265	GLN
29	5J	305	ASN
29	5J	307	HIS
29	5J	308	HIS
29	5J	326	GLN
29	5J	330	ASN
29	5J	353	GLN
29	5J	497	ASN
29	5J	508	GLN
29	5J	587	HIS
29	5J	655	ASN
29	5J	717	GLN
29	5J	733	ASN
29	5J	809	ASN
29	5J	839	HIS
29	5J	865	HIS
29	5J	887	GLN
29	5J	908	HIS
11	51	12	HIS
11	51	64	ASN
30	4D	27	GLN

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Mol	Chain	Res	Type
30	4D	111	GLN
25	2b	76	ASN
33	B3	5	ASN
33	B3	28	GLN
33	B3	138	GLN
33	B3	169	HIS
33	B3	260	ASN
33	B3	264	GLN
33	B3	304	GLN
33	B3	394	ASN
33	B3	518	GLN
33	B3	730	HIS
33	B3	760	ASN
33	B3	795	ASN
33	B3	796	ASN
33	B3	859	ASN
33	B3	885	ASN
33	B3	916	ASN
33	B3	988	ASN
33	B3	1172	ASN
5	23	40	ASN
5	23	45	ASN
25	5b	22	GLN
35	68	10	ASN
35	68	42	HIS
7	1e	65	HIS
36	5A	210	HIS
36	5A	221	ASN
36	5A	294	ASN
36	5A	325	HIS
36	5A	448	GLN
36	5A	579	GLN
36	5A	654	ASN
36	5A	703	GLN
36	5A	711	GLN
36	5A	752	ASN
36	5A	775	ASN
36	5A	875	HIS
36	5A	1003	HIS
36	5A	1014	ASN
36	5A	1066	GLN
36	5A	1121	ASN

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Mol	Chain	Res	Type
36	5A	1159	ASN
36	5A	1182	ASN
36	5A	1188	ASN
36	5A	1209	HIS
36	5A	1332	HIS
36	5A	1345	GLN
36	5A	1424	GLN
36	5A	1487	HIS
36	5A	1527	ASN
36	5A	1543	ASN
36	5A	1638	ASN
36	5A	1728	GLN
36	5A	1737	ASN
36	5A	1752	GLN
36	5A	1775	GLN
36	5A	1811	ASN
36	5A	1875	HIS
36	5A	1946	ASN
36	5A	1947	ASN
36	5A	2166	HIS
36	5A	2203	ASN
36	5A	2260	GLN
36	5A	2276	GLN
36	5A	2306	HIS
37	A3	143	HIS
37	A3	326	GLN
37	A3	448	ASN
38	U	158	GLN
38	U	200	GLN
38	U	234	ASN
38	U	242	GLN
38	U	294	HIS
38	U	413	GLN
38	U	531	GLN
38	U	551	GLN
34	2g	26	HIS
34	2g	55	ASN
34	2g	56	ASN
39	5D	7	HIS
39	5D	32	HIS
39	5D	89	HIS
16	52	34	GLN

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Mol	Chain	Res	Type
16	52	38	ASN
16	52	41	GLN
16	52	91	ASN
40	64	13	HIS
7	2e	19	ASN
7	2e	88	GLN
34	5g	26	HIS
34	5g	28	GLN
34	5g	55	ASN
43	K	678	ASN
43	K	695	GLN
43	K	707	ASN
43	K	711	ASN
43	K	740	ASN
43	K	840	HIS
43	K	895	ASN
43	K	896	HIS
43	K	921	GLN
43	K	926	ASN
43	K	928	ASN
43	K	950	ASN
43	K	995	ASN
44	4A	425	ASN
44	4A	524	GLN
44	4A	542	HIS
11	21	64	ASN
34	4g	26	HIS
34	4g	28	GLN
34	4g	55	ASN
46	2A	72	ASN
48	65	75	ASN
48	65	77	ASN
48	65	78	ASN
49	5B	202	ASN
49	5B	259	HIS
49	5B	304	ASN
49	5B	313	ASN
49	5B	485	GLN
49	5B	498	ASN
49	5B	524	HIS
49	5B	638	ASN
49	5B	702	GLN

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Mol	Chain	Res	Type
49	5B	807	GLN
49	5B	884	ASN
49	5B	885	GLN
49	5B	951	GLN
49	5B	968	ASN
49	5B	980	GLN
49	5B	1003	GLN
49	5B	1086	GLN
49	5B	1113	ASN
49	5B	1124	GLN
49	5B	1209	GLN
49	5B	1247	GLN
49	5B	1265	GLN
49	5B	1329	ASN
49	5B	1370	GLN
49	5B	1402	ASN
49	5B	1441	GLN
49	5B	1659	HIS
49	5B	1674	HIS
49	5B	1737	ASN
49	5B	1769	ASN
49	5B	1885	ASN
49	5B	1892	ASN
49	5B	1951	GLN
49	5B	1965	HIS
49	5B	2016	ASN
49	5B	2086	GLN
50	B1	457	ASN
50	B1	533	ASN
50	B1	662	HIS
50	B1	698	GLN
50	B1	832	GLN
50	B1	912	ASN
50	B1	919	ASN
50	B1	1002	ASN
50	B1	1069	HIS
50	B1	1100	ASN
50	B1	1107	GLN
50	B1	1108	ASN
50	B1	1218	ASN
50	B1	1252	GLN
50	B1	1270	ASN

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Mol	Chain	Res	Type
50	B1	1293	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	163/164 (99%)	49 (30%)	6 (3%)
17	5	101/117 (86%)	42 (41%)	4 (3%)
2	6	50/106 (47%)	5 (10%)	2 (4%)
32	2	90/188 (47%)	23 (25%)	4 (4%)
45	4	120/146 (82%)	25 (20%)	3 (2%)
8	I	23/62 (37%)	5 (21%)	0
All	All	547/783 (69%)	149 (27%)	19 (3%)

All (149) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	U
1	1	12	G
1	1	15	G
1	1	16	G
1	1	17	G
1	1	20	G
1	1	21	A
1	1	22	U
1	1	23	A
1	1	28	G
1	1	29	A
1	1	35	A
1	1	41	G
1	1	47	C
1	1	48	C
1	1	50	G
1	1	51	G
1	1	55	A
1	1	62	U
1	1	72	U
1	1	73	C
1	1	75	G
1	1	88	C
1	1	90	U
1	1	91	G

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Mol	Chain	Res	Type
1	1	92	C
1	1	93	G
1	1	94	A
1	1	103	A
1	1	105	U
1	1	108	G
1	1	112	A
1	1	114	C
1	1	115	U
1	1	117	G
1	1	118	A
1	1	119	C
1	1	123	A
1	1	124	U
1	1	126	A
1	1	128	U
1	1	130	G
1	1	132	G
1	1	133	G
1	1	135	A
1	1	136	G
1	1	137	U
1	1	138	G
1	1	158	U
2	6	48	A
2	6	49	G
2	6	74	U
2	6	77	C
2	6	106	U
8	I	0	G
8	I	5	G
8	I	92	U
8	I	100	A
8	I	101	C
17	5	4	C
17	5	5	U
17	5	6	C
17	5	7	U
17	5	9	G
17	5	20	G
17	5	21	A
17	5	22	U

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Mol	Chain	Res	Type
17	5	23	C
17	5	24	G
17	5	25	C
17	5	26	A
17	5	28	A
17	5	36	C
17	5	37	G
17	5	38	C
17	5	47	A
17	5	48	A
17	5	57	G
17	5	58	U
17	5	59	G
17	5	63	A
17	5	66	A
17	5	67	A
17	5	71	C
17	5	75	G
17	5	78	U
17	5	86	C
17	5	88	A
17	5	89	U
17	5	90	U
17	5	94	U
17	5	95	G
17	5	97	G
17	5	98	G
17	5	102	U
17	5	104	C
17	5	105	U
17	5	106	U
17	5	107	U
17	5	108	G
17	5	109	G
32	2	37	U
32	2	38	A
32	2	40	C
32	2	43	U
32	2	45	C
32	2	46	U
32	2	47	U
32	2	48	A

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Mol	Chain	Res	Type
32	2	49	U
32	2	63	G
32	2	65	U
32	2	98	G
32	2	100	U
32	2	101	U
32	2	102	U
32	2	103	U
32	2	104	U
32	2	105	G
32	2	106	G
32	2	107	A
32	2	157	G
32	2	171	U
32	2	178	A
45	4	2	G
45	4	19	U
45	4	20	A
45	4	25	A
45	4	26	G
45	4	30	A
45	4	36	U
45	4	37	U
45	4	38	U
45	4	40	U
45	4	44	A
45	4	45	G
45	4	51	A
45	4	52	U
45	4	67	A
45	4	68	A
45	4	69	C
45	4	114	U
45	4	115	G
45	4	121	U
45	4	122	U
45	4	123	U
45	4	125	G
45	4	126	A
45	4	140	G

All (19) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	15	G
1	1	90	U
1	1	92	C
1	1	123	A
1	1	126	A
1	1	128	U
2	6	47	A
2	6	104	U
17	5	57	G
17	5	58	U
17	5	96	A
17	5	105	U
32	2	37	U
32	2	46	U
32	2	103	U
32	2	106	G
45	4	1	A
45	4	68	A
45	4	114	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 9 ligands modelled in this entry, 7 are monoatomic - leaving 2 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
53	GTP	5C	1002	52	33,34,34	0.99	2 (6%)	50,54,54	1.64	9 (18%)
54	IHP	5A	2401	-	36,36,36	0.71	0	60,60,60	0.76	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
53	GTP	5C	1002	52	-	4/22/38/38	0/3/3/3
54	IHP	5A	2401	-	-	6/30/54/54	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	5C	1002	GTP	O4'-C4'	-2.12	1.40	1.45
53	5C	1002	GTP	C5-N7	-2.01	1.35	1.39

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	5C	1002	GTP	C5-C4-N3	-4.53	121.18	128.39
53	5C	1002	GTP	C2-N3-C4	4.47	119.99	112.30
53	5C	1002	GTP	C2-N1-C6	-3.05	119.58	125.11
53	5C	1002	GTP	N9-C8-N7	-3.00	107.85	113.40
53	5C	1002	GTP	N9-C4-N3	2.82	131.60	125.95
53	5C	1002	GTP	C5-C6-N1	2.71	120.14	113.25
53	5C	1002	GTP	O6-C6-C5	-2.56	119.79	126.53
53	5C	1002	GTP	C8-N7-C5	2.55	108.80	104.26
53	5C	1002	GTP	O2A-PA-O3A	2.27	113.42	107.27

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
53	5C	1002	GTP	O4'-C4'-C5'-O5'
53	5C	1002	GTP	PB-O3A-PA-O2A
53	5C	1002	GTP	C3'-C4'-C5'-O5'
54	5A	2401	IHP	C1-O11-P1-O41
54	5A	2401	IHP	C3-O13-P3-O23

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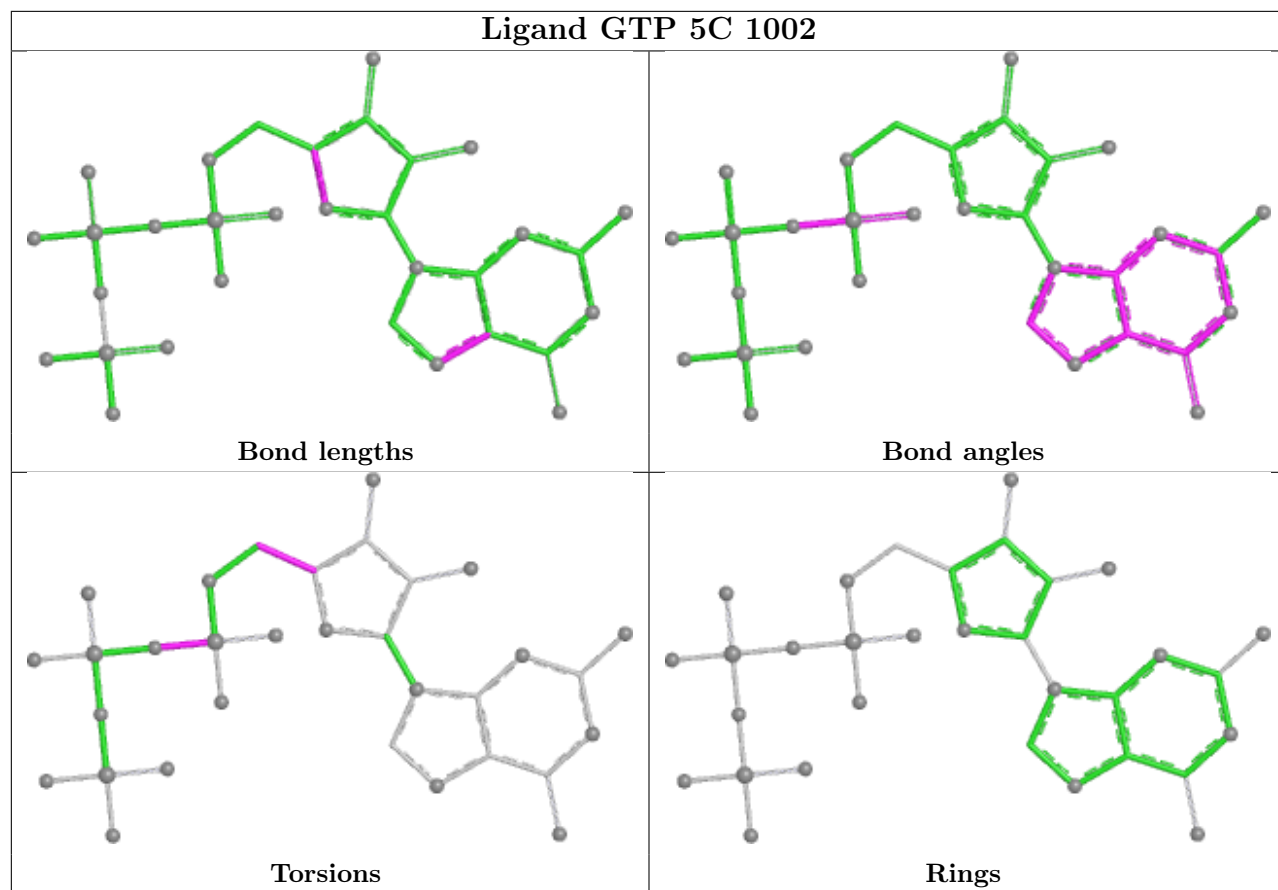
Mol	Chain	Res	Type	Atoms
54	5A	2401	IHP	C5-O15-P5-O25
54	5A	2401	IHP	C4-O14-P4-O34
54	5A	2401	IHP	C5-O15-P5-O35
54	5A	2401	IHP	C5-O15-P5-O45
53	5C	1002	GTP	PB-O3A-PA-O1A

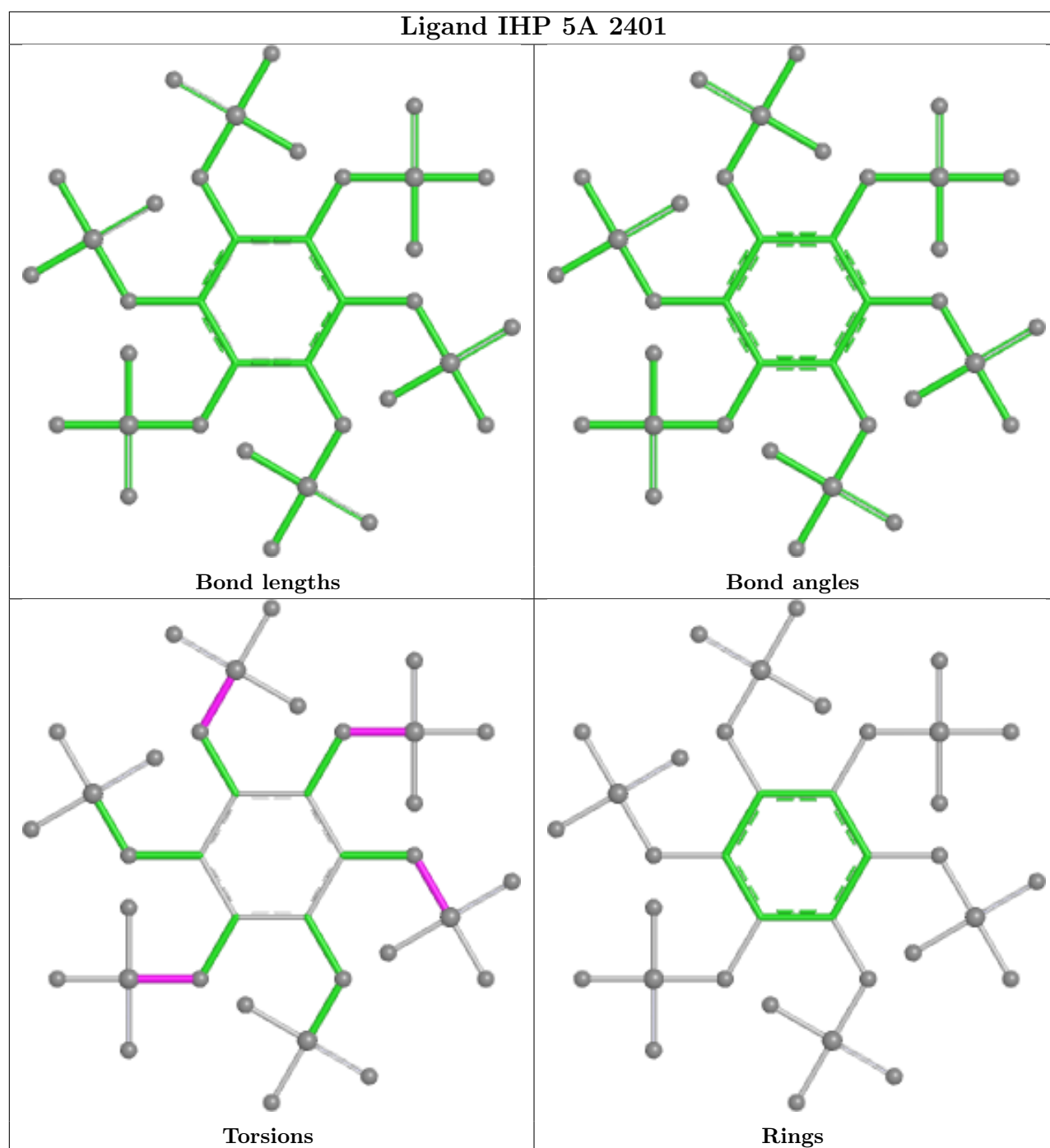
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	5A	2401	IHP	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
47	A1	2
1	1	2
29	5J	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A1	282:VAL	C	422:UNK	N	108.26
1	5J	165:ASP	C	236:GLY	N	34.19
1	A1	447:UNK	C	455:VAL	N	4.52
1	1	2:U	O3'	3:A	P	1.39
1	1	78:U	O3'	79:G	P	1.37

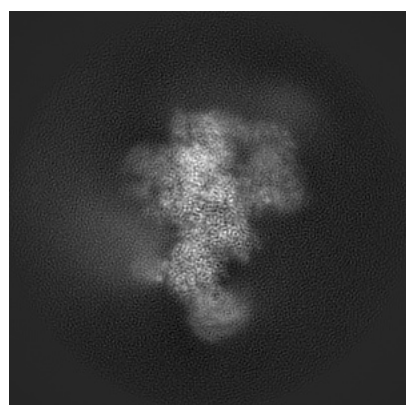
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4665. These allow visual inspection of the internal detail of the map and identification of artifacts.

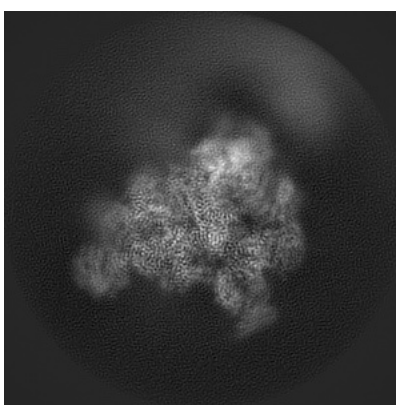
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

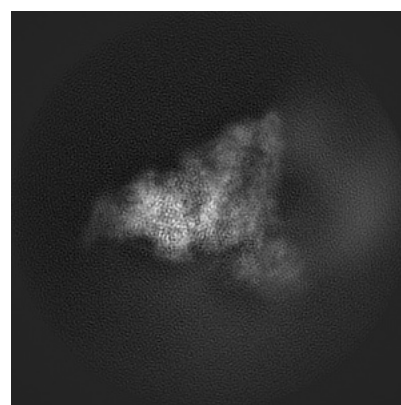
6.1.1 Primary map



X



Y

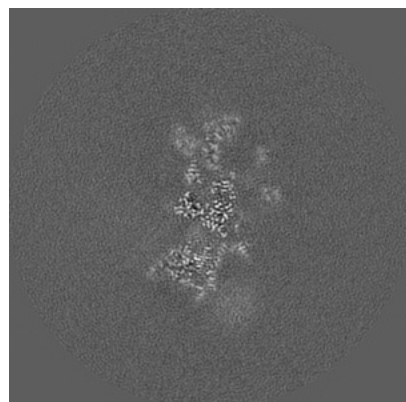


Z

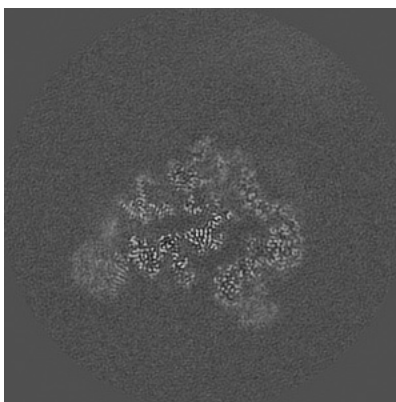
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

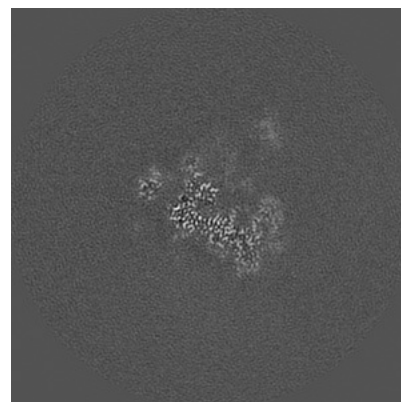
6.2.1 Primary map



X Index: 210



Y Index: 210

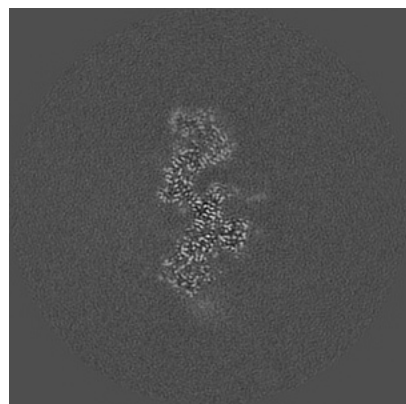


Z Index: 210

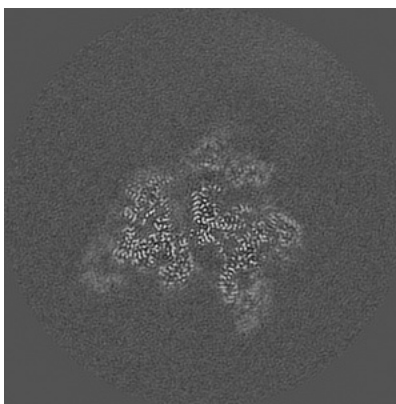
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

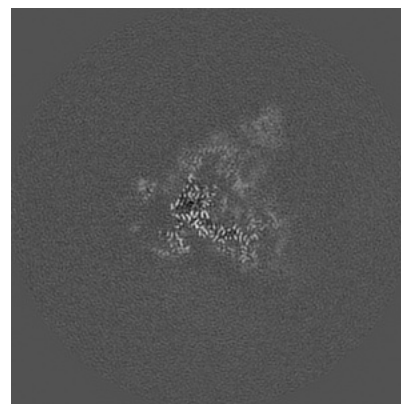
6.3.1 Primary map



X Index: 177



Y Index: 193

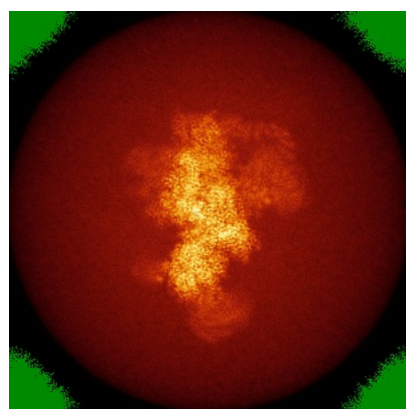


Z Index: 218

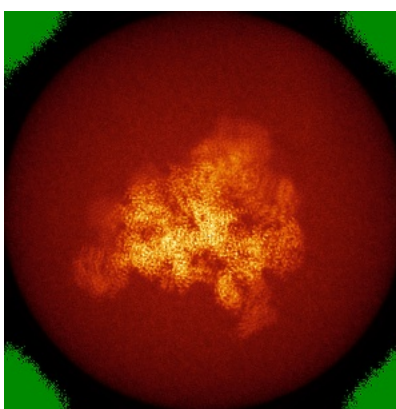
The images above show the largest variance slices of the map in three orthogonal directions.

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

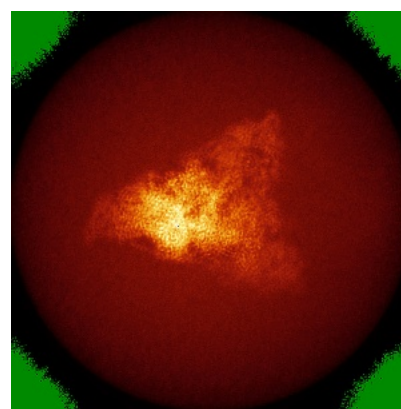
6.4.1 Primary map



X



Y

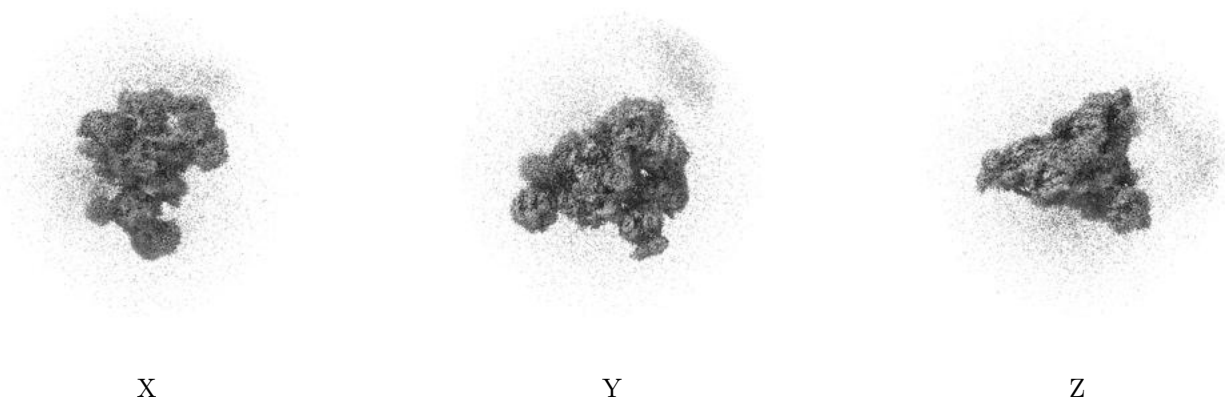


Z

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 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

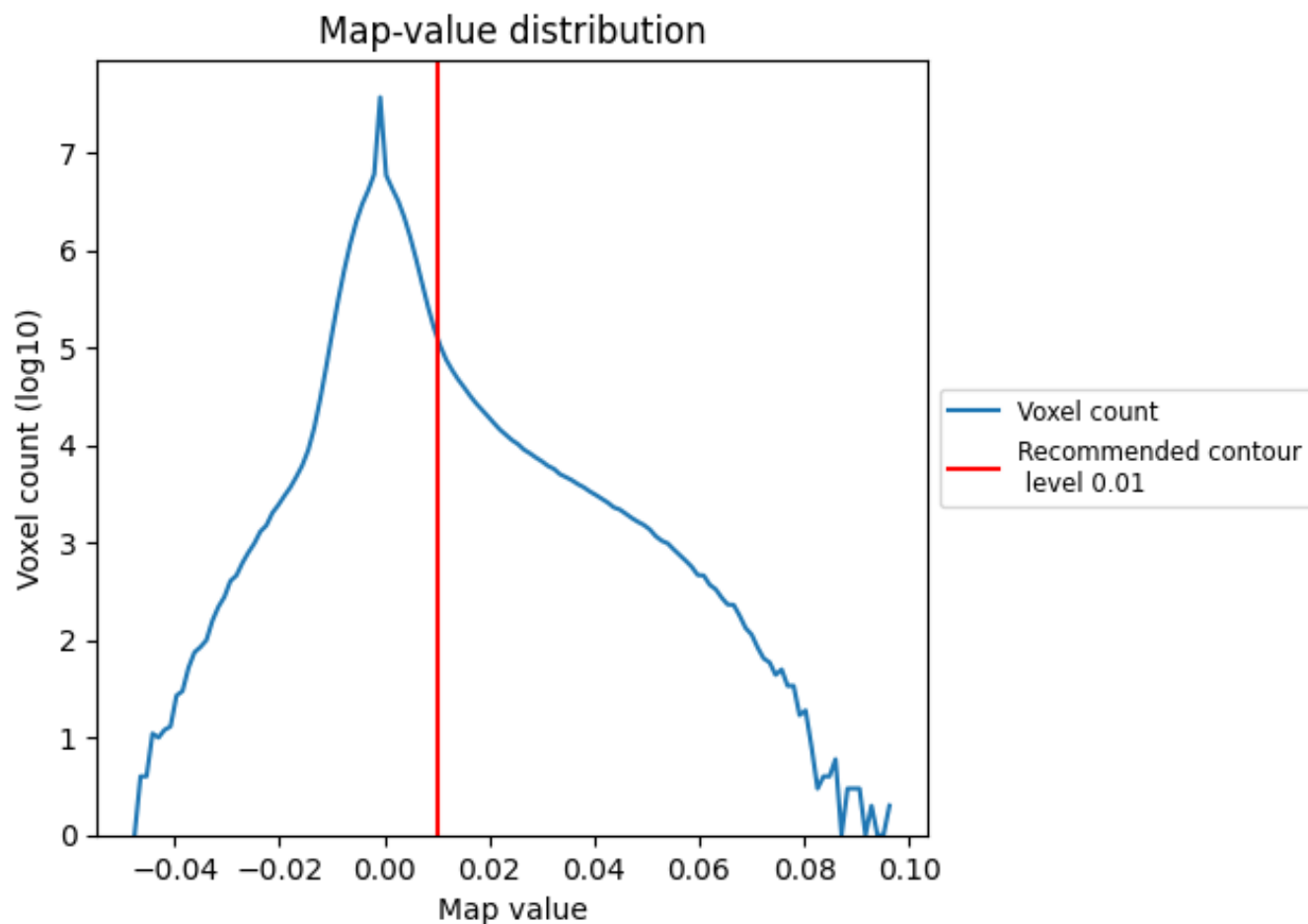
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

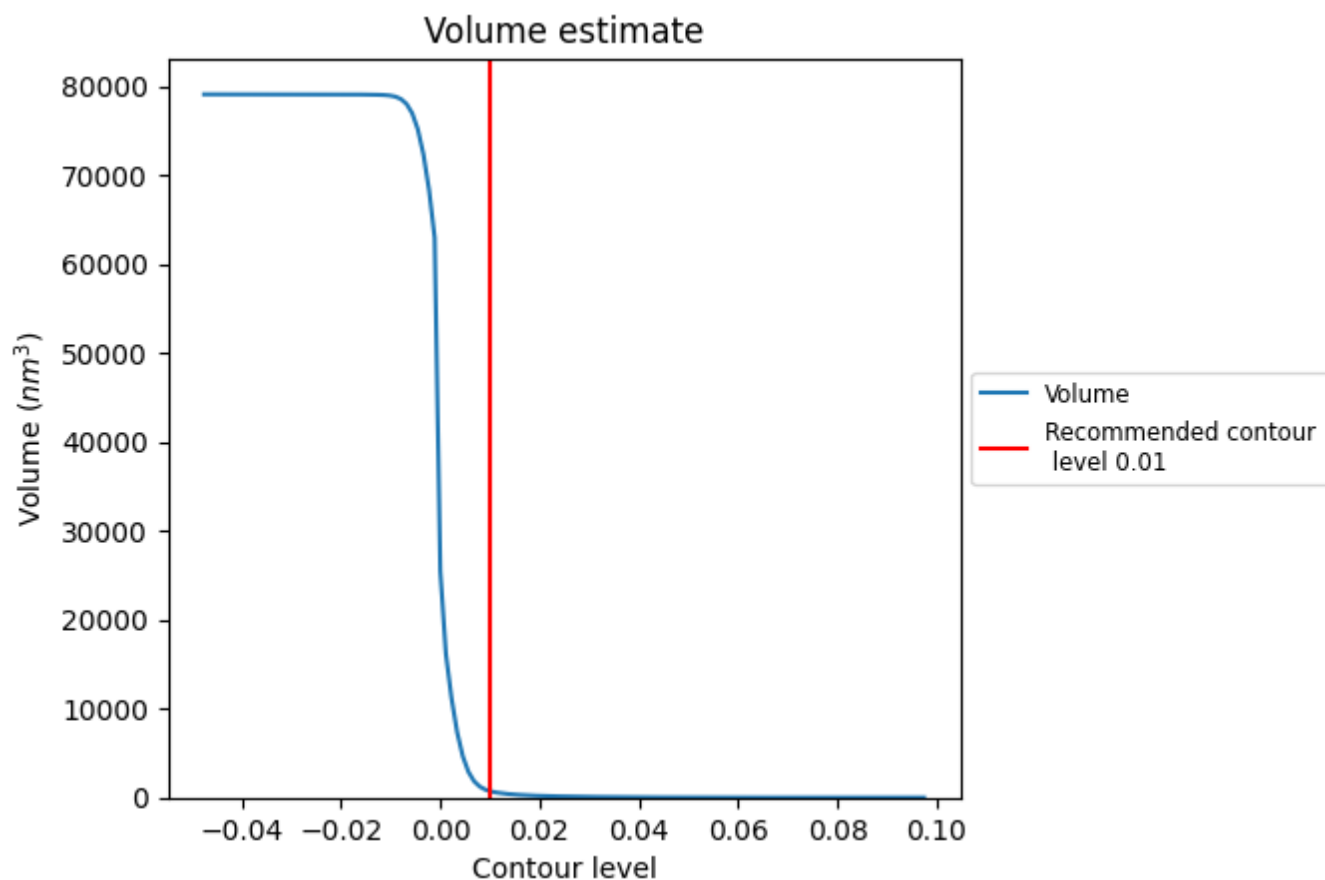
This section contains the results of statistical analysis of the map.

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.

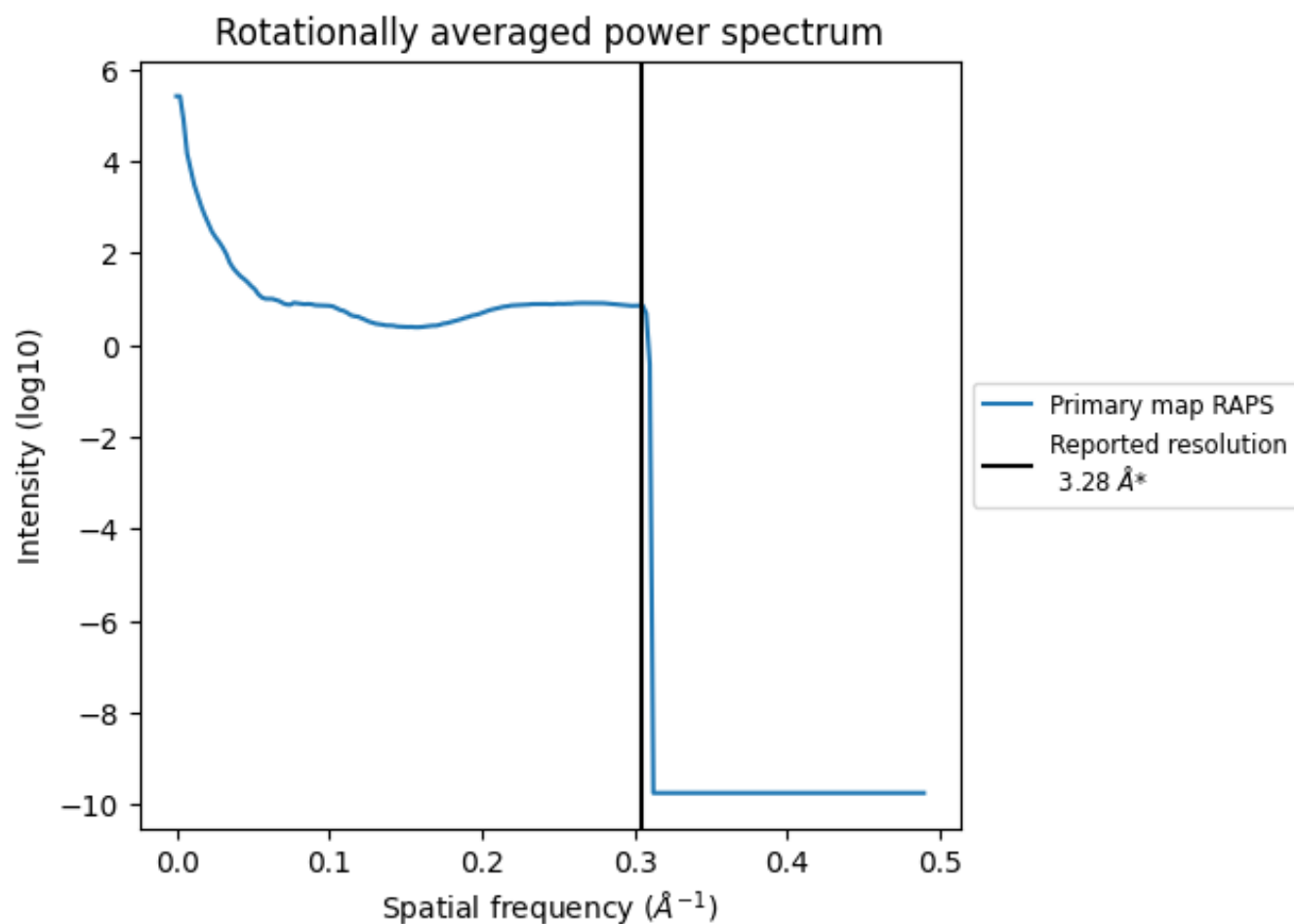
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 726 nm^3 ; this corresponds to an approximate mass of 656 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 ⓘ

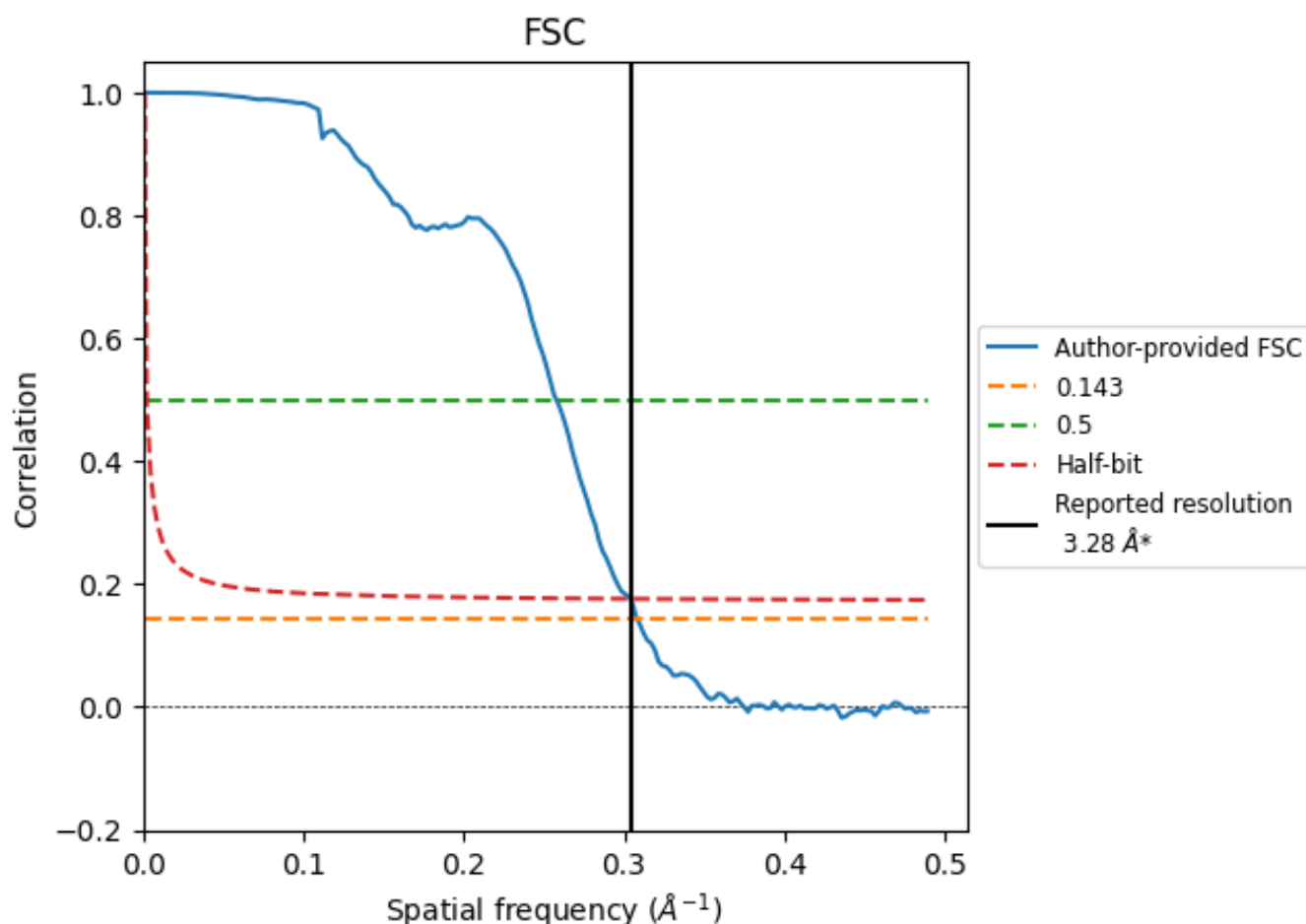


*Reported resolution corresponds to spatial frequency of 0.305 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.305 Å⁻¹

8.2 Resolution estimates [i](#)

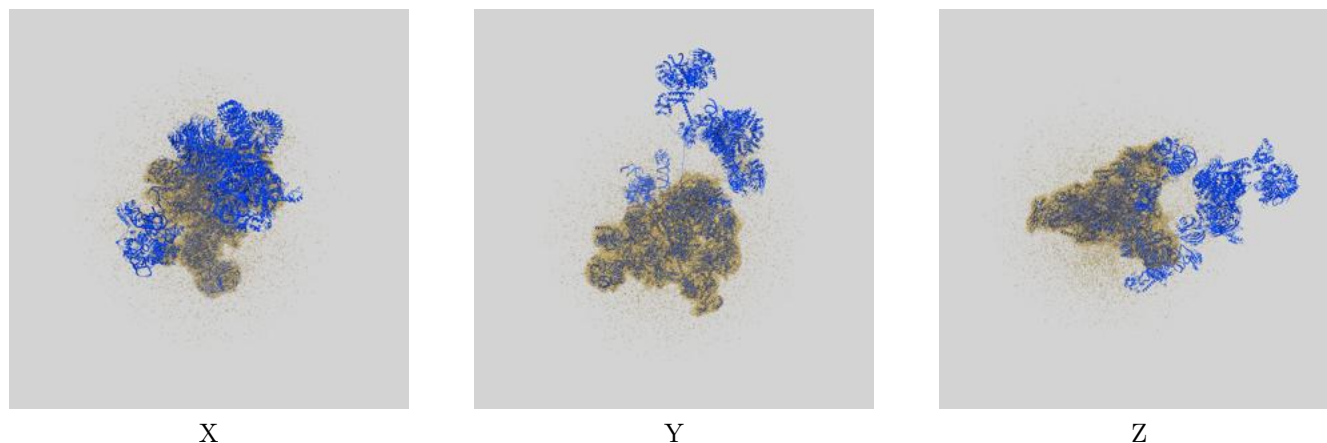
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.28	-	-
Author-provided FSC curve	3.24	3.88	3.29
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

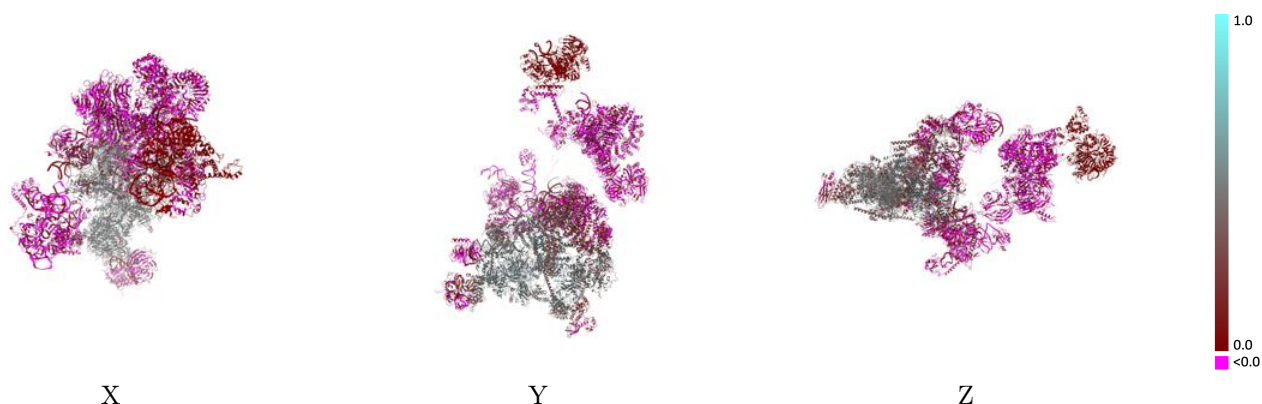
This section contains information regarding the fit between EMDB map EMD-4665 and PDB model 6QX9. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



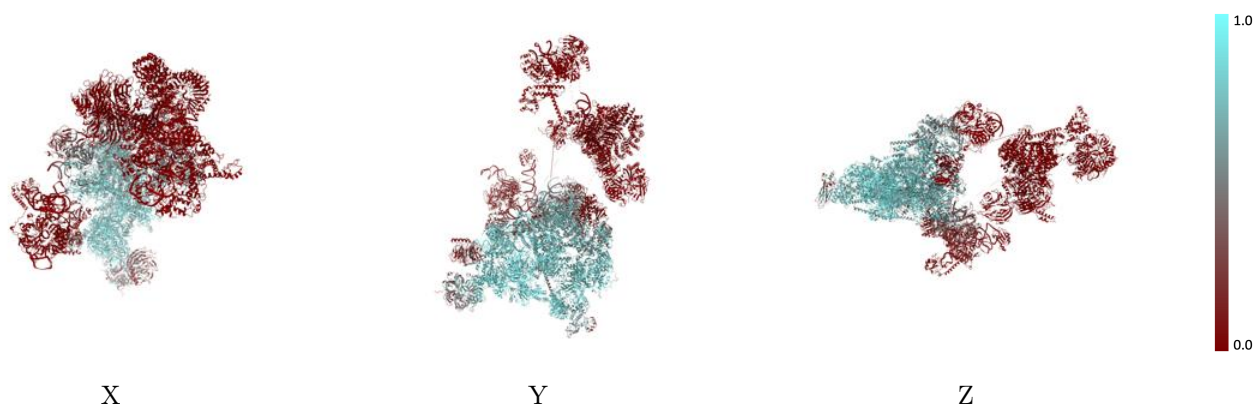
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



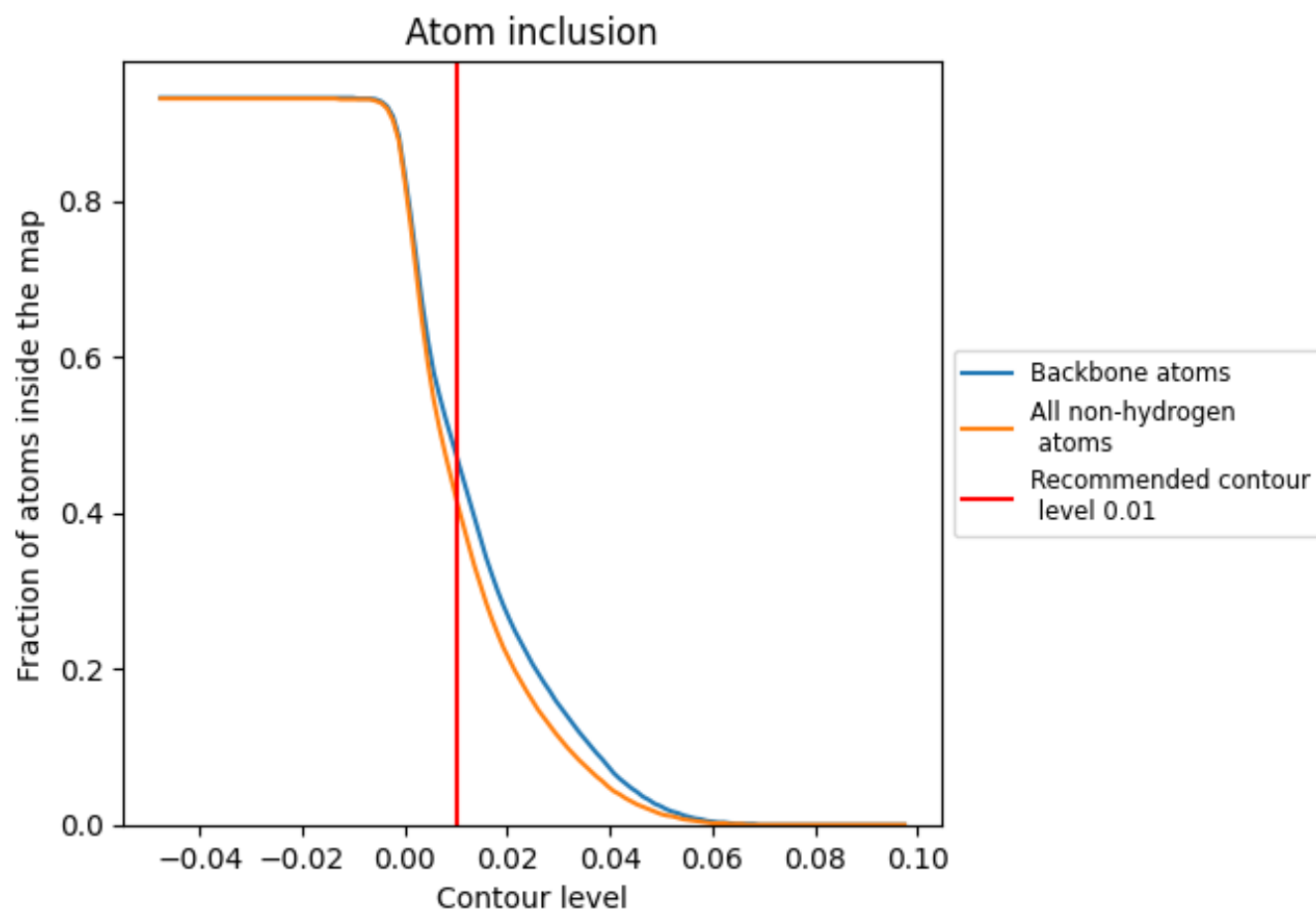
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 48% of all backbone atoms, 42% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4190	 0.2070
1	 0.0020	 0.0030
11	 0.0000	 -0.0020
12	 0.0000	 0.0170
13	 0.0000	 -0.0140
1A	 0.0000	 0.0280
1C	 0.0000	 0.0100
1K	 0.0010	 -0.0000
1b	 0.0030	 0.0140
1e	 0.0000	 0.0140
1f	 0.0020	 0.0020
1g	 0.0000	 0.0360
2	 0.0010	 0.0120
21	 0.0000	 0.0000
22	 0.0000	 0.0000
23	 0.0000	 0.0000
2A	 0.0000	 0.0000
2B	 0.0000	 0.0000
2b	 0.0000	 0.0000
2e	 0.0000	 0.0000
2f	 0.0000	 0.0000
2g	 0.0000	 0.0000
4	 0.6370	 0.2230
41	 0.4710	 0.2010
42	 0.4720	 0.2320
43	 0.2390	 0.0480
4A	 0.4880	 0.1430
4B	 0.5560	 0.1550
4C	 0.6880	 0.3260
4D	 0.6860	 0.3020
4b	 0.2840	 0.0870
4e	 0.2410	 0.0760
4f	 0.3330	 0.1270
4g	 0.2040	 0.0230
5	 0.7530	 0.2980



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Chain	Atom inclusion	Q-score
51	 0.4680	 0.1340
52	 0.4130	 0.1040
53	 0.7280	 0.3830
5A	 0.8230	 0.4690
5B	 0.7650	 0.3870
5C	 0.8730	 0.5100
5D	 0.8170	 0.4650
5J	 0.6500	 0.2450
5O	 0.1710	 0.0160
5X	 0.3060	 0.1470
5b	 0.5770	 0.2660
5e	 0.4730	 0.1160
5f	 0.3570	 0.0930
5g	 0.5680	 0.2690
6	 0.5610	 0.1990
62	 0.0050	 0.0140
63	 0.0100	 -0.0020
64	 0.0000	 -0.0470
65	 0.0020	 0.0290
66	 0.0000	 -0.0070
67	 0.0020	 -0.0100
68	 0.0010	 0.0250
A1	 0.1030	 0.0580
A2	 0.0000	 -0.0020
A3	 0.0000	 0.0040
B1	 0.0010	 0.0020
B2	 0.0020	 0.0090
B3	 0.0010	 -0.0030
B4	 0.0000	 -0.0010
B5	 0.0040	 -0.0090
BP	 0.0010	 -0.0110
I	 0.0040	 -0.0000
K	 0.0120	 0.0130
R	 0.6000	 0.2310
S	 0.6350	 0.3130
U	 0.8800	 0.5060
X	 0.5430	 0.2760