



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 05:50 AM UTC

PDB ID : 8BTR / pdb_00008btr
EMDB ID : EMD-16235
Title : Giardia Ribosome in PRE-T Hybrid State (D2)
Authors : Majumdar, S.; Emmerich, A.G.; Sanyal, S.
Deposited on : 2022-11-29
Resolution : 3.25 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
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

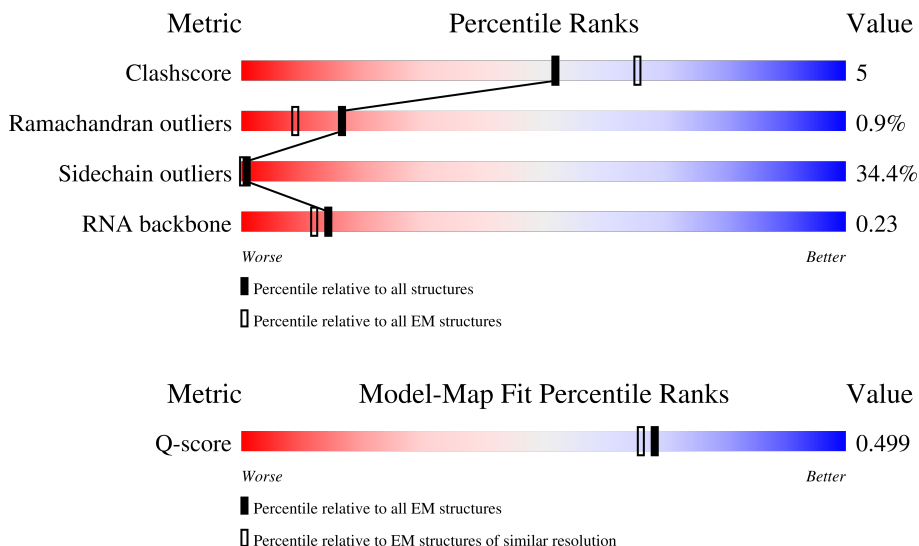
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.25 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.



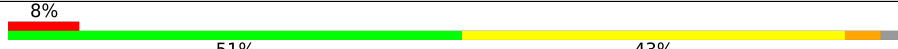
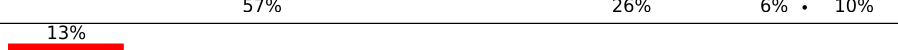
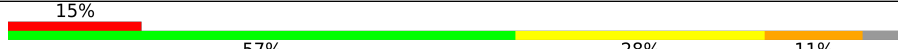
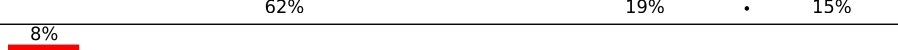
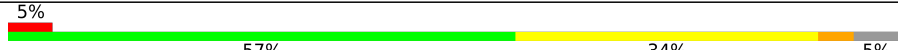
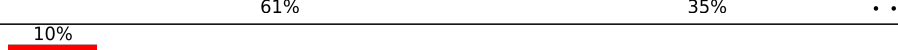
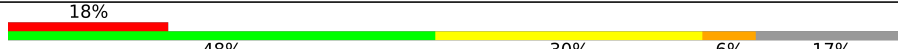
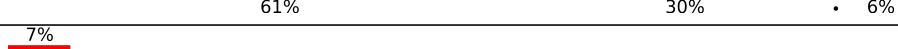
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14599 (2.75 - 3.75)

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	LA	251	 72% 24% . .
2	LB	379	 66% 28% 5% .
3	LC	316	 66% 28% . . .

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Mol	Chain	Length	Quality of chain
4	LD	142	
5	LE	121	
6	LF	297	
7	LG	51	
8	LH	235	
9	LI	225	
10	LJ	185	
11	LK	210	
12	LL	173	
13	LM	234	
14	LN	131	
15	LO	204	
16	LP	197	
17	LQ	164	
18	LR	179	
19	LS	196	
20	LT	173	
21	LU	159	
22	LV	124	
23	LW	142	
24	LX	189	
25	LY	141	
26	LZ	135	
27	La	135	
28	Lb	149	

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Mol	Chain	Length	Quality of chain
29	Lc	62	
30	Ld	109	
31	Le	106	
32	Lf	136	
33	Lg	123	
34	Lh	120	
35	Li	124	
36	Lj	90	
37	Lk	89	
38	Ll	77	
39	Ln	217	
40	Lo	25	
41	Lp	106	
42	Lq	94	
43	Ls	127	
44	Lt	2697	
45	SA	245	
46	SB	242	
47	SC	217	
48	SD	248	
49	SE	268	
50	SF	190	
51	SG	248	
52	SH	190	
53	SI	174	

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Mol	Chain	Length	Quality of chain
54	SJ	130	
55	SK	189	
56	SL	134	
57	SM	154	
58	SO	144	
59	SP	154	
60	SQ	145	
61	SR	145	
62	ST	158	
63	SU	137	
64	SV	154	
65	SW	139	
66	SX	126	
67	SY	89	
68	Sb	132	
69	Sc	88	
70	Sd	109	
71	Se	81	
72	Sg	64	
73	Sh	51	
74	Sj	69	
75	St	1454	
76	u	75	
77	v	75	
78	y	11	

2 Entry composition

There are 78 unique types of molecules in this entry. The entry contains 177509 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	LA	247	Total	C	N	O	S	0	0
			1855	1145	379	319	12		

- Molecule 2 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LB	378	Total	C	N	O	S	0	0
			2987	1886	566	514	21		

- Molecule 3 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LC	310	Total	C	N	O	S	0	0
			2415	1518	469	420	8		

- Molecule 4 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LD	142	Total	C	N	O	P	0	0
			3038	1350	563	983	142		

- Molecule 5 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LE	117	Total	C	N	O	P	0	0
			2502	1116	457	812	117		

- Molecule 6 is a protein called Ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LF	293	Total	C	N	O	S	0	0
			2355	1490	439	418	8		

- Molecule 7 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	LG	50	Total	C	N	O	0	0
			439	281	94	64		

- Molecule 8 is a protein called Ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LH	212	Total	C	N	O	S	0	0
			1717	1092	313	307	5		

- Molecule 9 is a protein called Ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LI	186	Total	C	N	O	S	0	0
			1487	947	273	262	5		

- Molecule 10 is a protein called Ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LJ	184	Total	C	N	O	S	0	0
			1452	917	264	261	10		

- Molecule 11 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LK	195	Total	C	N	O	S	0	0
			1594	1001	315	270	8		

- Molecule 12 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LL	166	Total	C	N	O	S	0	0
			1334	842	248	239	5		

- Molecule 13 is a protein called Ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LM	200	Total	C	N	O	S	0	0
			1600	996	324	273	7		

- Molecule 14 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LN	130	Total	C	N	O	S	0	0
			1024	649	186	183	6		

- Molecule 15 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LO	203	Total	C	N	O	S	0	0
			1708	1080	357	265	6		

- Molecule 16 is a protein called Ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LP	194	Total	C	N	O	S	0	0
			1578	994	306	266	12		

- Molecule 17 is a protein called Ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LQ	155	Total	C	N	O	S	0	0
			1247	788	241	214	4		

- Molecule 18 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LR	178	Total	C	N	O	S	0	0
			1402	871	279	243	9		

- Molecule 19 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LS	161	Total	C	N	O	S	0	0
			1342	829	283	226	4		

- Molecule 20 is a protein called Ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LT	170	Total	C	N	O	S	0	0
			1423	899	272	243	9		

- Molecule 21 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LU	156	Total	C	N	O	S	0	0
			1257	784	259	207	7		

- Molecule 22 is a protein called Ribosomal protein L22e.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LV	103	Total	C	N	O	S	0	0
			845	540	145	158	2		

- Molecule 23 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LW	133	Total	C	N	O	S	0	0
			1019	643	194	177	5		

- Molecule 24 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LX	63	Total	C	N	O	S	0	0
			538	340	109	82	7		

- Molecule 25 is a protein called Ribosomal protein L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LY	115	Total	C	N	O	S	0	0
			931	598	168	162	3		

- Molecule 26 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LZ	133	Total	C	N	O	S	0	0
			1076	665	219	184	8		

- Molecule 27 is a protein called Ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	La	126	Total	C	N	O	S	0	0
			1004	633	189	176	6		

- Molecule 28 is a protein called Ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Lb	148	Total	C	N	O	S	0	0
			1201	759	240	199	3		

- Molecule 29 is a protein called Ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Lc	55	Total	C	N	O	S	0	0
			456	275	103	76	2		

- Molecule 30 is a protein called Ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ld	100	Total	C	N	O	S	0	0
			753	473	131	145	4		

- Molecule 31 is a protein called Ribosomal protein L31B.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Le	100	Total	C	N	O		0	0
			818	518	158	142			

- Molecule 32 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lf	130	Total	C	N	O	S	0	0
			1077	683	215	173	6		

- Molecule 33 is a protein called Ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lg	98	Total	C	N	O	S	0	0
			778	498	147	130	3		

- Molecule 34 is a protein called Ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lh	101	Total	C	N	O	S	0	0
			815	504	169	138	4		

- Molecule 35 is a protein called Ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Li	122	Total	C	N	O	S	0	0
			983	623	192	163	5		

- Molecule 36 is a protein called Ribosomal protein L36-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lj	89	Total	C	N	O	S	0	0
			731	462	146	119	4		

- Molecule 37 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lk	88	Total	C	N	O	S	0	0
			711	435	152	117	7		

- Molecule 38 is a protein called Ribosomal protein L38e.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ll	72	Total	C	N	O	S	0	0
			558	353	99	102	4		

- Molecule 39 is a protein called Ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Ln	200	Total	C	N	O	S	0	0
			1592	1025	278	284	5		

- Molecule 40 is a protein called Ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lo	25	Total	C	N	O	S	0	0
			227	140	57	27	3		

- Molecule 41 is a protein called Ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lp	93	Total	C	N	O	S	0	0
			767	478	159	125	5		

- Molecule 42 is a protein called Ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lq	91	Total	C	N	O	S	0	0
			708	437	144	120	7		

- Molecule 43 is a protein called Ubiquitin/Ribosomal protein L40e.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Ls	47	Total	C	N	O	S	0	0
			388	234	83	64	7		

- Molecule 44 is a RNA chain called Large Subunit rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lt	2593	Total	C	N	O	P	0	0
			55643	24727	10311	18012	2593		

- Molecule 45 is a protein called Ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SA	197	Total	C	N	O	S	0	0
			1578	1018	276	276	8		

- Molecule 46 is a protein called Ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SB	216	Total	C	N	O	S	0	0
			1667	1059	302	301	5		

- Molecule 47 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SC	206	Total	C	N	O	S	0	0
			1636	1030	302	288	16		

- Molecule 48 is a protein called Ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SD	229	Total	C	N	O	S	0	0
			1855	1172	346	324	13		

- Molecule 49 is a protein called Ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SE	257	Total	C	N	O	S	0	0
			2055	1312	378	353	12		

- Molecule 50 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SF	179	Total	C	N	O	S	0	0
			1400	871	266	254	9		

- Molecule 51 is a protein called Ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SG	238	Total	C	N	O	S	0	0
			1889	1188	360	331	10		

- Molecule 52 is a protein called Ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SH	177	Total	C	N	O	S	0	0
			1430	918	248	258	6		

- Molecule 53 is a protein called Ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SI	168	Total	C	N	O	S	0	0
			1316	826	252	235	3		

- Molecule 54 is a protein called Ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SJ	129	Total	C	N	O	S	0	0
			1031	659	192	177	3		

- Molecule 55 is a protein called Ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SK	176	Total	C	N	O	S	0	0
			1423	889	281	247	6		

- Molecule 56 is a protein called Ribosomal protein S10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SL	97	Total	C	N	O	S	0	0
			798	515	135	144	4		

- Molecule 57 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SM	152	Total	C	N	O	S	0	0
			1260	799	247	208	6		

- Molecule 58 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SO	140	Total	C	N	O	S	0	0
			1089	688	216	182	3		

- Molecule 59 is a protein called Ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SP	150	Total	C	N	O	S	0	0
			1193	762	225	202	4		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SP	6	ALA	SER	conflict	UNP A8BE02
SP	7	PRO	LYS	conflict	UNP A8BE02
SP	38	TYR	CYS	conflict	UNP A8BE02
SP	49	GLN	ARG	conflict	UNP A8BE02

- Molecule 60 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SQ	126	Total	C	N	O	S	0	0
			920	566	189	162	3		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SQ	110	GLY	GLN	conflict	UNP E2RU83
SQ	112	SER	GLY	conflict	UNP E2RU83
SQ	113	ALA	SER	conflict	UNP E2RU83
SQ	115	GLY	ALA	conflict	UNP E2RU83

- Molecule 61 is a protein called Ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SR	113	Total	C	N	O	S	0	0
			921	588	179	146	8		

- Molecule 62 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	ST	151	Total	C	N	O	S	0	0
			1180	736	229	212	3		

- Molecule 63 is a protein called Ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SU	121	Total	C	N	O	S	0	0
			965	598	184	178	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SU	104	THR	ALA	conflict	UNP A8BRG5

- Molecule 64 is a protein called Ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SV	129	Total	C	N	O	S	0	0
			1027	627	210	184	6		

- Molecule 65 is a protein called Ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SW	138	Total	C	N	O	S	0	0
			1080	686	204	187	3		

- Molecule 66 is a protein called Ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SX	98	Total	C	N	O	S	0	0
			776	496	141	135	4		

- Molecule 67 is a protein called Ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SY	86	Total	C	N	O	S	0	0
			651	403	120	122	6		

- Molecule 68 is a protein called Ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Sb	116	Total	C	N	O	S	0	0
			923	587	172	158	6		

- Molecule 69 is a protein called Ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sc	74	Total	C	N	O	S	0	0
			588	371	105	106	6		

- Molecule 70 is a protein called Ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Sd	97	Total	C	N	O	S	0	0
			787	485	162	133	7		

- Molecule 71 is a protein called Ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Se	79	Total	C	N	O	S	0	0
			621	392	109	115	5		

- Molecule 72 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Sg	62	Total	C	N	O	S	0	0
			498	306	99	91	2		

- Molecule 73 is a protein called Ribosomal protein S29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sh	49	Total	C	N	O	S	0	0
			409	259	79	66	5		

- Molecule 74 is a protein called Ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sj	67	Total	C	N	O	S	0	0
			543	341	114	87	1		

- Molecule 75 is a RNA chain called Small Subunit rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	St	1454	Total	C	N	O	P	0	0
			31176	13861	5772	10090	1453		

- Molecule 76 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	u	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 77 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	v	75	Total	C	N	O	P	0	0
			1602	716	296	516	74		

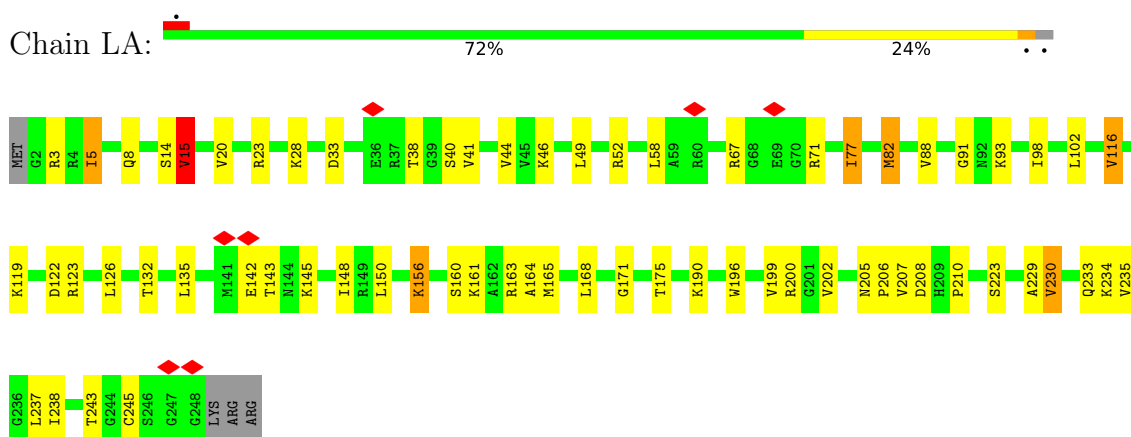
- Molecule 78 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	y	11	Total	C	N	O	P	0	0
			243	109	52	71	11		

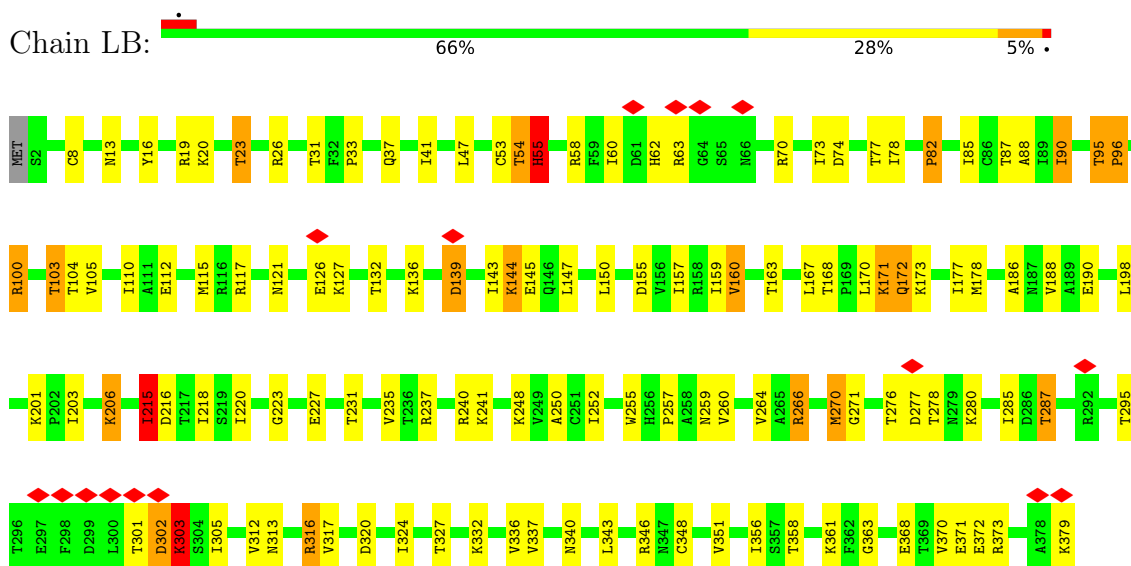
3 Residue-property plots

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

• Molecule 1: Ribosomal protein L2

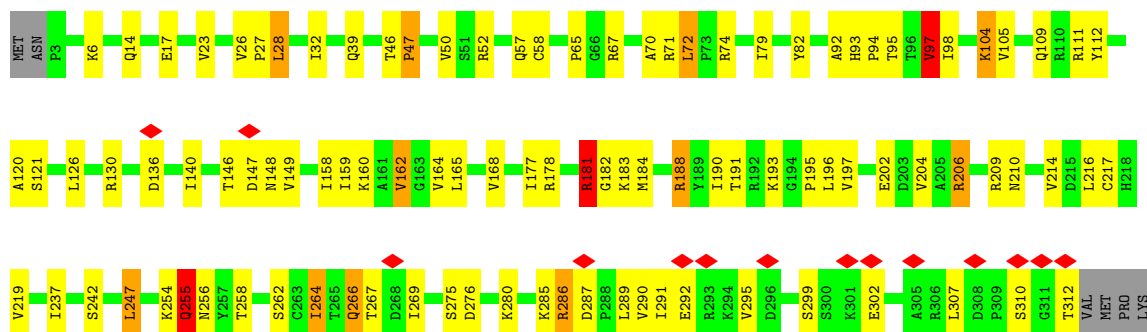


• Molecule 2: Ribosomal protein L3

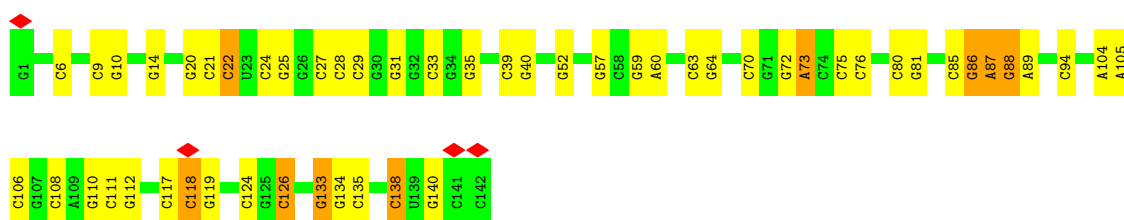


• Molecule 3: Ribosomal protein L4

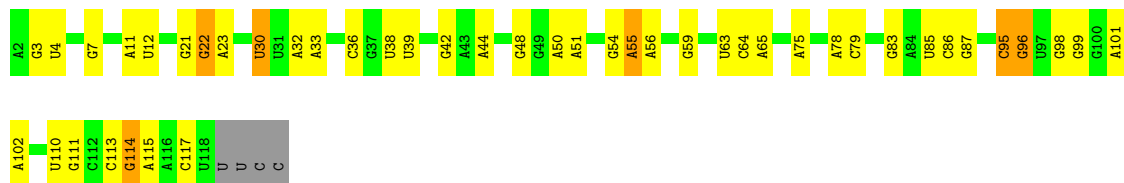




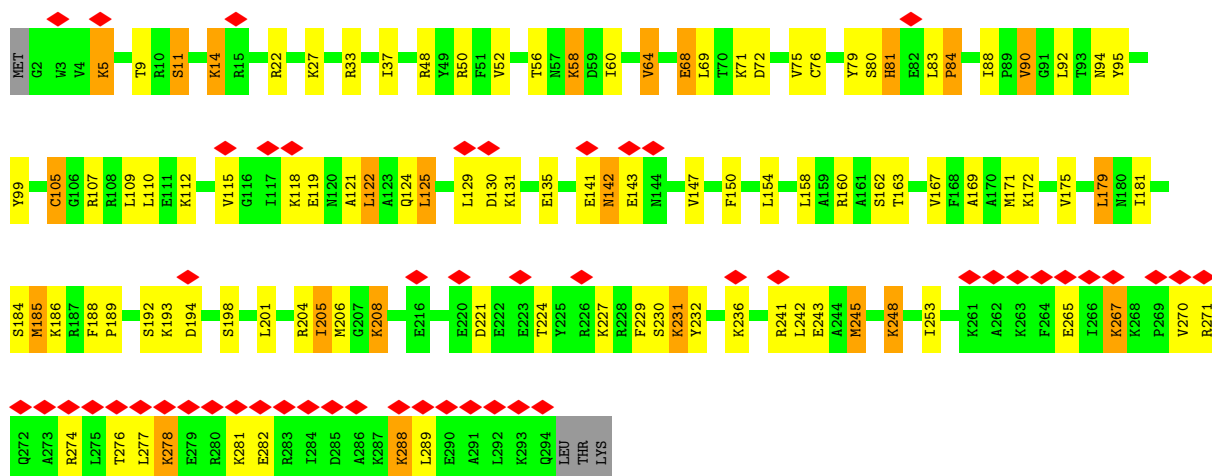
• Molecule 4: 5.8S rRNA



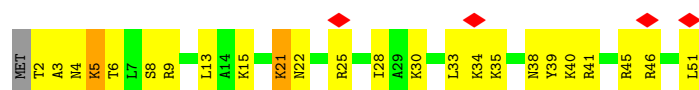
• Molecule 5: 5S rRNA



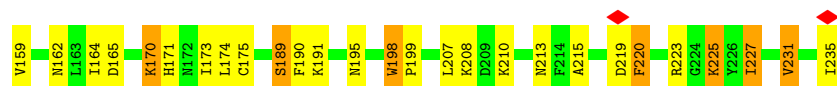
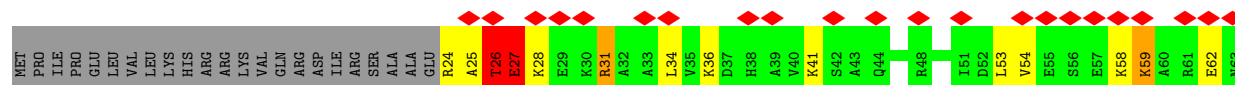
• Molecule 6: Ribosomal protein L5



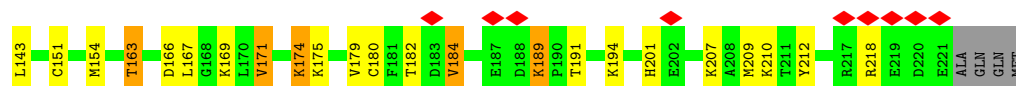
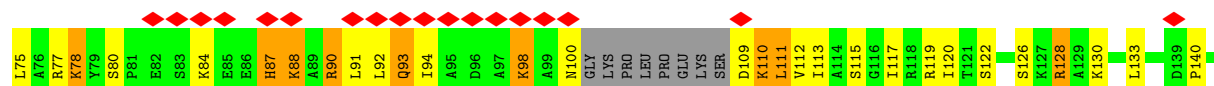
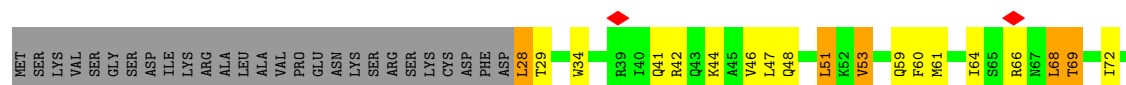
- Molecule 7: Ribosomal protein L39



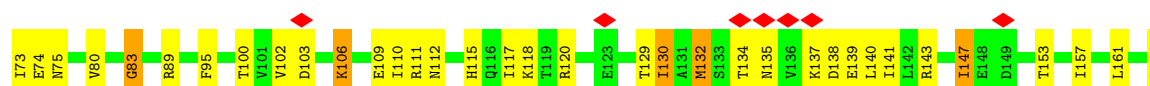
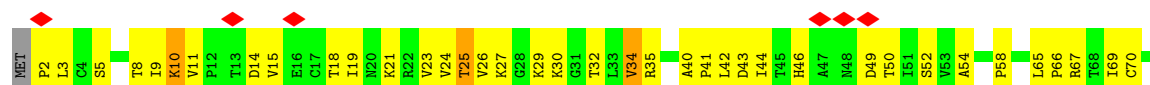
- Molecule 8: Ribosomal protein L7

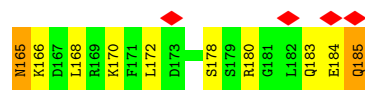


- Molecule 9: Ribosomal protein L7a

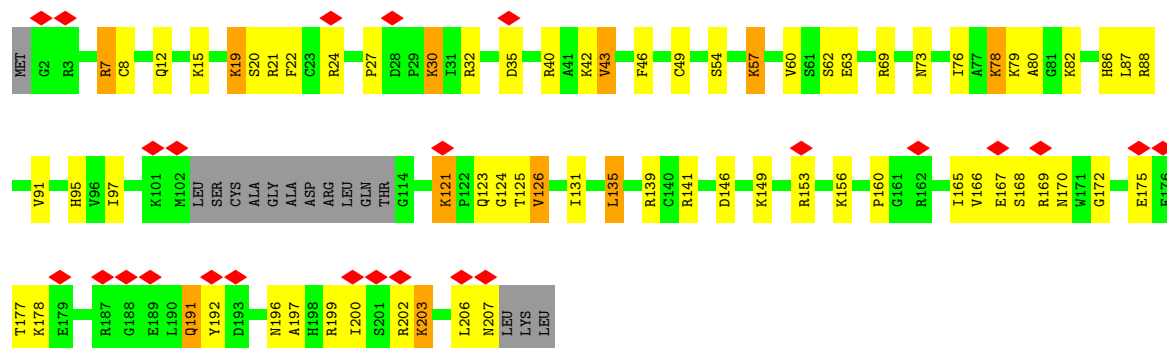


- Molecule 10: Ribosomal protein L6

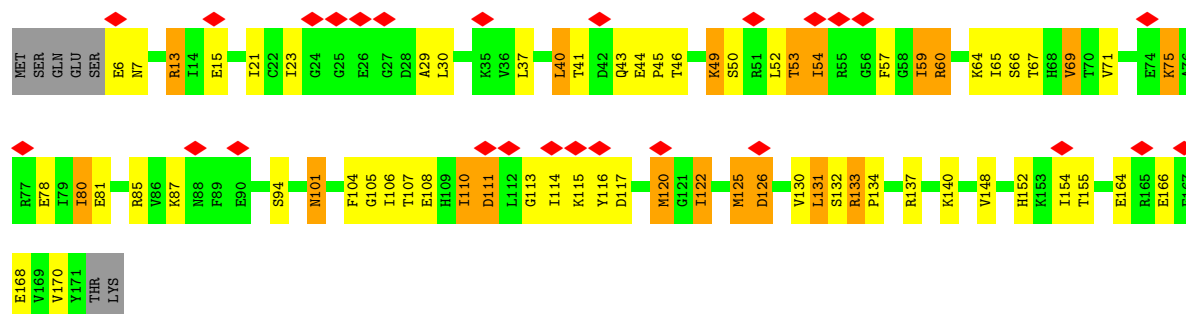




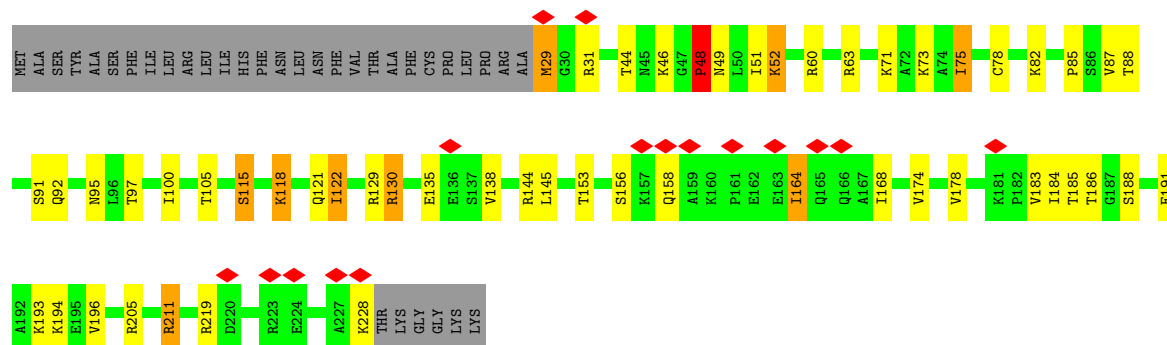
• Molecule 11: Ribosomal protein L10



• Molecule 12: Ribosomal protein L11

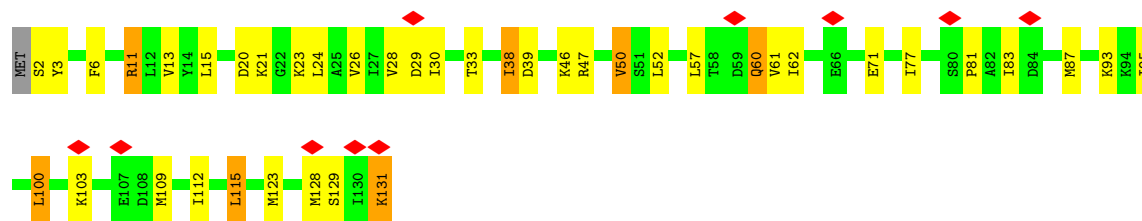


• Molecule 13: Ribosomal protein L13

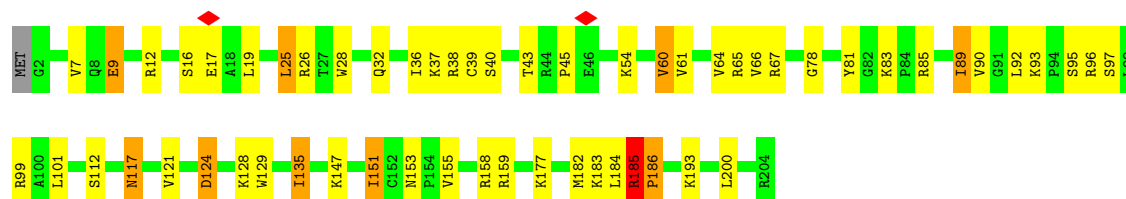
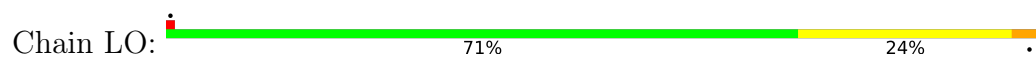


• Molecule 14: Ribosomal protein L14

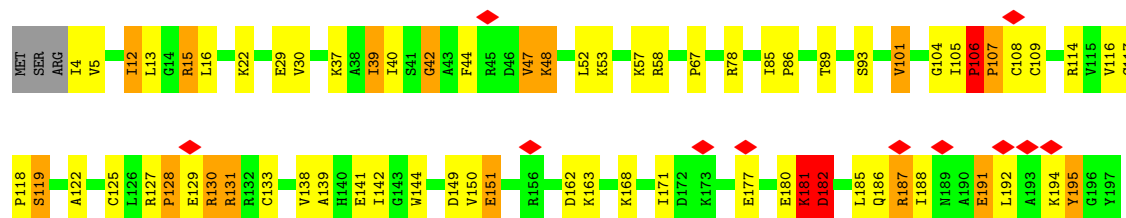




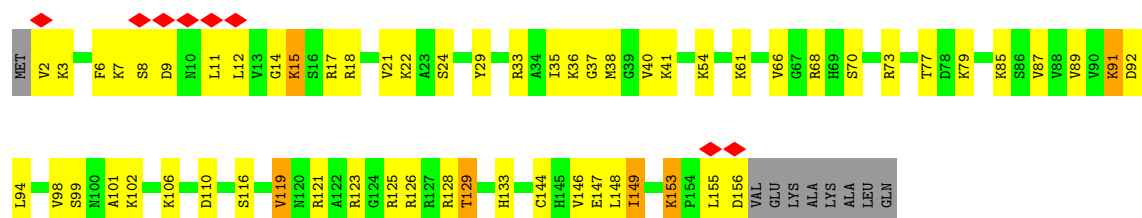
• Molecule 15: Ribosomal protein L15



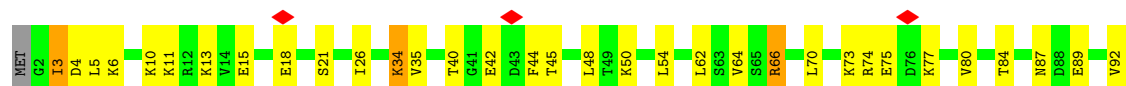
• Molecule 16: Ribosomal protein L13a



• Molecule 17: Ribosomal protein L17

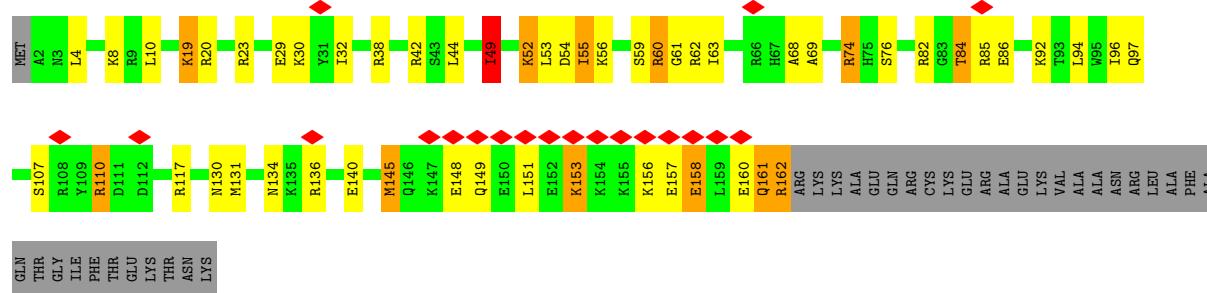


• Molecule 18: Ribosomal protein L18

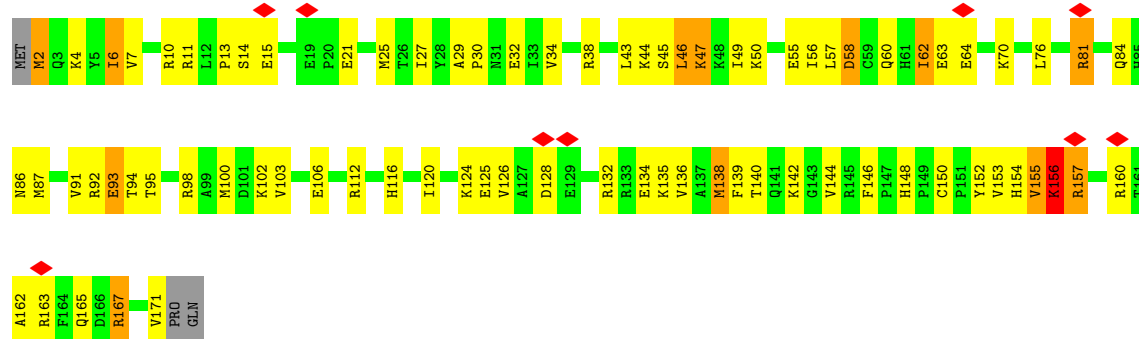




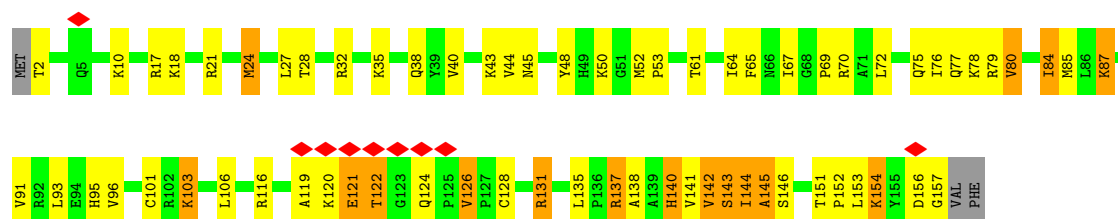
• Molecule 19: Ribosomal protein L19



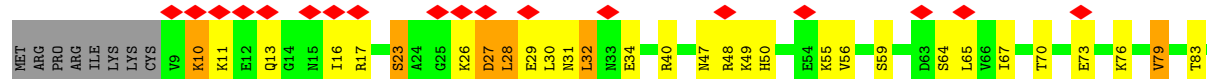
• Molecule 20: Ribosomal protein L18a



• Molecule 21: Ribosomal protein L21



• Molecule 22: Ribosomal protein L22e

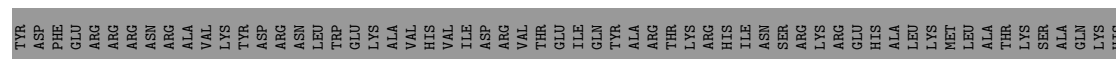
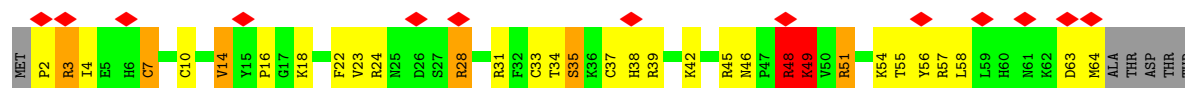




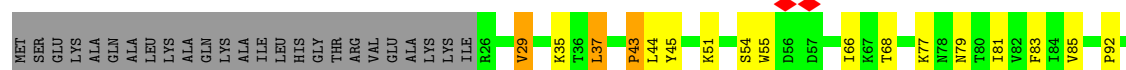
• Molecule 23: Ribosomal protein L23



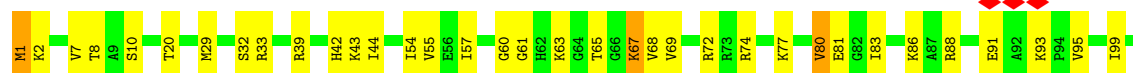
• Molecule 24: Ribosomal protein L24



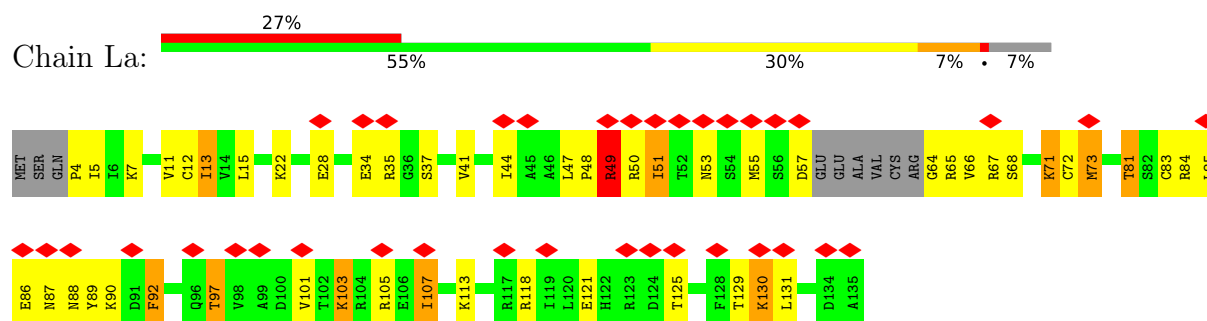
• Molecule 25: Ribosomal protein L23A



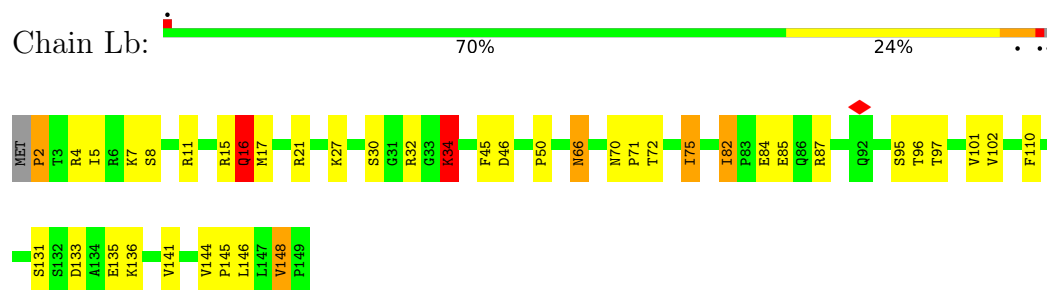
• Molecule 26: Ribosomal protein L26



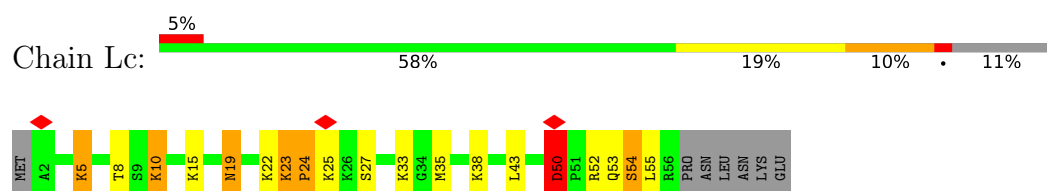
- Molecule 27: Ribosomal protein L27



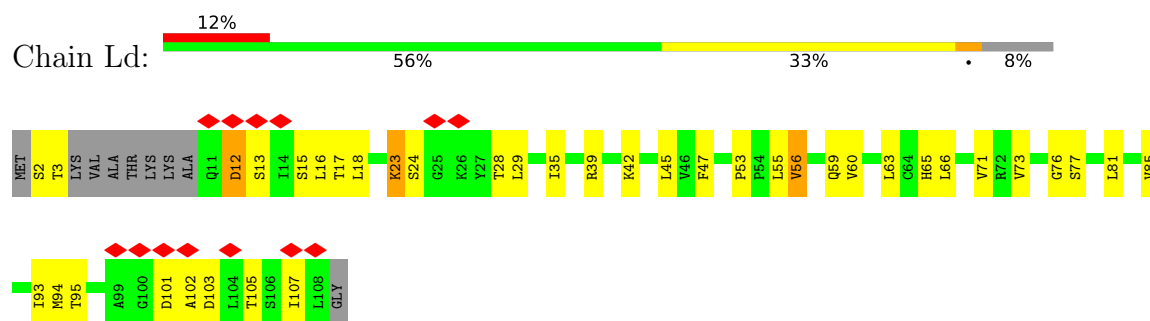
- Molecule 28: Ribosomal protein L27a



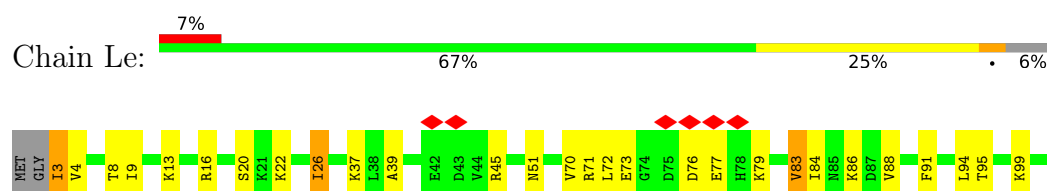
- Molecule 29: Ribosomal protein L29



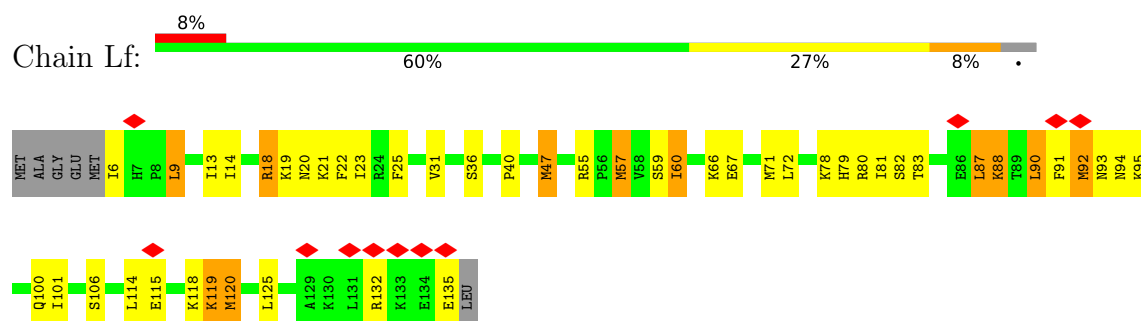
- Molecule 30: Ribosomal protein L30



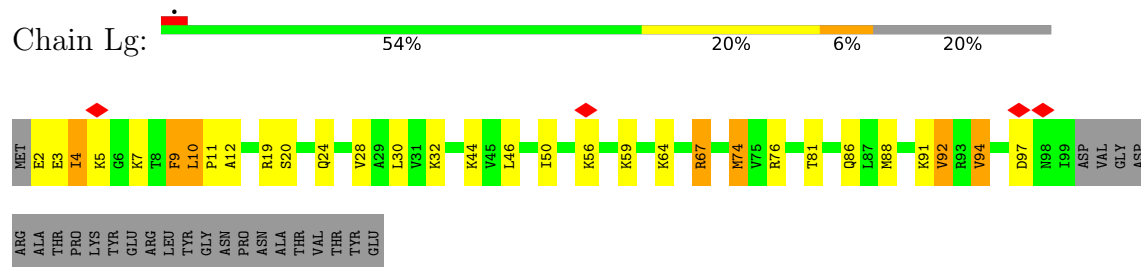
- Molecule 31: Ribosomal protein L31B



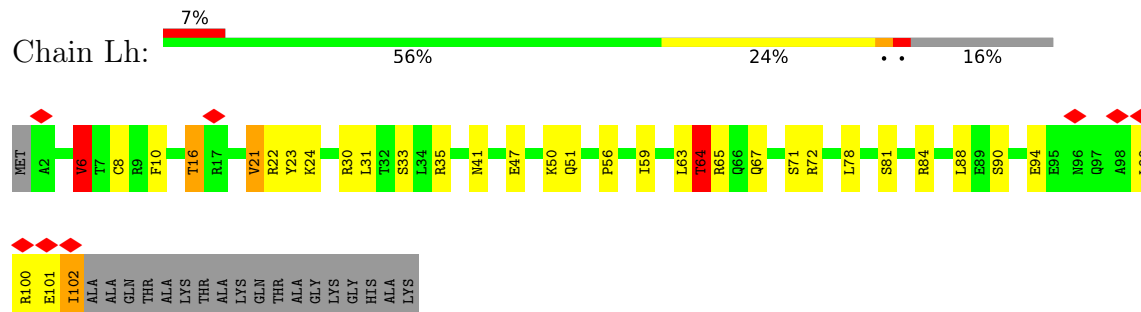
- Molecule 32: Ribosomal protein L32



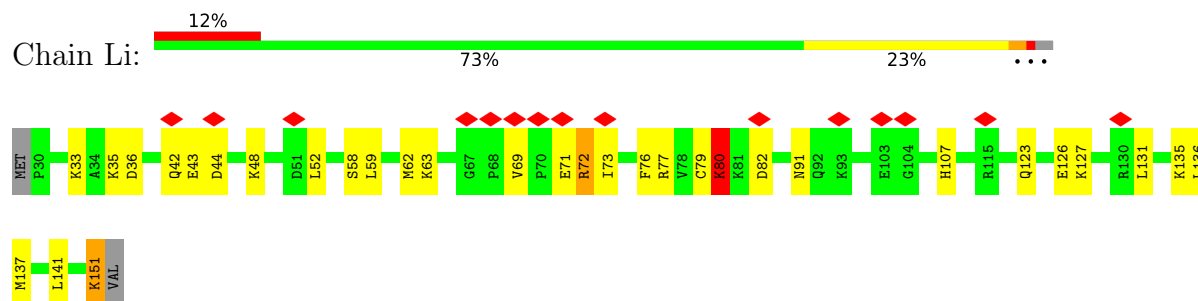
• Molecule 33: Ribosomal protein L35a



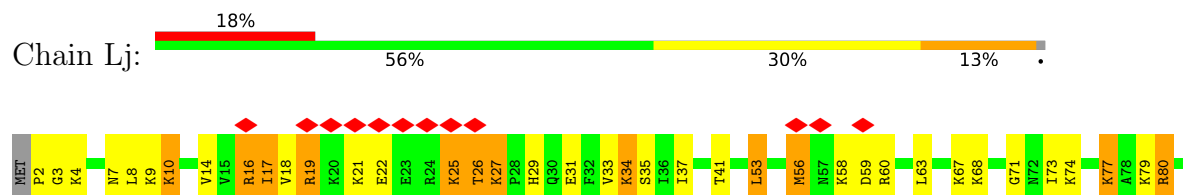
• Molecule 34: Ribosomal protein L34



• Molecule 35: Ribosomal protein L29

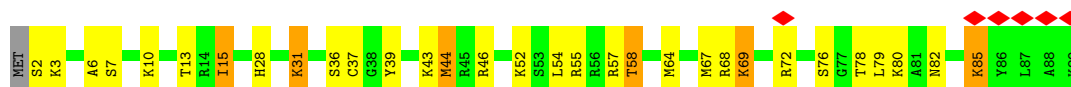


• Molecule 36: Ribosomal protein L36-1

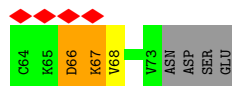
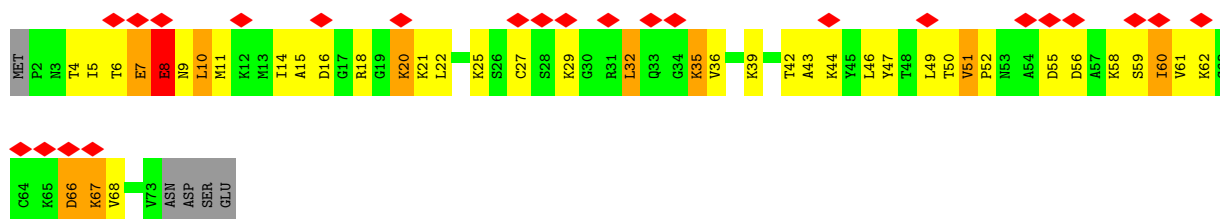




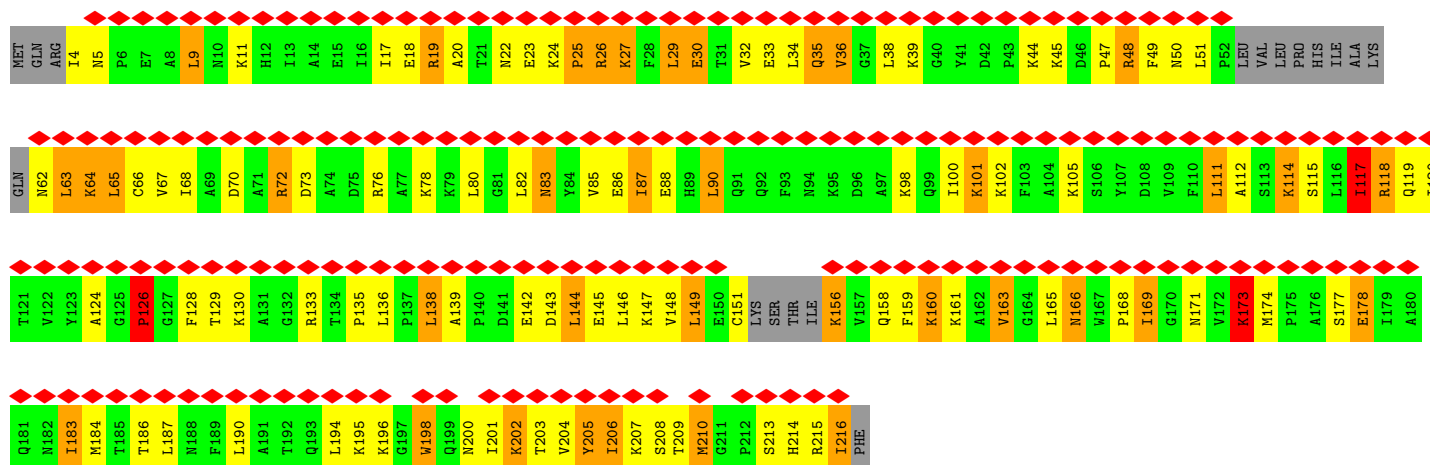
• Molecule 37: Ribosomal protein L37



• Molecule 38: Ribosomal protein L38e



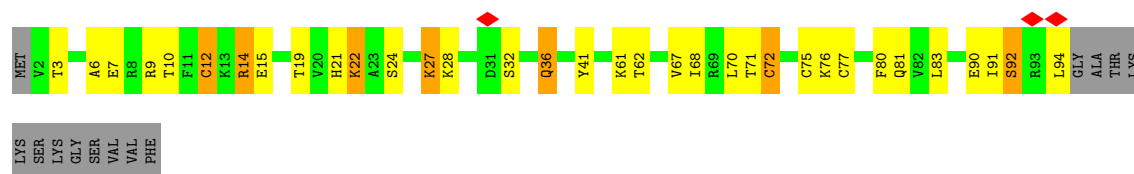
• Molecule 39: Ribosomal protein L10a



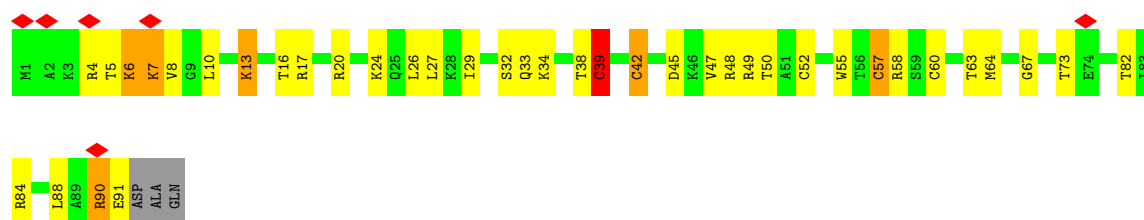
• Molecule 40: Ribosomal protein L41



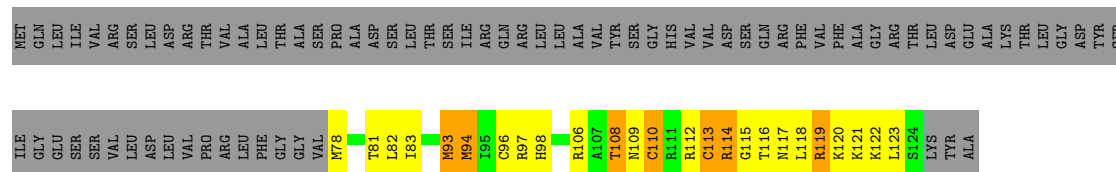
• Molecule 41: Ribosomal protein L44



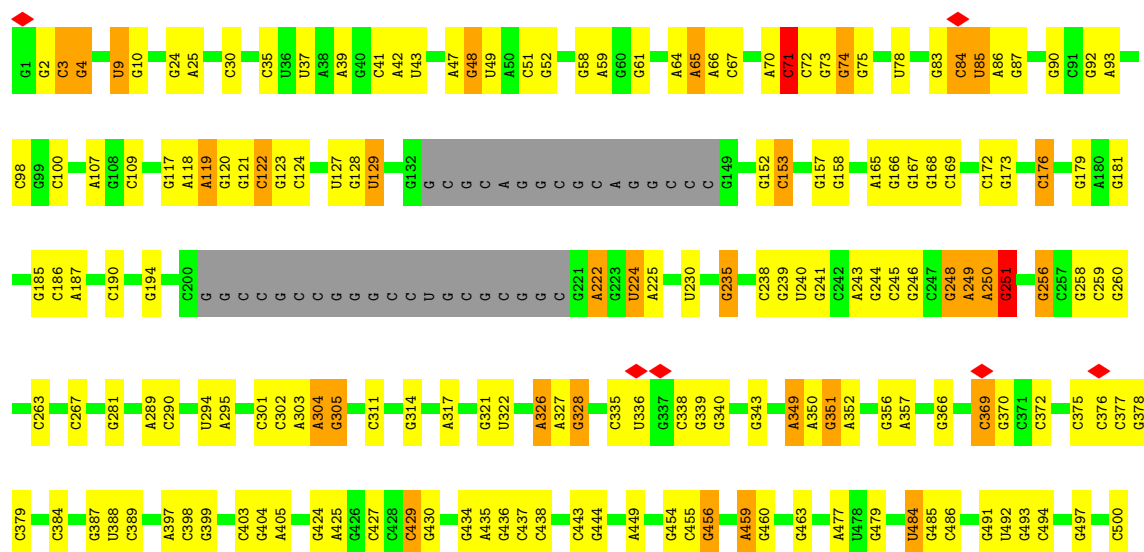
• Molecule 42: Ribosomal protein L37a



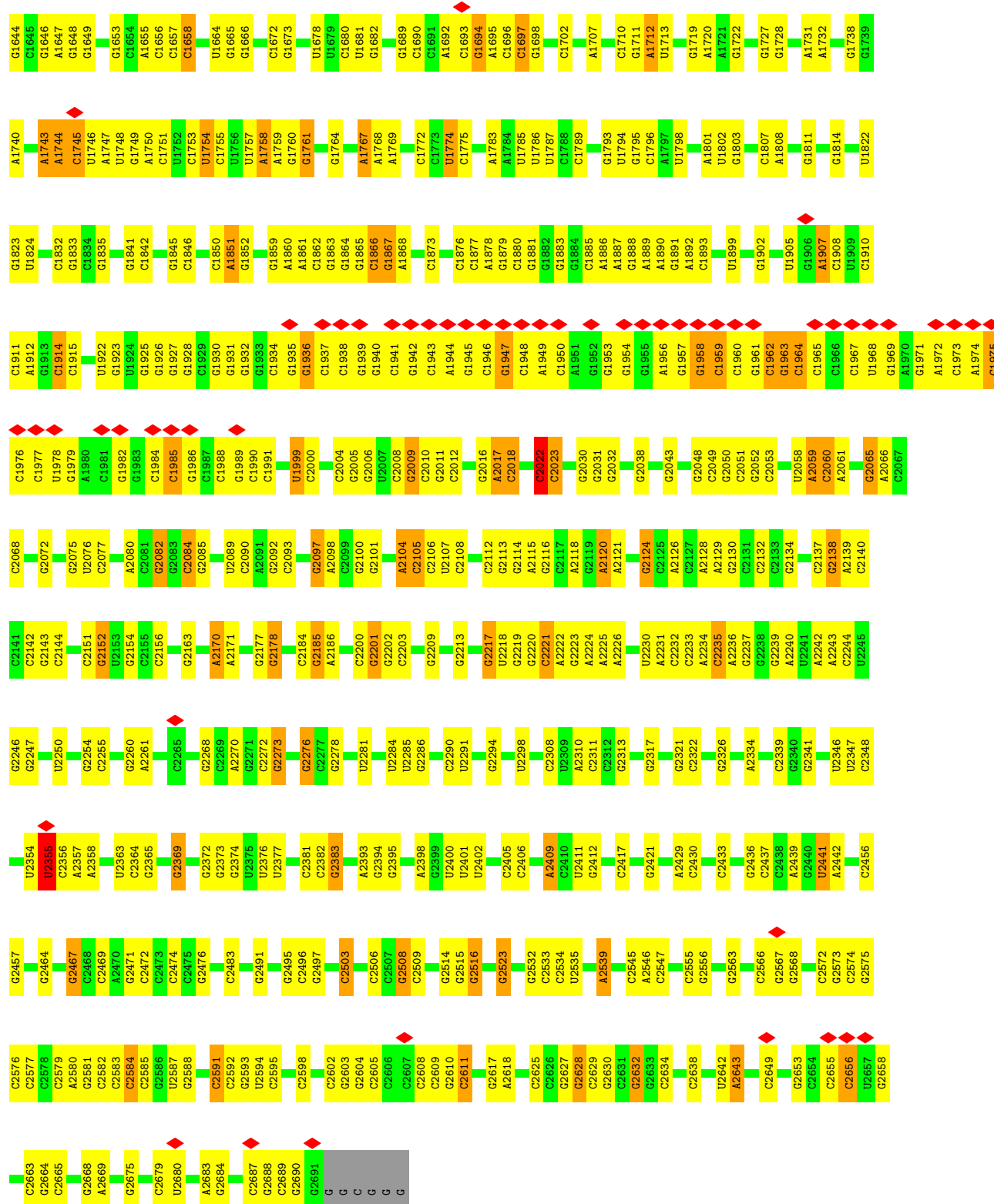
• Molecule 43: Ubiquitin/Ribosomal protein L40e



• Molecule 44: Large Subunit rRNA

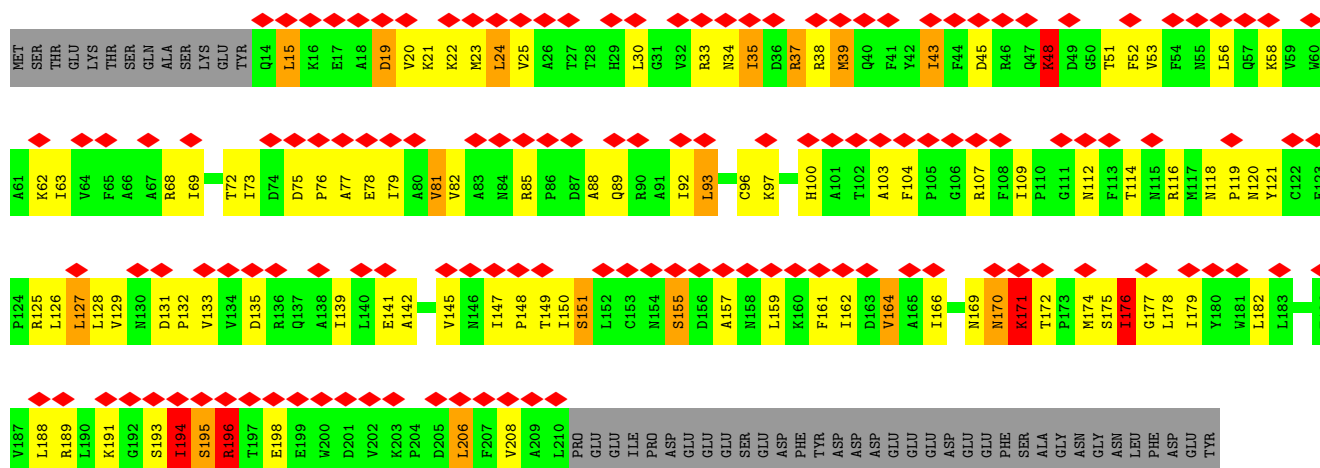




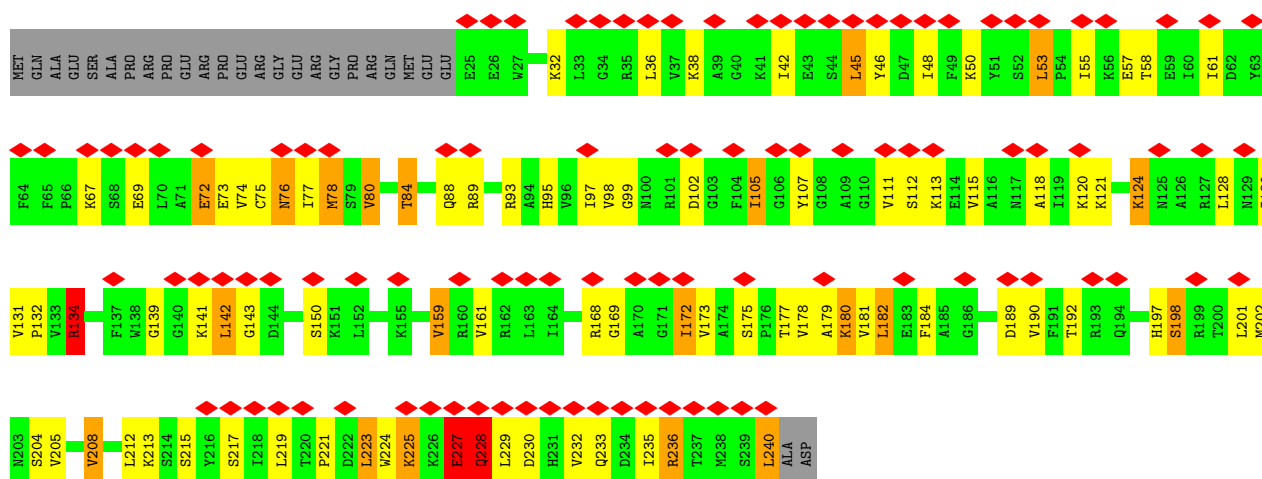


• Molecule 45: Ribosomal protein SA

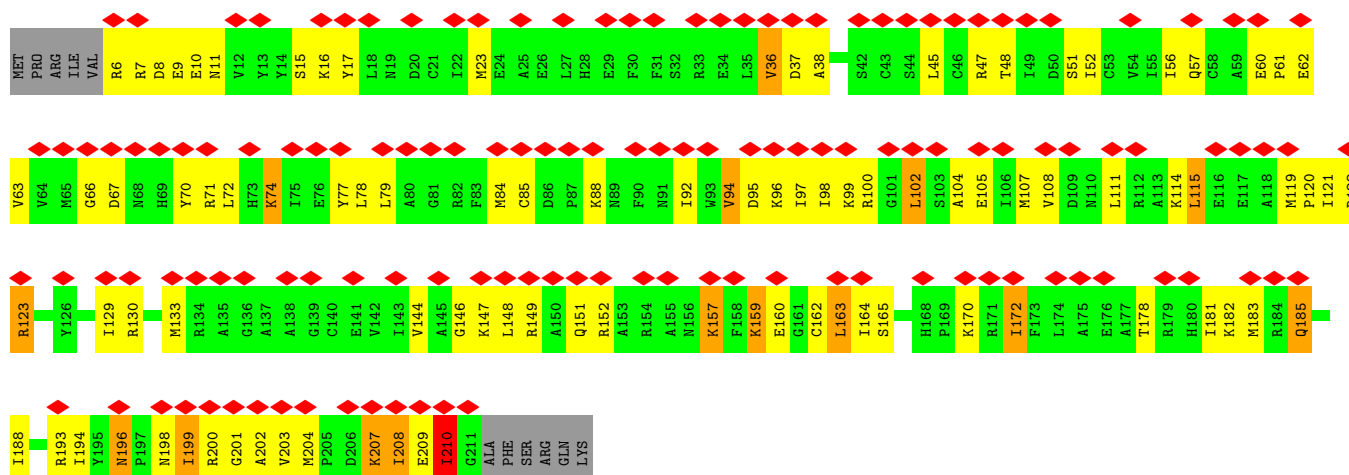




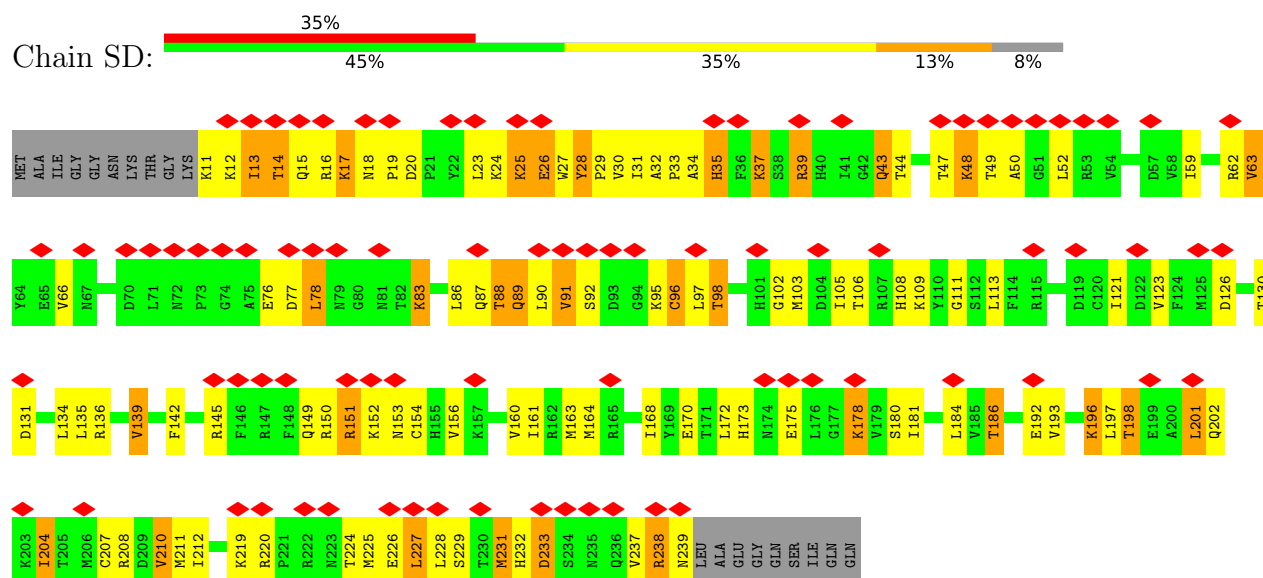
• Molecule 46: Ribosomal protein S2



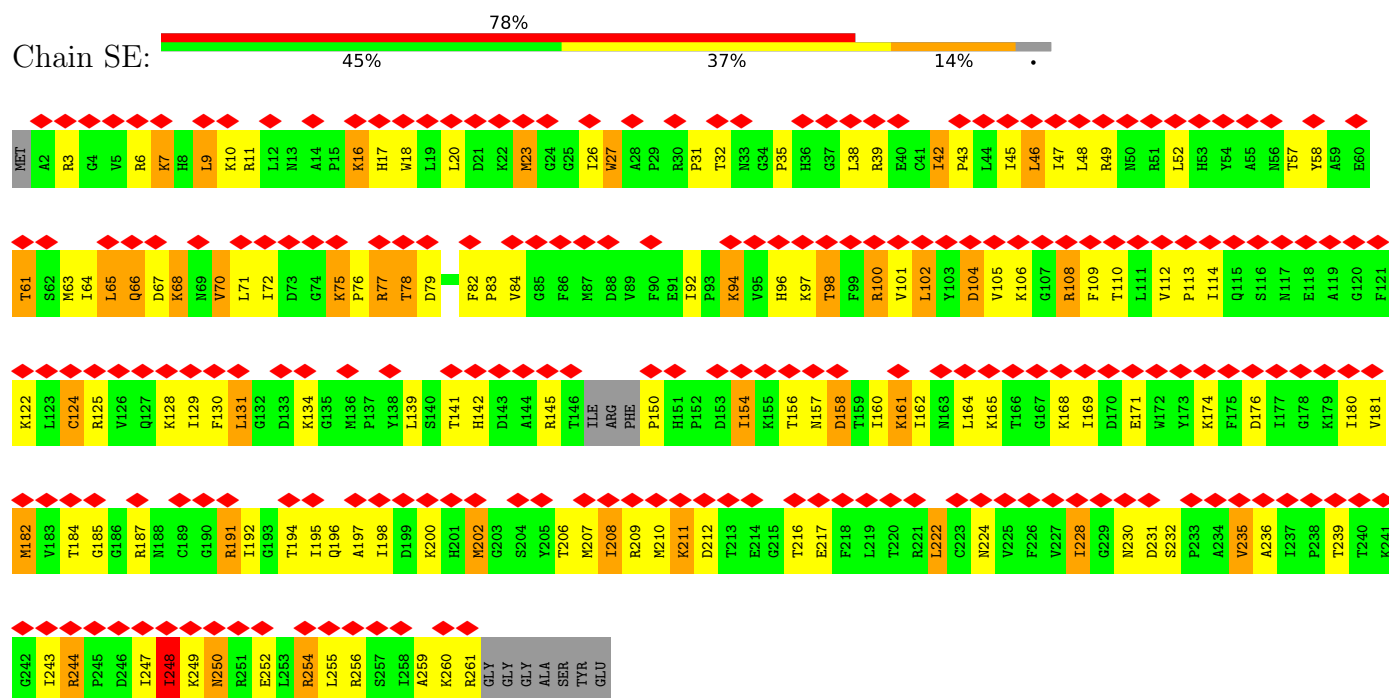
• Molecule 47: Ribosomal protein S3



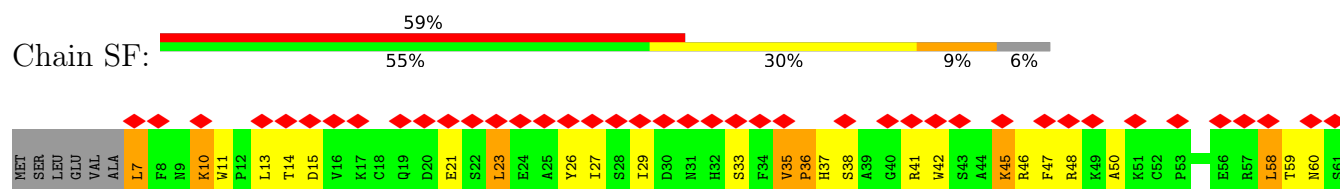
- Molecule 48: Ribosomal protein S3a

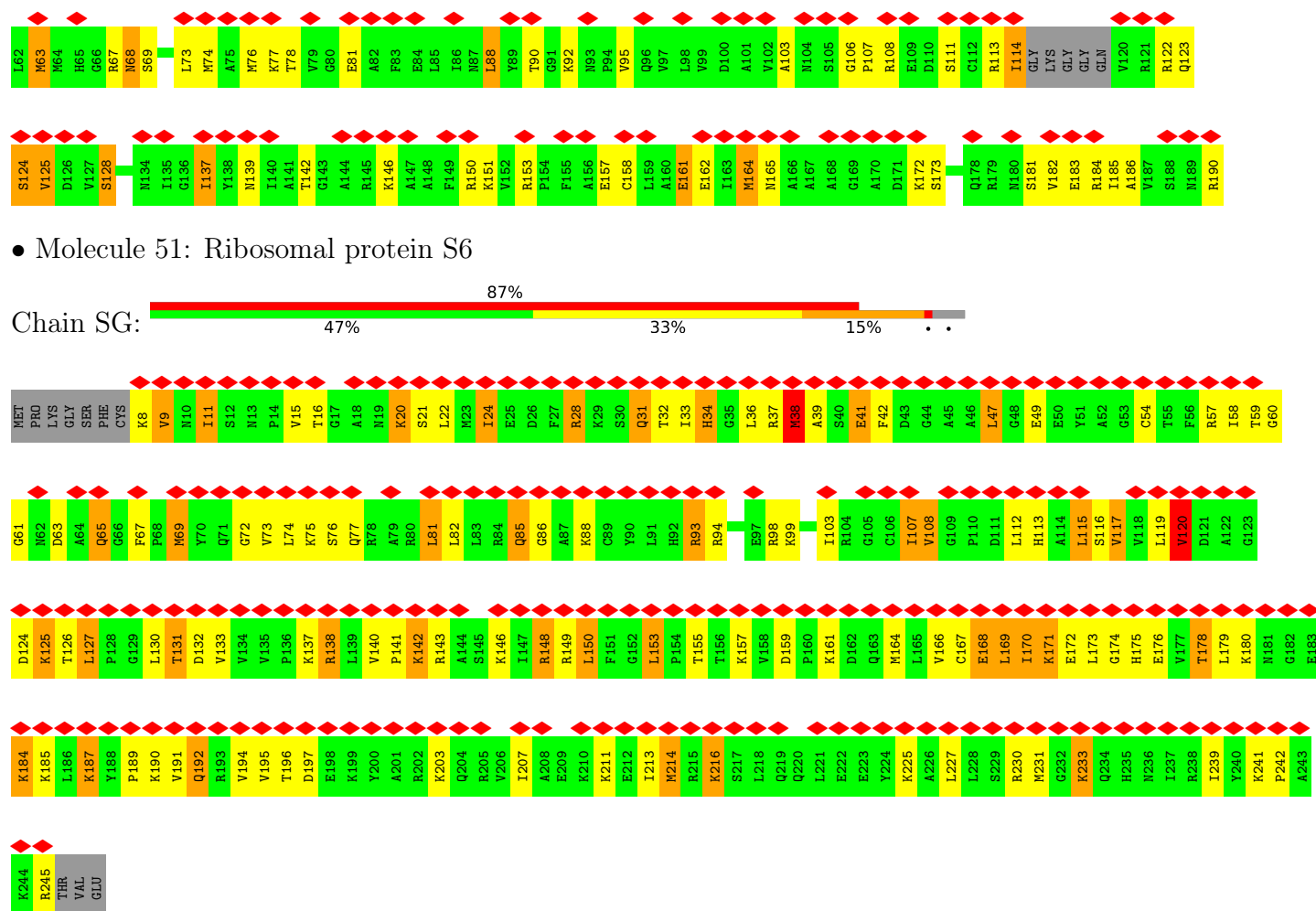


- Molecule 49: Ribosomal protein S4

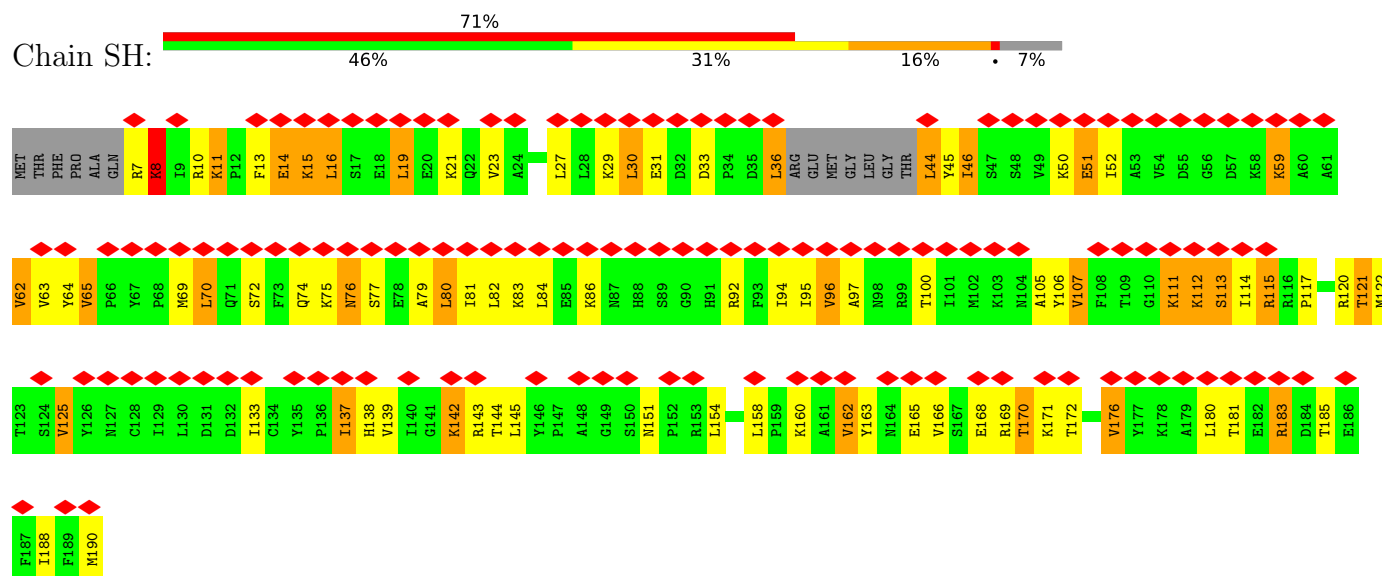


- Molecule 50: Ribosomal protein S5

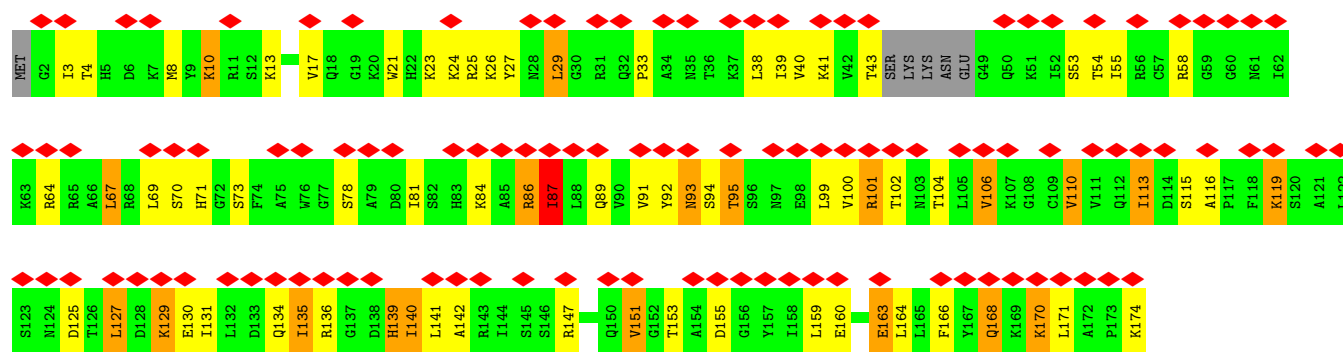




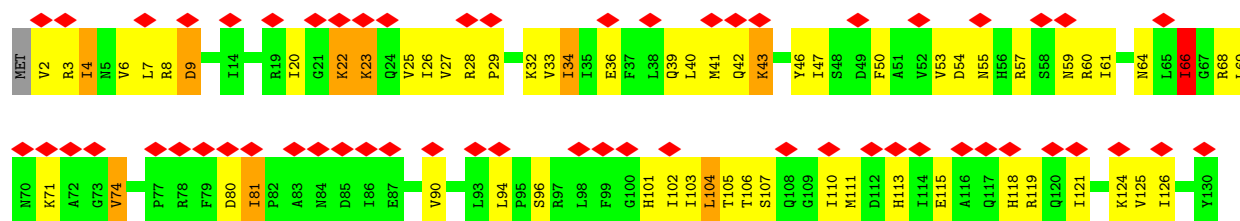
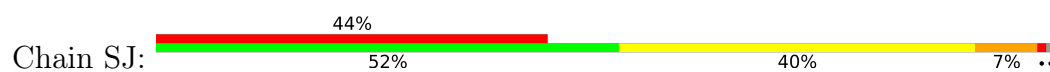
• Molecule 52: Ribosomal protein S7



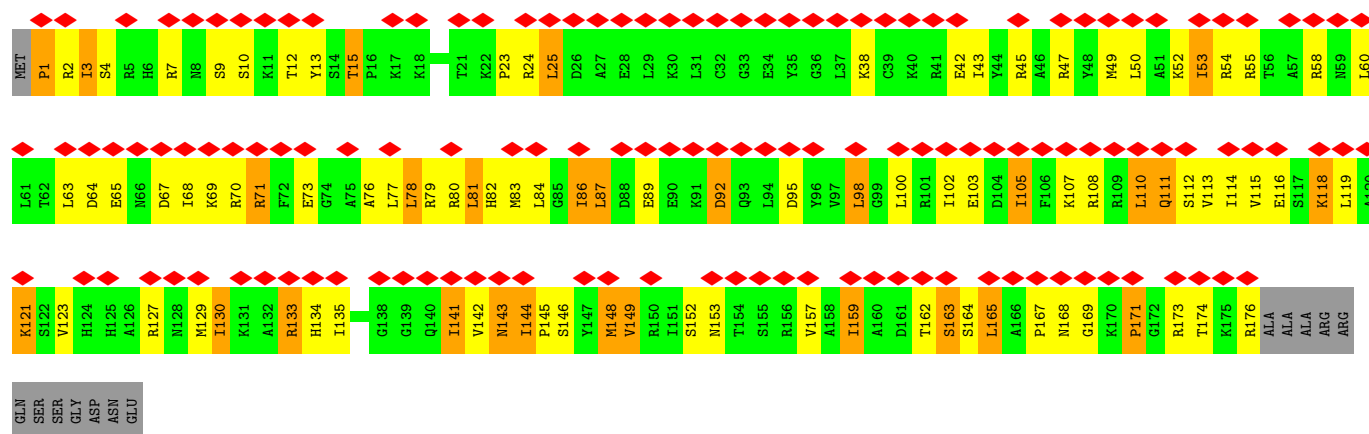
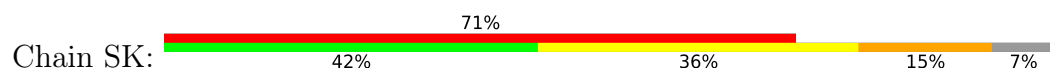
• Molecule 53: Ribosomal protein S8



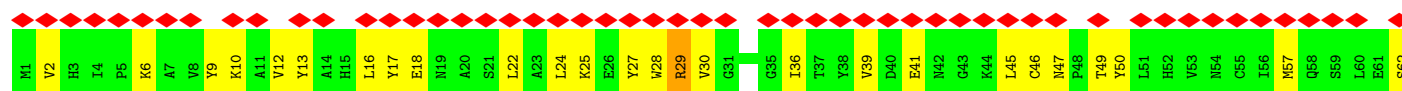
• Molecule 54: Ribosomal protein S15A

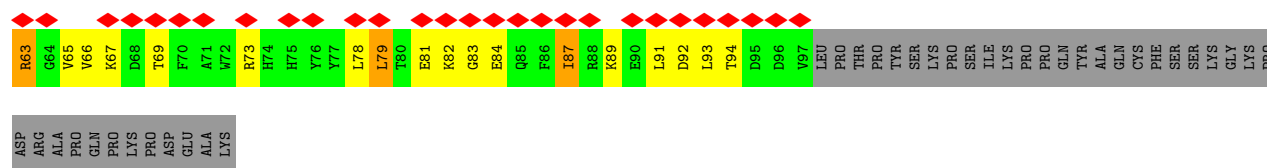


• Molecule 55: Ribosomal protein S9



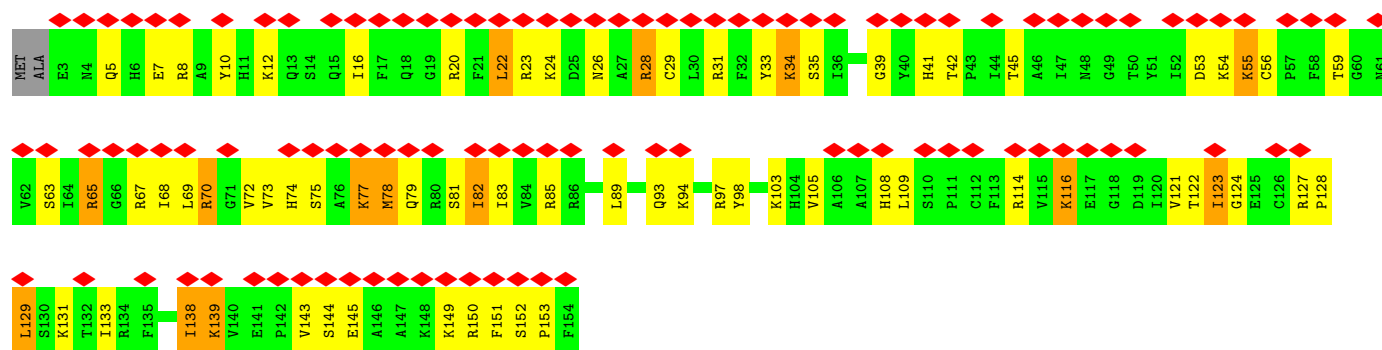
• Molecule 56: Ribosomal protein S10B





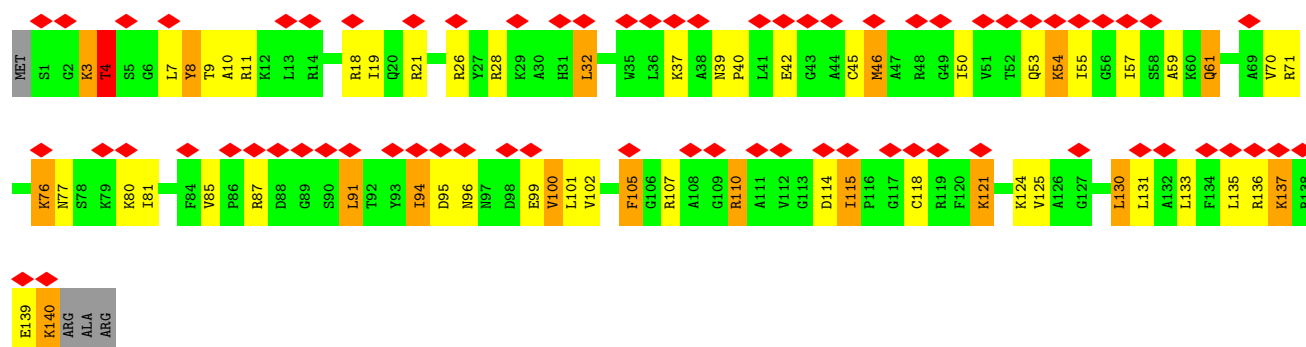
• Molecule 57: Ribosomal protein S11

Chain SM:



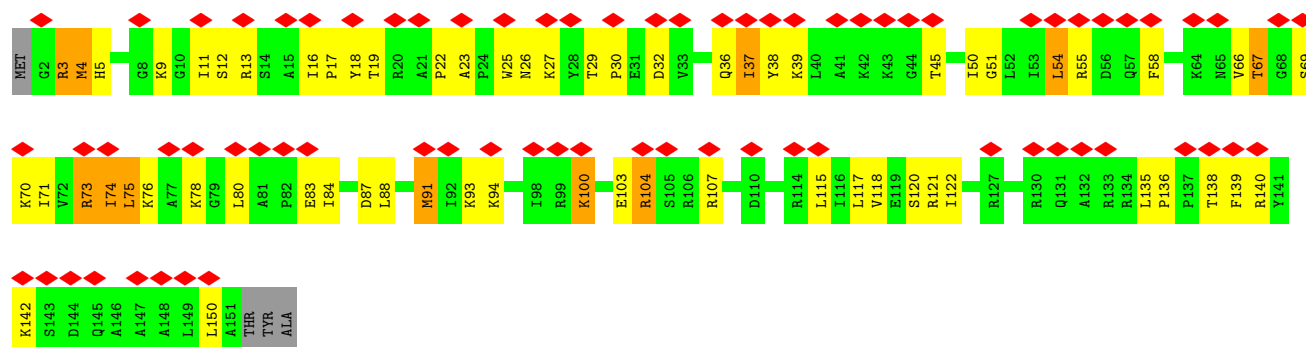
• Molecule 58: Ribosomal protein S23

Chain SO:

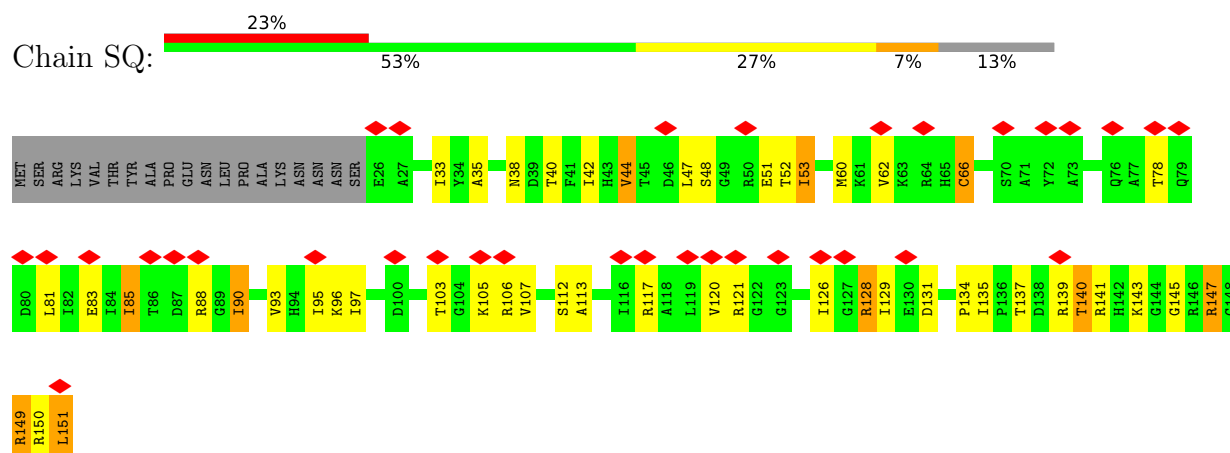


• Molecule 59: Ribosomal protein S13

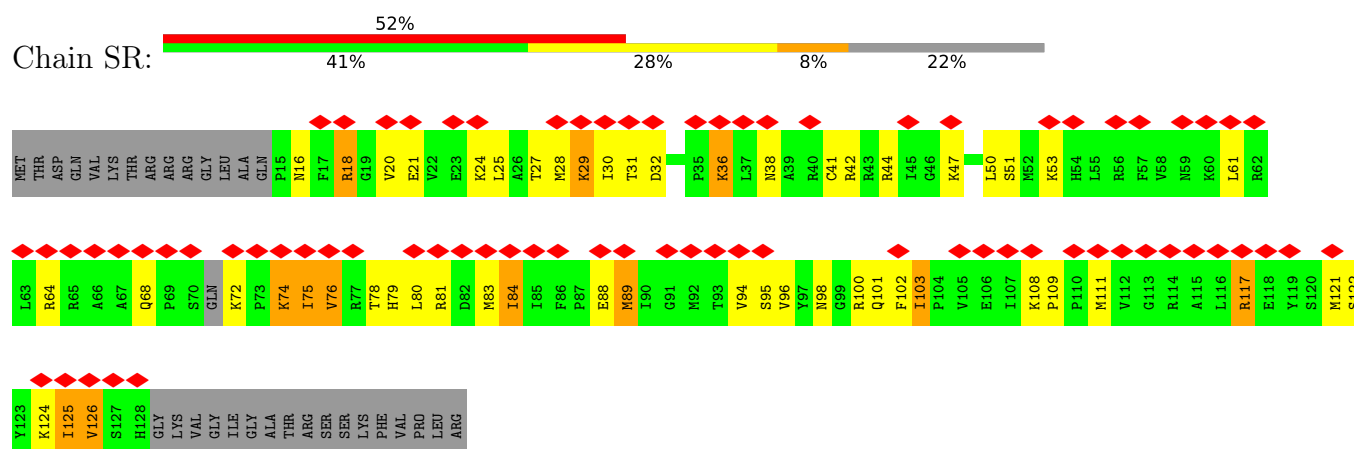
Chain SP:



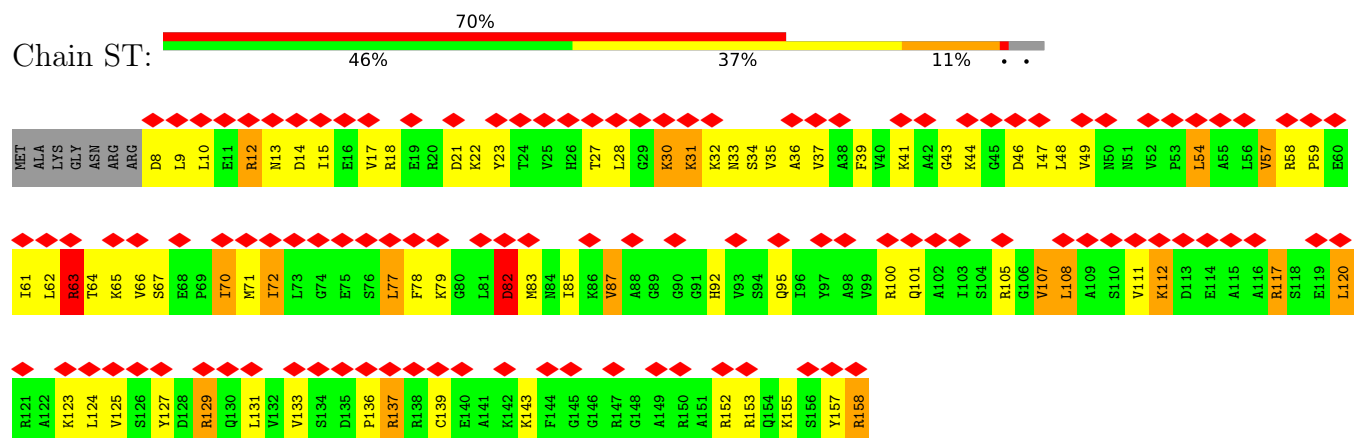
- Molecule 60: Ribosomal protein S14



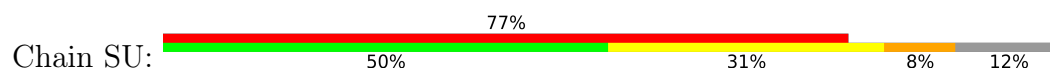
- Molecule 61: Ribosomal protein S15



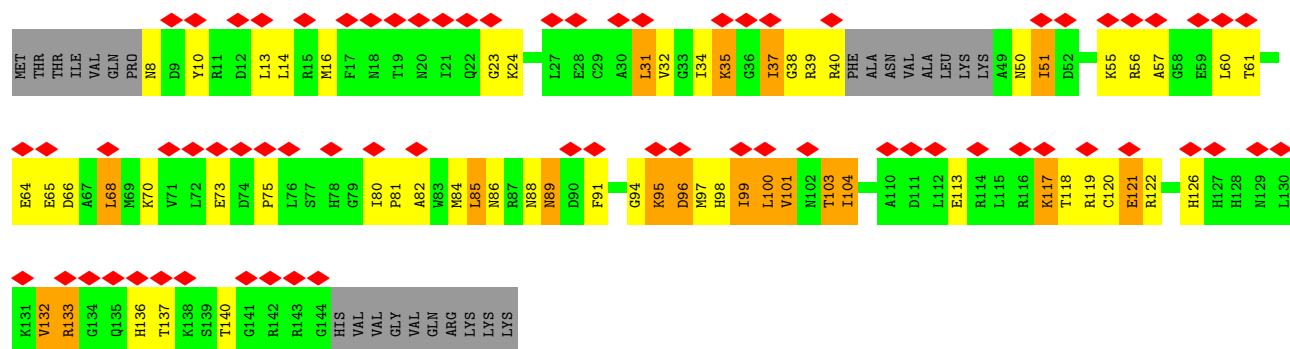
- Molecule 62: Ribosomal protein S16



- Molecule 63: Ribosomal protein S17



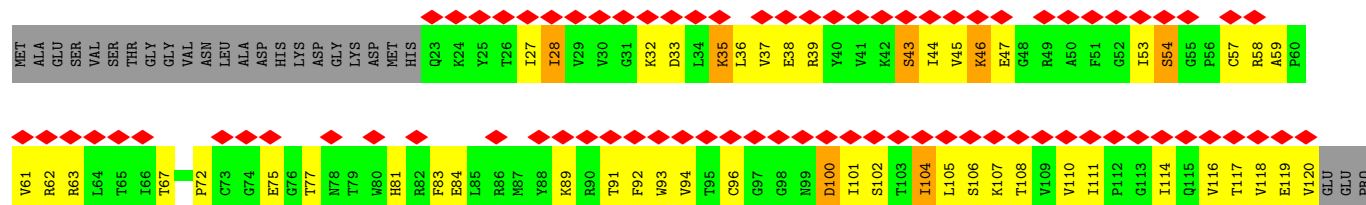
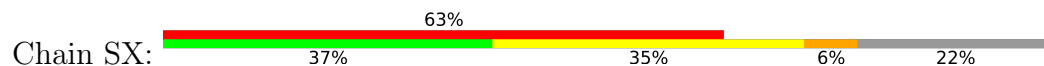
- Molecule 64: Ribosomal protein S18



- Molecule 65: Ribosomal protein S19e

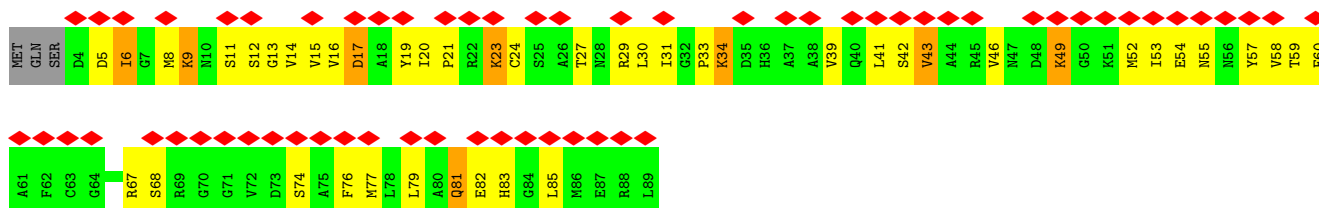


- Molecule 66: Ribosomal protein S20

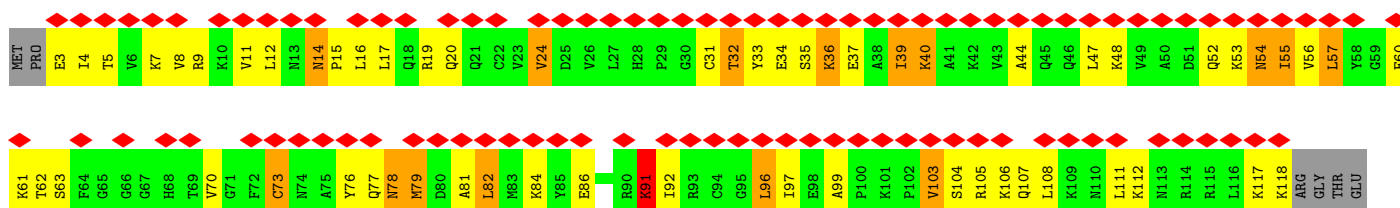


ASP
ASN
GLU

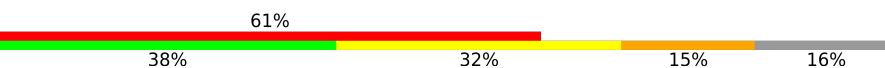
• Molecule 67: Ribosomal protein S21

Chain SY: 

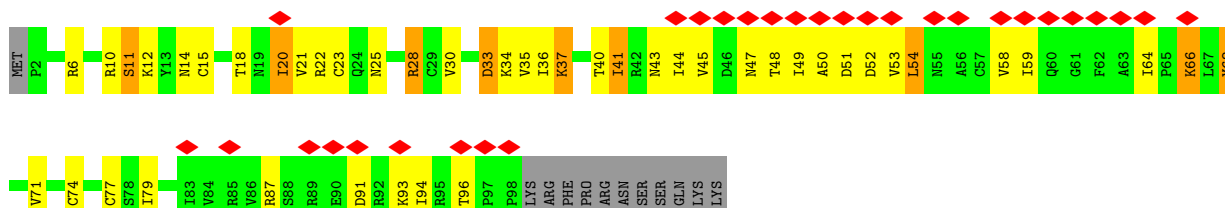
• Molecule 68: Ribosomal protein S24

Chain Sb: LYS
ALA
THR
VAL
THR
LEU
GLY
ALA
LYS
LYS

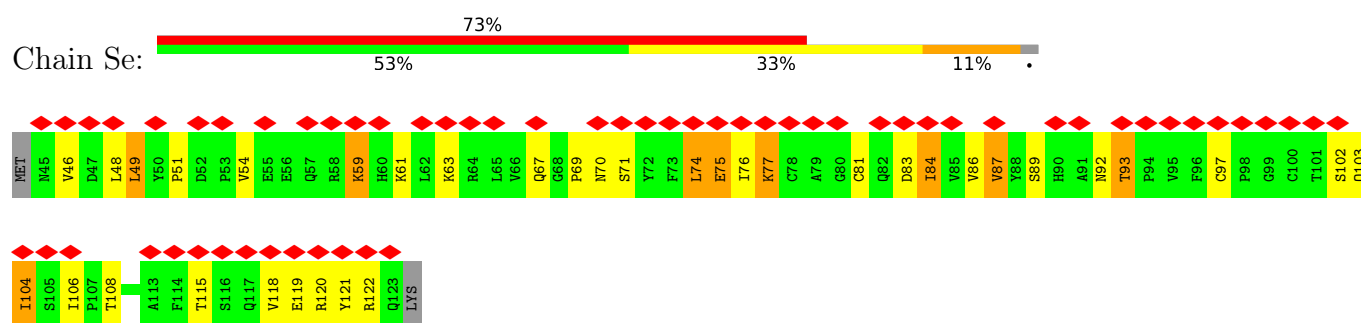
• Molecule 69: Ribosomal protein S25

Chain Sc: 

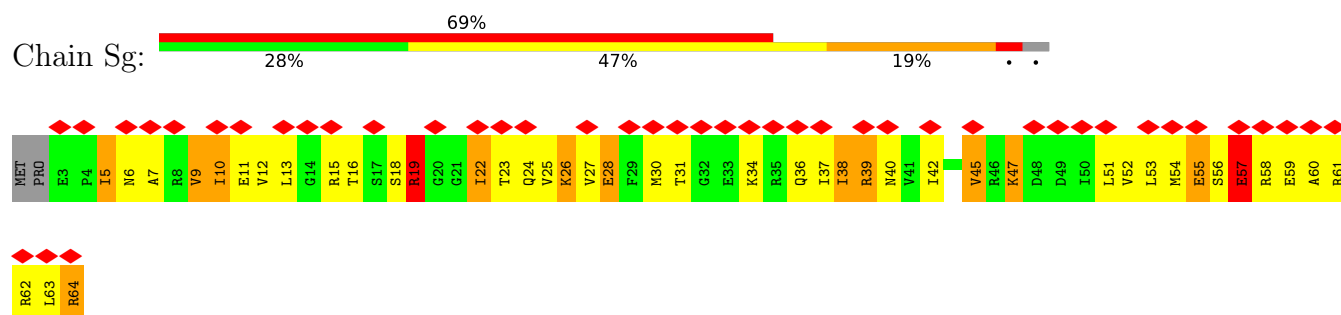
• Molecule 70: Ribosomal protein S26

Chain Sd: 

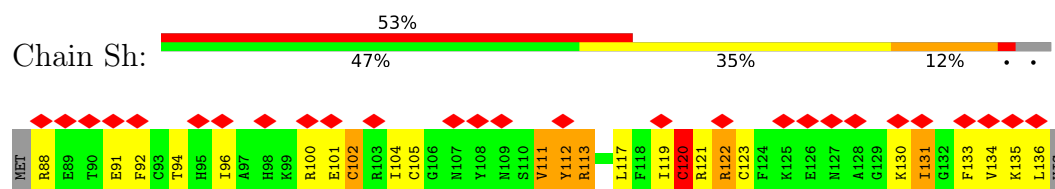
• Molecule 71: Ribosomal protein S27



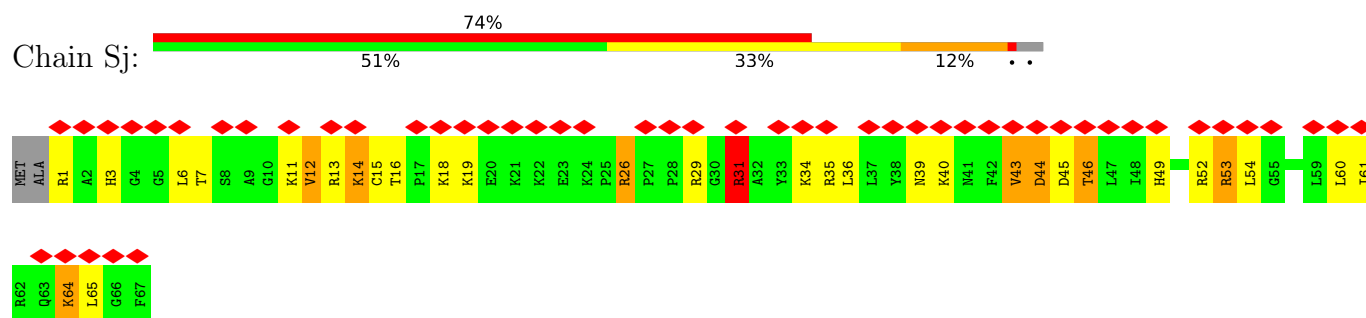
• Molecule 72: Ribosomal protein S28



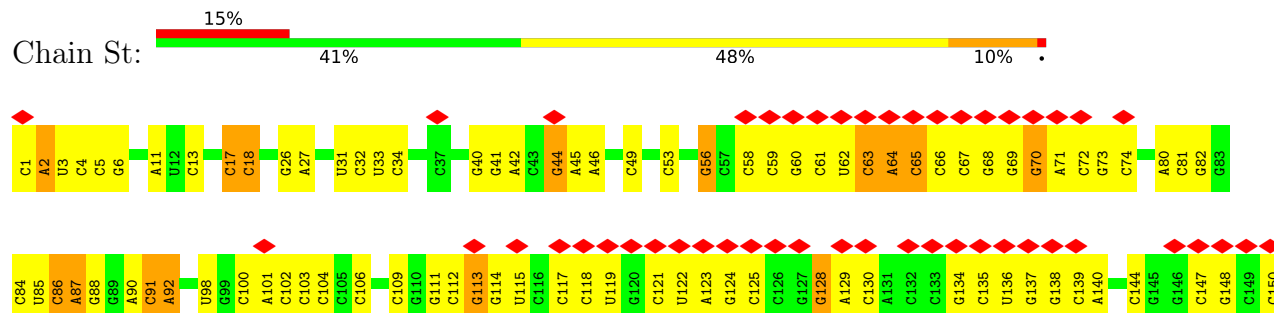
• Molecule 73: Ribosomal protein S29A

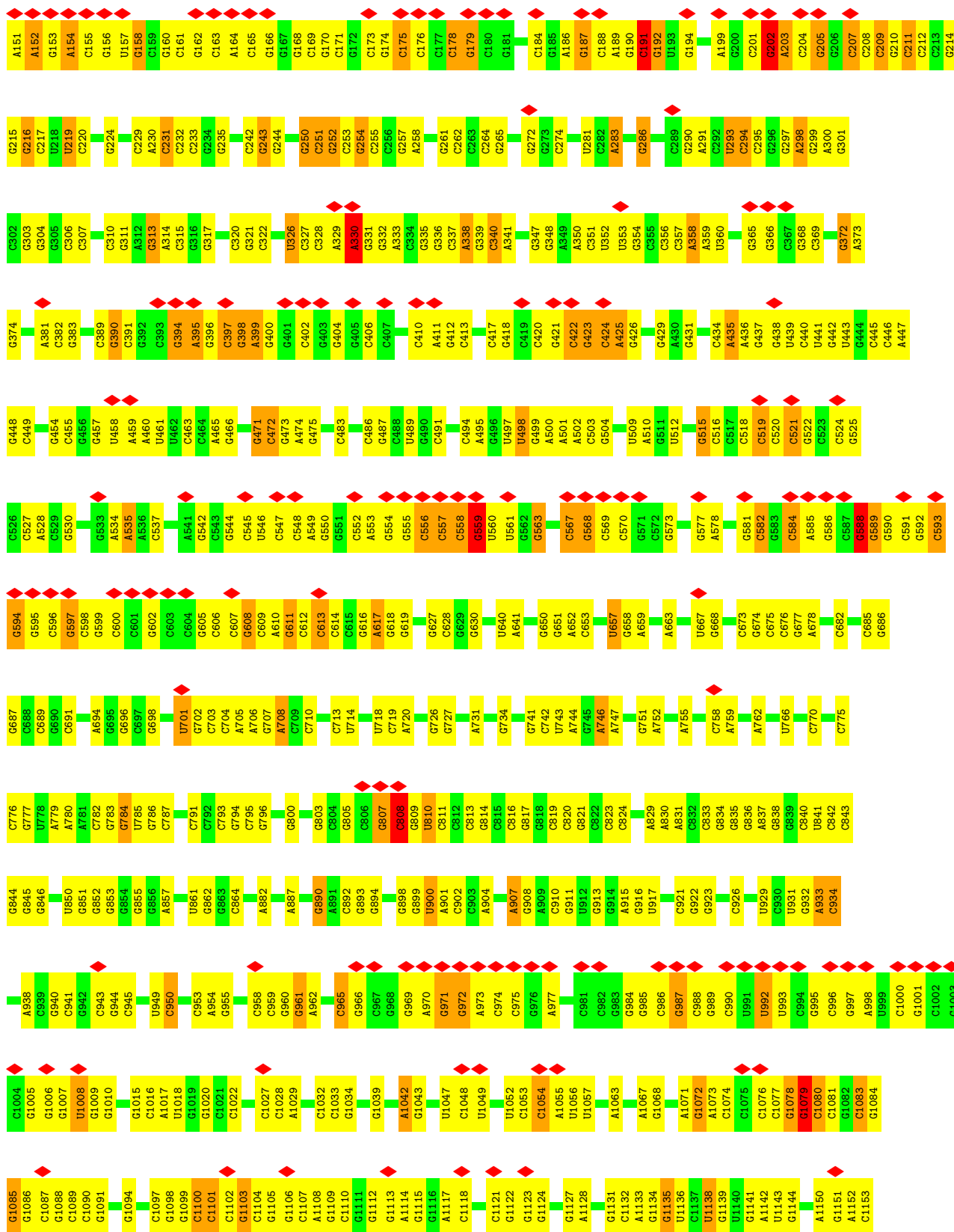


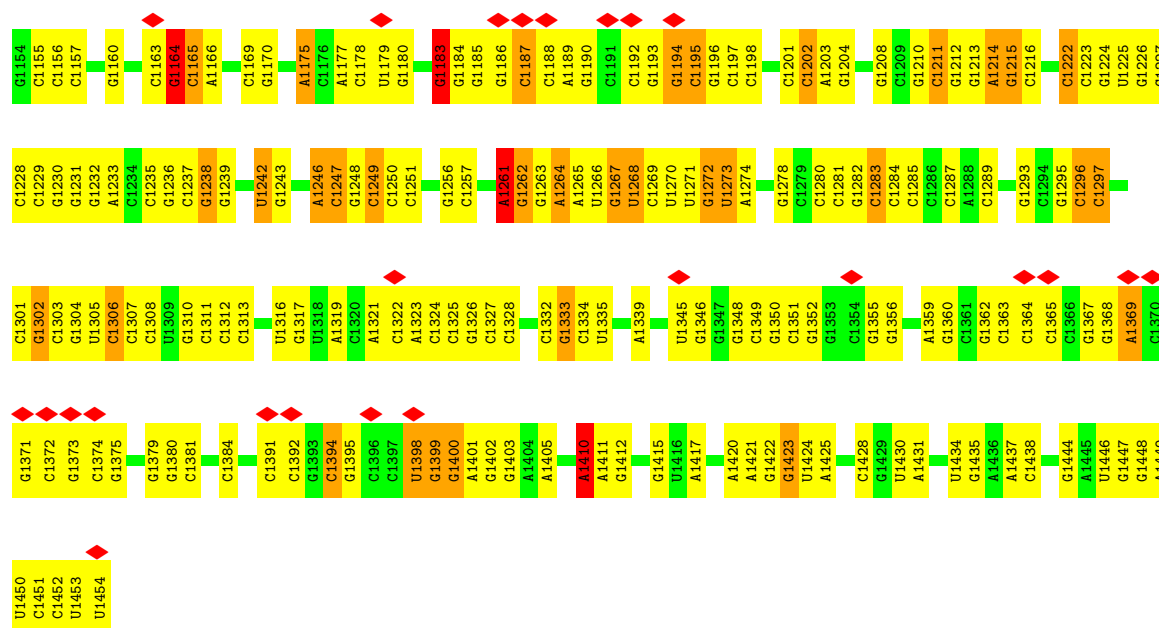
• Molecule 74: Ribosomal protein S30



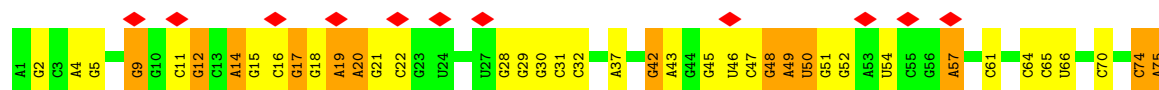
• Molecule 75: Small Subunit rRNA



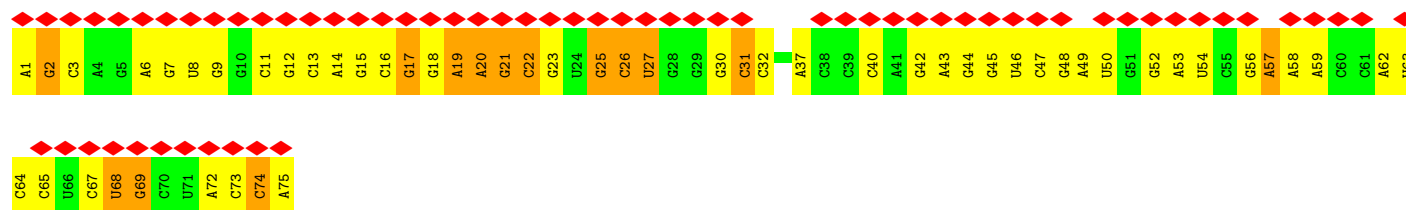
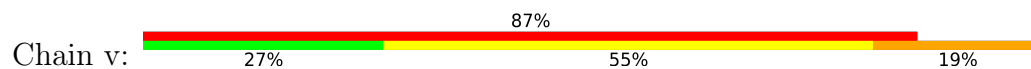




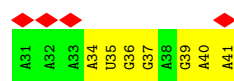
- Molecule 76: tRNA



- Molecule 77: tRNA



- Molecule 78: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31100	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1900	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	18.685	Depositor
Minimum map value	-9.239	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.87	Depositor
Map size (Å)	410.0, 410.0, 410.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	LA	0.90	0/1888	1.36	6/2538 (0.2%)
2	LB	0.90	0/3058	1.38	17/4129 (0.4%)
3	LC	0.90	0/2466	1.38	13/3345 (0.4%)
4	LD	0.56	0/3393	0.80	0/5292
5	LE	0.56	0/2798	0.77	1/4361 (0.0%)
6	LF	0.86	0/2398	1.32	3/3216 (0.1%)
7	LG	0.81	0/450	1.34	2/601 (0.3%)
8	LH	0.88	0/1747	1.40	7/2355 (0.3%)
9	LI	0.89	0/1513	1.37	6/2044 (0.3%)
10	LJ	0.89	0/1479	1.39	3/1997 (0.2%)
11	LK	0.86	0/1630	1.29	2/2181 (0.1%)
12	LL	0.87	0/1359	1.31	1/1825 (0.1%)
13	LM	0.88	0/1623	1.40	6/2173 (0.3%)
14	LN	0.87	0/1037	1.30	1/1390 (0.1%)
15	LO	0.88	0/1751	1.29	4/2346 (0.2%)
16	LP	0.86	0/1610	1.41	9/2160 (0.4%)
17	LQ	0.88	0/1273	1.36	0/1703
18	LR	0.90	0/1425	1.39	4/1907 (0.2%)
19	LS	0.83	0/1357	1.34	5/1796 (0.3%)
20	LT	0.85	0/1457	1.34	7/1957 (0.4%)
21	LU	0.87	0/1283	1.34	3/1725 (0.2%)
22	LV	0.84	0/861	1.39	4/1158 (0.3%)
23	LW	0.91	0/1039	1.32	1/1401 (0.1%)
24	LX	0.83	0/553	1.47	8/736 (1.1%)
25	LY	0.86	0/951	1.34	2/1286 (0.2%)
26	LZ	0.89	0/1091	1.32	4/1454 (0.3%)
27	La	0.91	0/1021	1.43	4/1376 (0.3%)
28	Lb	0.87	0/1231	1.37	5/1647 (0.3%)
29	Lc	0.89	0/463	1.45	4/612 (0.7%)
30	Ld	0.92	0/760	1.41	3/1027 (0.3%)
31	Le	0.89	0/832	1.30	1/1118 (0.1%)
32	Lf	0.88	0/1101	1.31	0/1467
33	Lg	0.87	0/793	1.40	4/1062 (0.4%)
34	Lh	0.91	0/830	1.38	2/1115 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Li	0.84	0/996	1.34	2/1328 (0.2%)
36	Lj	0.87	0/741	1.39	3/982 (0.3%)
37	Lk	0.89	0/727	1.33	3/963 (0.3%)
38	Ll	0.84	0/562	1.54	4/749 (0.5%)
39	Ln	0.95	0/1621	1.45	9/2183 (0.4%)
40	Lo	0.74	0/229	1.26	0/291
41	Lp	0.86	0/778	1.34	0/1029
42	Lq	0.87	0/717	1.43	1/955 (0.1%)
43	Ls	0.90	0/392	1.58	3/522 (0.6%)
44	Lt	0.57	0/62214	0.81	66/97098 (0.1%)
45	SA	0.92	0/1612	1.36	6/2190 (0.3%)
46	SB	0.92	0/1700	1.37	1/2293 (0.0%)
47	SC	0.90	0/1662	1.38	4/2231 (0.2%)
48	SD	0.88	0/1890	1.41	14/2546 (0.5%)
49	SE	0.94	0/2099	1.40	6/2829 (0.2%)
50	SF	0.91	0/1422	1.38	7/1912 (0.4%)
51	SG	0.91	0/1915	1.39	5/2560 (0.2%)
52	SH	0.89	0/1456	1.37	7/1962 (0.4%)
53	SI	0.95	0/1336	1.40	1/1792 (0.1%)
54	SJ	0.92	0/1048	1.41	7/1412 (0.5%)
55	SK	0.92	0/1443	1.41	7/1930 (0.4%)
56	SL	0.89	0/819	1.33	2/1112 (0.2%)
57	SM	0.94	0/1289	1.29	3/1724 (0.2%)
58	SO	0.88	0/1104	1.37	2/1478 (0.1%)
59	SP	0.91	0/1218	1.39	3/1640 (0.2%)
60	SQ	0.95	0/932	1.50	5/1251 (0.4%)
61	SR	0.90	0/938	1.35	2/1253 (0.2%)
62	ST	0.95	0/1192	1.36	4/1594 (0.3%)
63	SU	0.94	0/975	1.43	4/1303 (0.3%)
64	SV	0.88	0/1040	1.43	6/1392 (0.4%)
65	SW	0.94	0/1104	1.36	5/1484 (0.3%)
66	SX	0.94	0/790	1.34	2/1067 (0.2%)
67	SY	0.97	0/659	1.37	0/883
68	Sb	0.93	1/937 (0.1%)	1.39	3/1254 (0.2%)
69	Sc	0.90	0/594	1.56	6/791 (0.8%)
70	Sd	0.88	0/800	1.33	0/1077
71	Se	0.92	0/635	1.34	3/861 (0.3%)
72	Sg	0.94	1/500 (0.2%)	1.39	4/666 (0.6%)
73	Sh	0.86	0/417	1.42	2/553 (0.4%)
74	Sj	0.84	0/553	1.42	5/736 (0.7%)
75	St	0.59	0/34858	0.82	29/54401 (0.1%)
76	u	0.55	0/1795	0.76	1/2798 (0.0%)
77	v	0.54	0/1792	0.80	0/2793

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	y	0.55	0/274	0.89	0/426
All	All	0.73	2/190296 (0.0%)	1.07	389/278794 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
68	Sb	99	ALA	C-O	5.06	1.30	1.24
72	Sg	16	THR	N-CA	5.04	1.49	1.46

All (389) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	LP	106	PRO	N-CA-C	12.86	126.39	110.70
20	LT	155	VAL	N-CA-C	-11.50	101.86	112.90
49	SE	61	THR	N-CA-C	-10.84	99.89	113.55
44	Lt	1079	G	C2'-C3'-O3'	10.45	125.17	109.50
44	Lt	1277	G	C2'-C3'-O3'	10.38	125.07	109.50
44	Lt	691	G	C2'-C3'-O3'	10.32	129.18	113.70
44	Lt	776	G	C2'-C3'-O3'	10.25	124.87	109.50
44	Lt	1252	G	C2'-C3'-O3'	9.97	128.66	113.70
64	SV	81	PRO	N-CA-C	9.69	124.78	111.22
74	Sj	64	LYS	N-CA-C	-9.64	101.52	113.28
75	St	1079	G	C2'-C3'-O3'	9.58	128.07	113.70
28	Lb	2	PRO	CA-N-CD	-9.57	98.61	112.00
29	Lc	50	ASP	CB-CA-C	9.19	128.28	110.17
75	St	1400	G	C2'-C3'-O3'	-8.94	100.29	113.70
35	Li	72	ARG	CB-CA-C	8.92	118.66	109.83
55	SK	167	PRO	N-CA-C	8.89	125.00	111.14
38	Ll	8	GLU	N-CA-C	-8.74	101.92	112.59
44	Lt	2355	U	C4'-C3'-O3'	8.71	122.47	109.40
44	Lt	2017	A	C4'-C3'-O3'	8.67	122.40	109.40
37	Lk	39	TYR	CA-C-O	-8.52	111.74	119.75
44	Lt	1448	G	C2'-C3'-O3'	8.50	126.45	113.70
30	Ld	12	ASP	N-CA-C	-8.36	102.10	111.71
15	LO	186	PRO	N-CA-C	-8.33	101.55	113.47
56	SL	41	GLU	N-CA-C	-8.32	102.17	111.82
44	Lt	248	G	C2'-C3'-O3'	8.31	126.17	113.70
44	Lt	1356	C	C2'-C3'-O3'	8.30	126.14	113.70
44	Lt	349	A	C2'-C3'-O3'	-8.20	97.20	109.50
44	Lt	1999	U	C4'-C3'-O3'	8.15	121.63	109.40
44	Lt	2591	C	C2'-C3'-O3'	8.05	121.57	109.50
44	Lt	2022	C	C2'-C3'-O3'	8.00	125.70	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	LL	133	ARG	N-CA-C	-7.94	101.08	108.22
13	LM	164	ILE	N-CA-C	-7.91	103.19	111.58
59	SP	122	ILE	N-CA-C	-7.78	103.33	111.58
44	Lt	2508	G	C4'-C3'-O3'	7.75	121.02	109.40
2	LB	95	THR	CB-CA-C	7.74	120.75	108.91
44	Lt	1349	G	C2'-C3'-O3'	7.68	125.22	113.70
44	Lt	1914	C	C2'-C3'-O3'	7.66	125.19	113.70
2	LB	139	ASP	N-CA-C	-7.55	104.57	114.31
19	LS	29	GLU	N-CA-C	-7.51	104.25	113.41
75	St	1138	U	C4'-C3'-O3'	7.51	120.67	109.40
74	Sj	31	ARG	N-CA-C	-7.47	103.12	111.71
19	LS	68	ALA	N-CA-C	-7.46	104.30	113.41
47	SC	105	GLU	N-CA-C	-7.36	102.96	112.23
75	St	44	G	C2'-C3'-O3'	7.34	120.51	109.50
18	LR	40	THR	CB-CA-C	-7.29	99.01	110.74
44	Lt	1880	C	C4'-C3'-O3'	7.24	123.87	113.00
48	SD	76	GLU	N-CA-C	-7.19	105.04	114.31
44	Lt	898	C	C4'-C3'-O3'	7.18	120.17	109.40
3	LC	254	LYS	N-CA-C	-7.16	105.38	112.97
44	Lt	2574	C	C2'-C3'-O3'	7.16	124.43	113.70
75	St	588	G	C2'-C3'-O3'	7.10	124.34	113.70
49	SE	259	ALA	N-CA-C	-7.09	103.48	111.14
51	SG	67	PHE	CB-CA-C	7.08	121.36	109.67
33	Lg	86	GLN	N-CA-C	-7.08	104.38	113.16
63	SU	26	PRO	N-CA-C	7.07	123.36	113.53
7	LG	3	ALA	N-CA-C	-7.05	103.64	111.82
26	LZ	61	GLY	CA-C-O	-7.04	114.98	121.18
49	SE	248	ILE	N-CA-C	-7.03	104.13	111.58
10	LJ	83	GLY	CA-C-O	-7.00	117.40	122.23
22	LV	79	VAL	N-CA-C	-6.99	103.38	111.00
44	Lt	1135	G	C4'-C3'-O3'	6.98	119.88	109.40
33	Lg	9	PHE	CA-CB-CG	6.96	120.76	113.80
11	LK	7	ARG	N-CA-C	-6.96	104.26	112.89
75	St	1410	A	C2'-C3'-O3'	-6.96	99.06	109.50
20	LT	162	ALA	N-CA-C	-6.93	104.78	113.23
39	Ln	88	GLU	N-CA-C	-6.89	104.85	113.18
68	Sb	32	THR	CB-CA-C	-6.88	97.31	109.62
15	LO	12	ARG	N-CA-C	-6.85	103.93	112.90
18	LR	165	GLY	CA-C-O	-6.79	117.41	122.37
74	Sj	65	LEU	N-CA-C	-6.79	104.12	112.88
9	LI	60	PHE	CA-C-O	-6.77	113.68	121.47
44	Lt	1236	G	C2'-C3'-O3'	6.71	123.77	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	LG	40	LYS	N-CA-C	-6.71	104.31	113.30
2	LB	313	ASN	CB-CA-C	6.70	122.10	111.51
44	Lt	71	C	C2'-C3'-O3'	6.67	123.70	113.70
69	Sc	86	LYS	CB-CA-C	6.66	119.65	110.06
1	LA	77	ILE	N-CA-C	-6.64	101.02	109.58
63	SU	44	ILE	CA-C-O	-6.63	116.37	120.88
75	St	1261	A	C2'-C3'-O3'	6.62	119.43	109.50
22	LV	47	ASN	N-CA-C	-6.61	104.44	113.30
44	Lt	805	G	C2'-C3'-O3'	6.60	123.61	113.70
44	Lt	1317	C	C2'-C3'-O3'	6.60	123.60	113.70
44	Lt	2217	G	C2'-C3'-O3'	6.60	123.60	113.70
2	LB	55	HIS	CB-CA-C	6.59	123.54	110.42
34	Lh	47	GLU	N-CA-C	-6.59	101.66	110.55
47	SC	36	VAL	N-CA-C	-6.58	103.35	113.16
37	Lk	58	THR	CB-CA-C	-6.57	98.29	111.17
20	LT	156	LYS	N-CA-C	-6.55	104.17	111.71
19	LS	4	LEU	N-CA-C	-6.55	103.61	112.26
3	LC	112	TYR	N-CA-C	-6.53	103.37	112.45
8	LH	26	THR	CA-C-O	-6.50	114.46	121.94
1	LA	196	TRP	CA-C-O	-6.50	112.37	120.23
24	LX	48	ARG	CA-C-O	-6.50	113.64	121.05
44	Lt	1511	G	C2'-C3'-O3'	6.47	123.41	113.70
44	Lt	2508	G	C2'-C3'-O3'	6.45	119.18	109.50
27	La	101	VAL	N-CA-C	-6.43	100.40	108.89
33	Lg	20	SER	N-CA-C	-6.43	99.63	109.41
16	LP	52	LEU	N-CA-C	-6.43	105.56	113.41
75	St	175	C	C2'-C3'-O3'	6.43	119.14	109.50
30	Ld	81	LEU	N-CA-C	-6.38	104.19	112.23
37	Lk	78	THR	N-CA-C	-6.38	106.04	113.88
52	SH	117	PRO	N-CA-C	-6.35	101.21	111.19
62	ST	131	LEU	N-CA-C	-6.35	104.43	111.36
39	Ln	169	ILE	N-CA-C	-6.33	107.13	113.20
52	SH	180	LEU	N-CA-C	-6.32	105.59	113.55
64	SV	133	ARG	CB-CA-C	6.31	119.15	110.06
73	Sh	120	CYS	CB-CA-C	-6.30	99.27	109.72
2	LB	215	ILE	CA-C-N	-6.29	114.13	122.99
2	LB	215	ILE	C-N-CA	-6.29	114.13	122.99
16	LP	195	TYR	N-CA-C	-6.25	104.55	111.36
44	Lt	1080	C	C4'-C3'-O3'	6.22	118.73	109.40
62	ST	63	ARG	N-CA-C	-6.22	104.75	112.90
14	LN	81	PRO	N-CA-C	-6.21	107.53	114.92
60	SQ	147	ARG	N-CA-C	-6.20	105.71	113.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
69	Sc	84	MET	N-CA-C	-6.20	104.61	111.36
44	Lt	2022	C	C4'-C3'-O3'	6.18	122.27	113.00
54	SJ	80	ASP	CA-C-N	-6.17	116.64	123.43
54	SJ	80	ASP	C-N-CA	-6.17	116.64	123.43
55	SK	111	GLN	N-CA-C	-6.16	104.68	111.82
49	SE	66	GLN	N-CA-C	-6.15	104.57	111.28
19	LS	94	LEU	N-CA-C	-6.15	104.84	112.90
75	St	808	C	C4'-C3'-O3'	6.14	118.62	109.40
9	LI	151	CYS	N-CA-C	-6.14	103.92	112.45
3	LC	47	PRO	CB-CA-C	-6.13	104.05	111.46
13	LM	31	ARG	CA-C-N	-6.12	114.34	122.85
13	LM	31	ARG	C-N-CA	-6.12	114.34	122.85
44	Lt	1382	C	C2'-C3'-O3'	6.12	118.68	109.50
44	Lt	1257	U	C4'-C3'-O3'	6.11	118.56	109.40
75	St	950	C	C2'-C3'-O3'	-6.11	100.34	109.50
22	LV	83	THR	N-CA-C	-6.10	105.86	113.55
44	Lt	1306	C	C2'-C3'-O3'	-6.10	104.55	113.70
2	LB	23	THR	CB-CA-C	6.08	120.23	109.65
36	Lj	26	THR	CA-C-O	-6.06	114.12	120.55
50	SF	161	GLU	N-CA-C	-6.06	104.59	111.07
15	LO	99	ARG	N-CA-C	-6.05	104.80	111.82
44	Lt	1472	C	C2'-C3'-O3'	6.04	122.77	113.70
19	LS	49	ILE	N-CA-C	-6.04	104.80	113.07
29	Lc	54	SER	N-CA-C	-6.03	105.10	112.88
3	LC	158	ILE	N-CA-C	-6.03	104.43	111.00
28	Lb	66	ASN	CB-CA-C	6.02	119.78	109.24
25	LY	43	PRO	N-CA-C	6.02	124.87	112.47
28	Lb	46	ASP	N-CA-C	-6.00	106.00	113.55
39	Ln	126	PRO	N-CA-C	6.00	124.82	112.47
44	Lt	1356	C	C4'-C3'-O3'	5.99	121.99	113.00
45	SA	171	LYS	N-CA-C	-5.99	105.71	114.39
73	Sh	120	CYS	N-CA-CB	-5.99	100.79	109.83
61	SR	109	PRO	N-CA-C	5.98	118.00	110.70
16	LP	151	GLU	N-CA-C	-5.97	104.74	112.68
69	Sc	19	THR	CA-C-O	-5.97	114.22	120.55
75	St	969	G	C4'-C3'-O3'	5.97	121.95	113.00
76	u	28	G	C4'-C3'-O3'	-5.97	104.05	113.00
52	SH	114	ILE	CA-C-O	-5.95	114.76	120.95
58	SO	40	PRO	N-CA-C	-5.95	105.26	113.53
75	St	1303	C	C2'-C3'-O3'	5.95	122.62	113.70
43	Ls	97	ARG	CA-C-O	-5.93	115.56	122.37
44	Lt	694	C	C1'-C2'-O2'	-5.93	99.51	108.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	SD	78	LEU	CA-C-O	-5.91	114.45	120.71
27	La	55	MET	N-CA-C	-5.90	104.83	112.68
39	Ln	173	LYS	N-CA-C	-5.90	105.85	113.16
44	Lt	459	A	C2'-C3'-O3'	5.89	122.54	113.70
75	St	1183	G	C2'-C3'-O3'	-5.89	100.66	109.50
60	SQ	145	GLY	CA-C-O	-5.89	118.17	122.23
6	LF	121	ALA	N-CA-C	5.89	118.71	108.76
8	LH	220	PHE	CA-CB-CG	5.89	119.69	113.80
3	LC	82	TYR	CB-CA-C	-5.87	103.55	111.89
65	SW	39	VAL	N-CA-C	-5.87	105.02	113.07
16	LP	42	GLY	CA-C-O	-5.86	118.19	122.23
8	LH	75	GLU	CB-CA-C	5.86	118.70	109.27
44	Lt	1761	G	C3'-C2'-C1'	-5.86	95.64	101.50
48	SD	224	THR	N-CA-C	-5.85	106.38	112.93
60	SQ	48	SER	N-CA-C	-5.85	106.49	113.97
44	Lt	2584	C	C4'-C3'-O3'	5.84	118.17	109.40
28	Lb	34	LYS	N-CA-C	-5.84	105.97	112.57
50	SF	48	ARG	N-CA-C	-5.84	106.15	113.28
2	LB	155	ASP	N-CA-C	-5.84	106.70	113.88
20	LT	154	HIS	CB-CA-C	5.83	122.02	110.42
54	SJ	4	ILE	N-CA-C	-5.83	106.80	111.81
65	SW	49	ASP	N-CA-C	-5.82	104.85	112.41
1	LA	202	VAL	N-CA-C	-5.80	104.43	112.50
53	SI	168	GLN	N-CA-C	-5.80	104.86	111.07
21	LU	48	TYR	CB-CA-C	5.79	119.27	109.84
42	Lq	39	CYS	CB-CA-C	5.79	119.22	109.67
48	SD	89	GLN	N-CA-C	-5.79	104.78	112.94
24	LX	48	ARG	N-CA-C	-5.77	101.08	110.20
3	LC	47	PRO	N-CA-C	5.77	119.51	110.80
21	LU	69	PRO	CB-CA-C	-5.76	104.22	111.71
31	Le	76	ASP	CB-CA-C	5.76	120.06	111.89
26	LZ	112	ASN	CB-CA-C	-5.75	108.29	115.89
33	Lg	3	GLU	N-CA-C	-5.75	105.02	111.28
75	St	435	A	C4'-C3'-O3'	5.75	121.62	113.00
25	LY	55	TRP	N-CA-C	-5.74	105.60	113.30
72	Sg	10	ILE	N-CA-C	-5.74	106.87	111.81
64	SV	55	LYS	CA-C-O	-5.73	114.47	120.55
75	St	90	A	C4'-C3'-O3'	5.72	117.98	109.40
52	SH	170	THR	CB-CA-C	-5.71	101.92	110.88
44	Lt	326	A	C2'-C3'-O3'	-5.70	100.95	109.50
2	LB	55	HIS	CA-CB-CG	5.70	119.50	113.80
44	Lt	1135	G	C2'-C3'-O3'	5.70	118.04	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	Lt	1277	G	C4'-C3'-O3'	5.69	117.94	109.40
44	Lt	1166	G	C2'-C3'-O3'	5.69	118.04	109.50
48	SD	77	ASP	N-CA-C	-5.69	105.08	111.28
45	SA	48	LYS	N-CA-C	-5.68	105.60	112.54
13	LM	48	PRO	N-CA-C	5.68	124.18	112.47
2	LB	358	THR	N-CA-C	-5.68	105.66	112.59
18	LR	178	SER	CA-C-O	-5.67	114.29	120.81
29	Lc	24	PRO	CB-CA-C	-5.67	105.38	113.09
50	SF	36	PRO	CB-CA-C	-5.67	105.47	112.89
75	St	202	G	C3'-C2'-C1'	-5.66	95.84	101.50
54	SJ	66	ILE	N-CA-C	-5.66	107.23	112.83
75	St	1164	G	C2'-C3'-O3'	-5.66	105.21	113.70
75	St	1183	G	C1'-O4'-C4'	-5.66	104.04	109.70
2	LB	82	PRO	O-C-N	-5.62	118.72	121.31
23	LW	47	LYS	N-CA-C	-5.62	100.02	108.96
45	SA	176	ILE	N-CA-CB	5.62	117.12	110.55
68	Sb	34	GLU	CA-C-O	-5.61	115.62	122.64
3	LC	255	GLN	CB-CA-C	-5.61	110.09	116.54
54	SJ	9	ASP	CA-CB-CG	5.61	118.21	112.60
71	Se	93	THR	CB-CA-C	5.61	118.38	109.52
39	Ln	126	PRO	CA-N-CD	-5.61	104.15	112.00
44	Lt	2566	C	C2'-C3'-O3'	5.61	122.11	113.70
45	SA	45	ASP	CB-CA-C	-5.60	102.28	114.10
62	ST	12	ARG	N-CA-C	-5.59	106.49	113.15
6	LF	84	PRO	CB-CA-C	-5.58	102.93	112.64
15	LO	124	ASP	CA-CB-CG	5.58	118.17	112.60
56	SL	62	SER	N-CA-C	-5.57	105.99	112.89
48	SD	14	THR	CB-CA-C	5.56	120.30	110.85
66	SX	72	PRO	N-CA-C	-5.55	105.81	113.53
39	Ln	126	PRO	N-CA-CB	-5.55	97.42	103.25
72	Sg	55	GLU	N-CA-C	-5.55	105.23	111.28
8	LH	159	VAL	N-CA-C	-5.54	108.10	113.53
16	LP	128	PRO	N-CA-C	-5.54	102.39	111.21
75	St	567	C	C2'-C3'-O3'	5.54	117.81	109.50
75	St	1187	C	C4'-C3'-O3'	5.54	121.31	113.00
3	LC	111	ARG	N-CA-C	-5.54	106.52	113.72
72	Sg	19	ARG	N-CA-C	-5.53	106.43	114.12
8	LH	198	TRP	CA-C-O	-5.53	114.59	120.23
24	LX	35	SER	N-CA-C	-5.53	106.04	112.89
28	Lb	75	ILE	N-CA-C	-5.52	105.82	113.00
52	SH	14	GLU	CB-CA-C	-5.52	110.22	116.63
60	SQ	137	THR	CA-C-O	-5.52	115.52	122.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	SV	137	THR	N-CA-C	-5.50	106.56	113.28
48	SD	233	ASP	CA-C-N	-5.50	115.23	122.99
48	SD	233	ASP	C-N-CA	-5.50	115.23	122.99
8	LH	25	ALA	N-CA-C	-5.50	105.37	111.36
2	LB	302	ASP	CA-C-O	-5.50	115.04	120.70
2	LB	361	LYS	N-CA-C	-5.49	105.31	112.23
39	Ln	205	TYR	CB-CA-C	-5.49	101.68	110.14
43	Ls	113	CYS	N-CA-C	-5.49	106.56	113.20
44	Lt	2628	G	C4'-C3'-O3'	5.49	121.23	113.00
52	SH	8	LYS	N-CA-C	-5.49	104.16	111.24
75	St	330	A	C4'-C3'-O3'	5.48	117.62	109.40
44	Lt	805	G	C4'-C3'-O3'	5.48	121.22	113.00
55	SK	92	ASP	CB-CA-C	5.48	119.80	111.80
36	Lj	33	VAL	N-CA-C	-5.47	105.03	111.00
49	SE	78	THR	CA-C-O	-5.47	114.17	120.24
60	SQ	113	ALA	N-CA-C	-5.47	105.73	112.90
44	Lt	2011	G	C2'-C3'-O3'	-5.47	105.50	113.70
48	SD	50	ALA	N-CA-C	-5.46	106.61	113.28
61	SR	79	HIS	N-CA-C	-5.45	106.22	112.92
44	Lt	1080	C	C2'-C3'-O3'	5.44	117.66	109.50
6	LF	105	CYS	CB-CA-C	-5.44	102.34	110.88
38	Ll	43	ALA	N-CA-C	-5.43	104.22	112.04
3	LC	82	TYR	CA-C-O	-5.43	115.54	121.84
64	SV	31	LEU	N-CA-C	-5.42	106.71	113.38
71	Se	104	ILE	N-CA-C	-5.41	106.58	112.80
50	SF	42	TRP	N-CA-C	-5.41	106.66	113.20
59	SP	51	GLY	N-CA-C	-5.40	107.96	114.66
26	LZ	60	GLY	CA-C-N	-5.39	116.34	121.57
26	LZ	60	GLY	C-N-CA	-5.39	116.34	121.57
65	SW	117	GLU	CA-C-O	-5.39	115.46	121.23
55	SK	133	ARG	CB-CA-C	5.39	119.39	111.73
49	SE	130	PHE	CA-CB-CG	5.39	119.19	113.80
13	LM	85	PRO	N-CA-C	5.38	118.76	111.22
27	La	92	PHE	CB-CA-C	5.38	118.44	109.56
55	SK	1	PRO	CA-N-CD	-5.38	104.47	112.00
59	SP	22	PRO	N-CA-C	-5.38	103.34	111.41
57	SM	153	PRO	N-CA-C	-5.37	101.40	112.47
20	LT	152	TYR	N-CA-C	-5.37	106.68	113.18
36	Lj	56	MET	CA-C-O	-5.37	113.94	120.54
47	SC	146	GLY	CA-C-O	-5.37	117.21	120.91
50	SF	11	TRP	CA-C-O	-5.37	116.35	120.48
10	LJ	95	PHE	CB-CA-C	5.36	115.47	110.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
75	St	1073	A	C4'-C3'-O3'	-5.35	104.97	113.00
44	Lt	165	A	C2'-C3'-O3'	-5.35	105.68	113.70
68	Sb	91	LYS	N-CA-C	-5.34	105.50	112.23
2	LB	172	GLN	CA-C-O	-5.34	115.20	120.70
44	Lt	2060	C	N1-C1'-C2'	5.33	120.00	112.00
44	Lt	369	C	C2'-C3'-O3'	5.33	121.70	113.70
44	Lt	1448	G	C4'-C3'-C2'	-5.33	97.27	102.60
69	Sc	81	PHE	CB-CA-C	-5.33	99.96	109.71
9	LI	140	PRO	N-CA-C	-5.33	101.50	112.47
51	SG	38	MET	CA-C-O	-5.33	116.01	121.87
44	Lt	1620	A	C4'-C3'-O3'	5.32	120.98	113.00
43	Ls	108	THR	N-CA-C	-5.32	107.45	114.31
46	SB	198	SER	N-CA-C	-5.31	106.06	112.54
64	SV	121	GLU	N-CA-C	-5.31	105.49	111.28
44	Lt	1509	G	C2'-C3'-O3'	5.31	117.46	109.50
75	St	557	C	C2'-C3'-O3'	-5.31	105.74	113.70
39	Ln	90	LEU	N-CA-C	-5.30	105.50	111.28
48	SD	134	LEU	CA-C-N	-5.30	115.53	123.00
48	SD	134	LEU	C-N-CA	-5.30	115.53	123.00
58	SO	8	TYR	CB-CA-C	5.29	119.20	109.99
5	LE	55	A	C2'-C3'-O3'	-5.29	105.76	113.70
57	SM	39	GLY	CA-C-N	-5.29	115.74	122.77
57	SM	39	GLY	C-N-CA	-5.29	115.74	122.77
54	SJ	46	TYR	N-CA-C	-5.28	105.58	112.23
44	Lt	484	U	C2'-C3'-O3'	5.28	121.61	113.70
75	St	175	C	C4'-C3'-O3'	5.27	117.31	109.40
30	Ld	76	GLY	CA-C-O	-5.26	116.44	121.49
48	SD	102	GLY	CA-C-O	-5.25	117.45	122.13
63	SU	49	LEU	N-CA-C	-5.25	105.45	111.07
29	Lc	19	ASN	N-CA-C	-5.25	104.90	113.19
16	LP	182	ASP	N-CA-C	-5.25	106.66	113.16
9	LI	60	PHE	N-CA-C	-5.23	102.73	110.48
3	LC	97	VAL	N-CA-C	-5.23	106.79	112.80
16	LP	48	LYS	N-CA-C	-5.23	105.26	111.69
24	LX	10	CYS	CB-CA-C	-5.23	101.96	110.85
69	Sc	87	LYS	N-CA-C	-5.22	105.67	111.36
44	Lt	1619	G	C4'-C3'-C2'	-5.21	97.39	102.60
2	LB	186	ALA	N-CA-C	-5.21	105.78	111.82
24	LX	49	LYS	N-CA-CB	5.20	119.29	110.49
50	SF	60	ASN	N-CA-C	-5.20	106.09	112.90
75	St	1183	G	C3'-C2'-C1'	-5.20	96.30	101.50
1	LA	171	GLY	N-CA-C	-5.20	108.10	115.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	SF	183	GLU	N-CA-C	-5.20	106.78	113.01
34	Lh	47	GLU	CA-C-O	-5.19	115.69	121.81
65	SW	102	SER	CA-C-N	-5.19	117.63	122.66
65	SW	102	SER	C-N-CA	-5.19	117.63	122.66
3	LC	181	ARG	N-CA-C	-5.18	106.74	113.16
51	SG	197	ASP	N-CA-C	-5.18	106.47	112.89
38	Ll	66	ASP	N-CA-C	-5.17	105.64	111.28
1	LA	123	ARG	CA-C-O	-5.17	116.27	122.27
3	LC	46	THR	CA-C-O	-5.17	115.85	120.19
44	Lt	861	C	C2'-C3'-O3'	-5.17	105.94	113.70
22	LV	27	ASP	N-CA-C	-5.17	105.73	111.36
75	St	810	U	C3'-C2'-O2'	5.16	118.44	110.70
9	LI	163	THR	CB-CA-C	5.16	120.69	110.42
75	St	559	G	C4'-C3'-O3'	5.16	117.14	109.40
52	SH	8	LYS	CA-C-O	-5.16	115.39	120.80
38	Ll	9	ASN	N-CA-C	-5.15	105.31	111.03
55	SK	15	THR	CB-CA-C	5.14	116.82	109.11
9	LI	59	GLN	CB-CA-C	5.14	119.32	110.79
18	LR	167	HIS	CB-CA-C	5.13	120.63	110.42
51	SG	93	ARG	N-CA-C	-5.13	107.07	113.38
74	Sj	39	ASN	N-CA-C	-5.13	106.53	112.89
75	St	568	G	C4'-C3'-C2'	-5.12	97.47	102.60
63	SU	114	PHE	CB-CA-C	5.12	119.56	110.85
44	Lt	2097	G	C4'-C3'-C2'	-5.12	97.48	102.60
71	Se	70	ASN	N-CA-C	-5.12	106.81	113.16
44	Lt	1785	U	C4'-C3'-O3'	-5.12	105.32	113.00
20	LT	112	ARG	CB-CA-C	5.12	119.27	111.80
24	LX	7	CYS	N-CA-C	-5.12	102.47	110.10
69	Sc	52	SER	N-CA-C	-5.12	103.28	110.50
55	SK	23	PRO	CB-CA-C	-5.11	104.94	113.06
1	LA	122	ASP	N-CA-C	-5.10	106.46	113.30
16	LP	104	GLY	CA-C-O	-5.10	117.29	122.59
74	Sj	46	THR	N-CA-C	-5.10	107.01	113.43
75	St	191	C	C2'-C3'-O3'	5.10	121.35	113.70
8	LH	190	PHE	N-CA-C	-5.09	105.37	112.45
13	LM	85	PRO	CB-CA-C	-5.09	103.53	111.22
44	Lt	691	G	C4'-C3'-C2'	-5.09	97.51	102.60
44	Lt	1031	C	C2'-C3'-O3'	-5.08	106.08	113.70
48	SD	39	ARG	CA-C-N	-5.08	115.79	122.85
48	SD	39	ARG	C-N-CA	-5.08	115.79	122.85
10	LJ	164	PRO	CB-CA-C	-5.08	104.99	113.06
72	Sg	57	GLU	N-CA-C	-5.08	106.33	112.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	La	51	ILE	N-CA-C	5.07	115.84	110.72
51	SG	120	VAL	N-CA-C	-5.07	106.86	111.67
24	LX	22	PHE	CA-CB-CG	5.07	118.87	113.80
44	Lt	2584	C	C2'-C3'-O3'	5.06	117.09	109.50
54	SJ	50	PHE	CA-CB-CG	5.06	118.86	113.80
39	Ln	25	PRO	CB-CA-C	-5.06	103.21	111.56
44	Lt	2395	G	C4'-C3'-C2'	-5.05	97.55	102.60
11	LK	80	ALA	O-C-N	5.05	124.57	120.83
44	Lt	1298	C	N1-C1'-C2'	5.05	119.58	112.00
45	SA	119	PRO	CA-C-N	-5.05	115.99	123.05
45	SA	119	PRO	C-N-CA	-5.05	115.99	123.05
2	LB	96	PRO	N-CA-C	-5.04	107.83	114.03
47	SC	196	ASN	CA-C-O	-5.04	115.61	119.99
20	LT	81	ARG	N-CA-C	-5.03	106.40	112.54
66	SX	32	LYS	N-CA-C	-5.03	105.71	111.14
3	LC	295	VAL	CA-C-O	-5.03	116.65	121.63
35	Li	80	LYS	N-CA-C	-5.03	105.46	112.45
21	LU	137	ARG	CB-CA-C	-5.03	109.31	116.34
2	LB	257	PRO	CA-N-CD	-5.02	104.47	111.50
24	LX	57	ARG	N-CA-C	-5.01	105.92	112.23
44	Lt	387	G	C2'-C3'-O3'	5.01	121.22	113.70
44	Lt	251	G	C4'-C3'-C2'	-5.00	97.60	102.60
62	ST	82	ASP	CB-CA-C	-5.00	102.56	110.81

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	LA	1855	0	1909	16	0
2	LB	2987	0	3024	33	0
3	LC	2415	0	2498	31	0
4	LD	3038	0	1556	10	0
5	LE	2502	0	1268	9	0
6	LF	2355	0	2416	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	LG	439	0	479	7	0
8	LH	1717	0	1755	30	0
9	LI	1487	0	1566	26	0
10	LJ	1452	0	1495	23	0
11	LK	1594	0	1611	21	0
12	LL	1334	0	1351	32	0
13	LM	1600	0	1699	18	0
14	LN	1024	0	1091	15	0
15	LO	1708	0	1785	15	0
16	LP	1578	0	1616	31	0
17	LQ	1247	0	1280	19	0
18	LR	1402	0	1478	18	0
19	LS	1342	0	1433	22	0
20	LT	1423	0	1426	27	0
21	LU	1257	0	1294	33	0
22	LV	845	0	840	9	0
23	LW	1019	0	1060	13	0
24	LX	538	0	547	12	0
25	LY	931	0	979	9	0
26	LZ	1076	0	1140	10	0
27	La	1004	0	1038	15	0
28	Lb	1201	0	1233	13	0
29	Lc	456	0	482	7	0
30	Ld	753	0	781	6	0
31	Le	818	0	857	7	0
32	Lf	1077	0	1133	19	0
33	Lg	778	0	816	9	0
34	Lh	815	0	849	10	0
35	Li	983	0	1081	8	0
36	Lj	731	0	794	13	0
37	Lk	711	0	712	14	0
38	Ll	558	0	612	14	0
39	Ln	1592	0	1667	50	0
40	Lo	227	0	272	1	0
41	Lp	767	0	821	12	0
42	Lq	708	0	753	11	0
43	Ls	388	0	401	8	0
44	Lt	55643	0	28280	227	0
45	SA	1578	0	1618	45	0
46	SB	1667	0	1713	34	0
47	SC	1636	0	1677	28	0
48	SD	1855	0	1911	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	SE	2055	0	2141	47	0
50	SF	1400	0	1424	23	0
51	SG	1889	0	2011	46	0
52	SH	1430	0	1491	33	0
53	SI	1316	0	1377	31	0
54	SJ	1031	0	1082	15	0
55	SK	1423	0	1515	37	0
56	SL	798	0	786	9	0
57	SM	1260	0	1293	30	0
58	SO	1089	0	1177	23	0
59	SP	1193	0	1258	20	0
60	SQ	920	0	928	17	0
61	SR	921	0	995	13	0
62	ST	1180	0	1250	23	0
63	SU	965	0	1017	17	0
64	SV	1027	0	1039	23	0
65	SW	1080	0	1106	11	0
66	SX	776	0	820	15	0
67	SY	651	0	655	20	0
68	Sb	923	0	982	24	0
69	Sc	588	0	623	13	0
70	Sd	787	0	812	17	0
71	Se	621	0	614	7	0
72	Sg	498	0	532	16	0
73	Sh	409	0	407	10	0
74	Sj	543	0	587	10	0
75	St	31176	0	15856	203	0
76	u	1604	0	816	13	0
77	v	1602	0	816	17	0
78	y	243	0	121	0	0
All	All	177509	0	133628	1665	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 5.

All (1665) 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)
19:LS:161:GLN:HA	19:LS:161:GLN:OE1	1.55	1.04
23:LW:63:LEU:HD11	44:Lt:2354:U:OP1	1.70	0.91
62:ST:43:GLY:H	62:ST:82:ASP:HB2	1.36	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SK:84:LEU:HB3	55:SK:108:ARG:HD2	1.58	0.85
30:Ld:29:LEU:HD21	30:Ld:85:VAL:HG11	1.60	0.83
55:SK:114:ILE:HG23	55:SK:119:LEU:HB2	1.61	0.82
1:LA:234:LYS:HG2	1:LA:238:ILE:HG12	1.61	0.81
19:LS:158:GLU:OE1	19:LS:158:GLU:HA	1.82	0.81
39:Ln:112:ALA:HB2	39:Ln:135:PRO:HB2	1.63	0.80
39:Ln:120:ILE:HB	39:Ln:124:ALA:HB3	1.64	0.80
66:SX:27:ILE:HB	66:SX:92:PHE:HB2	1.63	0.79
73:Sh:102:CYS:HB3	73:Sh:120:CYS:H	1.47	0.78
50:SF:88:LEU:HD11	69:Sc:39:CYS:HB2	1.64	0.78
73:Sh:102:CYS:HB3	73:Sh:120:CYS:N	1.99	0.78
8:LH:70:LEU:HD13	20:LT:58:ASP:HB2	1.63	0.78
72:Sg:6:ASN:HB3	72:Sg:30:MET:HE2	1.66	0.77
39:Ln:17:ILE:HA	39:Ln:29:LEU:HG	1.67	0.77
62:ST:59:PRO:HB2	62:ST:62:LEU:HB2	1.67	0.76
39:Ln:48:ARG:HA	39:Ln:159:PHE:HB2	1.67	0.76
17:LQ:29:TYR:HA	17:LQ:119:VAL:HG11	1.67	0.76
46:SB:132:PRO:HD2	67:SY:33:PRO:HB2	1.67	0.76
13:LM:29:MET:HA	44:Lt:513:C:H4'	1.69	0.75
20:LT:29:ALA:HB1	20:LT:34:VAL:HG23	1.69	0.74
2:LB:88:ALA:HB3	2:LB:160:VAL:HB	1.69	0.74
49:SE:104:ASP:HB2	75:St:559:G:H1	1.52	0.74
49:SE:191:ARG:HG3	49:SE:244:ARG:HE	1.51	0.74
57:SM:97:ARG:HB2	58:SO:10:ALA:HB2	1.68	0.74
12:LL:53:THR:HB	12:LL:60:ARG:HA	1.72	0.72
44:Lt:235:G:H22	44:Lt:256:G:H21	1.36	0.72
21:LU:44:VAL:HG22	21:LU:53:PRO:HG2	1.72	0.72
39:Ln:205:TYR:HB3	39:Ln:213:SER:HB2	1.71	0.72
38:Ll:15:ALA:HA	38:Ll:20:LYS:HG3	1.71	0.72
75:St:113:G:H1'	75:St:207:C:H42	1.54	0.71
2:LB:227:GLU:HB2	2:LB:270:MET:HB2	1.72	0.71
51:SG:72:GLY:HA2	75:St:1369:A:H1'	1.72	0.71
16:LP:15:ARG:HH22	44:Lt:1017:G:H4'	1.53	0.71
19:LS:160:GLU:O	19:LS:160:GLU:HG3	1.89	0.71
70:Sd:41:ILE:HG22	70:Sd:68:TYR:HD1	1.56	0.70
13:LM:105:THR:HG22	13:LM:130:ARG:HB3	1.73	0.70
52:SH:137:ILE:HG21	52:SH:162:VAL:HG11	1.74	0.70
1:LA:15:VAL:HG22	44:Lt:539:G:H1'	1.74	0.69
73:Sh:120:CYS:HB3	73:Sh:123:CYS:H	1.55	0.69
4:LD:133:G:H1	44:Lt:9:U:H3	1.41	0.69
28:Lb:135:GLU:HG3	28:Lb:145:PRO:HG2	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:v:17:G:H21	77:v:57:A:H5'	1.58	0.69
52:SH:10:ARG:HG3	52:SH:11:LYS:HE2	1.73	0.69
31:Le:39:ALA:HB1	31:Le:72:LEU:HD21	1.75	0.69
39:Ln:27:LYS:HD2	39:Ln:171:ASN:HA	1.75	0.69
47:SC:210:ILE:HD13	63:SU:42:ALA:HB1	1.73	0.69
59:SP:37:ILE:HG23	59:SP:50:ILE:HG21	1.74	0.69
9:LI:115:SER:HB3	9:LI:171:VAL:HG11	1.75	0.69
2:LB:223:GLY:HA2	2:LB:271:GLY:HA3	1.74	0.68
47:SC:209:GLU:HB2	63:SU:43:ILE:HB	1.75	0.68
2:LB:78:ILE:HG12	2:LB:305:ILE:HD11	1.74	0.68
15:LO:9:GLU:HB3	36:Lj:37:ILE:HG13	1.74	0.68
32:Lf:106:SER:HB3	44:Lt:1078:G:H5''	1.76	0.68
44:Lt:157:G:H1	44:Lt:172:C:H5	1.40	0.68
64:SV:88:ASN:HA	64:SV:96:ASP:HB3	1.75	0.68
75:St:807:G:H1'	75:St:808:C:H2'	1.75	0.68
75:St:1242:U:H3	75:St:1246:A:H2	1.41	0.68
22:LV:31:ASN:HB3	22:LV:34:GLU:HB3	1.76	0.67
33:Lg:12:ALA:HB3	33:Lg:92:VAL:HG22	1.77	0.67
45:SA:24:LEU:HG	63:SU:101:VAL:HG12	1.77	0.67
43:Ls:112:ARG:HG3	44:Lt:2523:G:H5''	1.77	0.67
65:SW:82:LEU:HD21	75:St:1215:G:H4'	1.75	0.67
43:Ls:94:MET:HB3	43:Ls:119:ARG:HG3	1.78	0.66
51:SG:142:LYS:HB2	51:SG:192:GLN:HB2	1.78	0.66
13:LM:95:ASN:HD21	44:Lt:71:C:H4'	1.60	0.66
16:LP:192:LEU:C	16:LP:194:LYS:H	2.03	0.66
48:SD:131:ASP:HB3	48:SD:227:LEU:HD21	1.77	0.66
51:SG:28:ARG:HA	51:SG:31:GLN:HB3	1.78	0.66
2:LB:90:ILE:HD11	2:LB:160:VAL:HG23	1.79	0.65
2:LB:90:ILE:HG23	2:LB:104:THR:HG22	1.77	0.65
75:St:1246:A:H8	75:St:1247:C:H2'	1.61	0.65
20:LT:6:ILE:HG13	20:LT:62:ILE:HD13	1.78	0.65
55:SK:76:ALA:HB1	55:SK:80:ARG:HH21	1.60	0.65
44:Lt:1767:A:H2	44:Lt:1774:U:H3	1.43	0.65
60:SQ:44:VAL:HG11	60:SQ:85:ILE:HG22	1.78	0.65
32:Lf:72:LEU:HD11	32:Lf:78:LYS:HB2	1.78	0.65
12:LL:41:THR:HG21	12:LL:69:VAL:HG11	1.79	0.65
69:Sc:69:PHE:HA	69:Sc:83:ASN:HA	1.79	0.65
54:SJ:7:LEU:HD23	54:SJ:74:VAL:HG23	1.76	0.65
57:SM:131:LYS:HB2	75:St:250:G:H3'	1.78	0.65
75:St:399:A:H1'	75:St:424:C:H42	1.62	0.65
75:St:589:G:H2'	75:St:590:G:C8	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SQ:35:ALA:HB3	60:SQ:112:SER:HB3	1.78	0.65
15:LO:135:ILE:HG13	15:LO:151:ILE:HD13	1.79	0.65
64:SV:34:ILE:HB	64:SV:38:GLY:HA3	1.78	0.65
3:LC:184:MET:HE2	4:LD:22:C:H5''	1.79	0.64
37:Lk:28:HIS:HB3	37:Lk:31:LYS:HG2	1.79	0.64
49:SE:94:LYS:HB3	68:Sb:15:PRO:HB2	1.79	0.64
50:SF:23:LEU:HD12	50:SF:103:ALA:HA	1.78	0.64
43:Ls:115:GLY:HA3	44:Lt:907:G:H4'	1.78	0.64
75:St:202:G:H5'	75:St:205:G:H21	1.61	0.64
8:LH:130:THR:HB	8:LH:223:ARG:HD2	1.78	0.64
3:LC:178:ARG:HD2	3:LC:182:GLY:HA3	1.79	0.64
24:LX:45:ARG:HG3	44:Lt:1600:G:H2'	1.78	0.64
46:SB:46:TYR:HB3	67:SY:19:TYR:HB3	1.80	0.64
51:SG:31:GLN:HA	51:SG:34:HIS:HB3	1.80	0.64
26:LZ:2:LYS:HD2	26:LZ:7:VAL:HB	1.79	0.64
38:Ll:5:ILE:HB	38:Ll:47:TYR:HB3	1.80	0.64
19:LS:158:GLU:OE1	19:LS:158:GLU:CA	2.46	0.64
36:Lj:7:ASN:HB3	36:Lj:10:LYS:HG3	1.80	0.64
44:Lt:2221:C:H5''	44:Lt:2221:C:H6	1.63	0.64
1:LA:230:VAL:HG23	1:LA:233:GLN:HB2	1.79	0.63
76:u:17:G:H21	76:u:57:A:H5'	1.63	0.63
16:LP:118:PRO:HD2	20:LT:163:ARG:HA	1.81	0.63
39:Ln:174:MET:HB2	39:Ln:178:GLU:HG2	1.79	0.63
50:SF:128:SER:HB2	72:Sg:45:VAL:HG13	1.80	0.63
35:Li:73:ILE:HG13	35:Li:76:PHE:HB2	1.80	0.63
61:SR:76:VAL:HG13	61:SR:94:VAL:HA	1.79	0.63
37:Lk:2:SER:HA	37:Lk:6:ALA:HB3	1.81	0.63
75:St:1420:A:H2	75:St:1423:G:H1	1.46	0.63
39:Ln:206:ILE:HG13	39:Ln:214:HIS:HB3	1.80	0.63
71:Se:74:LEU:HB3	71:Se:87:VAL:HG23	1.81	0.63
75:St:590:G:H2'	75:St:591:C:C6	2.33	0.62
10:LJ:83:GLY:HA3	10:LJ:185:GLN:HA	1.80	0.62
44:Lt:1743:A:H2'	44:Lt:1744:A:H2'	1.82	0.62
44:Lt:1962:C:H2'	44:Lt:1963:G:H4'	1.81	0.62
61:SR:98:ASN:HB3	61:SR:103:ILE:HG13	1.79	0.62
13:LM:92:GLN:HB2	44:Lt:71:C:H5'	1.79	0.62
61:SR:81:ARG:HB3	61:SR:117:ARG:HB2	1.81	0.62
49:SE:124:CYS:HB2	49:SE:141:THR:HB	1.80	0.62
55:SK:118:LYS:HG3	55:SK:121:LYS:HD3	1.80	0.62
56:SL:17:TYR:HB2	56:SL:87:ILE:HG21	1.81	0.62
60:SQ:120:VAL:HG11	70:Sd:53:VAL:HG12	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SQ:103:THR:HG22	60:SQ:139:ARG:HB2	1.80	0.62
20:LT:165:GLN:HE21	20:LT:167:ARG:HH12	1.48	0.62
44:Lt:910:U:H5	44:Lt:995:G:H1	1.46	0.62
49:SE:208:ILE:HG13	49:SE:222:LEU:HA	1.81	0.62
47:SC:120:PRO:HB2	47:SC:123:ARG:HB2	1.80	0.62
49:SE:3:ARG:HB3	75:St:80:A:H1'	1.80	0.62
61:SR:95:SER:HB3	61:SR:102:PHE:HB3	1.81	0.62
57:SM:34:LYS:HG3	75:St:187:G:H2'	1.81	0.62
39:Ln:117:ILE:HG22	39:Ln:118:ARG:HG3	1.81	0.61
59:SP:23:ALA:HB3	59:SP:26:ASN:HB2	1.80	0.61
11:LK:170:ASN:HA	11:LK:177:THR:HA	1.81	0.61
48:SD:19:PRO:HG2	60:SQ:88:ARG:HE	1.65	0.61
75:St:1053:C:H2'	75:St:1054:C:H2'	1.81	0.61
75:St:64:A:H62	75:St:70:G:H21	1.48	0.61
75:St:921:C:H5''	75:St:933:A:H61	1.65	0.61
75:St:746:A:H2	75:St:766:U:H3	1.47	0.61
16:LP:39:ILE:HG12	16:LP:122:ALA:HB2	1.83	0.61
75:St:591:C:H2'	75:St:592:G:N2	2.15	0.61
45:SA:172:THR:HB	45:SA:175:SER:HB3	1.83	0.61
45:SA:35:ILE:HG12	45:SA:155:SER:HB2	1.83	0.61
75:St:128:G:H1	75:St:154:A:H61	1.49	0.61
52:SH:13:PHE:HE2	52:SH:45:TYR:HB3	1.65	0.61
39:Ln:38:LEU:H	39:Ln:163:VAL:HG13	1.65	0.61
72:Sg:5:ILE:HB	72:Sg:54:MET:HB2	1.82	0.60
16:LP:86:PRO:HD3	44:Lt:886:G:H4'	1.82	0.60
21:LU:84:ILE:HG12	29:Lc:24:PRO:HD3	1.83	0.60
12:LL:57:PHE:HB3	12:LL:59:ILE:HG12	1.83	0.60
43:Ls:109:ASN:HB3	43:Ls:115:GLY:HA2	1.83	0.60
9:LI:126:SER:HB2	9:LI:128:ARG:HG2	1.84	0.60
44:Lt:2354:U:H2'	44:Lt:2355:U:H3'	1.84	0.60
53:SI:87:ILE:HA	53:SI:113:ILE:HG22	1.84	0.60
75:St:1261:A:H4'	75:St:1262:G:H5'	1.84	0.60
9:LI:66:ARG:HA	9:LI:69:THR:HG23	1.83	0.60
16:LP:47:VAL:HG21	16:LP:133:CYS:SG	2.41	0.60
62:ST:47:ILE:HB	62:ST:54:LEU:HD22	1.84	0.60
75:St:87:A:H61	75:St:298:A:H1'	1.66	0.60
19:LS:44:LEU:HB3	19:LS:49:ILE:HG12	1.84	0.60
20:LT:30:PRO:HD2	20:LT:34:VAL:HG21	1.83	0.60
52:SH:50:LYS:HB3	52:SH:62:VAL:HG23	1.83	0.59
8:LH:215:ALA:HA	20:LT:34:VAL:HG12	1.82	0.59
12:LL:65:ILE:HD11	44:Lt:2105:C:H5'	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SM:53:ASP:HB3	57:SM:56:CYS:HB2	1.85	0.59
65:SW:46:ARG:HH12	75:St:1183:G:H4'	1.67	0.59
75:St:155:C:H2'	75:St:156:G:H8	1.66	0.59
77:v:19:A:H2'	77:v:20:A:H4'	1.84	0.59
8:LH:94:VAL:HG13	8:LH:125:VAL:HG12	1.84	0.59
10:LJ:19:ILE:HG12	10:LJ:24:VAL:HG12	1.83	0.59
20:LT:2:MET:HG2	20:LT:30:PRO:HA	1.85	0.59
47:SC:61:PRO:HB3	47:SC:94:VAL:HB	1.84	0.59
23:LW:82:VAL:HG23	23:LW:108:ILE:HG12	1.85	0.59
51:SG:63:ASP:HA	51:SG:112:LEU:HA	1.84	0.59
53:SI:147:ARG:HB2	53:SI:151:VAL:HG13	1.84	0.59
12:LL:105:GLY:HA2	12:LL:126:ASP:HA	1.85	0.59
44:Lt:1935:G:H21	44:Lt:1985:C:H5	1.50	0.58
51:SG:60:GLY:HA2	51:SG:69:MET:HE2	1.85	0.58
56:SL:28:TRP:HZ2	75:St:1155:C:H4'	1.68	0.58
21:LU:87:LYS:HZ1	44:Lt:2152:G:H22	1.48	0.58
47:SC:99:LYS:HB3	47:SC:102:LEU:HB2	1.85	0.58
50:SF:36:PRO:HD2	50:SF:76:MET:HG2	1.83	0.58
60:SQ:66:CYS:HB2	75:St:659:A:H5''	1.84	0.58
3:LC:92:ALA:HB1	44:Lt:520:C:H5''	1.86	0.58
75:St:707:G:H2'	75:St:708:A:C8	2.39	0.58
58:SO:61:GLN:HG3	75:St:1410:A:H5'	1.85	0.58
76:u:9:G:H2'	76:u:11:C:H41	1.69	0.58
48:SD:142:PHE:HB2	48:SD:208:ARG:HB3	1.86	0.58
66:SX:54:SER:HB3	66:SX:93:TRP:H	1.68	0.58
75:St:823:C:H42	75:St:834:G:H3'	1.69	0.58
49:SE:68:LYS:HZ1	49:SE:70:VAL:H	1.51	0.57
75:St:178:C:H2'	75:St:179:G:C8	2.39	0.57
19:LS:60:ARG:HA	19:LS:63:ILE:HD12	1.86	0.57
23:LW:84:VAL:HB	23:LW:123:VAL:HG22	1.86	0.57
69:Sc:35:LYS:HA	69:Sc:69:PHE:HE1	1.68	0.57
51:SG:175:HIS:HA	51:SG:178:THR:HG23	1.86	0.57
49:SE:158:ASP:HB2	49:SE:174:LYS:HA	1.86	0.57
55:SK:163:SER:HB3	55:SK:169:GLY:H	1.68	0.57
24:LX:39:ARG:HA	24:LX:42:LYS:HG2	1.84	0.57
33:Lg:10:LEU:HD23	33:Lg:11:PRO:HD2	1.86	0.57
70:Sd:14:ASN:HB2	75:St:819:C:H4'	1.86	0.57
51:SG:143:ARG:HB3	51:SG:146:LYS:HB2	1.86	0.57
30:Ld:13:SER:HA	30:Ld:17:THR:HG23	1.86	0.57
51:SG:54:CYS:HB3	51:SG:119:LEU:HD21	1.87	0.57
58:SO:9:THR:HG22	75:St:512:U:H4'	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Ln:34:LEU:HG	39:Ln:183:ILE:HD11	1.87	0.57
38:Ll:8:GLU:HA	38:Ll:11:MET:HB3	1.87	0.57
49:SE:206:THR:HB	49:SE:222:LEU:HD22	1.87	0.57
64:SV:100:LEU:HA	64:SV:104:ILE:HG13	1.87	0.57
20:LT:10:ARG:HG2	20:LT:57:LEU:HD21	1.87	0.57
62:ST:57:VAL:H	62:ST:63:ARG:HD3	1.69	0.57
77:v:53:A:H2	77:v:57:A:H8	1.52	0.57
75:St:915:A:H2'	75:St:916:G:C8	2.41	0.56
5:LE:117:C:H4'	6:LF:79:TYR:HE2	1.69	0.56
7:LG:25:ARG:HA	7:LG:28:ILE:HD12	1.87	0.56
7:LG:38:ASN:HB3	7:LG:41:ARG:HG3	1.87	0.56
22:LV:95:PHE:H	22:LV:109:PRO:HA	1.70	0.56
45:SA:208:VAL:HG21	63:SU:94:PHE:CZ	2.40	0.56
47:SC:70:TYR:CE2	47:SC:74:LYS:NZ	2.65	0.56
48:SD:13:ILE:HG21	48:SD:25:LYS:O	2.05	0.56
55:SK:1:PRO:HD2	75:St:293:U:H4'	1.86	0.56
55:SK:108:ARG:HE	55:SK:148:MET:HB3	1.71	0.56
64:SV:122:ARG:HA	64:SV:132:VAL:HG11	1.86	0.56
2:LB:82:PRO:HG3	2:LB:168:THR:HG22	1.87	0.56
39:Ln:65:LEU:HB2	39:Ln:82:LEU:HD22	1.86	0.56
39:Ln:67:VAL:HG11	39:Ln:144:LEU:HD11	1.86	0.56
75:St:390:G:H1	75:St:395:A:H61	1.53	0.56
17:LQ:66:VAL:HG23	17:LQ:79:LYS:HB3	1.87	0.56
39:Ln:9:LEU:HD11	39:Ln:216:ILE:HG12	1.87	0.56
39:Ln:111:LEU:HD22	39:Ln:148:VAL:HB	1.87	0.56
44:Lt:1937:C:H2'	44:Lt:1938:C:C6	2.40	0.56
52:SH:70:LEU:HG	52:SH:97:ALA:HB2	1.87	0.56
62:ST:30:LYS:HB3	62:ST:35:VAL:HG12	1.87	0.56
20:LT:10:ARG:HH12	20:LT:13:PRO:HD3	1.71	0.56
34:Lh:16:THR:HG21	44:Lt:1263:G:H5''	1.88	0.56
39:Ln:80:LEU:HD23	39:Ln:82:LEU:HD21	1.88	0.56
44:Lt:728:G:H1	44:Lt:749:C:H42	1.53	0.56
39:Ln:187:LEU:HB3	39:Ln:198:TRP:HZ3	1.71	0.56
44:Lt:1384:C:H4'	44:Lt:1397:G:H4'	1.87	0.56
12:LL:23:ILE:HD13	12:LL:29:ALA:HB3	1.88	0.56
12:LL:80:ILE:HG23	12:LL:104:PHE:HZ	1.70	0.56
21:LU:116:ARG:HE	21:LU:126:VAL:HG21	1.70	0.56
49:SE:16:LYS:HG2	75:St:535:A:H4'	1.87	0.56
64:SV:10:TYR:HB2	69:Sc:20:LEU:HD22	1.86	0.56
70:Sd:25:ASN:HD21	70:Sd:77:CYS:HB3	1.71	0.56
14:LN:3:TYR:HD1	44:Lt:2582:C:H41	1.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:SD:34:ALA:HA	48:SD:39:ARG:HD2	1.88	0.56
49:SE:256:ARG:O	49:SE:260:LYS:HD3	2.06	0.56
17:LQ:129:THR:HG22	44:Lt:1191:G:H21	1.71	0.55
55:SK:144:ILE:HG21	75:St:547:C:H1'	1.87	0.55
65:SW:60:ARG:HH21	65:SW:64:ILE:HG12	1.71	0.55
12:LL:108:GLU:HA	12:LL:122:ILE:HG23	1.88	0.55
16:LP:192:LEU:C	16:LP:194:LYS:N	2.62	0.55
75:St:498:U:H5''	75:St:784:G:C5	2.42	0.55
77:v:68:U:H2'	77:v:69:G:C8	2.41	0.55
17:LQ:18:ARG:HH22	44:Lt:338:C:H2'	1.71	0.55
49:SE:42:ILE:HD12	49:SE:109:PHE:HB2	1.88	0.55
57:SM:89:LEU:HD22	57:SM:98:TYR:HB3	1.87	0.55
58:SO:101:LEU:HB2	58:SO:124:LYS:HB2	1.88	0.55
75:St:1008:U:H2'	75:St:1009:G:C8	2.42	0.55
75:St:1079:G:H21	75:St:1118:C:H1'	1.70	0.55
15:LO:186:PRO:HB3	44:Lt:61:G:H21	1.72	0.55
72:Sg:7:ALA:HB1	72:Sg:27:VAL:HB	1.89	0.55
2:LB:343:LEU:HD21	44:Lt:2516:G:H5'	1.88	0.55
3:LC:28:LEU:HD21	3:LC:120:ALA:HB2	1.87	0.55
4:LD:126:C:H5''	15:LO:60:VAL:HG21	1.88	0.55
18:LR:44:PHE:HZ	18:LR:80:VAL:HG21	1.72	0.55
48:SD:88:THR:HA	48:SD:98:THR:HA	1.88	0.55
53:SI:67:LEU:HD13	75:St:1364:C:H5''	1.89	0.55
2:LB:96:PRO:HB3	16:LP:150:VAL:HG12	1.88	0.55
39:Ln:198:TRP:H	39:Ln:198:TRP:CD1	2.25	0.55
44:Lt:84:C:H1'	44:Lt:85:U:C6	2.41	0.55
44:Lt:1964:C:H4'	44:Lt:1964:C:OP1	2.07	0.55
75:St:326:U:H2'	75:St:327:C:C6	2.42	0.55
44:Lt:1935:G:H2'	44:Lt:1936:G:C8	2.41	0.55
37:Lk:36:SER:HB2	37:Lk:57:ARG:HH22	1.71	0.55
46:SB:169:GLY:HA2	55:SK:98:LEU:HG	1.88	0.55
47:SC:104:ALA:HB2	47:SC:194:ILE:HD12	1.88	0.55
49:SE:228:ILE:HD11	49:SE:235:VAL:HG11	1.89	0.55
28:Lb:32:ARG:HD2	44:Lt:37:U:H4'	1.89	0.55
44:Lt:2156:C:H5'	44:Lt:2185:G:H5''	1.89	0.55
45:SA:161:PHE:HA	67:SY:67:ARG:HG2	1.88	0.55
61:SR:21:GLU:HB2	61:SR:24:LYS:HG3	1.87	0.55
3:LC:104:LYS:HE3	44:Lt:507:G:H5''	1.89	0.55
12:LL:15:GLU:HB2	12:LL:132:SER:HB3	1.89	0.55
14:LN:109:MET:HA	14:LN:112:ILE:HD12	1.89	0.55
44:Lt:533:A:H5''	44:Lt:637:C:H41	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:St:251:C:H2'	75:St:252:G:C8	2.42	0.55
1:LA:14:SER:O	1:LA:15:VAL:HB	2.06	0.54
20:LT:10:ARG:HE	21:LU:142:VAL:HG11	1.71	0.54
29:Lc:53:GLN:HG2	29:Lc:55:LEU:H	1.72	0.54
75:St:202:G:H4'	75:St:203:A:H5'	1.89	0.54
64:SV:37:ILE:HB	64:SV:104:ILE:HD12	1.88	0.54
61:SR:64:ARG:HH21	61:SR:74:LYS:HG3	1.73	0.54
75:St:1080:C:H2'	75:St:1081:C:C6	2.42	0.54
75:St:1306:C:H1'	75:St:1307:C:H5	1.72	0.54
45:SA:43:ILE:HG12	45:SA:52:PHE:HD2	1.72	0.54
75:St:1273:U:H2'	75:St:1274:A:H8	1.72	0.54
27:La:15:LEU:HB3	34:Lh:84:ARG:HG3	1.90	0.54
44:Lt:304:A:H4'	44:Lt:305:G:H4'	1.89	0.54
44:Lt:2138:G:H4'	44:Lt:2139:A:H5''	1.89	0.54
46:SB:172:ILE:HA	46:SB:190:VAL:H	1.72	0.54
53:SI:134:GLN:HB3	53:SI:140:ILE:HG23	1.89	0.54
55:SK:81:LEU:HB3	55:SK:87:LEU:HB3	1.89	0.54
75:St:592:G:N2	75:St:592:G:OP1	2.36	0.54
27:La:53:ASN:HB3	27:La:57:ASP:HB2	1.88	0.54
55:SK:133:ARG:HB2	55:SK:141:ILE:HG23	1.89	0.54
2:LB:54:THR:HG21	2:LB:356:ILE:HG23	1.90	0.54
27:La:11:VAL:HB	27:La:83:CYS:HB3	1.90	0.54
39:Ln:67:VAL:HG22	39:Ln:111:LEU:HB2	1.89	0.54
48:SD:26:GLU:HG2	48:SD:48:LYS:HG3	1.89	0.54
51:SG:172:GLU:HG3	51:SG:174:GLY:H	1.72	0.54
53:SI:106:VAL:HG12	75:St:243:G:H5'	1.90	0.54
58:SO:76:LYS:HB3	75:St:347:G:H5''	1.90	0.54
75:St:329:A:H3'	75:St:330:A:H8	1.73	0.54
39:Ln:65:LEU:HB3	39:Ln:148:VAL:HG22	1.90	0.54
52:SH:51:GLU:HB2	52:SH:59:LYS:HD2	1.88	0.54
53:SI:33:PRO:HA	75:St:244:G:H5'	1.90	0.54
65:SW:72:VAL:HG11	65:SW:101:ARG:HA	1.89	0.54
9:LI:28:LEU:HG	25:LY:29:VAL:HG23	1.89	0.54
13:LM:87:VAL:HB	44:Lt:74:G:H5'	1.90	0.54
19:LS:134:ASN:HB3	44:Lt:1579:C:H5''	1.90	0.54
20:LT:93:GLU:HG2	20:LT:98:ARG:HB3	1.90	0.54
44:Lt:61:G:H22	44:Lt:78:U:H4'	1.73	0.54
45:SA:20:VAL:HG11	63:SU:114:PHE:HZ	1.73	0.54
47:SC:38:ALA:HB2	47:SC:63:VAL:HB	1.90	0.53
66:SX:28:ILE:H	66:SX:117:THR:HB	1.73	0.53
66:SX:53:ILE:HD11	66:SX:92:PHE:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LH:80:LEU:HD21	8:LH:231:VAL:HG21	1.91	0.53
21:LU:72:LEU:HD12	21:LU:96:VAL:HG11	1.90	0.53
44:Lt:1959:C:H4'	44:Lt:1975:C:H4'	1.90	0.53
49:SE:197:ALA:HB3	49:SE:209:ARG:HE	1.74	0.53
51:SG:16:THR:HG21	51:SG:131:THR:HA	1.91	0.53
16:LP:106:PRO:HD2	16:LP:107:PRO:HD3	1.89	0.53
24:LX:48:ARG:O	24:LX:49:LYS:HB2	2.08	0.53
26:LZ:68:VAL:HA	26:LZ:80:VAL:HA	1.90	0.53
70:Sd:43:ASN:HA	70:Sd:66:LYS:HA	1.90	0.53
13:LM:184:ILE:HD12	28:Lb:102:VAL:HG22	1.91	0.53
26:LZ:132:ARG:O	26:LZ:133:ILE:C	2.52	0.53
66:SX:104:ILE:HA	66:SX:107:LYS:HB2	1.90	0.53
68:Sb:112:LYS:HD2	75:St:56:G:H5'	1.90	0.53
75:St:340:C:H1'	75:St:372:G:H1'	1.91	0.53
77:v:1:A:H3'	77:v:2:G:H8	1.73	0.53
6:LF:206:MET:HB3	6:LF:243:GLU:HG2	1.90	0.53
29:Lc:52:ARG:HD3	44:Lt:799:G:H1'	1.90	0.53
44:Lt:83:G:H3'	44:Lt:84:C:H5''	1.90	0.53
45:SA:208:VAL:HG21	63:SU:94:PHE:HZ	1.74	0.53
66:SX:57:CYS:HB2	75:St:1086:G:H1'	1.91	0.53
48:SD:11:LYS:HB2	48:SD:27:TRP:HB2	1.90	0.53
63:SU:99:ILE:HD11	63:SU:121:LEU:HD12	1.89	0.53
46:SB:159:VAL:HG11	46:SB:204:SER:HA	1.91	0.53
48:SD:35:HIS:HD1	48:SD:186:THR:HG23	1.74	0.53
51:SG:171:LYS:HA	51:SG:184:LYS:HA	1.91	0.53
55:SK:102:ILE:HA	55:SK:105:ILE:HG13	1.90	0.53
18:LR:3:ILE:HG12	18:LR:5:LEU:HG	1.91	0.53
60:SQ:134:PRO:HB2	75:St:641:A:H5''	1.90	0.53
62:ST:36:ALA:HB2	62:ST:87:VAL:HG13	1.90	0.53
46:SB:223:LEU:HD13	67:SY:6:ILE:HD11	1.91	0.53
62:ST:108:LEU:HA	62:ST:120:LEU:HD21	1.91	0.53
4:LD:134:G:H21	9:LI:41:GLN:HE22	1.56	0.52
5:LE:95:C:H2'	5:LE:96:G:H8	1.73	0.52
44:Lt:1696:C:H1'	44:Lt:1697:C:H5	1.74	0.52
55:SK:127:ARG:HG2	74:Sj:31:ARG:HE	1.74	0.52
8:LH:171:HIS:HB3	8:LH:189:SER:HB3	1.91	0.52
44:Lt:119:A:H5'	44:Lt:122:C:H42	1.75	0.52
45:SA:76:PRO:HB2	45:SA:100:HIS:HB2	1.90	0.52
47:SC:159:LYS:HG3	47:SC:163:LEU:HD21	1.90	0.52
53:SI:119:LYS:HA	53:SI:135:ILE:HG23	1.90	0.52
64:SV:89:ASN:HB2	75:St:1238:G:H4'	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:Sb:54:ASN:HB2	68:Sb:76:TYR:H	1.72	0.52
74:Sj:31:ARG:HH22	75:St:391:C:H5'	1.74	0.52
75:St:1394:C:H2'	75:St:1395:G:C8	2.44	0.52
16:LP:119:SER:HB2	20:LT:163:ARG:HG2	1.90	0.52
32:Lf:18:ARG:HH12	32:Lf:22:PHE:H	1.57	0.52
76:u:48:G:H3'	76:u:49:A:H8	1.74	0.52
44:Lt:224:U:H2'	44:Lt:225:A:C8	2.44	0.52
75:St:155:C:H2'	75:St:156:G:C8	2.44	0.52
12:LL:54:ILE:HD13	44:Lt:2104:A:H8	1.73	0.52
16:LP:58:ARG:HA	16:LP:67:PRO:HD2	1.91	0.52
47:SC:199:ILE:HG23	47:SC:201:GLY:H	1.75	0.52
75:St:590:G:C2	75:St:591:C:C2	2.97	0.52
45:SA:72:THR:HG21	67:SY:42:SER:HB3	1.90	0.52
68:Sb:57:LEU:HA	68:Sb:73:CYS:HA	1.92	0.52
3:LC:168:VAL:HG22	3:LC:195:PRO:HG2	1.92	0.52
4:LD:86:G:H4'	4:LD:87:A:H5'	1.92	0.52
17:LQ:14:GLY:HA3	17:LQ:101:ALA:HB2	1.92	0.52
31:Le:3:ILE:HG22	31:Le:102:GLU:HG2	1.92	0.52
44:Lt:243:A:H2'	44:Lt:244:G:C8	2.45	0.52
22:LV:23:SER:HA	22:LV:26:LYS:HD3	1.91	0.52
33:Lg:10:LEU:HB3	33:Lg:94:VAL:HG13	1.92	0.52
45:SA:189:ARG:HG3	45:SA:194:ILE:HB	1.91	0.52
50:SF:59:THR:HG21	50:SF:76:MET:HG3	1.91	0.52
75:St:1281:C:H2'	75:St:1282:G:C8	2.45	0.52
6:LF:64:VAL:HG21	6:LF:109:LEU:HD22	1.92	0.51
33:Lg:50:ILE:HG22	33:Lg:94:VAL:HB	1.91	0.51
44:Lt:700:U:H2'	44:Lt:701:U:C6	2.45	0.51
45:SA:170:ASN:HA	45:SA:176:ILE:HG22	1.92	0.51
75:St:1107:C:H2'	75:St:1108:A:C8	2.44	0.51
39:Ln:27:LYS:HG3	39:Ln:30:GLU:HA	1.92	0.51
42:Lq:39:CYS:SG	42:Lq:42:CYS:N	2.74	0.51
46:SB:72:GLU:HB3	46:SB:98:VAL:HG12	1.92	0.51
48:SD:201:LEU:HD12	48:SD:204:ILE:HD11	1.93	0.51
51:SG:127:LEU:H	51:SG:131:THR:HG23	1.75	0.51
70:Sd:23:CYS:HB2	70:Sd:74:CYS:HB3	1.90	0.51
48:SD:86:LEU:HB3	48:SD:98:THR:HG21	1.93	0.51
49:SE:48:LEU:HD13	49:SE:64:ILE:HD11	1.93	0.51
56:SL:13:TYR:HB3	56:SL:87:ILE:HG23	1.92	0.51
6:LF:229:PHE:HB3	6:LF:232:TYR:HB2	1.91	0.51
12:LL:23:ILE:HG12	12:LL:30:LEU:HD13	1.91	0.51
34:Lh:56:PRO:HA	44:Lt:1404:C:H5''	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Lt:47:A:H4'	44:Lt:48:G:H5'	1.92	0.51
44:Lt:1711:G:H2'	44:Lt:1712:A:C8	2.45	0.51
49:SE:248:ILE:O	49:SE:252:GLU:HG2	2.11	0.51
12:LL:45:PRO:HA	12:LL:69:VAL:HG13	1.92	0.51
44:Lt:1292:G:H2'	44:Lt:1293:G:C8	2.46	0.51
68:Sb:44:ALA:HB2	68:Sb:55:ILE:HD12	1.93	0.51
75:St:320:C:H2'	75:St:321:G:H8	1.75	0.51
75:St:971:G:H1'	75:St:972:G:C8	2.46	0.51
31:Le:8:THR:O	44:Lt:2632:G:H5''	2.11	0.51
42:Lq:6:LYS:HB2	44:Lt:1558:C:H3'	1.91	0.51
44:Lt:1947:G:N3	44:Lt:1947:G:H3'	2.25	0.51
75:St:140:A:H1'	75:St:329:A:C8	2.45	0.51
75:St:593:C:N3	75:St:597:G:H5''	2.26	0.51
3:LC:196:LEU:HD23	3:LC:237:ILE:HG12	1.93	0.51
20:LT:57:LEU:HD22	21:LU:142:VAL:HG21	1.93	0.51
27:La:84:ARG:HG3	27:La:86:GLU:HG2	1.93	0.51
46:SB:169:GLY:CA	55:SK:98:LEU:HG	2.41	0.51
52:SH:106:TYR:HA	52:SH:115:ARG:HA	1.93	0.51
25:LY:112:LEU:HD23	25:LY:122:PHE:HE1	1.76	0.51
16:LP:139:ALA:HA	16:LP:142:ILE:HG12	1.92	0.50
32:Lf:47:MET:HE1	32:Lf:55:ARG:HB2	1.92	0.50
59:SP:69:SER:HB3	75:St:613:C:H42	1.76	0.50
75:St:338:A:C8	75:St:338:A:H5''	2.46	0.50
75:St:953:C:H2'	75:St:954:A:H8	1.76	0.50
65:SW:26:ILE:H	65:SW:110:GLN:HE22	1.60	0.50
5:LE:36:C:H5'	6:LF:163:THR:HB	1.92	0.50
10:LJ:3:LEU:HB3	10:LJ:58:PRO:HD2	1.93	0.50
11:LK:49:CYS:HB3	11:LK:168:SER:HB2	1.94	0.50
18:LR:161:VAL:HG12	18:LR:162:LYS:H	1.77	0.50
59:SP:5:HIS:HB3	59:SP:117:LEU:HD22	1.93	0.50
21:LU:79:ARG:HA	21:LU:84:ILE:HA	1.94	0.50
56:SL:65:VAL:HG13	56:SL:83:GLY:HA3	1.92	0.50
3:LC:147:ASP:O	3:LC:148:ASN:C	2.53	0.50
8:LH:81:VAL:HG22	8:LH:103:LEU:HD11	1.92	0.50
22:LV:88:TYR:HA	22:LV:92:GLN:HB3	1.94	0.50
35:Li:79:CYS:HA	35:Li:82:ASP:HB2	1.92	0.50
50:SF:58:LEU:HD23	50:SF:137:ILE:HG23	1.92	0.50
50:SF:111:SER:HB3	50:SF:186:ALA:HA	1.94	0.50
8:LH:116:LYS:HG2	44:Lt:702:G:H4'	1.94	0.50
18:LR:163:PRO:HB2	18:LR:167:HIS:CE1	2.47	0.50
27:La:13:ILE:HG21	27:La:131:LEU:HD22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:Lq:6:LYS:HE2	44:Lt:1558:C:H5''	1.93	0.50
44:Lt:328:G:H1'	44:Lt:351:G:H21	1.76	0.50
46:SB:223:LEU:HD11	67:SY:21:PRO:HD2	1.92	0.50
2:LB:218:ILE:HG23	2:LB:276:THR:HG22	1.92	0.50
19:LS:92:LYS:O	19:LS:96:ILE:HG12	2.12	0.50
44:Lt:1877:C:H2'	44:Lt:1878:A:C8	2.46	0.50
51:SG:61:GLY:HA2	51:SG:115:LEU:HA	1.92	0.50
58:SO:53:GLN:HA	58:SO:96:ASN:HD21	1.77	0.50
75:St:734:G:H4'	75:St:1431:A:H4'	1.94	0.50
77:v:22:C:H2'	77:v:23:G:C8	2.47	0.50
15:LO:28:TRP:O	15:LO:32:GLN:HG2	2.11	0.50
17:LQ:73:ARG:HG2	44:Lt:2611:C:H4'	1.94	0.50
25:LY:29:VAL:HG11	44:Lt:2009:G:H3'	1.93	0.50
44:Lt:1244:G:H2'	44:Lt:1245:C:C2	2.47	0.50
45:SA:127:LEU:HB3	45:SA:149:THR:HG23	1.92	0.50
52:SH:46:ILE:HG22	52:SH:65:VAL:HG12	1.94	0.50
59:SP:17:PRO:HA	71:Se:69:PRO:HD3	1.93	0.50
25:LY:45:TYR:HB3	35:Li:107:HIS:O	2.12	0.50
44:Lt:1362:A:H2'	44:Lt:1363:A:C8	2.47	0.50
75:St:1071:A:H3'	75:St:1072:G:H8	1.77	0.50
5:LE:95:C:H2'	5:LE:96:G:C8	2.47	0.49
6:LF:83:LEU:HD13	6:LF:88:ILE:HD12	1.94	0.49
6:LF:277:LEU:HG	6:LF:281:LYS:HD2	1.93	0.49
68:Sb:19:ARG:HA	68:Sb:76:TYR:HA	1.93	0.49
68:Sb:82:LEU:HD21	68:Sb:96:LEU:HG	1.94	0.49
71:Se:75:GLU:O	71:Se:119:GLU:HB3	2.12	0.49
75:St:861:U:H2'	75:St:862:G:C8	2.47	0.49
5:LE:95:C:H4'	20:LT:116:HIS:HB3	1.95	0.49
11:LK:95:HIS:HB3	11:LK:126:VAL:HG23	1.94	0.49
20:LT:156:LYS:HE2	20:LT:157:ARG:HH12	1.76	0.49
44:Lt:1421:G:H2'	44:Lt:1422:C:C6	2.47	0.49
44:Lt:1681:U:H5''	44:Lt:1682:G:H5'	1.94	0.49
45:SA:112:ASN:O	45:SA:121:TYR:HA	2.12	0.49
46:SB:131:VAL:HG12	67:SY:34:LYS:HD3	1.94	0.49
49:SE:254:ARG:HE	75:St:558:C:H5	1.60	0.49
62:ST:23:TYR:CG	62:ST:39:PHE:HB3	2.47	0.49
12:LL:110:ILE:HD13	12:LL:116:TYR:HB2	1.94	0.49
23:LW:63:LEU:HD11	44:Lt:2354:U:P	2.51	0.49
44:Lt:1302:G:H1'	44:Lt:1306:C:H42	1.77	0.49
49:SE:43:PRO:HG2	49:SE:46:LEU:HB3	1.94	0.49
75:St:253:C:H2'	75:St:254:G:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LK:8:CYS:HB3	44:Lt:838:U:H4'	1.93	0.49
47:SC:208:ILE:HD13	63:SU:12:ALA:HB2	1.94	0.49
55:SK:163:SER:HB2	55:SK:171:PRO:HB3	1.95	0.49
58:SO:18:ARG:HA	58:SO:21:ARG:HE	1.76	0.49
75:St:548:C:H2'	75:St:549:A:C8	2.47	0.49
75:St:1284:C:H1'	75:St:1287:C:H41	1.77	0.49
19:LS:55:ILE:HG12	44:Lt:1357:C:H5''	1.95	0.49
25:LY:126:ALA:HB3	25:LY:129:VAL:HG13	1.93	0.49
46:SB:223:LEU:HA	67:SY:6:ILE:HG13	1.94	0.49
53:SI:115:SER:HA	53:SI:140:ILE:HD11	1.93	0.49
15:LO:78:GLY:HA2	15:LO:89:ILE:HD13	1.95	0.49
17:LQ:37:GLY:HA2	17:LQ:155:LEU:HD13	1.95	0.49
32:Lf:88:LYS:HA	32:Lf:91:PHE:HB3	1.94	0.49
45:SA:195:SER:HB2	45:SA:198:GLU:HB2	1.94	0.49
50:SF:88:LEU:HD12	69:Sc:82:LYS:HB3	1.95	0.49
54:SJ:105:THR:HB	54:SJ:126:ILE:HD11	1.95	0.49
75:St:358:A:H2'	75:St:359:A:H8	1.77	0.49
75:St:373:A:H3'	75:St:374:G:H8	1.77	0.49
75:St:399:A:H1'	75:St:424:C:N4	2.25	0.49
3:LC:27:PRO:HD3	3:LC:262:SER:HA	1.94	0.49
30:Ld:2:SER:HB3	75:St:701:U:H4'	1.95	0.49
32:Lf:31:VAL:HB	44:Lt:403:C:H5''	1.93	0.49
34:Lh:6:VAL:HG11	34:Lh:23:TYR:CE1	2.48	0.49
51:SG:39:ALA:HA	51:SG:57:ARG:HB2	1.94	0.49
55:SK:82:HIS:HB2	55:SK:89:GLU:HG3	1.95	0.49
55:SK:149:VAL:HG23	55:SK:153:ASN:HB2	1.95	0.49
20:LT:135:LYS:HA	20:LT:138:MET:HE3	1.95	0.49
44:Lt:839:A:H2'	44:Lt:840:A:C8	2.48	0.49
44:Lt:2043:G:H1	77:v:74:C:H42	1.59	0.49
52:SH:8:LYS:HE3	52:SH:21:LYS:HA	1.94	0.49
57:SM:98:TYR:O	58:SO:8:TYR:HA	2.12	0.49
5:LE:21:G:H2'	5:LE:22:G:C8	2.48	0.49
8:LH:101:LEU:O	8:LH:110:VAL:HG21	2.12	0.49
18:LR:98:THR:HG23	18:LR:118:ARG:HB3	1.95	0.49
27:La:49:ARG:HB2	27:La:64:GLY:HA2	1.95	0.49
33:Lg:4:ILE:HG22	33:Lg:7:LYS:HG3	1.95	0.49
44:Lt:92:G:H2'	44:Lt:93:A:C8	2.48	0.49
46:SB:99:GLY:HA3	46:SB:184:PHE:HB3	1.95	0.49
51:SG:38:MET:HE1	51:SG:108:VAL:HG23	1.94	0.49
51:SG:168:GLU:HB2	51:SG:187:LYS:HD3	1.93	0.49
64:SV:8:ASN:HB2	69:Sc:21:PHE:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:Sb:54:ASN:HB2	68:Sb:76:TYR:HB2	1.95	0.49
21:LU:65:PHE:HB3	21:LU:75:GLN:HG3	1.95	0.48
61:SR:84:ILE:H	61:SR:84:ILE:HG12	1.45	0.48
75:St:400:G:H21	75:St:422:C:H41	1.60	0.48
3:LC:104:LYS:HA	44:Lt:429:C:H5	1.78	0.48
11:LK:43:VAL:HG21	11:LK:197:ALA:HB2	1.94	0.48
36:Lj:80:ARG:HE	36:Lj:80:ARG:HB3	1.40	0.48
39:Ln:26:ARG:HH11	39:Ln:62:ASN:HB3	1.79	0.48
39:Ln:36:VAL:HG22	39:Ln:165:LEU:HB2	1.95	0.48
44:Lt:152:G:H2'	44:Lt:153:C:C6	2.48	0.48
49:SE:114:ILE:HG22	49:SE:236:ALA:HB3	1.95	0.48
49:SE:202:MET:HE3	49:SE:202:MET:HB3	1.73	0.48
4:LD:94:C:H5''	37:Lk:76:SER:HB3	1.95	0.48
12:LL:37:LEU:O	12:LL:41:THR:HG22	2.13	0.48
37:Lk:69:LYS:HE3	37:Lk:69:LYS:HB3	1.36	0.48
44:Lt:328:G:H1'	44:Lt:351:G:N2	2.29	0.48
45:SA:116:ARG:HA	45:SA:121:TYR:CD2	2.48	0.48
53:SI:170:LYS:HA	53:SI:170:LYS:HD3	1.63	0.48
55:SK:60:LEU:HD21	55:SK:73:GLU:HB2	1.95	0.48
12:LL:108:GLU:HB3	12:LL:110:ILE:HG22	1.95	0.48
14:LN:38:ILE:HG12	14:LN:50:VAL:HB	1.95	0.48
19:LS:23:ARG:HD3	19:LS:23:ARG:HA	1.67	0.48
19:LS:84:THR:HG21	44:Lt:550:G:H5''	1.95	0.48
44:Lt:398:C:H2'	44:Lt:399:G:C8	2.48	0.48
44:Lt:2382:C:H2'	44:Lt:2383:G:C8	2.48	0.48
51:SG:20:LYS:HA	51:SG:20:LYS:HD3	1.44	0.48
55:SK:159:ILE:HG21	55:SK:165:LEU:HB2	1.96	0.48
60:SQ:81:LEU:O	60:SQ:85:ILE:HG23	2.14	0.48
62:ST:92:HIS:CE1	75:St:1216:C:H42	2.32	0.48
5:LE:114:G:H21	6:LF:72:ASP:H	1.61	0.48
9:LI:53:VAL:HG11	9:LI:61:MET:HE1	1.95	0.48
12:LL:111:ASP:C	12:LL:113:GLY:H	2.21	0.48
42:Lq:42:CYS:HB3	42:Lq:60:CYS:HB3	1.72	0.48
48:SD:63:VAL:HG23	48:SD:87:GLN:HB2	1.94	0.48
74:Sj:12:VAL:HG13	75:St:447:A:H1'	1.95	0.48
75:St:1:C:H2'	75:St:283:A:H4'	1.95	0.48
75:St:677:G:H2'	75:St:678:A:C8	2.49	0.48
9:LI:143:LEU:HD11	15:LO:45:PRO:HG2	1.96	0.48
11:LK:63:GLU:HB3	44:Lt:2276:G:H5'	1.95	0.48
44:Lt:2555:C:H2'	44:Lt:2556:G:O4'	2.13	0.48
53:SI:26:LYS:O	53:SI:29:LEU:HB3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SR:125:ILE:HD12	61:SR:125:ILE:HA	1.75	0.48
62:ST:58:ARG:HE	75:St:1186:G:H8	1.60	0.48
75:St:147:C:H2'	75:St:148:G:C8	2.49	0.48
10:LJ:165:ASN:HB3	10:LJ:166:LYS:H	1.42	0.48
12:LL:41:THR:HG23	12:LL:43:GLN:H	1.79	0.48
18:LR:159:SER:HB2	18:LR:161:VAL:HG23	1.95	0.48
21:LU:154:LYS:HB2	21:LU:154:LYS:HE2	1.68	0.48
23:LW:38:LEU:HD22	23:LW:64:ILE:HD13	1.96	0.48
32:Lf:66:LYS:HB2	32:Lf:66:LYS:HE2	1.70	0.48
44:Lt:1963:G:H3'	44:Lt:1964:C:O4'	2.13	0.48
45:SA:82:VAL:HG12	45:SA:104:PHE:HB2	1.95	0.48
47:SC:157:LYS:HB3	47:SC:157:LYS:HE3	1.53	0.48
67:SY:23:LYS:H	67:SY:23:LYS:HG3	1.50	0.48
75:St:440:C:H42	75:St:465:A:H61	1.61	0.48
2:LB:100:ARG:HA	2:LB:100:ARG:HD3	1.60	0.48
45:SA:177:GLY:HA3	45:SA:208:VAL:HG22	1.95	0.48
46:SB:132:PRO:HD2	67:SY:33:PRO:CB	2.40	0.48
50:SF:124:SER:HB3	50:SF:190:ARG:HA	1.96	0.48
2:LB:206:LYS:H	2:LB:206:LYS:HG2	1.41	0.48
8:LH:207:LEU:HD23	8:LH:219:ASP:HB2	1.96	0.48
10:LJ:10:LYS:HE2	10:LJ:10:LYS:HB2	1.46	0.48
10:LJ:67:ARG:HD2	10:LJ:67:ARG:HA	1.63	0.48
34:Lh:63:LEU:O	34:Lh:64:THR:HB	2.12	0.48
34:Lh:99:LEU:HA	34:Lh:102:ILE:HG12	1.95	0.48
37:Lk:44:MET:HE1	37:Lk:57:ARG:HD2	1.96	0.48
44:Lt:65:A:N6	44:Lt:75:G:H1'	2.29	0.48
44:Lt:84:C:H4'	44:Lt:84:C:OP1	2.14	0.48
49:SE:75:LYS:HE2	49:SE:75:LYS:HB3	1.48	0.48
50:SF:164:MET:HE2	50:SF:164:MET:HB2	1.75	0.48
57:SM:70:ARG:HE	57:SM:70:ARG:HB2	1.51	0.48
68:Sb:40:LYS:HE3	68:Sb:40:LYS:HB3	1.53	0.48
75:St:1169:C:H2'	75:St:1170:G:H8	1.79	0.48
9:LI:174:LYS:HB2	9:LI:174:LYS:HE2	1.42	0.48
29:Lc:10:LYS:HB2	29:Lc:10:LYS:HE2	1.47	0.48
42:Lq:7:LYS:HB2	42:Lq:27:LEU:HD22	1.95	0.48
44:Lt:1198:G:H21	44:Lt:1474:A:H8	1.60	0.48
46:SB:134:ARG:HB2	46:SB:215:SER:HB2	1.96	0.48
57:SM:144:SER:HB3	75:St:584:C:H1'	1.95	0.48
23:LW:46:TRP:CE2	23:LW:54:PRO:HA	2.49	0.47
35:Li:59:LEU:HD13	35:Li:76:PHE:HA	1.95	0.47
48:SD:25:LYS:HB2	48:SD:25:LYS:HE2	1.53	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:SO:54:LYS:HB3	58:SO:91:LEU:HD11	1.95	0.47
65:SW:62:PHE:HD1	65:SW:113:LEU:HD21	1.79	0.47
66:SX:83:PHE:HB3	73:Sh:133:PHE:HB3	1.95	0.47
75:St:961:G:H5'	75:St:962:A:H5'	1.96	0.47
10:LJ:153:THR:O	10:LJ:157:ILE:HG13	2.13	0.47
14:LN:24:LEU:HD11	14:LN:87:MET:HE3	1.96	0.47
23:LW:74:LEU:H	23:LW:74:LEU:HG	1.48	0.47
42:Lq:57:CYS:SG	42:Lq:60:CYS:N	2.79	0.47
53:SI:142:ALA:HA	53:SI:159:LEU:H	1.79	0.47
60:SQ:140:THR:HB	60:SQ:141:ARG:H	1.51	0.47
75:St:588:G:H1'	75:St:608:G:N2	2.29	0.47
75:St:953:C:H2'	75:St:954:A:C8	2.50	0.47
75:St:1201:C:H2'	75:St:1202:C:O4'	2.14	0.47
2:LB:259:ASN:HD22	44:Lt:2409:A:H4'	1.78	0.47
15:LO:182:MET:HG3	44:Lt:98:C:H4'	1.96	0.47
44:Lt:533:A:H5''	44:Lt:637:C:N4	2.29	0.47
45:SA:188:LEU:HB2	45:SA:194:ILE:HD11	1.96	0.47
54:SJ:81:ILE:HD12	54:SJ:104:LEU:HD11	1.96	0.47
58:SO:3:LYS:O	58:SO:4:THR:C	2.57	0.47
70:Sd:20:ILE:HD12	70:Sd:20:ILE:HA	1.75	0.47
74:Sj:26:ARG:HB3	74:Sj:29:ARG:HH12	1.79	0.47
1:LA:82:MET:HB2	1:LA:82:MET:HE2	1.61	0.47
45:SA:37:ARG:H	45:SA:37:ARG:HG2	1.39	0.47
58:SO:135:LEU:HB2	58:SO:137:LYS:HG2	1.97	0.47
62:ST:158:ARG:HD2	62:ST:158:ARG:HA	1.37	0.47
64:SV:86:ASN:HD22	64:SV:99:ILE:HG13	1.78	0.47
70:Sd:50:ALA:HA	70:Sd:53:VAL:HG22	1.97	0.47
75:St:64:A:C2	75:St:65:C:H1'	2.49	0.47
75:St:1263:G:H2'	75:St:1264:A:C8	2.48	0.47
12:LL:54:ILE:HD13	44:Lt:2104:A:C8	2.50	0.47
27:La:92:PHE:HD2	27:La:107:ILE:HG13	1.78	0.47
27:La:113:LYS:HE2	27:La:113:LYS:HB2	1.65	0.47
44:Lt:2235:C:H2'	44:Lt:2236:A:C8	2.49	0.47
46:SB:221:PRO:HA	46:SB:224:TRP:CE2	2.49	0.47
63:SU:66:LYS:HD2	63:SU:66:LYS:HA	1.59	0.47
70:Sd:41:ILE:HG22	70:Sd:68:TYR:CD1	2.44	0.47
71:Se:49:LEU:O	71:Se:51:PRO:HD3	2.14	0.47
11:LK:30:LYS:HG3	11:LK:63:GLU:HG2	1.96	0.47
44:Lt:1181:C:H2'	44:Lt:1182:G:C8	2.50	0.47
62:ST:31:LYS:HB3	62:ST:101:GLN:HE22	1.79	0.47
6:LF:83:LEU:HB2	6:LF:92:LEU:HD22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LH:198:TRP:O	8:LH:199:PRO:C	2.58	0.47
14:LN:112:ILE:HG12	16:LP:195:TYR:HB3	1.95	0.47
14:LN:115:LEU:HD13	16:LP:186:GLN:HG2	1.95	0.47
16:LP:12:ILE:HD13	16:LP:39:ILE:HD11	1.97	0.47
21:LU:80:VAL:HG23	21:LU:85:MET:HG3	1.97	0.47
23:LW:44:LYS:HE3	23:LW:44:LYS:HB3	1.36	0.47
31:Le:22:LYS:O	31:Le:26:ILE:HB	2.15	0.47
44:Lt:2441:U:H2'	44:Lt:2442:A:H8	1.78	0.47
45:SA:48:LYS:HB2	45:SA:48:LYS:HE2	1.61	0.47
46:SB:225:LYS:HB2	67:SY:6:ILE:HB	1.97	0.47
54:SJ:55:ASN:HA	59:SP:18:TYR:HE1	1.80	0.47
59:SP:100:LYS:HB3	59:SP:100:LYS:HE2	1.42	0.47
68:Sb:78:ASN:HD22	68:Sb:81:ALA:HB2	1.79	0.47
73:Sh:120:CYS:HB2	73:Sh:123:CYS:HB2	1.28	0.47
76:u:14:A:H3'	76:u:15:G:H8	1.80	0.47
77:v:1:A:H3'	77:v:2:G:C8	2.50	0.47
6:LF:11:SER:HB2	44:Lt:716:G:H4'	1.97	0.47
16:LP:117:CYS:HB3	20:LT:163:ARG:HB3	1.95	0.47
24:LX:46:ASN:HB3	24:LX:48:ARG:O	2.15	0.47
29:Lc:43:LEU:HD12	29:Lc:43:LEU:HA	1.76	0.47
44:Lt:837:G:N2	44:Lt:839:A:H3'	2.30	0.47
44:Lt:1302:G:H1'	44:Lt:1306:C:N4	2.29	0.47
47:SC:66:GLY:HA3	47:SC:71:ARG:HD3	1.96	0.47
48:SD:17:LYS:HB2	48:SD:17:LYS:HE2	1.61	0.47
52:SH:50:LYS:HB2	52:SH:64:TYR:HE1	1.79	0.47
73:Sh:100:ARG:HB3	73:Sh:111:VAL:HG11	1.96	0.47
3:LC:181:ARG:HE	3:LC:184:MET:HE3	1.80	0.47
12:LL:75:LYS:HD3	12:LL:75:LYS:HA	1.77	0.47
37:Lk:55:ARG:HD2	44:Lt:305:G:N7	2.30	0.47
39:Ln:210:MET:HG2	44:Lt:1958:G:H4'	1.97	0.47
44:Lt:695:C:H2'	44:Lt:696:G:H4'	1.96	0.47
45:SA:85:ARG:HG2	45:SA:88:ALA:H	1.79	0.47
51:SG:9:VAL:HG21	51:SG:47:LEU:HD11	1.97	0.47
54:SJ:101:HIS:HA	54:SJ:113:HIS:CE1	2.50	0.47
75:St:907:A:H1'	75:St:1302:G:H5'	1.97	0.47
3:LC:47:PRO:HB3	3:LC:97:VAL:HG22	1.97	0.47
8:LH:31:ARG:HD2	8:LH:31:ARG:HA	1.68	0.47
10:LJ:2:PRO:HD3	20:LT:139:PHE:CE2	2.50	0.47
11:LK:54:SER:HB2	11:LK:135:LEU:HD21	1.95	0.47
14:LN:6:PHE:H	14:LN:11:ARG:HH21	1.63	0.47
25:LY:95:ARG:HE	25:LY:95:ARG:HB2	1.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Ln:27:LYS:HD3	39:Ln:62:ASN:O	2.15	0.47
41:Lp:21:HIS:HB3	41:Lp:70:LEU:HB3	1.97	0.47
44:Lt:737:G:H1	44:Lt:743:C:H2'	1.80	0.47
44:Lt:1758:A:H2'	44:Lt:1759:A:C8	2.50	0.47
44:Lt:2355:U:N3	44:Lt:2433:C:O2'	2.46	0.47
45:SA:75:ASP:C	45:SA:77:ALA:H	2.23	0.47
47:SC:74:LYS:HE3	47:SC:74:LYS:HB3	1.52	0.47
52:SH:19:LEU:HD22	52:SH:19:LEU:HA	1.70	0.47
74:Sj:14:LYS:HB3	74:Sj:14:LYS:HE2	1.52	0.47
74:Sj:45:ASP:O	74:Sj:49:HIS:HB2	2.15	0.47
6:LF:99:TYR:HB2	6:LF:205:ILE:HD12	1.96	0.46
6:LF:125:LEU:HD22	6:LF:125:LEU:HA	1.77	0.46
24:LX:51:ARG:HA	24:LX:56:TYR:HD2	1.81	0.46
29:Lc:5:LYS:HB2	29:Lc:5:LYS:HE2	1.72	0.46
44:Lt:1448:G:H2'	44:Lt:1449:G:C8	2.49	0.46
44:Lt:1448:G:H2'	44:Lt:1449:G:H8	1.80	0.46
44:Lt:1653:G:H1	44:Lt:1658:C:H5	1.60	0.46
60:SQ:128:ARG:HA	60:SQ:128:ARG:HD3	1.44	0.46
61:SR:18:ARG:HG3	64:SV:94:GLY:HA2	1.96	0.46
71:Se:77:LYS:H	71:Se:119:GLU:HB2	1.80	0.46
75:St:830:A:H2'	75:St:831:A:C8	2.50	0.46
75:St:1085:G:H2'	75:St:1086:G:C8	2.50	0.46
3:LC:65:PRO:HG2	44:Lt:2236:A:OP1	2.16	0.46
16:LP:42:GLY:H	16:LP:130:ARG:HH12	1.63	0.46
18:LR:66:ARG:HD2	18:LR:66:ARG:HA	1.53	0.46
21:LU:137:ARG:HB3	21:LU:138:ALA:H	1.55	0.46
44:Lt:51:C:H2'	44:Lt:52:G:H8	1.80	0.46
44:Lt:1270:C:H5'	44:Lt:1362:A:H1'	1.96	0.46
52:SH:106:TYR:HB3	52:SH:113:SER:HB2	1.98	0.46
53:SI:91:VAL:O	53:SI:110:VAL:HB	2.16	0.46
64:SV:35:LYS:HG2	64:SV:101:VAL:HG23	1.97	0.46
68:Sb:82:LEU:O	68:Sb:86:GLU:HB2	2.15	0.46
75:St:1135:G:H2'	75:St:1136:U:C6	2.50	0.46
2:LB:171:LYS:HB3	2:LB:171:LYS:HE3	1.52	0.46
7:LG:5:LYS:HB2	7:LG:5:LYS:HE2	1.58	0.46
10:LJ:184:GLU:O	10:LJ:185:GLN:C	2.58	0.46
12:LL:37:LEU:HD13	12:LL:69:VAL:HG22	1.96	0.46
12:LL:49:LYS:HB3	12:LL:49:LYS:HE3	1.47	0.46
18:LR:174:ARG:HD2	18:LR:174:ARG:HA	1.41	0.46
27:La:71:LYS:HB3	27:La:71:LYS:HE3	1.35	0.46
32:Lf:119:LYS:HB2	32:Lf:119:LYS:HE3	1.68	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Lt:250:A:O3'	44:Lt:251:G:H4'	2.16	0.46
44:Lt:590:C:H3'	44:Lt:591:U:H4'	1.96	0.46
45:SA:68:ARG:HB2	67:SY:43:VAL:HG23	1.97	0.46
52:SH:8:LYS:O	52:SH:10:ARG:HG2	2.16	0.46
57:SM:82:ILE:HG12	57:SM:83:ILE:N	2.28	0.46
58:SO:115:ILE:H	58:SO:115:ILE:HG12	1.33	0.46
59:SP:30:PRO:HB3	59:SP:67:THR:HG23	1.97	0.46
75:St:61:C:H4'	75:St:152:A:H4'	1.97	0.46
75:St:915:A:H2'	75:St:916:G:H8	1.80	0.46
76:u:50:U:H2'	76:u:51:G:C8	2.50	0.46
3:LC:291:ILE:HD12	8:LH:156:ILE:HD12	1.98	0.46
19:LS:52:LYS:HB3	19:LS:52:LYS:HE2	1.49	0.46
44:Lt:1429:G:H2'	44:Lt:1430:G:C8	2.51	0.46
47:SC:199:ILE:HD12	47:SC:199:ILE:HA	1.82	0.46
48:SD:91:VAL:HA	48:SD:96:CYS:HA	1.97	0.46
51:SG:85:GLN:H	51:SG:85:GLN:HG3	1.57	0.46
55:SK:176:ARG:HH22	75:St:397:C:H41	1.63	0.46
57:SM:73:VAL:HG13	57:SM:82:ILE:HG13	1.98	0.46
75:St:219:U:H2'	75:St:220:C:C6	2.50	0.46
35:Li:80:LYS:HB3	35:Li:80:LYS:HE3	1.64	0.46
42:Lq:20:ARG:HD3	44:Lt:1678:U:H5'	1.97	0.46
44:Lt:222:A:H61	44:Lt:249:A:H5''	1.80	0.46
53:SI:151:VAL:HG11	75:St:168:G:H4'	1.96	0.46
75:St:1194:G:H1'	75:St:1211:C:C6	2.50	0.46
75:St:1243:G:H22	75:St:1246:A:H5''	1.80	0.46
2:LB:250:ALA:HB1	44:Lt:2369:G:N3	2.31	0.46
2:LB:287:THR:HA	2:LB:320:ASP:HA	1.98	0.46
6:LF:160:ARG:HE	6:LF:160:ARG:HB2	1.51	0.46
8:LH:75:GLU:HG2	21:LU:137:ARG:HD3	1.98	0.46
32:Lf:57:MET:HE3	32:Lf:57:MET:HB2	1.67	0.46
44:Lt:1218:A:H2'	44:Lt:1219:A:C8	2.50	0.46
48:SD:172:LEU:HD23	48:SD:172:LEU:HA	1.80	0.46
52:SH:105:ALA:HB3	75:St:521:C:H42	1.80	0.46
68:Sb:54:ASN:HA	68:Sb:82:LEU:HD13	1.98	0.46
71:Se:84:ILE:H	71:Se:84:ILE:HG12	1.48	0.46
2:LB:55:HIS:HB3	44:Lt:2467:G:H1'	1.98	0.46
12:LL:101:ASN:HB3	12:LL:130:VAL:HA	1.97	0.46
46:SB:180:LYS:HD2	46:SB:180:LYS:HA	1.42	0.46
55:SK:130:ILE:HD12	55:SK:145:PRO:HA	1.98	0.46
56:SL:16:LEU:HD22	56:SL:79:LEU:HD23	1.98	0.46
58:SO:105:PHE:HA	58:SO:121:LYS:HG2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:ST:70:ILE:H	62:ST:70:ILE:HG12	1.53	0.46
70:Sd:66:LYS:HB3	70:Sd:66:LYS:HE3	1.52	0.46
11:LK:46:PHE:HB3	11:LK:139:ARG:HG2	1.98	0.46
19:LS:69:ALA:HB1	19:LS:74:ARG:HB2	1.98	0.46
32:Lf:40:PRO:HG3	32:Lf:47:MET:HG2	1.96	0.46
36:Lj:25:LYS:HE2	36:Lj:25:LYS:HB2	1.35	0.46
42:Lq:13:LYS:H	42:Lq:13:LYS:HG3	1.49	0.46
45:SA:189:ARG:HG2	45:SA:196:ARG:HG3	1.98	0.46
66:SX:35:LYS:HD2	66:SX:35:LYS:HA	1.74	0.46
69:Sc:77:ARG:H	69:Sc:77:ARG:HG3	1.50	0.46
72:Sg:10:ILE:HD11	72:Sg:28:GLU:HB3	1.97	0.46
75:St:113:G:H1'	75:St:207:C:N4	2.26	0.46
3:LC:70:ALA:H	3:LC:74:ARG:HH21	1.63	0.46
11:LK:19:LYS:HB3	11:LK:19:LYS:HE3	1.54	0.46
23:LW:130:ARG:HB3	23:LW:131:TRP:CD1	2.51	0.46
44:Lt:1962:C:C2	44:Lt:1963:G:H1'	2.51	0.46
45:SA:174:MET:HG3	63:SU:94:PHE:CZ	2.50	0.46
54:SJ:6:VAL:HG13	54:SJ:29:PRO:HB2	1.96	0.46
63:SU:99:ILE:HD11	63:SU:121:LEU:HA	1.97	0.46
6:LF:33:ARG:HH11	21:LU:27:LEU:HD12	1.80	0.46
13:LM:75:ILE:HB	13:LM:78:CYS:HB2	1.97	0.46
19:LS:110:ARG:HE	19:LS:110:ARG:HB3	1.58	0.46
37:Lk:79:LEU:O	37:Lk:82:ASN:HB3	2.15	0.46
39:Ln:206:ILE:O	39:Ln:213:SER:HA	2.16	0.46
46:SB:173:VAL:HG11	75:St:2:A:H5'	1.97	0.46
51:SG:85:GLN:HA	51:SG:86:GLY:HA2	1.58	0.46
53:SI:25:ARG:HA	75:St:313:G:H5''	1.97	0.46
55:SK:3:ILE:H	55:SK:3:ILE:HG13	1.41	0.46
55:SK:54:ARG:HB3	55:SK:58:ARG:HH21	1.81	0.46
59:SP:38:TYR:HE1	59:SP:74:ILE:HG23	1.81	0.46
59:SP:75:LEU:HD12	59:SP:75:LEU:HA	1.84	0.46
1:LA:116:VAL:HG13	1:LA:164:ALA:HB2	1.98	0.45
2:LB:260:VAL:HG11	2:LB:266:ARG:HH12	1.81	0.45
6:LF:278:LYS:HD2	6:LF:278:LYS:HA	1.72	0.45
9:LI:88:LYS:HA	9:LI:88:LYS:HD3	1.43	0.45
9:LI:110:LYS:HE2	9:LI:110:LYS:HB2	1.39	0.45
19:LS:161:GLN:OE1	19:LS:161:GLN:CA	2.43	0.45
21:LU:103:LYS:HE3	21:LU:103:LYS:HB2	1.73	0.45
44:Lt:61:G:N2	44:Lt:78:U:H4'	2.30	0.45
46:SB:240:LEU:H	46:SB:240:LEU:HG	1.49	0.45
51:SG:42:PHE:HE1	51:SG:117:VAL:HG21	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SH:62:VAL:HG11	52:SH:176:VAL:HG21	1.98	0.45
63:SU:99:ILE:HG23	63:SU:100:THR:H	1.81	0.45
72:Sg:39:ARG:HD2	72:Sg:39:ARG:HA	1.68	0.45
75:St:320:C:H2'	75:St:321:G:C8	2.51	0.45
76:u:74:C:H3'	76:u:75:A:H3'	1.97	0.45
2:LB:13:ASN:HB3	2:LB:16:TYR:HD2	1.81	0.45
6:LF:231:LYS:HA	6:LF:231:LYS:HD3	1.69	0.45
9:LI:94:ILE:HA	9:LI:98:LYS:HB2	1.98	0.45
17:LQ:8:SER:HB2	17:LQ:11:LEU:HB2	1.97	0.45
19:LS:19:LYS:HE2	19:LS:19:LYS:HB2	1.48	0.45
22:LV:28:LEU:HD13	22:LV:28:LEU:HA	1.80	0.45
24:LX:2:PRO:HB2	24:LX:3:ARG:H	1.52	0.45
27:La:97:THR:HG23	27:La:103:LYS:HD2	1.96	0.45
33:Lg:30:LEU:HB3	33:Lg:74:MET:HE1	1.98	0.45
38:Ll:67:LYS:H	38:Ll:67:LYS:HG2	1.46	0.45
44:Lt:1553:A:H2'	44:Lt:1554:A:C8	2.51	0.45
45:SA:142:ALA:HB1	45:SA:147:ILE:O	2.16	0.45
49:SE:161:LYS:HE3	49:SE:161:LYS:HB3	1.62	0.45
52:SH:51:GLU:H	52:SH:51:GLU:HG3	1.59	0.45
75:St:17:C:H2'	75:St:18:C:C6	2.51	0.45
75:St:230:A:H4'	75:St:231:C:H4'	1.97	0.45
9:LI:68:LEU:O	9:LI:72:ILE:HG13	2.17	0.45
11:LK:139:ARG:HG3	11:LK:172:GLY:HA2	1.98	0.45
15:LO:117:ASN:HD22	15:LO:117:ASN:HA	1.49	0.45
18:LR:153:SER:HB3	18:LR:156:ARG:HG2	1.97	0.45
19:LS:162:ARG:H	19:LS:162:ARG:HG2	1.47	0.45
39:Ln:63:LEU:HB2	39:Ln:64:LYS:H	1.62	0.45
39:Ln:156:LYS:HD3	39:Ln:168:PRO:HD2	1.98	0.45
44:Lt:240:U:H2'	44:Lt:241:G:C8	2.51	0.45
44:Lt:981:A:H2'	44:Lt:982:G:H8	1.82	0.45
44:Lt:1579:C:H2'	44:Lt:1580:G:C8	2.51	0.45
47:SC:56:ILE:HG13	47:SC:94:VAL:HG13	1.97	0.45
48:SD:32:ALA:HA	48:SD:98:THR:HG22	1.98	0.45
50:SF:63:MET:HB2	50:SF:63:MET:HE2	1.55	0.45
51:SG:127:LEU:HD13	51:SG:130:LEU:HD23	1.98	0.45
52:SH:11:LYS:H	52:SH:11:LYS:HG2	1.48	0.45
52:SH:16:LEU:H	52:SH:16:LEU:HG	1.27	0.45
2:LB:115:MET:HE3	2:LB:115:MET:HB3	1.88	0.45
6:LF:221:ASP:HB3	6:LF:224:THR:HB	1.97	0.45
9:LI:78:LYS:HB2	9:LI:78:LYS:HE2	1.31	0.45
10:LJ:26:VAL:HG12	10:LJ:80:VAL:HG11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LM:87:VAL:HB	44:Lt:74:G:C5'	2.46	0.45
21:LU:131:ARG:HE	21:LU:131:ARG:HB2	1.48	0.45
34:Lh:65:ARG:HD2	44:Lt:1311:G:H5'	1.98	0.45
36:Lj:17:ILE:H	36:Lj:17:ILE:HG12	1.32	0.45
51:SG:108:VAL:HG22	51:SG:112:LEU:HD13	1.98	0.45
59:SP:4:MET:HB3	59:SP:5:HIS:H	1.66	0.45
62:ST:112:LYS:HA	62:ST:117:ARG:HB3	1.98	0.45
69:Sc:57:LYS:HE3	69:Sc:57:LYS:HB2	1.72	0.45
74:Sj:43:VAL:O	74:Sj:44:ASP:HB2	2.16	0.45
75:St:628:C:H4'	75:St:800:G:H4'	1.97	0.45
75:St:922:G:H5'	75:St:934:C:H42	1.80	0.45
6:LF:79:TYR:HB2	6:LF:81:HIS:HD2	1.82	0.45
9:LI:34:TRP:CD1	9:LI:42:ARG:HH12	2.35	0.45
37:Lk:15:ILE:HD11	44:Lt:311:C:H1'	1.98	0.45
44:Lt:1694:G:H2'	44:Lt:1695:A:C8	2.52	0.45
50:SF:73:LEU:HD11	62:ST:62:LEU:HD11	1.99	0.45
53:SI:10:LYS:HB2	53:SI:10:LYS:HE2	1.57	0.45
59:SP:104:ARG:H	59:SP:104:ARG:HG3	1.48	0.45
75:St:593:C:O2'	75:St:594:G:O5'	2.31	0.45
1:LA:23:ARG:HG2	1:LA:52:ARG:HB3	1.99	0.45
6:LF:150:PHE:HB3	6:LF:179:LEU:HD22	1.99	0.45
6:LF:267:LYS:HB2	6:LF:267:LYS:HE2	1.42	0.45
22:LV:26:LYS:HA	22:LV:26:LYS:HD2	1.87	0.45
39:Ln:183:ILE:HD13	39:Ln:183:ILE:HA	1.53	0.45
44:Lt:41:C:O5'	44:Lt:41:C:H6	1.99	0.45
44:Lt:403:C:H2'	44:Lt:404:G:C8	2.51	0.45
45:SA:19:ASP:HB3	45:SA:182:LEU:HD21	1.98	0.45
46:SB:95:HIS:HB3	46:SB:107:TYR:HE1	1.82	0.45
49:SE:185:GLY:H	49:SE:224:ASN:HB3	1.81	0.45
50:SF:26:TYR:HD1	50:SF:50:ALA:HB2	1.80	0.45
58:SO:100:VAL:HG22	58:SO:125:VAL:HG22	1.98	0.45
75:St:1078:G:H2'	75:St:1079:G:C8	2.51	0.45
75:St:1249:C:H2'	75:St:1250:C:C6	2.51	0.45
11:LK:203:LYS:HB2	11:LK:203:LYS:HE2	1.41	0.45
22:LV:10:LYS:HA	22:LV:10:LYS:HD2	1.36	0.45
44:Lt:1100:C:H2'	44:Lt:1101:G:C8	2.52	0.45
44:Lt:1292:G:H2'	44:Lt:1293:G:H8	1.80	0.45
44:Lt:1963:G:N3	44:Lt:1963:G:H2'	2.31	0.45
54:SJ:6:VAL:HG12	54:SJ:34:ILE:HD11	1.99	0.45
56:SL:67:LYS:HB3	56:SL:67:LYS:HE2	1.83	0.45
64:SV:23:GLY:HA2	64:SV:57:ALA:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:St:1175:A:H4'	75:St:1231:G:H4'	1.98	0.45
7:LG:2:THR:HG21	44:Lt:1176:G:O6	2.17	0.45
10:LJ:103:ASP:O	10:LJ:106:LYS:HB2	2.17	0.45
18:LR:89:GLU:H	18:LR:89:GLU:CD	2.24	0.45
21:LU:61:THR:HG21	21:LU:101:CYS:SG	2.57	0.45
28:Lb:34:LYS:HB2	28:Lb:45:PHE:HZ	1.82	0.45
44:Lt:1907:A:H2'	44:Lt:1908:C:C6	2.52	0.45
44:Lt:2084:C:H2'	44:Lt:2085:G:C8	2.52	0.45
45:SA:81:VAL:HG23	45:SA:103:ALA:HA	1.99	0.45
49:SE:18:TRP:HH2	49:SE:31:PRO:HD3	1.81	0.45
50:SF:139:ASN:HA	50:SF:142:THR:HG22	1.98	0.45
64:SV:37:ILE:H	64:SV:37:ILE:HG12	1.60	0.45
64:SV:99:ILE:HB	64:SV:103:THR:HB	1.99	0.45
67:SY:8:MET:H	67:SY:17:ASP:HB2	1.82	0.45
67:SY:41:LEU:HD12	67:SY:41:LEU:HA	1.76	0.45
75:St:591:C:H2'	75:St:592:G:H21	1.82	0.45
76:u:42:G:H2'	76:u:43:A:C8	2.52	0.45
8:LH:59:LYS:HD2	8:LH:59:LYS:HA	1.62	0.45
18:LR:48:LEU:HD12	18:LR:48:LEU:HA	1.73	0.45
21:LU:24:MET:HE2	21:LU:24:MET:HB2	1.59	0.45
21:LU:87:LYS:HB3	21:LU:87:LYS:HE2	1.54	0.45
23:LW:58:VAL:HG11	23:LW:124:ALA:HB3	1.97	0.45
57:SM:65:ARG:HD3	75:St:100:C:H5'	1.99	0.45
75:St:1195:C:H2'	75:St:1196:G:H8	1.82	0.45
2:LB:252:ILE:HA	2:LB:264:VAL:HG11	1.99	0.45
3:LC:149:VAL:HG23	3:LC:204:VAL:HG12	1.99	0.45
3:LC:162:VAL:HG13	3:LC:164:VAL:HG23	1.99	0.45
3:LC:206:ARG:HE	3:LC:206:ARG:HB3	1.46	0.45
4:LD:118:C:H4'	4:LD:119:G:C8	2.52	0.45
8:LH:69:GLN:HG2	21:LU:143:SER:HA	1.99	0.45
14:LN:60:GLN:HE21	14:LN:60:GLN:HB3	1.50	0.45
20:LT:60:GLN:HE21	20:LT:60:GLN:HB2	1.52	0.45
28:Lb:71:PRO:HD2	28:Lb:110:PHE:CD2	2.52	0.45
38:Ll:5:ILE:HG21	38:Ll:11:MET:HB2	1.99	0.45
38:Ll:6:THR:HB	38:Ll:10:LEU:HB2	1.98	0.45
47:SC:185:GLN:H	47:SC:185:GLN:HG2	1.36	0.45
57:SM:124:GLY:HA3	57:SM:138:ILE:HD11	1.99	0.45
61:SR:89:MET:HE3	61:SR:89:MET:HB3	1.73	0.45
69:Sc:69:PHE:HD2	69:Sc:81:PHE:HB3	1.82	0.45
75:St:589:G:H2'	75:St:590:G:H8	1.78	0.45
21:LU:24:MET:H	21:LU:24:MET:HG3	1.40	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:LU:144:ILE:O	21:LU:145:ALA:C	2.60	0.44
30:Ld:12:ASP:O	30:Ld:16:LEU:HB3	2.17	0.44
45:SA:148:PRO:HG3	67:SY:39:VAL:HB	1.98	0.44
48:SD:198:THR:HG22	48:SD:202:GLN:HG2	1.98	0.44
53:SI:159:LEU:HB3	53:SI:164:LEU:HB2	2.00	0.44
57:SM:65:ARG:HH22	57:SM:127:ARG:N	2.15	0.44
57:SM:139:LYS:HA	57:SM:139:LYS:HD3	1.76	0.44
59:SP:38:TYR:CE1	59:SP:74:ILE:HG23	2.51	0.44
60:SQ:97:ILE:HD11	60:SQ:112:SER:HB2	1.98	0.44
16:LP:163:LYS:HB3	16:LP:163:LYS:HE2	1.88	0.44
17:LQ:66:VAL:CG2	17:LQ:79:LYS:HB3	2.47	0.44
24:LX:28:ARG:HA	24:LX:28:ARG:HD2	1.45	0.44
39:Ln:138:LEU:HD13	39:Ln:138:LEU:HA	1.71	0.44
41:Lp:36:GLN:HG2	44:Lt:2209:G:H5''	1.98	0.44
44:Lt:224:U:H2'	44:Lt:225:A:H8	1.82	0.44
44:Lt:822:C:H2'	44:Lt:823:G:C8	2.53	0.44
44:Lt:2016:G:H4'	44:Lt:2018:C:C2	2.52	0.44
47:SC:204:MET:HB2	47:SC:207:LYS:HB2	1.98	0.44
52:SH:46:ILE:H	52:SH:46:ILE:HG13	1.58	0.44
53:SI:71:HIS:CD2	53:SI:86:ARG:HA	2.52	0.44
54:SJ:43:LYS:HB3	54:SJ:43:LYS:HE3	1.78	0.44
55:SK:38:LYS:HA	74:Sj:31:ARG:HB3	2.00	0.44
64:SV:95:LYS:HB2	64:SV:95:LYS:HE2	1.45	0.44
68:Sb:7:LYS:HD2	75:St:556:C:H42	1.81	0.44
68:Sb:104:SER:C	68:Sb:106:LYS:H	2.25	0.44
72:Sg:19:ARG:HH21	75:St:1307:C:H1'	1.83	0.44
75:St:1143:U:H2'	75:St:1144:G:C8	2.52	0.44
76:u:17:G:N2	76:u:57:A:H5'	2.31	0.44
44:Lt:842:C:H2'	44:Lt:843:A:C8	2.52	0.44
44:Lt:1962:C:C2'	44:Lt:1963:G:H4'	2.47	0.44
57:SM:33:TYR:HB3	57:SM:59:THR:HG22	1.99	0.44
73:Sh:112:TYR:H	75:St:1283:C:H5''	1.82	0.44
2:LB:33:PRO:HG2	2:LB:340:ASN:HB2	1.98	0.44
2:LB:303:LYS:HB3	2:LB:303:LYS:HE3	1.73	0.44
4:LD:57:G:H21	4:LD:63:C:H5'	1.82	0.44
10:LJ:65:LEU:HD21	44:Lt:2539:A:H1'	2.00	0.44
13:LM:52:LYS:HD3	13:LM:52:LYS:HA	1.50	0.44
17:LQ:94:LEU:O	17:LQ:98:VAL:HG13	2.17	0.44
28:Lb:11:ARG:HD3	28:Lb:11:ARG:HA	1.76	0.44
36:Lj:34:LYS:HB3	36:Lj:34:LYS:HE3	1.46	0.44
37:Lk:52:LYS:HB3	37:Lk:52:LYS:HE3	1.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Lt:2642:U:H4'	44:Lt:2643:A:H5'	1.98	0.44
49:SE:94:LYS:HD2	49:SE:94:LYS:HA	1.70	0.44
50:SF:7:LEU:HD13	50:SF:7:LEU:HA	1.78	0.44
51:SG:216:LYS:HE3	51:SG:216:LYS:HB3	1.49	0.44
52:SH:160:LYS:O	52:SH:163:TYR:HB2	2.18	0.44
53:SI:127:LEU:HD12	53:SI:127:LEU:HA	1.79	0.44
58:SO:107:ARG:HB3	58:SO:110:ARG:HB3	1.98	0.44
73:Sh:122:ARG:H	73:Sh:122:ARG:HG2	1.48	0.44
75:St:5:C:H2'	75:St:6:G:H8	1.82	0.44
75:St:1307:C:H2'	75:St:1308:C:C6	2.52	0.44
1:LA:5:ILE:HG12	1:LA:8:GLN:HG3	1.99	0.44
2:LB:96:PRO:HA	16:LP:149:ASP:HB3	1.98	0.44
2:LB:215:ILE:HD11	2:LB:324:ILE:HG21	2.00	0.44
8:LH:75:GLU:HB2	21:LU:137:ARG:HB2	1.99	0.44
9:LI:61:MET:HB2	9:LI:61:MET:HE2	1.68	0.44
10:LJ:15:VAL:HG11	10:LJ:26:VAL:HG13	2.00	0.44
12:LL:80:ILE:HG23	12:LL:104:PHE:CZ	2.52	0.44
32:Lf:90:LEU:HA	32:Lf:94:ASN:HB2	1.99	0.44
39:Ln:20:ALA:HA	39:Ln:29:LEU:HD21	1.99	0.44
45:SA:132:PRO:HG3	45:SA:157:ALA:HB1	1.99	0.44
48:SD:29:PRO:HA	48:SD:43:GLN:HA	1.99	0.44
49:SE:250:ASN:HD22	49:SE:250:ASN:HA	1.54	0.44
53:SI:39:ILE:HA	53:SI:39:ILE:HD13	1.76	0.44
59:SP:54:LEU:HA	59:SP:58:PHE:HD1	1.82	0.44
63:SU:90:LYS:H	63:SU:90:LYS:HG2	1.53	0.44
69:Sc:15:VAL:HG21	75:St:1226:G:H5'	1.99	0.44
3:LC:98:ILE:HB	15:LO:200:LEU:HD12	1.99	0.44
3:LC:255:GLN:HB3	3:LC:256:ASN:H	1.55	0.44
9:LI:210:LYS:HB3	9:LI:210:LYS:HE3	1.64	0.44
14:LN:57:LEU:HG	20:LT:148:HIS:HD2	1.82	0.44
26:LZ:67:LYS:HB3	26:LZ:67:LYS:HE3	1.55	0.44
36:Lj:3:GLY:HA3	44:Lt:2201:G:H5''	2.00	0.44
39:Ln:160:LYS:HD3	39:Ln:160:LYS:HA	1.67	0.44
39:Ln:173:LYS:HB3	39:Ln:173:LYS:HE3	1.56	0.44
44:Lt:1877:C:H2'	44:Lt:1878:A:H8	1.82	0.44
48:SD:28:TYR:HD1	48:SD:28:TYR:HA	1.73	0.44
48:SD:201:LEU:HB3	48:SD:207:CYS:SG	2.57	0.44
55:SK:50:LEU:O	55:SK:53:ILE:HG13	2.18	0.44
57:SM:34:LYS:HG3	75:St:187:G:H8	1.82	0.44
64:SV:51:ILE:HD11	64:SV:68:LEU:HB2	2.00	0.44
70:Sd:37:LYS:HE3	70:Sd:37:LYS:HB2	1.36	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:St:306:C:H2'	75:St:307:C:C6	2.53	0.44
75:St:471:G:H2'	75:St:472:C:C6	2.52	0.44
75:St:1280:C:H2'	75:St:1281:C:C6	2.53	0.44
8:LH:227:ILE:HD12	8:LH:227:ILE:HA	1.79	0.44
16:LP:188:ILE:O	16:LP:192:LEU:HB2	2.18	0.44
44:Lt:2243:A:H1'	77:v:75:A:H2'	2.00	0.44
48:SD:33:PRO:HB2	48:SD:35:HIS:CD2	2.53	0.44
48:SD:111:GLY:HA3	70:Sd:68:TYR:CD2	2.52	0.44
48:SD:227:LEU:HD13	48:SD:227:LEU:HA	1.72	0.44
49:SE:17:HIS:HB2	49:SE:108:ARG:HA	2.00	0.44
52:SH:44:LEU:N	52:SH:69:MET:SD	2.91	0.44
57:SM:116:LYS:HE3	57:SM:116:LYS:HB3	1.52	0.44
75:St:1273:U:H2'	75:St:1274:A:C8	2.52	0.44
6:LF:14:LYS:HB3	6:LF:14:LYS:HE2	1.76	0.44
18:LR:168:LYS:HB2	18:LR:168:LYS:HE2	1.47	0.44
21:LU:44:VAL:HA	21:LU:95:HIS:HB3	1.99	0.44
29:Lc:23:LYS:HB3	29:Lc:23:LYS:HE2	1.51	0.44
44:Lt:3:C:H2'	44:Lt:4:G:C8	2.53	0.44
44:Lt:403:C:H2'	44:Lt:404:G:H8	1.82	0.44
44:Lt:1630:A:H8	44:Lt:2398:A:H2	1.63	0.44
44:Lt:2355:U:H3	44:Lt:2433:C:HO2'	1.65	0.44
48:SD:178:LYS:H	48:SD:178:LYS:HZ2	1.66	0.44
49:SE:108:ARG:HH21	75:St:563:G:H5'	1.82	0.44
54:SJ:22:LYS:HE2	54:SJ:22:LYS:HB2	1.84	0.44
57:SM:77:LYS:H	57:SM:77:LYS:HG2	1.53	0.44
62:ST:107:VAL:HB	62:ST:120:LEU:HD13	1.99	0.44
68:Sb:91:LYS:HB3	68:Sb:91:LYS:HE3	1.77	0.44
75:St:390:G:H2'	75:St:391:C:O4'	2.17	0.44
75:St:394:G:H2'	75:St:395:A:H8	1.83	0.44
75:St:519:C:H6	75:St:519:C:H2'	1.65	0.44
75:St:1083:C:H2'	75:St:1084:G:C8	2.53	0.44
2:LB:144:LYS:HB2	2:LB:144:LYS:HE2	1.45	0.44
3:LC:93:HIS:HA	44:Lt:517:G:H22	1.83	0.44
6:LF:68:GLU:H	6:LF:68:GLU:HG2	1.62	0.44
6:LF:79:TYR:HB2	6:LF:81:HIS:CD2	2.53	0.44
9:LI:48:GLN:HG2	15:LO:25:LEU:HD21	1.98	0.44
12:LL:131:LEU:HD12	12:LL:131:LEU:HA	1.76	0.44
23:LW:64:ILE:HG12	23:LW:81:ALA:HB2	1.99	0.44
44:Lt:1738:G:H1	44:Lt:1754:U:H3	1.66	0.44
44:Lt:2534:C:H2'	44:Lt:2535:U:O4'	2.17	0.44
46:SB:45:LEU:HD23	46:SB:45:LEU:HA	1.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SI:93:ASN:C	53:SI:95:THR:H	2.26	0.44
53:SI:159:LEU:HD23	53:SI:159:LEU:HA	1.82	0.44
65:SW:62:PHE:HD2	65:SW:62:PHE:HA	1.58	0.44
75:St:1267:G:H2'	75:St:1268:U:C6	2.53	0.44
9:LI:72:ILE:HG21	9:LI:133:LEU:HD21	2.01	0.43
11:LK:78:LYS:HE3	11:LK:78:LYS:HB3	1.36	0.43
35:LI:52:LEU:HD13	35:LI:82:ASP:HB3	2.00	0.43
38:LI:5:ILE:HD12	38:LI:5:ILE:HA	1.90	0.43
51:SG:81:LEU:HD23	51:SG:81:LEU:HA	1.77	0.43
52:SH:111:LYS:HE2	52:SH:111:LYS:HB2	1.75	0.43
53:SI:116:ALA:HA	53:SI:119:LYS:HD2	2.00	0.43
68:Sb:33:TYR:HB2	68:Sb:39:ILE:HD11	2.00	0.43
75:St:527:C:H2'	75:St:528:A:C8	2.53	0.43
6:LF:248:LYS:HB2	6:LF:248:LYS:HE2	1.76	0.43
7:LG:21:LYS:HZ3	7:LG:21:LYS:HG3	1.72	0.43
8:LH:225:LYS:HB2	8:LH:225:LYS:HE3	1.76	0.43
12:LL:54:ILE:HG22	12:LL:57:PHE:H	1.82	0.43
15:LO:185:ARG:HA	15:LO:185:ARG:HD3	1.53	0.43
18:LR:163:PRO:HB3	28:Lb:50:PRO:HD2	2.00	0.43
21:LU:121:GLU:HB2	21:LU:122:THR:H	1.56	0.43
39:Ln:114:LYS:HB2	39:Ln:139:ALA:HA	1.99	0.43
41:Lp:72:CYS:SG	41:Lp:75:CYS:N	2.89	0.43
44:Lt:1911:C:H2'	44:Lt:1912:A:H8	1.84	0.43
46:SB:112:SER:HB3	46:SB:118:ALA:HB2	2.00	0.43
49:SE:23:MET:HE3	49:SE:23:MET:HB3	1.72	0.43
56:SL:29:ARG:HA	56:SL:29:ARG:HD3	1.58	0.43
58:SO:32:LEU:HD23	58:SO:32:LEU:HA	1.71	0.43
72:Sg:39:ARG:HH22	72:Sg:56:SER:H	1.66	0.43
75:St:298:A:H2'	75:St:299:G:C8	2.53	0.43
75:St:987:G:H1	75:St:992:U:H3	1.65	0.43
12:LL:13:ARG:HH21	12:LL:134:PRO:HA	1.83	0.43
13:LM:211:ARG:HE	13:LM:211:ARG:HB3	1.39	0.43
32:Lf:88:LYS:HA	32:Lf:88:LYS:HD3	1.47	0.43
44:Lt:2689:C:H2'	44:Lt:2690:G:C8	2.53	0.43
45:SA:24:LEU:HD12	45:SA:24:LEU:HA	1.82	0.43
47:SC:16:LYS:HZ2	47:SC:16:LYS:HG2	1.69	0.43
48:SD:37:LYS:H	48:SD:37:LYS:HG2	1.35	0.43
51:SG:150:LEU:HD22	51:SG:150:LEU:HA	1.82	0.43
51:SG:214:MET:HE3	51:SG:214:MET:HB3	1.78	0.43
55:SK:25:LEU:HD12	55:SK:25:LEU:HA	1.78	0.43
55:SK:71:ARG:HE	55:SK:71:ARG:HB3	1.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SW:13:ILE:HD11	65:SW:60:ARG:HB3	2.01	0.43
66:SX:47:GLU:HB3	66:SX:107:LYS:HB3	2.00	0.43
68:Sb:112:LYS:HB3	68:Sb:112:LYS:HE3	1.76	0.43
74:Sj:29:ARG:HG3	75:St:389:C:H2'	2.01	0.43
3:LC:247:LEU:HD23	3:LC:247:LEU:HA	1.75	0.43
8:LH:26:THR:O	8:LH:27:GLU:HB3	2.18	0.43
16:LP:78:ARG:HB2	16:LP:101:VAL:HG21	2.01	0.43
21:LU:80:VAL:HG11	44:Lt:2152:G:N7	2.33	0.43
39:Ln:65:LEU:HD13	39:Ln:149:LEU:HA	2.00	0.43
39:Ln:87:ILE:HG22	39:Ln:90:LEU:HB2	2.00	0.43
44:Lt:1194:U:H2'	44:Lt:1196:U:C5	2.53	0.43
46:SB:53:LEU:HD22	46:SB:53:LEU:HA	1.81	0.43
48:SD:237:VAL:C	48:SD:239:ASN:H	2.26	0.43
51:SG:107:ILE:H	51:SG:107:ILE:HG12	1.42	0.43
51:SG:241:LYS:HD3	51:SG:245:ARG:HH21	1.83	0.43
52:SH:30:LEU:HD22	52:SH:30:LEU:HA	1.68	0.43
62:ST:129:ARG:HA	62:ST:129:ARG:HD3	1.47	0.43
66:SX:54:SER:HB3	66:SX:93:TRP:N	2.33	0.43
68:Sb:24:VAL:O	68:Sb:70:VAL:HA	2.19	0.43
68:Sb:96:LEU:HD13	68:Sb:96:LEU:HA	1.76	0.43
72:Sg:26:LYS:HE3	72:Sg:26:LYS:HB2	1.25	0.43
4:LD:138:C:H1'	9:LI:163:THR:HG21	2.00	0.43
14:LN:15:LEU:HD21	14:LN:38:ILE:HD13	2.01	0.43
17:LQ:15:LYS:HB3	17:LQ:149:ILE:HG13	1.99	0.43
17:LQ:93:ILE:HG22	17:LQ:148:LEU:HB2	2.01	0.43
20:LT:38:ARG:HD2	20:LT:38:ARG:HA	1.67	0.43
20:LT:46:LEU:HD11	21:LU:152:PRO:HA	2.00	0.43
21:LU:78:LYS:HG2	21:LU:80:VAL:HG22	2.00	0.43
36:Lj:73:ILE:HG21	44:Lt:260:G:H5''	2.01	0.43
44:Lt:2058:U:H3'	44:Lt:2059:A:H5''	2.01	0.43
46:SB:80:VAL:HG21	75:St:1042:A:H5''	2.00	0.43
46:SB:182:LEU:HD12	46:SB:182:LEU:HA	1.78	0.43
56:SL:63:ARG:HD2	56:SL:63:ARG:HA	1.87	0.43
65:SW:77:ARG:HE	65:SW:77:ARG:HB2	1.58	0.43
75:St:211:C:H2'	75:St:212:C:O4'	2.19	0.43
75:St:358:A:H2'	75:St:359:A:C8	2.54	0.43
2:LB:260:VAL:HG11	2:LB:266:ARG:NH1	2.34	0.43
9:LI:93:GLN:HE21	9:LI:94:ILE:HB	1.84	0.43
28:Lb:66:ASN:HD22	28:Lb:66:ASN:HA	1.51	0.43
41:Lp:67:VAL:HG13	41:Lp:80:PHE:HB3	2.00	0.43
44:Lt:903:A:N6	44:Lt:1000:G:H2'	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:SA:56:LEU:HD23	45:SA:56:LEU:HA	1.81	0.43
45:SA:129:VAL:HG13	45:SA:135:ASP:HB2	2.01	0.43
53:SI:129:LYS:HD3	53:SI:129:LYS:HA	1.63	0.43
54:SJ:2:VAL:HG22	54:SJ:3:ARG:H	1.84	0.43
55:SK:86:ILE:HD12	55:SK:86:ILE:HA	1.80	0.43
57:SM:94:LYS:HA	75:St:286:G:OP1	2.19	0.43
63:SU:55:GLY:HA3	75:St:1097:C:O2'	2.19	0.43
70:Sd:22:ARG:HA	70:Sd:28:ARG:O	2.18	0.43
75:St:673:C:H2'	75:St:674:G:C8	2.53	0.43
3:LC:94:PRO:HD2	44:Lt:517:G:N1	2.33	0.43
7:LG:13:LEU:HD22	44:Lt:1177:G:H2'	2.01	0.43
8:LH:173:ILE:HD11	8:LH:189:SER:HB2	2.00	0.43
10:LJ:15:VAL:CG1	10:LJ:26:VAL:HG13	2.49	0.43
10:LJ:75:ASN:HB3	10:LJ:147:ILE:HG21	2.00	0.43
10:LJ:130:ILE:HD11	10:LJ:140:LEU:HB3	2.01	0.43
11:LK:24:ARG:HE	11:LK:24:ARG:HB2	1.73	0.43
17:LQ:153:LYS:C	17:LQ:155:LEU:H	2.27	0.43
18:LR:34:LYS:HE2	18:LR:34:LYS:HB3	1.64	0.43
21:LU:17:ARG:HG2	44:Lt:2124:G:H5''	2.01	0.43
26:LZ:33:ARG:HB3	26:LZ:105:ILE:HG12	1.99	0.43
26:LZ:42:HIS:HB3	26:LZ:119:ILE:HD12	2.00	0.43
49:SE:10:LYS:HA	49:SE:27:TRP:HB3	1.99	0.43
51:SG:242:PRO:HG3	51:SG:245:ARG:NH2	2.34	0.43
70:Sd:54:LEU:HD13	70:Sd:54:LEU:HA	1.75	0.43
75:St:1398:U:H2'	75:St:1399:G:H8	1.83	0.43
24:LX:3:ARG:HD2	24:LX:3:ARG:HA	1.31	0.43
25:LY:92:PRO:HD3	44:Lt:1465:G:H4'	2.00	0.43
28:Lb:126:LYS:HD2	28:Lb:148:VAL:HG23	2.00	0.43
42:Lq:47:VAL:HG13	42:Lq:55:TRP:HB3	2.01	0.43
48:SD:231:MET:HG3	48:SD:232:HIS:N	2.34	0.43
51:SG:11:ILE:H	51:SG:11:ILE:HG12	1.41	0.43
52:SH:112:LYS:HB3	52:SH:112:LYS:HE2	1.33	0.43
57:SM:69:LEU:HB2	57:SM:123:ILE:HD12	2.01	0.43
64:SV:82:ALA:O	64:SV:85:LEU:HB2	2.19	0.43
67:SY:60:PHE:HZ	67:SY:83:HIS:HB2	1.83	0.43
73:Sh:131:ILE:H	73:Sh:131:ILE:HG12	1.63	0.43
75:St:294:C:H2'	75:St:295:C:C6	2.54	0.43
77:v:53:A:C2	77:v:57:A:H8	2.35	0.43
6:LF:189:PRO:HD2	6:LF:201:LEU:HD13	2.01	0.43
8:LH:112:MET:HB3	8:LH:112:MET:HE2	1.64	0.43
9:LI:189:LYS:HB3	9:LI:189:LYS:HE2	1.72	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LN:131:LYS:HE3	14:LN:131:LYS:HB2	1.77	0.43
21:LU:119:ALA:O	21:LU:124:GLN:HA	2.19	0.43
24:LX:14:VAL:HG22	24:LX:33:CYS:HB3	2.00	0.43
28:Lb:21:ARG:HG3	44:Lt:1056:A:H4'	2.01	0.43
37:Lk:15:ILE:H	37:Lk:15:ILE:HG12	1.54	0.43
41:Lp:14:ARG:HB2	41:Lp:77:CYS:SG	2.58	0.43
44:Lt:235:G:H1	44:Lt:256:G:N2	2.17	0.43
44:Lt:671:U:H2'	44:Lt:672:G:H8	1.83	0.43
44:Lt:1643:C:H2'	44:Lt:1644:G:C8	2.54	0.43
48:SD:201:LEU:HD23	48:SD:210:VAL:HG11	2.00	0.43
50:SF:45:LYS:HB3	50:SF:46:ARG:H	1.56	0.43
51:SG:125:LYS:HB2	51:SG:125:LYS:HE2	1.34	0.43
51:SG:230:ARG:HA	51:SG:233:LYS:HD3	2.00	0.43
57:SM:127:ARG:O	57:SM:128:PRO:C	2.61	0.43
61:SR:126:VAL:HG21	75:St:1165:C:H4'	2.01	0.43
72:Sg:27:VAL:HG22	72:Sg:39:ARG:HB2	2.00	0.43
75:St:1169:C:H2'	75:St:1170:G:C8	2.53	0.43
1:LA:150:LEU:HD11	1:LA:156:LYS:HB2	2.00	0.43
2:LB:103:THR:HG22	2:LB:150:LEU:HD21	2.00	0.43
10:LJ:69:ILE:O	10:LJ:73:ILE:HG13	2.19	0.43
13:LM:135:GLU:HG3	36:Lj:16:ARG:HH22	1.84	0.43
18:LR:163:PRO:HB2	18:LR:167:HIS:ND1	2.34	0.43
28:Lb:146:LEU:HD23	28:Lb:146:LEU:HA	1.84	0.43
44:Lt:35:C:H4'	44:Lt:525:A:H2	1.84	0.43
44:Lt:989:C:H2'	44:Lt:990:G:O4'	2.19	0.43
44:Lt:2441:U:H2'	44:Lt:2442:A:C8	2.54	0.43
46:SB:124:LYS:HB2	46:SB:124:LYS:HE2	1.75	0.43
51:SG:24:ILE:H	51:SG:24:ILE:HG12	1.62	0.43
56:SL:63:ARG:HB3	56:SL:65:VAL:HG23	2.00	0.43
58:SO:46:MET:HE3	58:SO:46:MET:HB3	1.80	0.43
75:St:158:G:N1	75:St:202:G:H1'	2.33	0.43
1:LA:132:THR:HG21	44:Lt:1666:G:H5''	1.99	0.42
2:LB:53:CYS:HB2	44:Lt:2467:G:H5'	2.01	0.42
8:LH:122:LEU:HD23	8:LH:122:LEU:HA	1.80	0.42
9:LI:87:HIS:HA	9:LI:90:ARG:HG2	2.01	0.42
10:LJ:40:ALA:HA	10:LJ:41:PRO:HD3	1.91	0.42
13:LM:118:LYS:O	13:LM:122:ILE:HG13	2.19	0.42
15:LO:65:ARG:HB2	15:LO:129:TRP:CD1	2.54	0.42
32:Lf:25:PHE:CD1	32:Lf:47:MET:HE3	2.53	0.42
38:Ll:51:VAL:HG12	38:Ll:52:PRO:HD2	2.01	0.42
42:Lq:90:ARG:HD3	42:Lq:90:ARG:HA	1.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Lt:83:G:H3'	44:Lt:84:C:C5'	2.49	0.42
48:SD:229:SER:O	48:SD:233:ASP:HB2	2.19	0.42
49:SE:247:ILE:HB	75:St:563:G:H21	1.84	0.42
4:LD:73:A:N6	4:LD:88:G:H1'	2.34	0.42
12:LL:125:MET:HE2	12:LL:125:MET:HB3	1.66	0.42
27:La:130:LYS:HB2	27:La:130:LYS:HE3	1.72	0.42
34:Lh:90:SER:O	34:Lh:94:GLU:HG2	2.18	0.42
38:Ll:32:LEU:HD13	38:Ll:32:LEU:HA	1.75	0.42
38:Ll:60:ILE:H	38:Ll:60:ILE:HG13	1.64	0.42
39:Ln:64:LYS:HB2	39:Ln:64:LYS:HE3	1.77	0.42
41:Lp:3:THR:HG22	41:Lp:90:GLU:HB2	2.01	0.42
43:Ls:114:ARG:HH12	44:Lt:998:C:H1'	1.83	0.42
44:Lt:1442:A:H2'	44:Lt:1443:A:C8	2.54	0.42
47:SC:163:LEU:H	47:SC:163:LEU:HG	1.67	0.42
50:SF:68:ASN:ND2	50:SF:68:ASN:H	2.17	0.42
51:SG:148:ARG:HE	51:SG:148:ARG:HB3	1.28	0.42
53:SI:93:ASN:HB2	53:SI:100:VAL:HG22	2.00	0.42
64:SV:117:LYS:HD3	64:SV:117:LYS:HA	1.48	0.42
72:Sg:57:GLU:H	72:Sg:57:GLU:HG2	1.67	0.42
75:St:91:C:H4'	75:St:92:A:H8	1.83	0.42
75:St:397:C:H2'	75:St:398:G:C8	2.54	0.42
5:LE:75:A:H61	5:LE:101:A:H5''	1.84	0.42
13:LM:29:MET:HE3	13:LM:29:MET:HB3	1.74	0.42
17:LQ:91:LYS:HB2	17:LQ:91:LYS:HE3	1.60	0.42
19:LS:157:GLU:O	19:LS:161:GLN:N	2.52	0.42
32:Lf:87:LEU:HD13	32:Lf:87:LEU:HA	1.80	0.42
36:Lj:53:LEU:HD12	36:Lj:53:LEU:HA	1.86	0.42
45:SA:77:ALA:HA	45:SA:100:HIS:O	2.19	0.42
47:SC:115:LEU:HD23	47:SC:115:LEU:HA	1.72	0.42
48:SD:151:ARG:H	48:SD:151:ARG:HG2	1.40	0.42
54:SJ:23:LYS:H	54:SJ:23:LYS:HG2	1.52	0.42
57:SM:129:LEU:HD12	57:SM:129:LEU:HA	1.75	0.42
59:SP:73:ARG:HE	59:SP:73:ARG:HB3	1.50	0.42
64:SV:40:ARG:HG2	64:SV:98:HIS:CE1	2.54	0.42
66:SX:59:ALA:HB3	66:SX:89:LYS:HB3	2.01	0.42
67:SY:49:LYS:HA	67:SY:49:LYS:HD2	1.75	0.42
75:St:1102:C:H2'	75:St:1103:G:C8	2.55	0.42
76:u:48:G:C8	76:u:48:G:H5''	2.54	0.42
3:LC:266:GLN:HE21	3:LC:266:GLN:HB2	1.58	0.42
6:LF:288:LYS:HG3	11:LK:202:ARG:HH22	1.83	0.42
15:LO:89:ILE:HG12	44:Lt:1912:A:H4'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LP:22:LYS:HD2	16:LP:22:LYS:HA	1.83	0.42
30:Ld:23:LYS:HB2	30:Ld:23:LYS:HE2	1.58	0.42
32:Lf:60:ILE:HB	44:Lt:664:U:H5'	2.00	0.42
34:Lh:10:PHE:CE2	34:Lh:21:VAL:HG13	2.54	0.42
46:SB:84:THR:HA	75:St:890:G:H4'	2.01	0.42
53:SI:21:TRP:CD1	53:SI:21:TRP:H	2.36	0.42
61:SR:36:LYS:HA	61:SR:36:LYS:HD3	1.51	0.42
66:SX:47:GLU:HG3	66:SX:108:THR:HA	2.02	0.42
75:St:650:G:H2'	75:St:651:G:C8	2.55	0.42
75:St:850:U:H2'	75:St:851:G:H8	1.84	0.42
75:St:1100:C:H2'	75:St:1101:C:C6	2.54	0.42
75:St:1164:G:N3	75:St:1164:G:H2'	2.35	0.42
6:LF:5:LYS:HB2	6:LF:5:LYS:HE3	1.68	0.42
6:LF:245:MET:HE2	6:LF:245:MET:HB2	1.64	0.42
26:LZ:132:ARG:HD3	26:LZ:132:ARG:HA	1.84	0.42
37:Lk:44:MET:HB3	37:Lk:44:MET:HE3	1.55	0.42
44:Lt:245:C:H2'	44:Lt:246:G:C8	2.53	0.42
44:Lt:455:C:C5	44:Lt:456:G:H1'	2.55	0.42
44:Lt:749:C:H2'	44:Lt:750:C:C6	2.54	0.42
49:SE:76:PRO:O	49:SE:77:ARG:C	2.62	0.42
49:SE:154:ILE:HA	49:SE:174:LYS:HE3	2.00	0.42
52:SH:183:ARG:HE	52:SH:183:ARG:HB2	1.43	0.42
75:St:1203:A:H1'	75:St:1239:G:H21	1.85	0.42
75:St:1327:C:H2'	75:St:1328:C:O4'	2.19	0.42
1:LA:165:MET:HB2	1:LA:165:MET:HE2	1.75	0.42
9:LI:111:LEU:HD12	9:LI:111:LEU:HA	1.79	0.42
11:LK:121:LYS:H	11:LK:121:LYS:HG3	1.63	0.42
21:LU:18:LYS:HB2	21:LU:21:ARG:HB2	2.02	0.42
38:LI:27:CYS:HA	38:LI:35:LYS:O	2.20	0.42
44:Lt:745:C:H2'	44:Lt:746:U:C6	2.54	0.42
49:SE:131:LEU:HD23	49:SE:131:LEU:HA	1.78	0.42
49:SE:211:LYS:HB2	49:SE:211:LYS:HE3	1.47	0.42
53:SI:163:GLU:H	53:SI:163:GLU:HG2	1.51	0.42
66:SX:43:SER:HA	66:SX:46:LYS:HG2	2.01	0.42
67:SY:9:LYS:HB3	67:SY:13:GLY:HA2	2.02	0.42
69:Sc:42:HIS:CD2	69:Sc:57:LYS:HG2	2.54	0.42
75:St:394:G:H2'	75:St:395:A:C8	2.55	0.42
75:St:900:U:H2'	75:St:901:A:C8	2.54	0.42
6:LF:288:LYS:HD3	6:LF:288:LYS:HA	1.82	0.42
8:LH:100:LEU:HD22	44:Lt:812:G:H1'	2.01	0.42
13:LM:205:ARG:HD2	13:LM:205:ARG:HA	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:LY:37:LEU:HD22	25:LY:37:LEU:HA	1.73	0.42
31:Le:91:PHE:HA	31:Le:94:LEU:HD12	2.01	0.42
35:Li:35:LYS:HE2	35:Li:35:LYS:HB2	1.85	0.42
44:Lt:2655:C:H2'	44:Lt:2656:C:C6	2.54	0.42
49:SE:79:ASP:HB3	49:SE:82:PHE:HB2	2.00	0.42
52:SH:64:TYR:HA	52:SH:96:VAL:O	2.19	0.42
55:SK:60:LEU:HD23	55:SK:63:LEU:HD12	2.02	0.42
55:SK:153:ASN:O	55:SK:157:VAL:HG23	2.20	0.42
66:SX:36:LEU:HD23	66:SX:36:LEU:HA	1.80	0.42
72:Sg:64:ARG:HA	72:Sg:64:ARG:HD3	1.40	0.42
6:LF:172:LYS:HD3	6:LF:185:MET:HE1	2.02	0.42
10:LJ:132:MET:HE3	10:LJ:132:MET:HB3	1.64	0.42
20:LT:106:GLU:HG2	44:Lt:895:G:H4'	2.02	0.42
37:Lk:67:MET:HE3	37:Lk:67:MET:HB3	1.85	0.42
44:Lt:1850:C:H2'	44:Lt:1851:A:O4'	2.20	0.42
46:SB:142:LEU:HB3	46:SB:143:GLY:H	1.58	0.42
46:SB:161:VAL:HG11	46:SB:208:VAL:HG22	2.01	0.42
46:SB:172:ILE:HD11	46:SB:179:ALA:HA	2.00	0.42
46:SB:227:GLU:HB3	46:SB:228:GLN:H	1.56	0.42
47:SC:196:ASN:HB3	47:SC:199:ILE:HD13	2.01	0.42
48:SD:238:ARG:HD2	48:SD:238:ARG:HA	1.48	0.42
52:SH:121:THR:O	52:SH:125:VAL:HG13	2.20	0.42
54:SJ:90:VAL:HG13	54:SJ:94:LEU:HD12	2.01	0.42
57:SM:22:LEU:HD12	57:SM:22:LEU:HA	1.88	0.42
61:SR:29:LYS:HA	61:SR:29:LYS:HD3	1.40	0.42
66:SX:96:CYS:HB2	66:SX:100:ASP:HB2	2.02	0.42
72:Sg:9:VAL:HG22	72:Sg:47:LYS:HA	2.02	0.42
1:LA:40:SER:HA	1:LA:91:GLY:HA3	2.00	0.42
8:LH:130:THR:HG22	8:LH:220:PHE:HA	2.02	0.42
16:LP:44:PHE:HE1	16:LP:138:VAL:HA	1.85	0.42
32:Lf:47:MET:HE3	32:Lf:47:MET:HB2	1.62	0.42
37:Lk:85:LYS:HA	37:Lk:85:LYS:HD3	1.51	0.42
38:Ll:10:LEU:HD23	38:Ll:10:LEU:HA	1.85	0.42
39:Ln:190:LEU:O	39:Ln:194:LEU:HB2	2.19	0.42
41:Lp:41:TYR:CG	76:u:74:C:H1'	2.55	0.42
44:Lt:2120:A:H2'	44:Lt:2121:A:C8	2.55	0.42
51:SG:239:ILE:O	51:SG:242:PRO:HD2	2.19	0.42
57:SM:150:ARG:HD2	75:St:582:C:H5'	2.01	0.42
58:SO:59:ALA:HB1	58:SO:114:ASP:HB2	2.02	0.42
60:SQ:53:ILE:HA	60:SQ:88:ARG:NH1	2.35	0.42
69:Sc:65:LYS:HD2	69:Sc:65:LYS:HA	1.91	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:St:423:G:H4'	75:St:424:C:H5'	2.01	0.42
3:LC:183:LYS:HA	3:LC:188:ARG:HA	2.02	0.42
6:LF:5:LYS:H	6:LF:5:LYS:HG3	1.56	0.42
6:LF:185:MET:HA	6:LF:188:PHE:CD1	2.55	0.42
18:LR:62:LEU:HD13	18:LR:140:GLY:HA2	2.02	0.42
26:LZ:1:MET:HE2	26:LZ:1:MET:HB2	1.74	0.42
33:Lg:74:MET:HE3	33:Lg:74:MET:HB3	1.40	0.42
38:Ll:14:ILE:HG23	38:Ll:18:ARG:HB3	2.02	0.42
41:Lp:27:LYS:HB3	41:Lp:27:LYS:HE2	1.65	0.42
45:SA:93:LEU:HD13	45:SA:93:LEU:HA	1.84	0.42
48:SD:196:LYS:HA	48:SD:196:LYS:HD3	1.75	0.42
48:SD:201:LEU:HD12	48:SD:201:LEU:HA	1.83	0.42
50:SF:67:ARG:HB3	50:SF:68:ASN:H	1.71	0.42
53:SI:166:PHE:CD2	57:SM:10:TYR:HB2	2.55	0.42
62:ST:136:PRO:O	62:ST:137:ARG:C	2.62	0.42
65:SW:27:LYS:HA	65:SW:27:LYS:HD3	1.30	0.42
75:St:611:G:N3	75:St:611:G:H2'	2.35	0.42
1:LA:205:ASN:HB3	1:LA:206:PRO:HD2	2.01	0.41
2:LB:316:ARG:O	2:LB:317:VAL:C	2.63	0.41
3:LC:206:ARG:HA	3:LC:209:ARG:HD3	2.02	0.41
17:LQ:79:LYS:HE2	17:LQ:79:LYS:HB2	1.82	0.41
18:LR:54:LEU:HD22	44:Lt:692:C:H5''	2.02	0.41
20:LT:47:LYS:HB3	20:LT:47:LYS:HE2	1.86	0.41
39:Ln:196:LYS:H	39:Ln:200:ASN:HD22	1.68	0.41
44:Lt:2082:G:H5'	44:Lt:2178:G:H1'	2.01	0.41
46:SB:105:ILE:HG21	46:SB:212:LEU:HD12	2.02	0.41
49:SE:98:THR:O	49:SE:113:PRO:HA	2.20	0.41
52:SH:8:LYS:HE2	52:SH:8:LYS:HB2	1.33	0.41
52:SH:76:ASN:HD22	52:SH:80:LEU:HD22	1.84	0.41
59:SP:13:ARG:HH22	75:St:617:A:H3'	1.86	0.41
64:SV:51:ILE:HG12	64:SV:64:GLU:HB3	2.01	0.41
75:St:515:G:H2'	75:St:516:C:O4'	2.20	0.41
3:LC:72:LEU:HD21	44:Lt:1126:U:H5'	2.02	0.41
3:LC:286:ARG:HE	3:LC:286:ARG:HB3	1.44	0.41
6:LF:227:LYS:HB2	6:LF:227:LYS:HE2	1.63	0.41
7:LG:4:ASN:HB3	44:Lt:1261:A:C4	2.56	0.41
10:LJ:106:LYS:HD2	10:LJ:106:LYS:HA	1.48	0.41
17:LQ:85:LYS:HB2	44:Lt:1841:G:H5''	2.02	0.41
27:La:12:CYS:HA	27:La:81:THR:HG23	2.01	0.41
44:Lt:84:C:H42	44:Lt:98:C:H5	1.68	0.41
44:Lt:2260:G:N2	44:Lt:2273:G:H2'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:SA:151:SER:HB3	45:SA:162:ILE:HG21	2.02	0.41
53:SI:38:LEU:CD2	53:SI:89:GLN:HA	2.50	0.41
54:SJ:66:ILE:HG23	54:SJ:68:ARG:HB2	2.01	0.41
58:SO:140:LYS:HE2	58:SO:140:LYS:HB2	1.94	0.41
60:SQ:131:ASP:HB2	70:Sd:44:ILE:HD11	2.02	0.41
75:St:191:C:H2'	75:St:192:G:C8	2.54	0.41
75:St:1155:C:H2'	75:St:1156:C:C6	2.56	0.41
3:LC:210:ASN:HD22	44:Lt:176:C:H6	1.67	0.41
8:LH:84:ILE:HG21	8:LH:130:THR:HG23	2.02	0.41
13:LM:184:ILE:HG13	28:Lb:82:ILE:HA	2.01	0.41
19:LS:10:LEU:HD22	19:LS:38:ARG:HG3	2.02	0.41
22:LV:13:GLN:HE21	22:LV:73:GLU:HB2	1.84	0.41
23:LW:66:VAL:HG21	23:LW:74:LEU:HB2	2.01	0.41
27:La:49:ARG:HD3	27:La:49:ARG:HA	1.86	0.41
32:Lf:9:LEU:HD13	32:Lf:9:LEU:HA	1.87	0.41
33:Lg:67:ARG:HD3	33:Lg:76:ARG:HD2	2.02	0.41
43:Ls:114:ARG:HE	43:Ls:114:ARG:HB3	1.13	0.41
44:Lt:51:C:H2'	44:Lt:52:G:C8	2.55	0.41
49:SE:35:PRO:HD2	49:SE:83:PRO:HG2	2.03	0.41
49:SE:200:LYS:HE3	49:SE:200:LYS:HB3	1.82	0.41
54:SJ:55:ASN:C	54:SJ:57:ARG:H	2.28	0.41
62:ST:72:ILE:HD11	62:ST:127:TYR:CG	2.55	0.41
77:v:25:G:H1	77:v:43:A:H2	1.67	0.41
77:v:26:C:H2'	77:v:27:U:C6	2.55	0.41
9:LI:91:LEU:HD23	9:LI:91:LEU:HA	1.90	0.41
11:LK:22:PHE:CZ	44:Lt:761:A:H2'	2.56	0.41
16:LP:37:LYS:HA	16:LP:37:LYS:HD2	1.82	0.41
22:LV:32:LEU:HD12	22:LV:32:LEU:HA	1.83	0.41
34:Lh:31:LEU:HD23	34:Lh:31:LEU:HA	1.79	0.41
36:Lj:19:ARG:HD2	36:Lj:19:ARG:HA	1.50	0.41
44:Lt:2346:U:H2'	44:Lt:2347:U:C6	2.54	0.41
46:SB:78:MET:HE3	46:SB:78:MET:HB3	1.63	0.41
47:SC:159:LYS:HE3	47:SC:159:LYS:HB3	1.60	0.41
50:SF:114:ILE:HG13	50:SF:123:GLN:HB2	2.03	0.41
50:SF:125:VAL:HG22	72:Sg:42:ILE:HG22	2.01	0.41
55:SK:47:ARG:HG2	55:SK:102:ILE:HG21	2.02	0.41
55:SK:143:ASN:H	75:St:546:U:H5	1.68	0.41
58:SO:130:LEU:HA	58:SO:130:LEU:HD12	1.66	0.41
63:SU:47:LYS:HA	63:SU:50:ARG:HD3	2.01	0.41
68:Sb:79:MET:HE3	68:Sb:79:MET:HB3	1.72	0.41
69:Sc:47:GLU:H	69:Sc:47:GLU:HG3	1.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:Sj:49:HIS:HA	74:Sj:53:ARG:HA	2.02	0.41
75:St:191:C:H2'	75:St:192:G:H8	1.86	0.41
75:St:1222:C:H2'	75:St:1223:C:C6	2.55	0.41
75:St:1229:C:H6	75:St:1229:C:H2'	1.72	0.41
2:LB:363:GLY:HA2	44:Lt:2503:C:H5''	2.03	0.41
6:LF:58:LYS:HB3	6:LF:58:LYS:HE3	1.47	0.41
8:LH:154:GLN:HE22	44:Lt:1043:G:H21	1.69	0.41
9:LI:167:LEU:HD23	9:LI:167:LEU:HA	1.84	0.41
13:LM:115:SER:HB3	13:LM:118:LYS:HE3	2.03	0.41
17:LQ:6:PHE:CE2	17:LQ:8:SER:HB3	2.56	0.41
25:LY:138:MET:HE2	25:LY:138:MET:HB2	1.81	0.41
26:LZ:111:MET:O	26:LZ:115:ARG:HB3	2.21	0.41
32:Lf:92:MET:HE3	32:Lf:92:MET:HB3	1.61	0.41
39:Ln:35:GLN:HG2	39:Ln:166:ASN:HB3	2.03	0.41
40:Lo:16:LYS:HB3	40:Lo:16:LYS:HE2	1.85	0.41
44:Lt:2065:G:H5''	44:Lt:2065:G:H8	1.86	0.41
49:SE:9:LEU:HD23	49:SE:9:LEU:HA	1.77	0.41
51:SG:170:ILE:H	51:SG:170:ILE:HG13	1.40	0.41
53:SI:113:ILE:O	53:SI:139:HIS:HA	2.21	0.41
75:St:80:A:H3'	75:St:81:C:H6	1.86	0.41
75:St:1312:C:H2'	75:St:1313:C:C6	2.56	0.41
16:LP:42:GLY:N	16:LP:130:ARG:HH12	2.17	0.41
16:LP:128:PRO:O	16:LP:129:GLU:HB2	2.21	0.41
16:LP:171:ILE:HD13	16:LP:171:ILE:HA	1.89	0.41
19:LS:145:MET:O	19:LS:149:GLN:HG2	2.20	0.41
31:Le:70:VAL:HG22	31:Le:83:VAL:HG13	2.02	0.41
38:Ll:6:THR:O	38:Ll:7:GLU:C	2.64	0.41
39:Ln:30:GLU:OE1	39:Ln:209:THR:HG22	2.19	0.41
48:SD:126:ASP:HA	48:SD:136:ARG:HA	2.03	0.41
50:SF:10:LYS:HD2	50:SF:10:LYS:HA	1.59	0.41
51:SG:41:GLU:HB3	51:SG:120:VAL:HG21	2.03	0.41
51:SG:138:ARG:H	51:SG:138:ARG:HG2	1.57	0.41
54:SJ:41:MET:HB2	54:SJ:47:ILE:HG12	2.03	0.41
57:SM:28:ARG:HD3	57:SM:28:ARG:HA	1.41	0.41
58:SO:28:ARG:O	58:SO:32:LEU:HB2	2.21	0.41
62:ST:70:ILE:HA	62:ST:78:PHE:CE1	2.56	0.41
64:SV:85:LEU:HA	64:SV:85:LEU:HD12	1.86	0.41
65:SW:55:ALA:HA	65:SW:58:VAL:HG22	2.03	0.41
75:St:329:A:H3'	75:St:330:A:C8	2.54	0.41
10:LJ:25:THR:HG23	10:LJ:34:VAL:HG22	2.01	0.41
11:LK:57:LYS:HE2	11:LK:57:LYS:HB3	1.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LN:71:GLU:H	14:LN:71:GLU:HG3	1.58	0.41
16:LP:107:PRO:HB2	16:LP:108:CYS:H	1.37	0.41
16:LP:144:TRP:HH2	16:LP:150:VAL:HG21	1.84	0.41
19:LS:153:LYS:HA	19:LS:153:LYS:HD3	1.68	0.41
33:Lg:19:ARG:HB3	33:Lg:24:GLN:HG3	2.01	0.41
39:Ln:82:LEU:H	39:Ln:82:LEU:HG	1.66	0.41
39:Ln:202:LYS:HE3	39:Ln:202:LYS:HB3	1.43	0.41
44:Lt:1866:C:H2'	44:Lt:1867:G:H8	1.85	0.41
45:SA:125:ARG:HG2	46:SB:236:ARG:HG3	2.03	0.41
53:SI:113:ILE:HG13	53:SI:140:ILE:HB	2.03	0.41
57:SM:74:HIS:HB2	57:SM:85:ARG:HB2	2.03	0.41
60:SQ:44:VAL:HG11	60:SQ:85:ILE:CG2	2.49	0.41
60:SQ:149:ARG:HH21	75:St:657:U:H5''	1.85	0.41
62:ST:77:LEU:HD13	62:ST:77:LEU:HA	1.78	0.41
62:ST:137:ARG:HG2	75:St:1272:G:H5''	2.03	0.41
64:SV:75:PRO:HB2	64:SV:85:LEU:HD11	2.02	0.41
68:Sb:36:LYS:HB2	68:Sb:36:LYS:HE2	1.57	0.41
1:LA:229:ALA:HB3	1:LA:234:LYS:HE2	2.03	0.41
3:LC:94:PRO:HD2	44:Lt:517:G:H1	1.86	0.41
6:LF:154:LEU:HB3	44:Lt:2170:A:H2	1.86	0.41
8:LH:84:ILE:HG12	8:LH:130:THR:HG23	2.03	0.41
10:LJ:11:VAL:HG21	10:LJ:46:HIS:CE1	2.55	0.41
12:LL:37:LEU:HD23	12:LL:37:LEU:HA	1.86	0.41
23:LW:21:LEU:HD13	23:LW:27:ILE:HG21	2.02	0.41
24:LX:24:ARG:HE	24:LX:24:ARG:HB2	1.66	0.41
24:LX:51:ARG:HD2	44:Lt:2642:U:H2'	2.03	0.41
31:Le:72:LEU:HD23	31:Le:72:LEU:HA	1.70	0.41
43:Ls:110:CYS:SG	43:Ls:113:CYS:N	2.78	0.41
44:Lt:1630:A:H8	44:Lt:2398:A:C2	2.38	0.41
45:SA:206:LEU:HD13	45:SA:206:LEU:HA	1.74	0.41
47:SC:172:ILE:H	47:SC:172:ILE:HG13	1.52	0.41
52:SH:36:LEU:HG	52:SH:79:ALA:HB3	2.01	0.41
52:SH:142:LYS:HB3	52:SH:154:LEU:HD11	2.03	0.41
58:SO:54:LYS:HA	58:SO:70:VAL:HG12	2.03	0.41
68:Sb:103:VAL:HB	68:Sb:107:GLN:HB3	2.02	0.41
75:St:251:C:H2'	75:St:252:G:H8	1.85	0.41
11:LK:27:PRO:HG2	11:LK:124:GLY:HA2	2.03	0.41
12:LL:40:LEU:HG	12:LL:114:ILE:HD11	2.03	0.41
12:LL:104:PHE:HB2	12:LL:105:GLY:H	1.72	0.41
12:LL:108:GLU:HG2	12:LL:122:ILE:HG13	2.03	0.41
12:LL:120:MET:HE2	12:LL:120:MET:HB2	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LN:100:LEU:HA	14:LN:100:LEU:HD12	1.80	0.41
17:LQ:35:ILE:O	17:LQ:38:MET:HB2	2.21	0.41
17:LQ:133:HIS:HA	44:Lt:600:G:H5'	2.03	0.41
19:LS:61:GLY:HA3	44:Lt:1355:G:H5''	2.02	0.41
20:LT:134:GLU:O	20:LT:138:MET:HG2	2.21	0.41
27:La:73:MET:HE2	27:La:73:MET:HB2	1.79	0.41
27:La:87:ASN:HD22	27:La:118:ARG:HH21	1.69	0.41
42:Lq:67:GLY:HA3	42:Lq:73:THR:HG23	2.02	0.41
44:Lt:1362:A:N6	44:Lt:1413:G:H2'	2.36	0.41
44:Lt:1911:C:H2'	44:Lt:1912:A:C8	2.56	0.41
45:SA:15:LEU:HD12	45:SA:20:VAL:HG21	2.01	0.41
45:SA:150:ILE:HG12	45:SA:164:VAL:HG23	2.03	0.41
45:SA:169:ASN:C	45:SA:171:LYS:H	2.29	0.41
47:SC:72:LEU:HD11	47:SC:92:ILE:HB	2.02	0.41
47:SC:119:MET:HE3	47:SC:119:MET:HB2	1.86	0.41
47:SC:133:MET:HE3	47:SC:133:MET:HB3	1.80	0.41
48:SD:83:LYS:HE3	48:SD:83:LYS:HB3	1.33	0.41
51:SG:169:LEU:H	51:SG:169:LEU:HG	1.80	0.41
51:SG:189:PRO:HB3	75:St:63:C:C4	2.56	0.41
52:SH:14:GLU:HB3	52:SH:15:LYS:H	1.67	0.41
55:SK:76:ALA:HB1	55:SK:80:ARG:NH2	2.33	0.41
55:SK:110:LEU:HD22	55:SK:110:LEU:HA	1.76	0.41
60:SQ:53:ILE:HG21	60:SQ:90:ILE:HD13	2.02	0.41
62:ST:47:ILE:HG23	62:ST:83:MET:HB2	2.03	0.41
64:SV:40:ARG:HB2	64:SV:86:ASN:HB2	2.02	0.41
70:Sd:11:SER:H	70:Sd:33:ASP:HB2	1.86	0.41
75:St:209:C:H2'	75:St:210:G:C8	2.56	0.41
77:v:64:C:H2'	77:v:65:C:C6	2.56	0.41
2:LB:255:TRP:CD1	44:Lt:1883:G:H5''	2.56	0.41
3:LC:264:ILE:H	3:LC:264:ILE:HG13	1.61	0.41
8:LH:135:THR:HG23	8:LH:138:THR:H	1.86	0.41
8:LH:170:LYS:H	8:LH:170:LYS:HG2	1.42	0.41
10:LJ:5:SER:HB3	10:LJ:66:PRO:HG3	2.03	0.41
11:LK:60:VAL:HG13	11:LK:160:PRO:HD2	2.03	0.41
16:LP:187:ARG:O	16:LP:191:GLU:HG2	2.21	0.41
35:Li:151:LYS:HD2	35:Li:151:LYS:HA	1.72	0.41
44:Lt:119:A:C2	44:Lt:129:U:H5	2.39	0.41
44:Lt:1109:G:H2'	44:Lt:1110:G:C8	2.56	0.41
44:Lt:2043:G:H1	77:v:74:C:N4	2.18	0.41
48:SD:204:ILE:H	48:SD:204:ILE:HG13	1.52	0.41
55:SK:12:THR:HB	55:SK:45:ARG:HD3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:SO:94:ILE:HG12	58:SO:125:VAL:HG21	2.03	0.41
59:SP:136:PRO:HG2	59:SP:139:PHE:HB2	2.03	0.41
67:SY:21:PRO:HB2	67:SY:30:LEU:HB3	2.03	0.41
70:Sd:91:ASP:HA	70:Sd:94:ILE:HG13	2.03	0.41
73:Sh:113:ARG:H	73:Sh:113:ARG:HG3	1.39	0.41
75:St:965:C:H2'	75:St:966:G:C8	2.56	0.41
76:u:11:C:H2'	76:u:12:G:H8	1.85	0.41
1:LA:210:PRO:HD2	1:LA:235:VAL:HG11	2.03	0.40
13:LM:48:PRO:HB3	15:LO:193:LYS:HD2	2.04	0.40
21:LU:156:ASP:HB3	21:LU:157:GLY:H	1.61	0.40
24:LX:2:PRO:HG2	24:LX:16:PRO:HG2	2.03	0.40
28:Lb:15:ARG:HB3	28:Lb:16:GLN:H	1.67	0.40
39:Ln:19:ARG:HE	39:Ln:19:ARG:HB3	1.65	0.40
39:Ln:187:LEU:HB3	39:Ln:198:TRP:CZ3	2.53	0.40
44:Lt:588:U:H2'	44:Lt:589:G:C8	2.56	0.40
51:SG:36:LEU:HD23	51:SG:36:LEU:HA	1.78	0.40
52:SH:44:LEU:HD12	52:SH:44:LEU:HA	1.80	0.40
53:SI:101:ARG:HE	53:SI:101:ARG:HB3	1.60	0.40
59:SP:91:MET:HE2	59:SP:91:MET:HB2	1.59	0.40
59:SP:115:LEU:HA	59:SP:118:VAL:HG22	2.02	0.40
67:SY:81:GLN:HE21	67:SY:81:GLN:HB2	1.65	0.40
68:Sb:104:SER:C	68:Sb:106:LYS:N	2.79	0.40
71:Se:59:LYS:HB2	71:Se:59:LYS:HE2	1.83	0.40
75:St:85:U:H2'	75:St:86:C:C6	2.56	0.40
75:St:216:G:H2'	75:St:217:C:O4'	2.21	0.40
75:St:590:G:H2'	75:St:591:C:H6	1.82	0.40
75:St:1311:C:H2'	75:St:1312:C:C6	2.56	0.40
75:St:1332:C:H2'	75:St:1333:G:H8	1.86	0.40
76:u:11:C:H2'	76:u:12:G:C8	2.56	0.40
1:LA:58:LEU:HD23	1:LA:58:LEU:HA	1.88	0.40
5:LE:30:U:H3	5:LE:48:G:H1	1.68	0.40
6:LF:95:TYR:CZ	6:LF:169:ALA:HB2	2.57	0.40
14:LN:39:ASP:HB2	14:LN:47:ARG:HG3	2.02	0.40
16:LP:181:LYS:HB3	16:LP:182:ASP:H	1.53	0.40
41:Lp:6:ALA:HB2	41:Lp:92:SER:O	2.21	0.40
41:Lp:12:CYS:SG	41:Lp:15:GLU:HG2	2.60	0.40
41:Lp:76:LYS:HD3	41:Lp:76:LYS:HA	1.98	0.40
44:Lt:760:A:H2'	44:Lt:761:A:C8	2.57	0.40
44:Lt:1245:C:H2'	44:Lt:1248:G:C8	2.56	0.40
45:SA:38:ARG:HB3	45:SA:159:LEU:HD12	2.03	0.40
47:SC:199:ILE:C	47:SC:201:GLY:H	2.29	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:SE:100:ARG:HB3	49:SE:102:LEU:HD23	2.04	0.40
49:SE:182:MET:HE2	49:SE:182:MET:HB3	1.89	0.40
49:SE:260:LYS:HE2	49:SE:260:LYS:HB2	1.92	0.40
55:SK:78:LEU:HD13	55:SK:78:LEU:HA	1.73	0.40
57:SM:55:LYS:HB2	57:SM:108:HIS:CE1	2.57	0.40
57:SM:78:MET:HB2	57:SM:81:SER:HB2	2.03	0.40
57:SM:150:ARG:O	57:SM:151:PHE:C	2.64	0.40
72:Sg:38:ILE:HB	72:Sg:60:ALA:HB3	2.03	0.40
75:St:1196:G:H2'	75:St:1197:C:C6	2.56	0.40
75:St:1316:U:H2'	75:St:1317:G:C8	2.56	0.40
76:u:19:A:C5	76:u:20:A:H1'	2.56	0.40
77:v:17:G:H4'	77:v:59:A:C2	2.56	0.40
6:LF:142:ASN:HD22	6:LF:142:ASN:HA	1.70	0.40
11:LK:191:GLN:H	11:LK:191:GLN:HG3	1.66	0.40
18:LR:66:ARG:HH21	18:LR:70:LEU:HD21	1.86	0.40
39:Ln:48:ARG:H	39:Ln:48:ARG:HG2	1.33	0.40
39:Ln:67:VAL:HG13	39:Ln:111:LEU:HB3	2.03	0.40
39:Ln:72:ARG:HH22	39:Ln:143:ASP:HA	1.86	0.40
41:Lp:22:LYS:HE2	41:Lp:22:LYS:HB3	1.58	0.40
44:Lt:645:C:H2'	44:Lt:646:G:C8	2.57	0.40
50:SF:114:ILE:HA	72:Sg:22:ILE:HD13	2.03	0.40
51:SG:65:GLN:HE22	75:St:140:A:H62	1.68	0.40
63:SU:32:ASN:HD22	63:SU:57:VAL:HG13	1.86	0.40
75:St:1296:C:H2'	75:St:1297:C:C6	2.55	0.40
77:v:31:C:H2'	77:v:32:C:C6	2.57	0.40
6:LF:90:VAL:HG21	6:LF:232:TYR:HA	2.04	0.40
9:LI:51:LEU:HD12	9:LI:51:LEU:HA	1.80	0.40
13:LM:29:MET:HB2	44:Lt:822:C:OP1	2.20	0.40
14:LN:30:ILE:HG21	20:LT:146:PHE:HE1	1.85	0.40
30:Ld:53:PRO:HB2	30:Ld:56:VAL:HG13	2.02	0.40
36:Lj:8:LEU:HD23	36:Lj:8:LEU:HA	1.96	0.40
36:Lj:63:LEU:HD11	36:Lj:77:LYS:HG3	2.03	0.40
39:Ln:101:LYS:HZ3	39:Ln:101:LYS:HG3	1.77	0.40
44:Lt:1745:C:H6	44:Lt:1745:C:H2'	1.61	0.40
44:Lt:1964:C:OP1	44:Lt:1964:C:C4'	2.70	0.40
48:SD:139:VAL:HG13	48:SD:212:ILE:HG12	2.03	0.40
48:SD:156:VAL:HG23	48:SD:161:ILE:HG13	2.03	0.40
49:SE:68:LYS:HD2	49:SE:68:LYS:HA	1.43	0.40
49:SE:122:LYS:HB2	49:SE:164:LEU:HD11	2.02	0.40
68:Sb:14:ASN:HB2	68:Sb:19:ARG:HG3	2.04	0.40
21:LU:135:LEU:HD23	21:LU:135:LEU:HA	1.91	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LZ:120:LYS:HE3	26:LZ:120:LYS:HB3	1.47	0.40
32:Lf:120:MET:HE2	32:Lf:120:MET:HB2	1.61	0.40
39:Ln:34:LEU:HD11	39:Ln:206:ILE:HG12	2.04	0.40
43:Ls:116:THR:HG22	43:Ls:118:LEU:H	1.87	0.40
44:Lt:2022:C:H2'	44:Lt:2023:C:C6	2.56	0.40
44:Lt:2664:G:H2'	44:Lt:2665:C:C6	2.56	0.40
45:SA:38:ARG:HB2	45:SA:39:MET:HE2	2.02	0.40
45:SA:73:ILE:HG23	45:SA:125:ARG:HD3	2.04	0.40
48:SD:35:HIS:CD2	48:SD:35:HIS:H	2.39	0.40
48:SD:113:LEU:HB3	48:SD:142:PHE:CE1	2.57	0.40
49:SE:7:LYS:HA	49:SE:7:LYS:HD2	1.69	0.40
49:SE:65:LEU:H	49:SE:65:LEU:HG	1.58	0.40
50:SF:106:GLY:HA2	50:SF:107:PRO:HD3	1.88	0.40
51:SG:146:LYS:O	51:SG:150:LEU:HB2	2.21	0.40
51:SG:184:LYS:HB2	51:SG:184:LYS:HE2	1.66	0.40
55:SK:79:ARG:HA	55:SK:82:HIS:NE2	2.36	0.40
59:SP:91:MET:SD	59:SP:121:ARG:HB3	2.60	0.40
60:SQ:149:ARG:HH11	60:SQ:151:LEU:HD22	1.85	0.40
63:SU:47:LYS:HB3	63:SU:47:LYS:HE2	1.95	0.40
75:St:425:A:H61	75:St:473:G:H2'	1.86	0.40
75:St:1214:A:H2'	75:St:1215:G:C8	2.57	0.40
77:v:21:G:H2'	77:v:22:C:C6	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	LA	245/251 (98%)	234 (96%)	10 (4%)	1 (0%)	30	59
2	LB	376/379 (99%)	358 (95%)	16 (4%)	2 (0%)	24	55
3	LC	308/316 (98%)	298 (97%)	10 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	LF	291/297 (98%)	276 (95%)	12 (4%)	3 (1%)	12	40
7	LG	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
8	LH	210/235 (89%)	201 (96%)	6 (3%)	3 (1%)	9	33
9	LI	182/225 (81%)	171 (94%)	9 (5%)	2 (1%)	11	38
10	LJ	182/185 (98%)	168 (92%)	11 (6%)	3 (2%)	7	30
11	LK	191/210 (91%)	180 (94%)	11 (6%)	0	100	100
12	LL	164/173 (95%)	157 (96%)	7 (4%)	0	100	100
13	LM	198/234 (85%)	187 (94%)	8 (4%)	3 (2%)	8	32
14	LN	128/131 (98%)	121 (94%)	7 (6%)	0	100	100
15	LO	201/204 (98%)	193 (96%)	7 (4%)	1 (0%)	24	55
16	LP	192/197 (98%)	182 (95%)	6 (3%)	4 (2%)	5	25
17	LQ	153/164 (93%)	146 (95%)	7 (5%)	0	100	100
18	LR	176/179 (98%)	168 (96%)	8 (4%)	0	100	100
19	LS	159/196 (81%)	158 (99%)	1 (1%)	0	100	100
20	LT	168/173 (97%)	164 (98%)	3 (2%)	1 (1%)	21	51
21	LU	154/159 (97%)	140 (91%)	12 (8%)	2 (1%)	9	34
22	LV	101/124 (82%)	92 (91%)	8 (8%)	1 (1%)	12	40
23	LW	131/142 (92%)	125 (95%)	6 (5%)	0	100	100
24	LX	61/189 (32%)	60 (98%)	0	1 (2%)	7	30
25	LY	113/141 (80%)	105 (93%)	6 (5%)	2 (2%)	6	29
26	LZ	131/135 (97%)	123 (94%)	8 (6%)	0	100	100
27	La	122/135 (90%)	110 (90%)	10 (8%)	2 (2%)	7	30
28	Lb	146/149 (98%)	135 (92%)	9 (6%)	2 (1%)	9	33
29	Lc	53/62 (86%)	49 (92%)	3 (6%)	1 (2%)	6	28
30	Ld	96/109 (88%)	91 (95%)	3 (3%)	2 (2%)	5	25
31	Le	98/106 (92%)	91 (93%)	7 (7%)	0	100	100
32	Lf	128/136 (94%)	119 (93%)	9 (7%)	0	100	100
33	Lg	96/123 (78%)	92 (96%)	4 (4%)	0	100	100
34	Lh	99/120 (82%)	90 (91%)	6 (6%)	3 (3%)	3	19
35	Li	120/124 (97%)	114 (95%)	6 (5%)	0	100	100
36	Lj	87/90 (97%)	78 (90%)	7 (8%)	2 (2%)	5	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	Lk	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
38	Ll	70/77 (91%)	63 (90%)	7 (10%)	0	100	100
39	Ln	194/217 (89%)	176 (91%)	13 (7%)	5 (3%)	4	21
40	Lo	23/25 (92%)	23 (100%)	0	0	100	100
41	Lp	91/106 (86%)	90 (99%)	1 (1%)	0	100	100
42	Lq	89/94 (95%)	82 (92%)	7 (8%)	0	100	100
43	Ls	45/127 (35%)	40 (89%)	2 (4%)	3 (7%)	1	6
45	SA	195/245 (80%)	183 (94%)	9 (5%)	3 (2%)	8	32
46	SB	214/242 (88%)	203 (95%)	6 (3%)	5 (2%)	5	24
47	SC	204/217 (94%)	191 (94%)	10 (5%)	3 (2%)	8	32
48	SD	227/248 (92%)	218 (96%)	8 (4%)	1 (0%)	30	59
49	SE	253/268 (94%)	233 (92%)	19 (8%)	1 (0%)	30	59
50	SF	175/190 (92%)	165 (94%)	8 (5%)	2 (1%)	11	38
51	SG	236/248 (95%)	221 (94%)	13 (6%)	2 (1%)	16	44
52	SH	173/190 (91%)	165 (95%)	6 (4%)	2 (1%)	10	36
53	SI	164/174 (94%)	153 (93%)	8 (5%)	3 (2%)	6	29
54	SJ	127/130 (98%)	118 (93%)	7 (6%)	2 (2%)	7	30
55	SK	174/189 (92%)	167 (96%)	4 (2%)	3 (2%)	7	29
56	SL	95/134 (71%)	90 (95%)	5 (5%)	0	100	100
57	SM	150/154 (97%)	133 (89%)	17 (11%)	0	100	100
58	SO	138/144 (96%)	133 (96%)	4 (3%)	1 (1%)	18	48
59	SP	148/154 (96%)	139 (94%)	8 (5%)	1 (1%)	18	48
60	SQ	124/145 (86%)	110 (89%)	11 (9%)	3 (2%)	4	23
61	SR	109/145 (75%)	102 (94%)	5 (5%)	2 (2%)	6	29
62	ST	149/158 (94%)	142 (95%)	6 (4%)	1 (1%)	18	48
63	SU	119/137 (87%)	111 (93%)	5 (4%)	3 (2%)	4	22
64	SV	125/154 (81%)	107 (86%)	16 (13%)	2 (2%)	7	30
65	SW	136/139 (98%)	127 (93%)	9 (7%)	0	100	100
66	SX	96/126 (76%)	95 (99%)	1 (1%)	0	100	100
67	SY	84/89 (94%)	77 (92%)	7 (8%)	0	100	100
68	Sb	114/132 (86%)	103 (90%)	9 (8%)	2 (2%)	6	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	Sc	72/88 (82%)	69 (96%)	3 (4%)	0	100	100
70	Sd	95/109 (87%)	91 (96%)	3 (3%)	1 (1%)	11	38
71	Se	77/81 (95%)	74 (96%)	3 (4%)	0	100	100
72	Sg	60/64 (94%)	52 (87%)	7 (12%)	1 (2%)	7	29
73	Sh	47/51 (92%)	46 (98%)	1 (2%)	0	100	100
74	Sj	65/69 (94%)	60 (92%)	4 (6%)	1 (2%)	8	32
All	All	10051/11193 (90%)	9452 (94%)	505 (5%)	94 (1%)	16	42

All (94) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	LA	15	VAL
2	LB	303	LYS
16	LP	181	LYS
29	Lc	50	ASP
34	Lh	6	VAL
36	Lj	27	LYS
39	Ln	117	ILE
39	Ln	126	PRO
43	Ls	98	HIS
6	LF	122	LEU
8	LH	208	LYS
9	LI	184	VAL
16	LP	107	PRO
21	LU	145	ALA
24	LX	49	LYS
28	Lb	16	GLN
39	Ln	47	PRO
43	Ls	121	LYS
46	SB	227	GLU
47	SC	202	ALA
51	SG	132	ASP
53	SI	40	VAL
54	SJ	59	ASN
55	SK	164	SER
58	SO	4	THR
59	SP	3	ARG
61	SR	76	VAL
62	ST	137	ARG
63	SU	46	SER

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Mol	Chain	Res	Type
64	SV	56	ARG
6	LF	271	ARG
15	LO	185	ARG
16	LP	106	PRO
27	La	48	PRO
30	Ld	102	ALA
34	Lh	41	ASN
34	Lh	64	THR
39	Ln	25	PRO
46	SB	76	ASN
46	SB	228	GLN
2	LB	55	HIS
6	LF	208	LYS
8	LH	27	GLU
8	LH	213	ASN
9	LI	53	VAL
10	LJ	21	LYS
13	LM	49	ASN
13	LM	91	SER
25	LY	54	SER
45	SA	109	ILE
49	SE	157	ASN
50	SF	38	SER
52	SH	115	ARG
53	SI	87	ILE
53	SI	92	TYR
60	SQ	38	ASN
63	SU	99	ILE
64	SV	101	VAL
68	Sb	8	VAL
72	Sg	53	LEU
10	LJ	137	LYS
13	LM	158	GLN
16	LP	131	ARG
20	LT	4	LYS
25	LY	43	PRO
27	La	49	ARG
28	Lb	124	ILE
39	Ln	83	ASN
45	SA	196	ARG
46	SB	134	ARG
46	SB	139	GLY

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Mol	Chain	Res	Type
47	SC	52	ILE
54	SJ	96	SER
55	SK	2	ARG
60	SQ	149	ARG
63	SU	100	THR
10	LJ	54	ALA
21	LU	140	HIS
30	Ld	77	SER
43	Ls	93	MET
45	SA	194	ILE
74	Sj	44	ASP
47	SC	210	ILE
55	SK	171	PRO
61	SR	75	ILE
68	Sb	103	VAL
52	SH	107	VAL
22	LV	94	VAL
36	Lj	71	GLY
48	SD	18	ASN
50	SF	35	VAL
51	SG	153	LEU
60	SQ	126	ILE
70	Sd	96	THR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	LA	188/192 (98%)	145 (77%)	43 (23%)	1	4
2	LB	312/313 (100%)	221 (71%)	91 (29%)	0	1
3	LC	257/263 (98%)	191 (74%)	66 (26%)	0	2
6	LF	238/242 (98%)	162 (68%)	76 (32%)	0	1
7	LG	47/48 (98%)	32 (68%)	15 (32%)	0	1
8	LH	183/204 (90%)	134 (73%)	49 (27%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
9	LI	164/198 (83%)	114 (70%)	50 (30%)	0	1	
10	LJ	163/164 (99%)	111 (68%)	52 (32%)	0	1	
11	LK	165/177 (93%)	115 (70%)	50 (30%)	0	1	
12	LL	142/149 (95%)	93 (66%)	49 (34%)	0	0	
13	LM	169/197 (86%)	128 (76%)	41 (24%)	1	3	
14	LN	110/111 (99%)	82 (74%)	28 (26%)	0	2	
15	LO	174/175 (99%)	128 (74%)	46 (26%)	0	2	
16	LP	162/165 (98%)	124 (76%)	38 (24%)	1	3	
17	LQ	132/139 (95%)	91 (69%)	41 (31%)	0	1	
18	LR	154/155 (99%)	107 (70%)	47 (30%)	0	1	
19	LS	139/167 (83%)	102 (73%)	37 (27%)	0	2	
20	LT	151/154 (98%)	95 (63%)	56 (37%)	0	0	
21	LU	130/133 (98%)	91 (70%)	39 (30%)	0	1	
22	LV	91/110 (83%)	58 (64%)	33 (36%)	0	0	
23	LW	108/114 (95%)	76 (70%)	32 (30%)	0	1	
24	LX	61/174 (35%)	42 (69%)	19 (31%)	0	1	
25	LY	104/123 (85%)	84 (81%)	20 (19%)	1	6	
26	LZ	114/115 (99%)	79 (69%)	35 (31%)	0	1	
27	La	111/119 (93%)	76 (68%)	35 (32%)	0	1	
28	Lb	126/127 (99%)	97 (77%)	29 (23%)	1	3	
29	Lc	50/57 (88%)	36 (72%)	14 (28%)	0	1	
30	Ld	86/92 (94%)	59 (69%)	27 (31%)	0	1	
31	Le	88/92 (96%)	68 (77%)	20 (23%)	1	4	
32	Lf	116/120 (97%)	79 (68%)	37 (32%)	0	1	
33	Lg	82/103 (80%)	62 (76%)	20 (24%)	1	3	
34	Lh	89/100 (89%)	67 (75%)	22 (25%)	1	3	
35	Li	105/107 (98%)	81 (77%)	24 (23%)	1	4	
36	Lj	77/78 (99%)	46 (60%)	31 (40%)	0	0	
37	Lk	73/74 (99%)	55 (75%)	18 (25%)	1	3	
38	Ll	63/68 (93%)	33 (52%)	30 (48%)	0	0	
39	Ln	173/189 (92%)	85 (49%)	88 (51%)	0	0	

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
40	Lo	22/22 (100%)	15 (68%)	7 (32%)	0	1	
41	Lp	83/93 (89%)	61 (74%)	22 (26%)	0	2	
42	Lq	71/73 (97%)	39 (55%)	32 (45%)	0	0	
43	Ls	43/110 (39%)	27 (63%)	16 (37%)	0	0	
45	SA	172/217 (79%)	116 (67%)	56 (33%)	0	1	
46	SB	179/201 (89%)	107 (60%)	72 (40%)	0	0	
47	SC	172/182 (94%)	100 (58%)	72 (42%)	0	0	
48	SD	207/220 (94%)	124 (60%)	83 (40%)	0	0	
49	SE	225/232 (97%)	123 (55%)	102 (45%)	0	0	
50	SF	150/157 (96%)	99 (66%)	51 (34%)	0	1	
51	SG	204/213 (96%)	111 (54%)	93 (46%)	0	0	
52	SH	160/170 (94%)	90 (56%)	70 (44%)	0	0	
53	SI	142/148 (96%)	86 (61%)	56 (39%)	0	0	
54	SJ	114/115 (99%)	73 (64%)	41 (36%)	0	0	
55	SK	155/164 (94%)	92 (59%)	63 (41%)	0	0	
56	SL	86/119 (72%)	51 (59%)	35 (41%)	0	0	
57	SM	135/136 (99%)	87 (64%)	48 (36%)	0	0	
58	SO	111/114 (97%)	69 (62%)	42 (38%)	0	0	
59	SP	124/129 (96%)	80 (64%)	44 (36%)	0	0	
60	SQ	86/112 (77%)	55 (64%)	31 (36%)	0	0	
61	SR	102/128 (80%)	60 (59%)	42 (41%)	0	0	
62	ST	125/130 (96%)	64 (51%)	61 (49%)	0	0	
63	SU	109/124 (88%)	68 (62%)	41 (38%)	0	0	
64	SV	109/131 (83%)	68 (62%)	41 (38%)	0	0	
65	SW	114/115 (99%)	68 (60%)	46 (40%)	0	0	
66	SX	87/110 (79%)	52 (60%)	35 (40%)	0	0	
67	SY	69/72 (96%)	35 (51%)	34 (49%)	0	0	
68	Sb	101/113 (89%)	56 (55%)	45 (45%)	0	0	
69	Sc	66/79 (84%)	32 (48%)	34 (52%)	0	0	
70	Sd	91/103 (88%)	58 (64%)	33 (36%)	0	0	
71	Se	71/73 (97%)	39 (55%)	32 (45%)	0	0	

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	Sg	55/57 (96%)	22 (40%)	33 (60%)	0	0
73	Sh	43/45 (96%)	21 (49%)	22 (51%)	0	0
74	Sj	57/58 (98%)	31 (54%)	26 (46%)	0	0
All	All	8737/9573 (91%)	5728 (66%)	3009 (34%)	1	0

All (3009) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	LA	3	ARG
1	LA	5	ILE
1	LA	15	VAL
1	LA	20	VAL
1	LA	28	LYS
1	LA	33	ASP
1	LA	38	THR
1	LA	41	VAL
1	LA	44	VAL
1	LA	46	LYS
1	LA	49	LEU
1	LA	67	ARG
1	LA	71	ARG
1	LA	77	ILE
1	LA	82	MET
1	LA	88	VAL
1	LA	93	LYS
1	LA	98	ILE
1	LA	102	LEU
1	LA	116	VAL
1	LA	119	LYS
1	LA	126	LEU
1	LA	135	LEU
1	LA	142	GLU
1	LA	143	THR
1	LA	145	LYS
1	LA	148	ILE
1	LA	156	LYS
1	LA	160	SER
1	LA	161	LYS
1	LA	163	ARG
1	LA	168	LEU
1	LA	175	THR

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Mol	Chain	Res	Type
1	LA	190	LYS
1	LA	199	VAL
1	LA	200	ARG
1	LA	207	VAL
1	LA	208	ASP
1	LA	223	SER
1	LA	230	VAL
1	LA	237	LEU
1	LA	243	THR
1	LA	245	CYS
2	LB	8	CYS
2	LB	19	ARG
2	LB	20	LYS
2	LB	23	THR
2	LB	26	ARG
2	LB	31	THR
2	LB	37	GLN
2	LB	41	ILE
2	LB	47	LEU
2	LB	54	THR
2	LB	55	HIS
2	LB	58	ARG
2	LB	60	ILE
2	LB	62	HIS
2	LB	63	ARG
2	LB	70	ARG
2	LB	73	ILE
2	LB	74	ASP
2	LB	77	THR
2	LB	85	ILE
2	LB	87	THR
2	LB	90	ILE
2	LB	95	THR
2	LB	100	ARG
2	LB	103	THR
2	LB	105	VAL
2	LB	110	ILE
2	LB	112	GLU
2	LB	117	ARG
2	LB	121	ASN
2	LB	126	GLU
2	LB	127	LYS

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Mol	Chain	Res	Type
2	LB	132	THR
2	LB	136	LYS
2	LB	139	ASP
2	LB	143	ILE
2	LB	144	LYS
2	LB	145	GLU
2	LB	147	LEU
2	LB	157	ILE
2	LB	159	ILE
2	LB	160	VAL
2	LB	163	THR
2	LB	167	LEU
2	LB	170	LEU
2	LB	171	LYS
2	LB	172	GLN
2	LB	173	LYS
2	LB	177	ILE
2	LB	178	MET
2	LB	188	VAL
2	LB	190	GLU
2	LB	198	LEU
2	LB	201	LYS
2	LB	203	ILE
2	LB	206	LYS
2	LB	215	ILE
2	LB	216	ASP
2	LB	220	ILE
2	LB	231	THR
2	LB	235	VAL
2	LB	237	ARG
2	LB	240	ARG
2	LB	241	LYS
2	LB	248	LYS
2	LB	266	ARG
2	LB	270	MET
2	LB	277	ASP
2	LB	278	THR
2	LB	280	LYS
2	LB	285	ILE
2	LB	287	THR
2	LB	295	THR
2	LB	301	THR

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Mol	Chain	Res	Type
2	LB	302	ASP
2	LB	303	LYS
2	LB	312	VAL
2	LB	316	ARG
2	LB	327	THR
2	LB	332	LYS
2	LB	336	VAL
2	LB	337	VAL
2	LB	346	ARG
2	LB	348	CYS
2	LB	351	VAL
2	LB	368	GLU
2	LB	370	VAL
2	LB	371	GLU
2	LB	372	GLU
2	LB	373	ARG
2	LB	379	LYS
3	LC	6	LYS
3	LC	14	GLN
3	LC	17	GLU
3	LC	23	VAL
3	LC	26	VAL
3	LC	28	LEU
3	LC	32	ILE
3	LC	39	GLN
3	LC	50	VAL
3	LC	52	ARG
3	LC	57	GLN
3	LC	58	CYS
3	LC	67	ARG
3	LC	71	ARG
3	LC	72	LEU
3	LC	79	ILE
3	LC	95	THR
3	LC	97	VAL
3	LC	104	LYS
3	LC	105	VAL
3	LC	109	GLN
3	LC	121	SER
3	LC	126	LEU
3	LC	130	ARG
3	LC	136	ASP

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Mol	Chain	Res	Type
3	LC	140	ILE
3	LC	146	THR
3	LC	159	ILE
3	LC	160	LYS
3	LC	162	VAL
3	LC	165	LEU
3	LC	177	ILE
3	LC	181	ARG
3	LC	188	ARG
3	LC	190	ILE
3	LC	191	THR
3	LC	193	LYS
3	LC	197	VAL
3	LC	202	GLU
3	LC	206	ARG
3	LC	214	VAL
3	LC	216	LEU
3	LC	217	CYS
3	LC	219	VAL
3	LC	242	SER
3	LC	247	LEU
3	LC	255	GLN
3	LC	258	THR
3	LC	264	ILE
3	LC	266	GLN
3	LC	267	THR
3	LC	269	ILE
3	LC	275	SER
3	LC	276	ASP
3	LC	280	LYS
3	LC	285	LYS
3	LC	286	ARG
3	LC	287	ASP
3	LC	289	LEU
3	LC	290	VAL
3	LC	292	GLU
3	LC	299	SER
3	LC	302	GLU
3	LC	307	LEU
3	LC	310	SER
3	LC	312	THR
6	LF	5	LYS

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Mol	Chain	Res	Type
6	LF	9	THR
6	LF	11	SER
6	LF	14	LYS
6	LF	22	ARG
6	LF	27	LYS
6	LF	37	ILE
6	LF	48	ARG
6	LF	50	ARG
6	LF	52	VAL
6	LF	56	THR
6	LF	58	LYS
6	LF	60	ILE
6	LF	64	VAL
6	LF	68	GLU
6	LF	69	LEU
6	LF	71	LYS
6	LF	75	VAL
6	LF	76	CYS
6	LF	80	SER
6	LF	81	HIS
6	LF	84	PRO
6	LF	90	VAL
6	LF	94	ASN
6	LF	105	CYS
6	LF	107	ARG
6	LF	110	LEU
6	LF	112	LYS
6	LF	115	VAL
6	LF	118	LYS
6	LF	119	GLU
6	LF	122	LEU
6	LF	124	GLN
6	LF	125	LEU
6	LF	129	LEU
6	LF	130	ASP
6	LF	131	LYS
6	LF	135	GLU
6	LF	141	GLU
6	LF	142	ASN
6	LF	143	GLU
6	LF	147	VAL
6	LF	158	LEU

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Mol	Chain	Res	Type
6	LF	162	SER
6	LF	167	VAL
6	LF	171	MET
6	LF	175	VAL
6	LF	179	LEU
6	LF	181	ILE
6	LF	184	SER
6	LF	185	MET
6	LF	186	LYS
6	LF	192	SER
6	LF	193	LYS
6	LF	194	ASP
6	LF	198	SER
6	LF	204	ARG
6	LF	205	ILE
6	LF	208	LYS
6	LF	230	SER
6	LF	231	LYS
6	LF	236	LYS
6	LF	241	ARG
6	LF	242	LEU
6	LF	245	MET
6	LF	248	LYS
6	LF	253	ILE
6	LF	265	GLU
6	LF	267	LYS
6	LF	270	VAL
6	LF	274	ARG
6	LF	276	THR
6	LF	278	LYS
6	LF	282	GLU
6	LF	288	LYS
6	LF	289	LEU
7	LG	5	LYS
7	LG	6	THR
7	LG	8	SER
7	LG	9	ARG
7	LG	15	LYS
7	LG	21	LYS
7	LG	22	ASN
7	LG	30	LYS
7	LG	33	LEU

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Mol	Chain	Res	Type
7	LG	34	LYS
7	LG	35	LYS
7	LG	39	TYR
7	LG	45	ARG
7	LG	46	ARG
7	LG	51	LEU
8	LH	24	ARG
8	LH	26	THR
8	LH	27	GLU
8	LH	28	LYS
8	LH	31	ARG
8	LH	34	LEU
8	LH	36	LYS
8	LH	41	LYS
8	LH	53	LEU
8	LH	54	VAL
8	LH	58	LYS
8	LH	59	LYS
8	LH	62	GLU
8	LH	65	LEU
8	LH	75	GLU
8	LH	77	LYS
8	LH	81	VAL
8	LH	82	VAL
8	LH	84	ILE
8	LH	85	ARG
8	LH	93	LYS
8	LH	99	SER
8	LH	101	LEU
8	LH	102	ARG
8	LH	112	MET
8	LH	119	LEU
8	LH	124	ILE
8	LH	126	ASP
8	LH	133	GLU
8	LH	136	VAL
8	LH	137	GLU
8	LH	138	THR
8	LH	139	ILE
8	LH	145	LYS
8	LH	152	ASN
8	LH	162	ASN

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Mol	Chain	Res	Type
8	LH	164	ILE
8	LH	165	ASP
8	LH	170	LYS
8	LH	174	LEU
8	LH	175	CYS
8	LH	189	SER
8	LH	191	LYS
8	LH	195	ASN
8	LH	210	LYS
8	LH	225	LYS
8	LH	227	ILE
8	LH	231	VAL
8	LH	235	ILE
9	LI	28	LEU
9	LI	29	THR
9	LI	44	LYS
9	LI	46	VAL
9	LI	47	LEU
9	LI	51	LEU
9	LI	64	ILE
9	LI	68	LEU
9	LI	69	THR
9	LI	75	LEU
9	LI	77	ARG
9	LI	78	LYS
9	LI	80	SER
9	LI	84	LYS
9	LI	87	HIS
9	LI	88	LYS
9	LI	90	ARG
9	LI	92	LEU
9	LI	93	GLN
9	LI	98	LYS
9	LI	100	ASN
9	LI	109	ASP
9	LI	110	LYS
9	LI	111	LEU
9	LI	112	VAL
9	LI	113	ILE
9	LI	117	ILE
9	LI	119	ARG
9	LI	120	ILE

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Mol	Chain	Res	Type
9	LI	122	SER
9	LI	128	ARG
9	LI	130	LYS
9	LI	154	MET
9	LI	166	ASP
9	LI	169	LYS
9	LI	171	VAL
9	LI	174	LYS
9	LI	175	LYS
9	LI	179	VAL
9	LI	180	CYS
9	LI	182	THR
9	LI	184	VAL
9	LI	189	LYS
9	LI	191	THR
9	LI	194	LYS
9	LI	201	HIS
9	LI	207	LYS
9	LI	209	MET
9	LI	212	TYR
9	LI	218	ARG
10	LJ	8	THR
10	LJ	9	ILE
10	LJ	10	LYS
10	LJ	14	ASP
10	LJ	18	THR
10	LJ	23	VAL
10	LJ	25	THR
10	LJ	27	LYS
10	LJ	29	LYS
10	LJ	30	LYS
10	LJ	32	THR
10	LJ	34	VAL
10	LJ	35	ARG
10	LJ	42	LEU
10	LJ	43	ASP
10	LJ	44	ILE
10	LJ	49	ASP
10	LJ	50	THR
10	LJ	52	SER
10	LJ	70	CYS
10	LJ	74	GLU

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Mol	Chain	Res	Type
10	LJ	89	ARG
10	LJ	100	THR
10	LJ	102	VAL
10	LJ	106	LYS
10	LJ	109	GLU
10	LJ	110	ILE
10	LJ	111	ARG
10	LJ	112	ASN
10	LJ	115	HIS
10	LJ	117	ILE
10	LJ	118	LYS
10	LJ	120	ARG
10	LJ	129	THR
10	LJ	130	ILE
10	LJ	132	MET
10	LJ	134	THR
10	LJ	135	ASN
10	LJ	138	ASP
10	LJ	139	GLU
10	LJ	141	ILE
10	LJ	143	ARG
10	LJ	147	ILE
10	LJ	161	LEU
10	LJ	165	ASN
10	LJ	168	LEU
10	LJ	170	LYS
10	LJ	172	LEU
10	LJ	178	SER
10	LJ	180	ARG
10	LJ	183	GLN
10	LJ	185	GLN
11	LK	7	ARG
11	LK	12	GLN
11	LK	15	LYS
11	LK	19	LYS
11	LK	20	SER
11	LK	21	ARG
11	LK	30	LYS
11	LK	32	ARG
11	LK	35	ASP
11	LK	40	ARG
11	LK	42	LYS

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Mol	Chain	Res	Type
11	LK	43	VAL
11	LK	57	LYS
11	LK	62	SER
11	LK	69	ARG
11	LK	73	ASN
11	LK	76	ILE
11	LK	78	LYS
11	LK	79	LYS
11	LK	82	LYS
11	LK	86	HIS
11	LK	87	LEU
11	LK	88	ARG
11	LK	91	VAL
11	LK	97	ILE
11	LK	121	LYS
11	LK	123	GLN
11	LK	125	THR
11	LK	126	VAL
11	LK	131	ILE
11	LK	135	LEU
11	LK	141	ARG
11	LK	146	ASP
11	LK	149	LYS
11	LK	153	ARG
11	LK	156	LYS
11	LK	165	ILE
11	LK	166	VAL
11	LK	167	GLU
11	LK	169	ARG
11	LK	175	GLU
11	LK	178	LYS
11	LK	191	GLN
11	LK	192	TYR
11	LK	196	ASN
11	LK	199	ARG
11	LK	200	ILE
11	LK	203	LYS
11	LK	206	LEU
11	LK	207	ASN
12	LL	6	GLU
12	LL	7	ASN
12	LL	13	ARG

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Mol	Chain	Res	Type
12	LL	21	ILE
12	LL	40	LEU
12	LL	44	GLU
12	LL	46	THR
12	LL	49	LYS
12	LL	50	SER
12	LL	52	LEU
12	LL	53	THR
12	LL	54	ILE
12	LL	59	ILE
12	LL	60	ARG
12	LL	64	LYS
12	LL	66	SER
12	LL	67	THR
12	LL	69	VAL
12	LL	71	VAL
12	LL	75	LYS
12	LL	78	GLU
12	LL	80	ILE
12	LL	81	GLU
12	LL	85	ARG
12	LL	87	LYS
12	LL	94	SER
12	LL	101	ASN
12	LL	106	ILE
12	LL	107	THR
12	LL	110	ILE
12	LL	111	ASP
12	LL	115	LYS
12	LL	117	ASP
12	LL	120	MET
12	LL	122	ILE
12	LL	125	MET
12	LL	126	ASP
12	LL	131	LEU
12	LL	133	ARG
12	LL	137	ARG
12	LL	140	LYS
12	LL	148	VAL
12	LL	152	HIS
12	LL	154	ILE
12	LL	155	THR

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Mol	Chain	Res	Type
12	LL	164	GLU
12	LL	166	GLU
12	LL	168	GLU
12	LL	170	VAL
13	LM	29	MET
13	LM	44	THR
13	LM	46	LYS
13	LM	48	PRO
13	LM	51	ILE
13	LM	52	LYS
13	LM	60	ARG
13	LM	63	ARG
13	LM	71	LYS
13	LM	73	LYS
13	LM	75	ILE
13	LM	82	LYS
13	LM	88	THR
13	LM	97	THR
13	LM	100	ILE
13	LM	115	SER
13	LM	118	LYS
13	LM	121	GLN
13	LM	122	ILE
13	LM	129	ARG
13	LM	130	ARG
13	LM	138	VAL
13	LM	144	ARG
13	LM	145	LEU
13	LM	153	THR
13	LM	156	SER
13	LM	164	ILE
13	LM	168	ILE
13	LM	174	VAL
13	LM	178	VAL
13	LM	183	VAL
13	LM	185	THR
13	LM	186	THR
13	LM	188	SER
13	LM	191	GLU
13	LM	193	LYS
13	LM	194	LYS
13	LM	196	VAL

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Mol	Chain	Res	Type
13	LM	211	ARG
13	LM	219	ARG
13	LM	228	LYS
14	LN	2	SER
14	LN	11	ARG
14	LN	13	VAL
14	LN	20	ASP
14	LN	21	LYS
14	LN	23	LYS
14	LN	26	VAL
14	LN	28	VAL
14	LN	29	ASP
14	LN	33	THR
14	LN	38	ILE
14	LN	46	LYS
14	LN	50	VAL
14	LN	52	LEU
14	LN	60	GLN
14	LN	61	VAL
14	LN	62	ILE
14	LN	77	ILE
14	LN	83	ILE
14	LN	93	LYS
14	LN	95	ILE
14	LN	100	LEU
14	LN	103	LYS
14	LN	115	LEU
14	LN	123	MET
14	LN	128	MET
14	LN	129	SER
14	LN	131	LYS
15	LO	7	VAL
15	LO	9	GLU
15	LO	16	SER
15	LO	17	GLU
15	LO	19	LEU
15	LO	25	LEU
15	LO	26	ARG
15	LO	36	ILE
15	LO	37	LYS
15	LO	38	ARG
15	LO	39	CYS

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Mol	Chain	Res	Type
15	LO	40	SER
15	LO	43	THR
15	LO	54	LYS
15	LO	60	VAL
15	LO	61	VAL
15	LO	64	VAL
15	LO	66	VAL
15	LO	67	ARG
15	LO	81	TYR
15	LO	83	LYS
15	LO	85	ARG
15	LO	89	ILE
15	LO	90	VAL
15	LO	92	LEU
15	LO	93	LYS
15	LO	95	SER
15	LO	96	ARG
15	LO	97	SER
15	LO	101	LEU
15	LO	112	SER
15	LO	117	ASN
15	LO	121	VAL
15	LO	124	ASP
15	LO	128	LYS
15	LO	135	ILE
15	LO	147	LYS
15	LO	151	ILE
15	LO	153	ASN
15	LO	155	VAL
15	LO	158	ARG
15	LO	159	ARG
15	LO	177	LYS
15	LO	183	LYS
15	LO	184	LEU
15	LO	185	ARG
16	LP	4	ILE
16	LP	5	VAL
16	LP	12	ILE
16	LP	13	LEU
16	LP	15	ARG
16	LP	16	LEU
16	LP	29	GLU

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Mol	Chain	Res	Type
16	LP	30	VAL
16	LP	39	ILE
16	LP	40	ILE
16	LP	47	VAL
16	LP	48	LYS
16	LP	53	LYS
16	LP	57	LYS
16	LP	85	ILE
16	LP	89	THR
16	LP	93	SER
16	LP	101	VAL
16	LP	105	ILE
16	LP	109	CYS
16	LP	114	ARG
16	LP	116	VAL
16	LP	119	SER
16	LP	125	CYS
16	LP	127	ARG
16	LP	130	ARG
16	LP	131	ARG
16	LP	141	GLU
16	LP	151	GLU
16	LP	162	ASP
16	LP	168	LYS
16	LP	177	GLU
16	LP	180	GLU
16	LP	181	LYS
16	LP	182	ASP
16	LP	185	LEU
16	LP	187	ARG
16	LP	191	GLU
17	LQ	2	VAL
17	LQ	3	LYS
17	LQ	7	LYS
17	LQ	9	ASP
17	LQ	12	LEU
17	LQ	15	LYS
17	LQ	17	ARG
17	LQ	21	VAL
17	LQ	22	LYS
17	LQ	24	SER
17	LQ	33	ARG

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Mol	Chain	Res	Type
17	LQ	36	LYS
17	LQ	40	VAL
17	LQ	41	LYS
17	LQ	54	LYS
17	LQ	61	LYS
17	LQ	68	ARG
17	LQ	70	SER
17	LQ	77	THR
17	LQ	87	VAL
17	LQ	89	VAL
17	LQ	91	LYS
17	LQ	92	ASP
17	LQ	99	SER
17	LQ	102	LYS
17	LQ	106	LYS
17	LQ	110	ASP
17	LQ	116	SER
17	LQ	119	VAL
17	LQ	121	ARG
17	LQ	123	ARG
17	LQ	125	ARG
17	LQ	126	ARG
17	LQ	128	ARG
17	LQ	129	THR
17	LQ	144	CYS
17	LQ	146	VAL
17	LQ	147	GLU
17	LQ	149	ILE
17	LQ	153	LYS
17	LQ	156	ASP
18	LR	3	ILE
18	LR	4	ASP
18	LR	6	LYS
18	LR	10	LYS
18	LR	11	LYS
18	LR	13	LYS
18	LR	15	GLU
18	LR	18	GLU
18	LR	21	SER
18	LR	26	ILE
18	LR	34	LYS
18	LR	35	VAL

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Mol	Chain	Res	Type
18	LR	42	GLU
18	LR	45	THR
18	LR	50	LYS
18	LR	64	VAL
18	LR	66	ARG
18	LR	73	LYS
18	LR	74	ARG
18	LR	75	GLU
18	LR	77	LYS
18	LR	84	THR
18	LR	87	ASN
18	LR	92	VAL
18	LR	93	THR
18	LR	94	ILE
18	LR	96	ARG
18	LR	97	MET
18	LR	99	ILE
18	LR	100	CYS
18	LR	105	SER
18	LR	107	THR
18	LR	111	ARG
18	LR	114	LYS
18	LR	120	MET
18	LR	121	SER
18	LR	123	ASP
18	LR	131	THR
18	LR	134	ASN
18	LR	137	LEU
18	LR	150	LYS
18	LR	162	LYS
18	LR	166	GLU
18	LR	168	LYS
18	LR	171	ARG
18	LR	176	ARG
18	LR	179	TRP
19	LS	8	LYS
19	LS	19	LYS
19	LS	20	ARG
19	LS	30	LYS
19	LS	32	ILE
19	LS	42	ARG
19	LS	49	ILE

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Mol	Chain	Res	Type
19	LS	52	LYS
19	LS	53	LEU
19	LS	54	ASP
19	LS	55	ILE
19	LS	56	LYS
19	LS	59	SER
19	LS	60	ARG
19	LS	62	ARG
19	LS	74	ARG
19	LS	76	SER
19	LS	82	ARG
19	LS	84	THR
19	LS	85	ARG
19	LS	86	GLU
19	LS	97	GLN
19	LS	107	SER
19	LS	110	ARG
19	LS	117	ARG
19	LS	130	ASN
19	LS	131	MET
19	LS	136	ARG
19	LS	140	GLU
19	LS	145	MET
19	LS	148	GLU
19	LS	151	LEU
19	LS	153	LYS
19	LS	156	LYS
19	LS	158	GLU
19	LS	161	GLN
19	LS	162	ARG
20	LT	2	MET
20	LT	6	ILE
20	LT	7	VAL
20	LT	11	ARG
20	LT	14	SER
20	LT	15	GLU
20	LT	21	GLU
20	LT	25	MET
20	LT	27	ILE
20	LT	32	GLU
20	LT	43	LEU
20	LT	44	LYS

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Mol	Chain	Res	Type
20	LT	45	SER
20	LT	46	LEU
20	LT	47	LYS
20	LT	49	ILE
20	LT	50	LYS
20	LT	55	GLU
20	LT	56	ILE
20	LT	58	ASP
20	LT	62	ILE
20	LT	63	GLU
20	LT	64	GLU
20	LT	70	LYS
20	LT	76	LEU
20	LT	81	ARG
20	LT	84	GLN
20	LT	86	ASN
20	LT	87	MET
20	LT	91	VAL
20	LT	92	ARG
20	LT	93	GLU
20	LT	94	THR
20	LT	95	THR
20	LT	100	MET
20	LT	102	LYS
20	LT	103	VAL
20	LT	120	ILE
20	LT	124	LYS
20	LT	125	GLU
20	LT	126	VAL
20	LT	128	ASP
20	LT	132	ARG
20	LT	136	VAL
20	LT	138	MET
20	LT	140	THR
20	LT	142	LYS
20	LT	144	VAL
20	LT	150	CYS
20	LT	153	VAL
20	LT	155	VAL
20	LT	156	LYS
20	LT	157	ARG
20	LT	160	ARG

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Mol	Chain	Res	Type
20	LT	167	ARG
20	LT	171	VAL
21	LU	2	THR
21	LU	10	LYS
21	LU	24	MET
21	LU	28	THR
21	LU	32	ARG
21	LU	35	LYS
21	LU	38	GLN
21	LU	40	VAL
21	LU	43	LYS
21	LU	45	ASN
21	LU	50	LYS
21	LU	52	MET
21	LU	64	ILE
21	LU	67	ILE
21	LU	70	ARG
21	LU	76	ILE
21	LU	77	GLN
21	LU	80	VAL
21	LU	84	ILE
21	LU	87	LYS
21	LU	91	VAL
21	LU	93	LEU
21	LU	103	LYS
21	LU	106	LEU
21	LU	120	LYS
21	LU	121	GLU
21	LU	122	THR
21	LU	126	VAL
21	LU	128	CYS
21	LU	131	ARG
21	LU	140	HIS
21	LU	141	VAL
21	LU	142	VAL
21	LU	143	SER
21	LU	144	ILE
21	LU	146	SER
21	LU	151	THR
21	LU	153	LEU
21	LU	154	LYS
22	LV	10	LYS

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Mol	Chain	Res	Type
22	LV	11	LYS
22	LV	16	ILE
22	LV	17	ARG
22	LV	23	SER
22	LV	27	ASP
22	LV	28	LEU
22	LV	29	GLU
22	LV	30	LEU
22	LV	32	LEU
22	LV	40	ARG
22	LV	48	ARG
22	LV	49	LYS
22	LV	50	HIS
22	LV	55	LYS
22	LV	56	VAL
22	LV	59	SER
22	LV	64	SER
22	LV	65	LEU
22	LV	67	ILE
22	LV	70	THR
22	LV	76	LYS
22	LV	79	VAL
22	LV	89	GLN
22	LV	90	ASP
22	LV	91	TYR
22	LV	92	GLN
22	LV	96	ARG
22	LV	97	VAL
22	LV	100	THR
22	LV	103	GLU
22	LV	104	THR
22	LV	111	THR
23	LW	11	ILE
23	LW	14	LYS
23	LW	15	PHE
23	LW	16	ARG
23	LW	18	SER
23	LW	36	LYS
23	LW	44	LYS
23	LW	45	ASN
23	LW	49	HIS
23	LW	50	LEU

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Mol	Chain	Res	Type
23	LW	61	MET
23	LW	62	VAL
23	LW	65	THR
23	LW	71	LYS
23	LW	74	LEU
23	LW	77	LYS
23	LW	79	THR
23	LW	93	LYS
23	LW	94	ASP
23	LW	98	ILE
23	LW	103	ASN
23	LW	108	ILE
23	LW	111	LYS
23	LW	114	LEU
23	LW	123	VAL
23	LW	125	LYS
23	LW	130	ARG
23	LW	133	LYS
23	LW	134	ILE
23	LW	135	SER
23	LW	139	GLU
23	LW	140	CYS
24	LX	3	ARG
24	LX	4	ILE
24	LX	7	CYS
24	LX	14	VAL
24	LX	18	LYS
24	LX	23	VAL
24	LX	28	ARG
24	LX	31	ARG
24	LX	34	THR
24	LX	35	SER
24	LX	37	CYS
24	LX	38	HIS
24	LX	48	ARG
24	LX	51	ARG
24	LX	54	LYS
24	LX	55	THR
24	LX	58	LEU
24	LX	63	ASP
24	LX	64	MET
25	LY	29	VAL

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Mol	Chain	Res	Type
25	LY	35	LYS
25	LY	37	LEU
25	LY	44	LEU
25	LY	51	LYS
25	LY	66	ILE
25	LY	68	THR
25	LY	77	LYS
25	LY	79	ASN
25	LY	81	ILE
25	LY	83	PHE
25	LY	85	VAL
25	LY	95	ARG
25	LY	104	THR
25	LY	105	LYS
25	LY	109	VAL
25	LY	116	LEU
25	LY	118	LEU
25	LY	129	VAL
25	LY	140	LEU
26	LZ	1	MET
26	LZ	8	THR
26	LZ	10	SER
26	LZ	20	THR
26	LZ	29	MET
26	LZ	32	SER
26	LZ	39	ARG
26	LZ	43	LYS
26	LZ	44	ILE
26	LZ	54	ILE
26	LZ	55	VAL
26	LZ	57	ILE
26	LZ	63	LYS
26	LZ	65	THR
26	LZ	67	LYS
26	LZ	69	VAL
26	LZ	72	ARG
26	LZ	74	ARG
26	LZ	77	LYS
26	LZ	80	VAL
26	LZ	81	GLU
26	LZ	83	ILE
26	LZ	86	LYS

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Mol	Chain	Res	Type
26	LZ	88	ARG
26	LZ	91	GLU
26	LZ	93	LYS
26	LZ	95	VAL
26	LZ	99	ILE
26	LZ	102	SER
26	LZ	105	ILE
26	LZ	107	LYS
26	LZ	111	MET
26	LZ	114	SER
26	LZ	120	LYS
26	LZ	133	ILE
27	La	4	PRO
27	La	5	ILE
27	La	7	LYS
27	La	13	ILE
27	La	22	LYS
27	La	28	GLU
27	La	34	GLU
27	La	35	ARG
27	La	37	SER
27	La	41	VAL
27	La	44	ILE
27	La	47	LEU
27	La	49	ARG
27	La	50	ARG
27	La	51	ILE
27	La	65	ARG
27	La	66	VAL
27	La	67	ARG
27	La	68	SER
27	La	71	LYS
27	La	72	CYS
27	La	73	MET
27	La	81	THR
27	La	85	LEU
27	La	88	ASN
27	La	89	TYR
27	La	90	LYS
27	La	97	THR
27	La	103	LYS
27	La	105	ARG

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Mol	Chain	Res	Type
27	La	107	ILE
27	La	121	GLU
27	La	125	THR
27	La	129	THR
27	La	130	LYS
28	Lb	2	PRO
28	Lb	4	ARG
28	Lb	5	ILE
28	Lb	7	LYS
28	Lb	8	SER
28	Lb	16	GLN
28	Lb	17	MET
28	Lb	27	LYS
28	Lb	30	SER
28	Lb	34	LYS
28	Lb	70	ASN
28	Lb	72	THR
28	Lb	75	ILE
28	Lb	82	ILE
28	Lb	84	GLU
28	Lb	85	GLU
28	Lb	87	ARG
28	Lb	95	SER
28	Lb	96	THR
28	Lb	97	THR
28	Lb	101	VAL
28	Lb	123	ILE
28	Lb	126	LYS
28	Lb	131	SER
28	Lb	133	ASP
28	Lb	136	LYS
28	Lb	141	VAL
28	Lb	144	VAL
28	Lb	148	VAL
29	Lc	5	LYS
29	Lc	8	THR
29	Lc	10	LYS
29	Lc	15	LYS
29	Lc	19	ASN
29	Lc	22	LYS
29	Lc	23	LYS
29	Lc	25	LYS

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Mol	Chain	Res	Type
29	Lc	27	SER
29	Lc	33	LYS
29	Lc	35	MET
29	Lc	38	LYS
29	Lc	50	ASP
29	Lc	54	SER
30	Ld	3	THR
30	Ld	15	SER
30	Ld	18	LEU
30	Ld	23	LYS
30	Ld	24	SER
30	Ld	28	THR
30	Ld	35	ILE
30	Ld	39	ARG
30	Ld	42	LYS
30	Ld	45	LEU
30	Ld	47	PHE
30	Ld	55	LEU
30	Ld	56	VAL
30	Ld	59	GLN
30	Ld	60	VAL
30	Ld	63	LEU
30	Ld	65	HIS
30	Ld	66	LEU
30	Ld	71	VAL
30	Ld	73	VAL
30	Ld	93	ILE
30	Ld	94	MET
30	Ld	95	THR
30	Ld	101	ASP
30	Ld	103	ASP
30	Ld	105	THR
30	Ld	107	ILE
31	Le	3	ILE
31	Le	4	VAL
31	Le	9	ILE
31	Le	13	LYS
31	Le	16	ARG
31	Le	20	SER
31	Le	26	ILE
31	Le	37	LYS
31	Le	45	ARG

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Mol	Chain	Res	Type
31	Le	51	ASN
31	Le	71	ARG
31	Le	73	GLU
31	Le	77	GLU
31	Le	79	LYS
31	Le	83	VAL
31	Le	84	ILE
31	Le	86	LYS
31	Le	88	VAL
31	Le	95	THR
31	Le	99	LYS
32	Lf	6	ILE
32	Lf	9	LEU
32	Lf	13	ILE
32	Lf	14	ILE
32	Lf	18	ARG
32	Lf	19	LYS
32	Lf	20	ASN
32	Lf	21	LYS
32	Lf	23	ILE
32	Lf	36	SER
32	Lf	47	MET
32	Lf	57	MET
32	Lf	59	SER
32	Lf	60	ILE
32	Lf	67	GLU
32	Lf	71	MET
32	Lf	79	HIS
32	Lf	80	ARG
32	Lf	81	ILE
32	Lf	82	SER
32	Lf	83	THR
32	Lf	87	LEU
32	Lf	88	LYS
32	Lf	90	LEU
32	Lf	92	MET
32	Lf	93	ASN
32	Lf	95	LYS
32	Lf	100	GLN
32	Lf	101	ILE
32	Lf	114	LEU
32	Lf	115	GLU

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Mol	Chain	Res	Type
32	Lf	118	LYS
32	Lf	119	LYS
32	Lf	120	MET
32	Lf	125	LEU
32	Lf	132	ARG
32	Lf	135	GLU
33	Lg	2	GLU
33	Lg	4	ILE
33	Lg	5	LYS
33	Lg	9	PHE
33	Lg	10	LEU
33	Lg	28	VAL
33	Lg	32	LYS
33	Lg	44	LYS
33	Lg	46	LEU
33	Lg	56	LYS
33	Lg	59	LYS
33	Lg	64	LYS
33	Lg	67	ARG
33	Lg	74	MET
33	Lg	81	THR
33	Lg	88	MET
33	Lg	91	LYS
33	Lg	92	VAL
33	Lg	94	VAL
33	Lg	97	ASP
34	Lh	6	VAL
34	Lh	8	CYS
34	Lh	16	THR
34	Lh	21	VAL
34	Lh	22	ARG
34	Lh	24	LYS
34	Lh	30	ARG
34	Lh	33	SER
34	Lh	35	ARG
34	Lh	50	LYS
34	Lh	51	GLN
34	Lh	59	ILE
34	Lh	64	THR
34	Lh	67	GLN
34	Lh	71	SER
34	Lh	72	ARG

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Mol	Chain	Res	Type
34	Lh	78	LEU
34	Lh	81	SER
34	Lh	88	LEU
34	Lh	100	ARG
34	Lh	101	GLU
34	Lh	102	ILE
35	Li	33	LYS
35	Li	36	ASP
35	Li	42	GLN
35	Li	43	GLU
35	Li	44	ASP
35	Li	48	LYS
35	Li	58	SER
35	Li	62	MET
35	Li	63	LYS
35	Li	69	VAL
35	Li	71	GLU
35	Li	72	ARG
35	Li	77	ARG
35	Li	80	LYS
35	Li	91	ASN
35	Li	123	GLN
35	Li	126	GLU
35	Li	127	LYS
35	Li	131	LEU
35	Li	135	LYS
35	Li	136	LEU
35	Li	137	MET
35	Li	141	LEU
35	Li	151	LYS
36	Lj	2	PRO
36	Lj	4	LYS
36	Lj	9	LYS
36	Lj	10	LYS
36	Lj	14	VAL
36	Lj	16	ARG
36	Lj	17	ILE
36	Lj	18	VAL
36	Lj	19	ARG
36	Lj	21	LYS
36	Lj	22	GLU
36	Lj	25	LYS

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Mol	Chain	Res	Type
36	Lj	26	THR
36	Lj	27	LYS
36	Lj	29	HIS
36	Lj	31	GLU
36	Lj	34	LYS
36	Lj	35	SER
36	Lj	41	THR
36	Lj	53	LEU
36	Lj	56	MET
36	Lj	58	LYS
36	Lj	59	ASP
36	Lj	60	ARG
36	Lj	67	LYS
36	Lj	68	LYS
36	Lj	74	LYS
36	Lj	77	LYS
36	Lj	79	LYS
36	Lj	80	ARG
36	Lj	88	ARG
37	Lk	3	LYS
37	Lk	7	SER
37	Lk	10	LYS
37	Lk	13	THR
37	Lk	15	ILE
37	Lk	31	LYS
37	Lk	37	CYS
37	Lk	43	LYS
37	Lk	44	MET
37	Lk	46	ARG
37	Lk	54	LEU
37	Lk	58	THR
37	Lk	64	MET
37	Lk	68	ARG
37	Lk	69	LYS
37	Lk	72	ARG
37	Lk	80	LYS
37	Lk	85	LYS
38	Ll	4	THR
38	Ll	7	GLU
38	Ll	8	GLU
38	Ll	10	LEU
38	Ll	16	ASP

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Mol	Chain	Res	Type
38	Ll	20	LYS
38	Ll	21	LYS
38	Ll	22	LEU
38	Ll	25	LYS
38	Ll	29	LYS
38	Ll	32	LEU
38	Ll	35	LYS
38	Ll	36	VAL
38	Ll	39	LYS
38	Ll	42	THR
38	Ll	44	LYS
38	Ll	46	LEU
38	Ll	49	LEU
38	Ll	50	THR
38	Ll	51	VAL
38	Ll	55	ASP
38	Ll	56	ASP
38	Ll	58	LYS
38	Ll	59	SER
38	Ll	60	ILE
38	Ll	61	VAL
38	Ll	62	LYS
38	Ll	66	ASP
38	Ll	67	LYS
38	Ll	68	VAL
39	Ln	4	ILE
39	Ln	5	ASN
39	Ln	9	LEU
39	Ln	11	LYS
39	Ln	18	GLU
39	Ln	19	ARG
39	Ln	22	ASN
39	Ln	23	GLU
39	Ln	24	LYS
39	Ln	26	ARG
39	Ln	27	LYS
39	Ln	29	LEU
39	Ln	30	GLU
39	Ln	32	VAL
39	Ln	33	GLU
39	Ln	35	GLN
39	Ln	36	VAL

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Mol	Chain	Res	Type
39	Ln	39	LYS
39	Ln	44	LYS
39	Ln	45	LYS
39	Ln	48	ARG
39	Ln	49	PHE
39	Ln	50	ASN
39	Ln	51	LEU
39	Ln	63	LEU
39	Ln	64	LYS
39	Ln	65	LEU
39	Ln	66	CYS
39	Ln	68	ILE
39	Ln	70	ASP
39	Ln	72	ARG
39	Ln	73	ASP
39	Ln	76	ARG
39	Ln	78	LYS
39	Ln	83	ASN
39	Ln	85	VAL
39	Ln	86	GLU
39	Ln	87	ILE
39	Ln	98	LYS
39	Ln	100	ILE
39	Ln	101	LYS
39	Ln	102	LYS
39	Ln	105	LYS
39	Ln	111	LEU
39	Ln	114	LYS
39	Ln	115	SER
39	Ln	117	ILE
39	Ln	118	ARG
39	Ln	119	GLN
39	Ln	126	PRO
39	Ln	128	PHE
39	Ln	129	THR
39	Ln	130	LYS
39	Ln	133	ARG
39	Ln	136	LEU
39	Ln	138	LEU
39	Ln	142	GLU
39	Ln	144	LEU
39	Ln	145	GLU

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Mol	Chain	Res	Type
39	Ln	146	LEU
39	Ln	147	LYS
39	Ln	149	LEU
39	Ln	151	CYS
39	Ln	156	LYS
39	Ln	158	GLN
39	Ln	160	LYS
39	Ln	161	LYS
39	Ln	163	VAL
39	Ln	166	ASN
39	Ln	169	ILE
39	Ln	173	LYS
39	Ln	177	SER
39	Ln	178	GLU
39	Ln	183	ILE
39	Ln	184	MET
39	Ln	186	THR
39	Ln	195	LYS
39	Ln	198	TRP
39	Ln	201	ILE
39	Ln	202	LYS
39	Ln	203	THR
39	Ln	204	VAL
39	Ln	206	ILE
39	Ln	207	LYS
39	Ln	208	SER
39	Ln	210	MET
39	Ln	215	ARG
39	Ln	216	ILE
40	Lo	1	MET
40	Lo	8	LYS
40	Lo	14	LYS
40	Lo	18	ARG
40	Lo	23	ARG
40	Lo	24	SER
40	Lo	25	LYS
41	Lp	7	GLU
41	Lp	9	ARG
41	Lp	10	THR
41	Lp	12	CYS
41	Lp	14	ARG
41	Lp	19	THR

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Mol	Chain	Res	Type
41	Lp	22	LYS
41	Lp	24	SER
41	Lp	27	LYS
41	Lp	28	LYS
41	Lp	32	SER
41	Lp	36	GLN
41	Lp	61	LYS
41	Lp	62	THR
41	Lp	68	ILE
41	Lp	71	THR
41	Lp	72	CYS
41	Lp	81	GLN
41	Lp	83	LEU
41	Lp	91	ILE
41	Lp	92	SER
41	Lp	94	LEU
42	Lq	4	ARG
42	Lq	5	THR
42	Lq	6	LYS
42	Lq	7	LYS
42	Lq	8	VAL
42	Lq	10	LEU
42	Lq	13	LYS
42	Lq	16	THR
42	Lq	17	ARG
42	Lq	24	LYS
42	Lq	26	LEU
42	Lq	29	ILE
42	Lq	32	SER
42	Lq	33	GLN
42	Lq	34	LYS
42	Lq	38	THR
42	Lq	39	CYS
42	Lq	42	CYS
42	Lq	45	ASP
42	Lq	48	ARG
42	Lq	49	ARG
42	Lq	50	THR
42	Lq	52	CYS
42	Lq	57	CYS
42	Lq	58	ARG
42	Lq	63	THR

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Mol	Chain	Res	Type
42	Lq	64	MET
42	Lq	82	THR
42	Lq	84	ARG
42	Lq	88	LEU
42	Lq	90	ARG
42	Lq	91	GLU
43	Ls	78	MET
43	Ls	81	THR
43	Ls	82	LEU
43	Ls	83	ILE
43	Ls	93	MET
43	Ls	94	MET
43	Ls	96	CYS
43	Ls	106	ARG
43	Ls	108	THR
43	Ls	110	CYS
43	Ls	114	ARG
43	Ls	117	ASN
43	Ls	119	ARG
43	Ls	120	LYS
43	Ls	122	LYS
43	Ls	123	LEU
45	SA	15	LEU
45	SA	19	ASP
45	SA	21	LYS
45	SA	22	LYS
45	SA	23	MET
45	SA	24	LEU
45	SA	25	VAL
45	SA	30	LEU
45	SA	33	ARG
45	SA	34	ASN
45	SA	35	ILE
45	SA	37	ARG
45	SA	39	MET
45	SA	43	ILE
45	SA	48	LYS
45	SA	51	THR
45	SA	53	VAL
45	SA	58	LYS
45	SA	62	LYS
45	SA	63	ILE

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Mol	Chain	Res	Type
45	SA	69	ILE
45	SA	78	GLU
45	SA	79	ILE
45	SA	81	VAL
45	SA	89	GLN
45	SA	92	ILE
45	SA	93	LEU
45	SA	96	CYS
45	SA	97	LYS
45	SA	107	ARG
45	SA	114	THR
45	SA	118	ASN
45	SA	120	ASN
45	SA	126	LEU
45	SA	127	LEU
45	SA	128	LEU
45	SA	131	ASP
45	SA	133	VAL
45	SA	139	ILE
45	SA	141	GLU
45	SA	145	VAL
45	SA	151	SER
45	SA	155	SER
45	SA	164	VAL
45	SA	166	ILE
45	SA	170	ASN
45	SA	171	LYS
45	SA	176	ILE
45	SA	178	LEU
45	SA	179	ILE
45	SA	191	LYS
45	SA	193	SER
45	SA	194	ILE
45	SA	195	SER
45	SA	196	ARG
45	SA	206	LEU
46	SB	32	LYS
46	SB	36	LEU
46	SB	38	LYS
46	SB	42	ILE
46	SB	45	LEU
46	SB	48	ILE

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Mol	Chain	Res	Type
46	SB	50	LYS
46	SB	53	LEU
46	SB	55	ILE
46	SB	57	GLU
46	SB	58	THR
46	SB	61	ILE
46	SB	67	LYS
46	SB	69	GLU
46	SB	72	GLU
46	SB	73	GLU
46	SB	74	VAL
46	SB	75	CYS
46	SB	76	ASN
46	SB	77	ILE
46	SB	78	MET
46	SB	80	VAL
46	SB	84	THR
46	SB	88	GLN
46	SB	89	ARG
46	SB	93	ARG
46	SB	97	ILE
46	SB	102	ASP
46	SB	105	ILE
46	SB	111	VAL
46	SB	113	LYS
46	SB	115	VAL
46	SB	120	LYS
46	SB	121	LYS
46	SB	124	LYS
46	SB	128	LEU
46	SB	130	ILE
46	SB	134	ARG
46	SB	141	LYS
46	SB	142	LEU
46	SB	150	SER
46	SB	159	VAL
46	SB	168	ARG
46	SB	172	ILE
46	SB	175	SER
46	SB	177	THR
46	SB	178	VAL
46	SB	180	LYS

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Mol	Chain	Res	Type
46	SB	181	VAL
46	SB	182	LEU
46	SB	189	ASP
46	SB	192	THR
46	SB	197	HIS
46	SB	198	SER
46	SB	201	LEU
46	SB	202	MET
46	SB	205	VAL
46	SB	208	VAL
46	SB	213	LYS
46	SB	217	SER
46	SB	219	LEU
46	SB	223	LEU
46	SB	225	LYS
46	SB	227	GLU
46	SB	228	GLN
46	SB	229	LEU
46	SB	230	ASP
46	SB	232	VAL
46	SB	233	GLN
46	SB	235	ILE
46	SB	236	ARG
46	SB	240	LEU
47	SC	6	ARG
47	SC	7	ARG
47	SC	8	ASP
47	SC	9	GLU
47	SC	10	GLU
47	SC	11	ASN
47	SC	15	SER
47	SC	17	TYR
47	SC	23	MET
47	SC	36	VAL
47	SC	37	ASP
47	SC	45	LEU
47	SC	47	ARG
47	SC	48	THR
47	SC	51	SER
47	SC	57	GLN
47	SC	60	GLU
47	SC	62	GLU

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Mol	Chain	Res	Type
47	SC	67	ASP
47	SC	74	LYS
47	SC	77	TYR
47	SC	78	LEU
47	SC	79	LEU
47	SC	84	MET
47	SC	85	CYS
47	SC	88	LYS
47	SC	94	VAL
47	SC	95	ASP
47	SC	96	LYS
47	SC	97	ILE
47	SC	98	ILE
47	SC	100	ARG
47	SC	102	LEU
47	SC	107	MET
47	SC	108	VAL
47	SC	111	LEU
47	SC	114	LYS
47	SC	115	LEU
47	SC	121	ILE
47	SC	122	ARG
47	SC	123	ARG
47	SC	129	ILE
47	SC	130	ARG
47	SC	144	VAL
47	SC	147	LYS
47	SC	148	LEU
47	SC	149	ARG
47	SC	151	GLN
47	SC	152	ARG
47	SC	157	LYS
47	SC	159	LYS
47	SC	160	GLU
47	SC	162	CYS
47	SC	163	LEU
47	SC	164	ILE
47	SC	165	SER
47	SC	170	LYS
47	SC	172	ILE
47	SC	178	THR
47	SC	181	ILE

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Mol	Chain	Res	Type
47	SC	182	LYS
47	SC	183	MET
47	SC	185	GLN
47	SC	188	ILE
47	SC	193	ARG
47	SC	198	ASN
47	SC	199	ILE
47	SC	200	ARG
47	SC	203	VAL
47	SC	207	LYS
47	SC	208	ILE
47	SC	210	ILE
48	SD	12	LYS
48	SD	13	ILE
48	SD	14	THR
48	SD	15	GLN
48	SD	16	ARG
48	SD	17	LYS
48	SD	20	ASP
48	SD	23	LEU
48	SD	24	LYS
48	SD	25	LYS
48	SD	26	GLU
48	SD	28	TYR
48	SD	30	VAL
48	SD	31	ILE
48	SD	35	HIS
48	SD	37	LYS
48	SD	43	GLN
48	SD	44	THR
48	SD	47	THR
48	SD	48	LYS
48	SD	49	THR
48	SD	52	LEU
48	SD	59	ILE
48	SD	62	ARG
48	SD	63	VAL
48	SD	66	VAL
48	SD	78	LEU
48	SD	83	LYS
48	SD	88	THR
48	SD	89	GLN

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Mol	Chain	Res	Type
48	SD	90	LEU
48	SD	91	VAL
48	SD	92	SER
48	SD	95	LYS
48	SD	96	CYS
48	SD	97	LEU
48	SD	98	THR
48	SD	103	MET
48	SD	105	ILE
48	SD	106	THR
48	SD	108	HIS
48	SD	109	LYS
48	SD	121	ILE
48	SD	123	VAL
48	SD	130	THR
48	SD	135	LEU
48	SD	139	VAL
48	SD	145	ARG
48	SD	149	GLN
48	SD	150	ARG
48	SD	151	ARG
48	SD	152	LYS
48	SD	153	ASN
48	SD	154	CYS
48	SD	160	VAL
48	SD	163	MET
48	SD	164	MET
48	SD	168	ILE
48	SD	170	GLU
48	SD	173	HIS
48	SD	175	GLU
48	SD	178	LYS
48	SD	180	SER
48	SD	181	ILE
48	SD	184	LEU
48	SD	186	THR
48	SD	192	GLU
48	SD	193	VAL
48	SD	196	LYS
48	SD	197	LEU
48	SD	198	THR
48	SD	201	LEU

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Mol	Chain	Res	Type
48	SD	204	ILE
48	SD	210	VAL
48	SD	211	MET
48	SD	219	LYS
48	SD	220	ARG
48	SD	225	MET
48	SD	226	GLU
48	SD	227	LEU
48	SD	228	LEU
48	SD	231	MET
48	SD	238	ARG
49	SE	6	ARG
49	SE	7	LYS
49	SE	9	LEU
49	SE	11	ARG
49	SE	16	LYS
49	SE	20	LEU
49	SE	23	MET
49	SE	26	ILE
49	SE	27	TRP
49	SE	32	THR
49	SE	38	LEU
49	SE	39	ARG
49	SE	42	ILE
49	SE	45	ILE
49	SE	46	LEU
49	SE	47	ILE
49	SE	49	ARG
49	SE	52	LEU
49	SE	57	THR
49	SE	58	TYR
49	SE	61	THR
49	SE	63	MET
49	SE	65	LEU
49	SE	66	GLN
49	SE	67	ASP
49	SE	68	LYS
49	SE	70	VAL
49	SE	71	LEU
49	SE	72	ILE
49	SE	75	LYS
49	SE	77	ARG

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Mol	Chain	Res	Type
49	SE	78	THR
49	SE	84	VAL
49	SE	92	ILE
49	SE	94	LYS
49	SE	96	HIS
49	SE	97	LYS
49	SE	98	THR
49	SE	100	ARG
49	SE	101	VAL
49	SE	102	LEU
49	SE	104	ASP
49	SE	105	VAL
49	SE	106	LYS
49	SE	108	ARG
49	SE	110	THR
49	SE	112	VAL
49	SE	124	CYS
49	SE	125	ARG
49	SE	128	LYS
49	SE	129	ILE
49	SE	131	LEU
49	SE	134	LYS
49	SE	139	LEU
49	SE	142	HIS
49	SE	145	ARG
49	SE	150	PRO
49	SE	154	ILE
49	SE	156	THR
49	SE	158	ASP
49	SE	160	ILE
49	SE	161	LYS
49	SE	162	ILE
49	SE	165	LYS
49	SE	168	LYS
49	SE	169	ILE
49	SE	171	GLU
49	SE	176	ASP
49	SE	180	ILE
49	SE	181	VAL
49	SE	182	MET
49	SE	184	THR
49	SE	187	ARG

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Mol	Chain	Res	Type
49	SE	191	ARG
49	SE	192	ILE
49	SE	194	THR
49	SE	195	ILE
49	SE	196	GLN
49	SE	198	ILE
49	SE	202	MET
49	SE	207	MET
49	SE	208	ILE
49	SE	210	MET
49	SE	211	LYS
49	SE	212	ASP
49	SE	216	THR
49	SE	217	GLU
49	SE	222	LEU
49	SE	228	ILE
49	SE	230	ASN
49	SE	231	ASP
49	SE	232	SER
49	SE	235	VAL
49	SE	239	THR
49	SE	243	ILE
49	SE	244	ARG
49	SE	248	ILE
49	SE	249	LYS
49	SE	250	ASN
49	SE	254	ARG
49	SE	255	LEU
49	SE	261	ARG
50	SF	7	LEU
50	SF	10	LYS
50	SF	13	LEU
50	SF	14	THR
50	SF	15	ASP
50	SF	21	GLU
50	SF	23	LEU
50	SF	27	ILE
50	SF	29	ILE
50	SF	33	SER
50	SF	35	VAL
50	SF	37	HIS
50	SF	41	ARG

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Mol	Chain	Res	Type
50	SF	45	LYS
50	SF	47	PHE
50	SF	58	LEU
50	SF	63	MET
50	SF	68	ASN
50	SF	69	SER
50	SF	74	MET
50	SF	77	LYS
50	SF	78	THR
50	SF	81	GLU
50	SF	88	LEU
50	SF	90	THR
50	SF	92	LYS
50	SF	95	VAL
50	SF	108	ARG
50	SF	113	ARG
50	SF	114	ILE
50	SF	122	ARG
50	SF	124	SER
50	SF	125	VAL
50	SF	128	SER
50	SF	137	ILE
50	SF	146	LYS
50	SF	150	ARG
50	SF	151	LYS
50	SF	153	ARG
50	SF	157	GLU
50	SF	158	CYS
50	SF	161	GLU
50	SF	162	GLU
50	SF	164	MET
50	SF	165	ASN
50	SF	172	LYS
50	SF	173	SER
50	SF	181	SER
50	SF	182	VAL
50	SF	184	ARG
50	SF	185	ILE
51	SG	8	LYS
51	SG	9	VAL
51	SG	11	ILE
51	SG	15	VAL

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Mol	Chain	Res	Type
51	SG	20	LYS
51	SG	21	SER
51	SG	22	LEU
51	SG	24	ILE
51	SG	28	ARG
51	SG	31	GLN
51	SG	32	THR
51	SG	33	ILE
51	SG	34	HIS
51	SG	37	ARG
51	SG	38	MET
51	SG	41	GLU
51	SG	47	LEU
51	SG	49	GLU
51	SG	58	ILE
51	SG	59	THR
51	SG	65	GLN
51	SG	69	MET
51	SG	73	VAL
51	SG	74	LEU
51	SG	75	LYS
51	SG	76	SER
51	SG	77	GLN
51	SG	81	LEU
51	SG	82	LEU
51	SG	85	GLN
51	SG	88	LYS
51	SG	93	ARG
51	SG	94	ARG
51	SG	98	ARG
51	SG	99	LYS
51	SG	103	ILE
51	SG	107	ILE
51	SG	108	VAL
51	SG	113	HIS
51	SG	115	LEU
51	SG	116	SER
51	SG	117	VAL
51	SG	120	VAL
51	SG	124	ASP
51	SG	125	LYS
51	SG	126	THR

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Mol	Chain	Res	Type
51	SG	127	LEU
51	SG	131	THR
51	SG	133	VAL
51	SG	137	LYS
51	SG	138	ARG
51	SG	140	VAL
51	SG	141	PRO
51	SG	142	LYS
51	SG	148	ARG
51	SG	149	ARG
51	SG	150	LEU
51	SG	153	LEU
51	SG	155	THR
51	SG	157	LYS
51	SG	159	ASP
51	SG	161	LYS
51	SG	164	MET
51	SG	166	VAL
51	SG	167	CYS
51	SG	168	GLU
51	SG	169	LEU
51	SG	170	ILE
51	SG	171	LYS
51	SG	173	LEU
51	SG	176	GLU
51	SG	178	THR
51	SG	179	LEU
51	SG	180	LYS
51	SG	184	LYS
51	SG	185	LYS
51	SG	187	LYS
51	SG	190	LYS
51	SG	191	VAL
51	SG	192	GLN
51	SG	194	VAL
51	SG	195	VAL
51	SG	196	THR
51	SG	203	LYS
51	SG	207	ILE
51	SG	211	LYS
51	SG	213	ILE
51	SG	214	MET

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Mol	Chain	Res	Type
51	SG	216	LYS
51	SG	225	LYS
51	SG	227	LEU
51	SG	231	MET
51	SG	233	LYS
52	SH	7	ARG
52	SH	8	LYS
52	SH	11	LYS
52	SH	15	LYS
52	SH	16	LEU
52	SH	19	LEU
52	SH	23	VAL
52	SH	27	LEU
52	SH	29	LYS
52	SH	30	LEU
52	SH	31	GLU
52	SH	33	ASP
52	SH	36	LEU
52	SH	44	LEU
52	SH	46	ILE
52	SH	51	GLU
52	SH	52	ILE
52	SH	59	LYS
52	SH	62	VAL
52	SH	63	VAL
52	SH	65	VAL
52	SH	70	LEU
52	SH	72	SER
52	SH	74	GLN
52	SH	75	LYS
52	SH	76	ASN
52	SH	77	SER
52	SH	80	LEU
52	SH	81	ILE
52	SH	82	LEU
52	SH	83	LYS
52	SH	84	LEU
52	SH	86	LYS
52	SH	92	ARG
52	SH	94	ILE
52	SH	95	ILE
52	SH	96	VAL

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Mol	Chain	Res	Type
52	SH	100	THR
52	SH	107	VAL
52	SH	111	LYS
52	SH	112	LYS
52	SH	113	SER
52	SH	120	ARG
52	SH	121	THR
52	SH	122	MET
52	SH	125	VAL
52	SH	133	ILE
52	SH	137	ILE
52	SH	138	HIS
52	SH	139	VAL
52	SH	142	LYS
52	SH	143	ARG
52	SH	144	THR
52	SH	145	LEU
52	SH	151	ASN
52	SH	158	LEU
52	SH	162	VAL
52	SH	165	GLU
52	SH	166	VAL
52	SH	168	GLU
52	SH	169	ARG
52	SH	170	THR
52	SH	171	LYS
52	SH	172	THR
52	SH	176	VAL
52	SH	181	THR
52	SH	183	ARG
52	SH	185	THR
52	SH	188	ILE
52	SH	190	MET
53	SI	3	ILE
53	SI	4	THR
53	SI	8	MET
53	SI	10	LYS
53	SI	13	LYS
53	SI	17	VAL
53	SI	23	LYS
53	SI	24	LYS
53	SI	27	TYR

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Mol	Chain	Res	Type
53	SI	29	LEU
53	SI	41	LYS
53	SI	43	THR
53	SI	53	SER
53	SI	54	THR
53	SI	55	ILE
53	SI	58	ARG
53	SI	64	ARG
53	SI	67	LEU
53	SI	69	LEU
53	SI	70	SER
53	SI	73	SER
53	SI	78	SER
53	SI	81	ILE
53	SI	84	LYS
53	SI	86	ARG
53	SI	87	ILE
53	SI	93	ASN
53	SI	94	SER
53	SI	95	THR
53	SI	99	LEU
53	SI	101	ARG
53	SI	102	THR
53	SI	104	THR
53	SI	106	VAL
53	SI	110	VAL
53	SI	113	ILE
53	SI	119	LYS
53	SI	125	ASP
53	SI	127	LEU
53	SI	129	LYS
53	SI	130	GLU
53	SI	131	ILE
53	SI	135	ILE
53	SI	136	ARG
53	SI	139	HIS
53	SI	140	ILE
53	SI	141	LEU
53	SI	151	VAL
53	SI	153	THR
53	SI	155	ASP
53	SI	160	GLU

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Mol	Chain	Res	Type
53	SI	163	GLU
53	SI	168	GLN
53	SI	170	LYS
53	SI	171	LEU
53	SI	174	LYS
54	SJ	4	ILE
54	SJ	8	ARG
54	SJ	9	ASP
54	SJ	20	ILE
54	SJ	22	LYS
54	SJ	23	LYS
54	SJ	25	VAL
54	SJ	26	ILE
54	SJ	27	VAL
54	SJ	28	ARG
54	SJ	32	LYS
54	SJ	33	VAL
54	SJ	34	ILE
54	SJ	36	GLU
54	SJ	39	GLN
54	SJ	40	LEU
54	SJ	42	GLN
54	SJ	43	LYS
54	SJ	53	VAL
54	SJ	54	ASP
54	SJ	60	ARG
54	SJ	61	ILE
54	SJ	64	ASN
54	SJ	66	ILE
54	SJ	69	LEU
54	SJ	71	LYS
54	SJ	74	VAL
54	SJ	81	ILE
54	SJ	102	ILE
54	SJ	103	ILE
54	SJ	104	LEU
54	SJ	106	THR
54	SJ	107	SER
54	SJ	110	ILE
54	SJ	111	MET
54	SJ	115	GLU
54	SJ	118	HIS

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Mol	Chain	Res	Type
54	SJ	119	ARG
54	SJ	121	ILE
54	SJ	124	LYS
54	SJ	125	VAL
55	SK	3	ILE
55	SK	4	SER
55	SK	7	ARG
55	SK	9	SER
55	SK	10	SER
55	SK	13	TYR
55	SK	15	THR
55	SK	24	ARG
55	SK	25	LEU
55	SK	42	GLU
55	SK	43	ILE
55	SK	49	MET
55	SK	52	LYS
55	SK	53	ILE
55	SK	55	ARG
55	SK	64	ASP
55	SK	65	GLU
55	SK	67	ASP
55	SK	68	ILE
55	SK	69	LYS
55	SK	70	ARG
55	SK	71	ARG
55	SK	77	LEU
55	SK	78	LEU
55	SK	81	LEU
55	SK	83	MET
55	SK	86	ILE
55	SK	87	LEU
55	SK	92	ASP
55	SK	95	ASP
55	SK	98	LEU
55	SK	100	LEU
55	SK	103	GLU
55	SK	105	ILE
55	SK	107	LYS
55	SK	110	LEU
55	SK	111	GLN
55	SK	112	SER

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Mol	Chain	Res	Type
55	SK	113	VAL
55	SK	115	VAL
55	SK	116	GLU
55	SK	118	LYS
55	SK	121	LYS
55	SK	123	VAL
55	SK	129	MET
55	SK	130	ILE
55	SK	134	HIS
55	SK	135	ILE
55	SK	141	ILE
55	SK	142	VAL
55	SK	143	ASN
55	SK	144	ILE
55	SK	146	SER
55	SK	148	MET
55	SK	149	VAL
55	SK	152	SER
55	SK	159	ILE
55	SK	162	THR
55	SK	163	SER
55	SK	165	LEU
55	SK	168	ASN
55	SK	173	ARG
55	SK	174	THR
56	SL	2	VAL
56	SL	6	LYS
56	SL	9	TYR
56	SL	10	LYS
56	SL	12	VAL
56	SL	18	GLU
56	SL	22	LEU
56	SL	24	LEU
56	SL	25	LYS
56	SL	27	TYR
56	SL	29	ARG
56	SL	30	VAL
56	SL	36	ILE
56	SL	39	VAL
56	SL	45	LEU
56	SL	46	CYS
56	SL	47	ASN

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Mol	Chain	Res	Type
56	SL	49	THR
56	SL	50	TYR
56	SL	57	MET
56	SL	63	ARG
56	SL	66	VAL
56	SL	69	THR
56	SL	73	ARG
56	SL	78	LEU
56	SL	79	LEU
56	SL	81	GLU
56	SL	82	LYS
56	SL	84	GLU
56	SL	87	ILE
56	SL	89	LYS
56	SL	91	LEU
56	SL	92	ASP
56	SL	93	LEU
56	SL	94	THR
57	SM	5	GLN
57	SM	7	GLU
57	SM	8	ARG
57	SM	12	LYS
57	SM	16	ILE
57	SM	20	ARG
57	SM	22	LEU
57	SM	23	ARG
57	SM	24	LYS
57	SM	26	ASN
57	SM	28	ARG
57	SM	29	CYS
57	SM	31	ARG
57	SM	34	LYS
57	SM	35	SER
57	SM	41	HIS
57	SM	42	THR
57	SM	45	THR
57	SM	54	LYS
57	SM	55	LYS
57	SM	63	SER
57	SM	65	ARG
57	SM	67	ARG
57	SM	68	ILE

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Mol	Chain	Res	Type
57	SM	70	ARG
57	SM	72	VAL
57	SM	75	SER
57	SM	77	LYS
57	SM	78	MET
57	SM	79	GLN
57	SM	82	ILE
57	SM	93	GLN
57	SM	103	LYS
57	SM	105	VAL
57	SM	109	LEU
57	SM	114	ARG
57	SM	116	LYS
57	SM	121	VAL
57	SM	122	THR
57	SM	123	ILE
57	SM	129	LEU
57	SM	133	ILE
57	SM	138	ILE
57	SM	139	LYS
57	SM	143	VAL
57	SM	145	GLU
57	SM	149	LYS
57	SM	152	SER
58	SO	3	LYS
58	SO	4	THR
58	SO	7	LEU
58	SO	11	ARG
58	SO	19	ILE
58	SO	26	ARG
58	SO	32	LEU
58	SO	37	LYS
58	SO	39	ASN
58	SO	42	GLU
58	SO	45	CYS
58	SO	46	MET
58	SO	50	ILE
58	SO	54	LYS
58	SO	55	ILE
58	SO	57	ILE
58	SO	61	GLN
58	SO	71	ARG

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Mol	Chain	Res	Type
58	SO	76	LYS
58	SO	77	ASN
58	SO	80	LYS
58	SO	81	ILE
58	SO	85	VAL
58	SO	87	ARG
58	SO	91	LEU
58	SO	94	ILE
58	SO	95	ASP
58	SO	99	GLU
58	SO	100	VAL
58	SO	102	VAL
58	SO	105	PHE
58	SO	110	ARG
58	SO	115	ILE
58	SO	118	CYS
58	SO	121	LYS
58	SO	130	LEU
58	SO	131	LEU
58	SO	133	LEU
58	SO	136	ARG
58	SO	137	LYS
58	SO	139	GLU
58	SO	140	LYS
59	SP	3	ARG
59	SP	4	MET
59	SP	9	LYS
59	SP	11	ILE
59	SP	12	SER
59	SP	16	ILE
59	SP	19	THR
59	SP	25	TRP
59	SP	27	LYS
59	SP	29	THR
59	SP	32	ASP
59	SP	36	GLN
59	SP	37	ILE
59	SP	39	LYS
59	SP	45	THR
59	SP	54	LEU
59	SP	55	ARG
59	SP	66	VAL

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Mol	Chain	Res	Type
59	SP	67	THR
59	SP	70	LYS
59	SP	71	ILE
59	SP	73	ARG
59	SP	74	ILE
59	SP	75	LEU
59	SP	76	LYS
59	SP	78	LYS
59	SP	80	LEU
59	SP	83	GLU
59	SP	84	ILE
59	SP	87	ASP
59	SP	88	LEU
59	SP	91	MET
59	SP	93	LYS
59	SP	94	LYS
59	SP	100	LYS
59	SP	103	GLU
59	SP	104	ARG
59	SP	107	ARG
59	SP	120	SER
59	SP	135	LEU
59	SP	138	THR
59	SP	140	ARG
59	SP	142	LYS
59	SP	150	LEU
60	SQ	33	ILE
60	SQ	40	THR
60	SQ	42	ILE
60	SQ	44	VAL
60	SQ	47	LEU
60	SQ	51	GLU
60	SQ	52	THR
60	SQ	53	ILE
60	SQ	60	MET
60	SQ	62	VAL
60	SQ	66	CYS
60	SQ	78	THR
60	SQ	83	GLU
60	SQ	85	ILE
60	SQ	90	ILE
60	SQ	93	VAL

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Mol	Chain	Res	Type
60	SQ	95	ILE
60	SQ	96	LYS
60	SQ	105	LYS
60	SQ	106	ARG
60	SQ	107	VAL
60	SQ	117	ARG
60	SQ	121	ARG
60	SQ	128	ARG
60	SQ	129	ILE
60	SQ	135	ILE
60	SQ	140	THR
60	SQ	143	LYS
60	SQ	147	ARG
60	SQ	150	ARG
60	SQ	151	LEU
61	SR	16	ASN
61	SR	18	ARG
61	SR	20	VAL
61	SR	25	LEU
61	SR	27	THR
61	SR	28	MET
61	SR	29	LYS
61	SR	30	ILE
61	SR	31	THR
61	SR	32	ASP
61	SR	36	LYS
61	SR	38	ASN
61	SR	41	CYS
61	SR	42	ARG
61	SR	44	ARG
61	SR	47	LYS
61	SR	50	LEU
61	SR	51	SER
61	SR	53	LYS
61	SR	61	LEU
61	SR	68	GLN
61	SR	72	LYS
61	SR	74	LYS
61	SR	75	ILE
61	SR	78	THR
61	SR	80	LEU
61	SR	83	MET

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Mol	Chain	Res	Type
61	SR	84	ILE
61	SR	88	GLU
61	SR	89	MET
61	SR	96	VAL
61	SR	100	ARG
61	SR	101	GLN
61	SR	103	ILE
61	SR	108	LYS
61	SR	111	MET
61	SR	117	ARG
61	SR	121	MET
61	SR	122	SER
61	SR	124	LYS
61	SR	125	ILE
61	SR	126	VAL
62	ST	8	ASP
62	ST	9	LEU
62	ST	10	LEU
62	ST	12	ARG
62	ST	13	ASN
62	ST	14	ASP
62	ST	15	ILE
62	ST	17	VAL
62	ST	18	ARG
62	ST	21	ASP
62	ST	22	LYS
62	ST	27	THR
62	ST	28	LEU
62	ST	30	LYS
62	ST	31	LYS
62	ST	32	LYS
62	ST	33	ASN
62	ST	34	SER
62	ST	37	VAL
62	ST	41	LYS
62	ST	44	LYS
62	ST	46	ASP
62	ST	48	LEU
62	ST	49	VAL
62	ST	54	LEU
62	ST	57	VAL
62	ST	61	ILE

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Mol	Chain	Res	Type
62	ST	63	ARG
62	ST	64	THR
62	ST	65	LYS
62	ST	66	VAL
62	ST	67	SER
62	ST	70	ILE
62	ST	71	MET
62	ST	72	ILE
62	ST	77	LEU
62	ST	79	LYS
62	ST	82	ASP
62	ST	85	ILE
62	ST	87	VAL
62	ST	95	GLN
62	ST	100	ARG
62	ST	105	ARG
62	ST	107	VAL
62	ST	108	LEU
62	ST	111	VAL
62	ST	112	LYS
62	ST	117	ARG
62	ST	120	LEU
62	ST	123	LYS
62	ST	124	LEU
62	ST	125	VAL
62	ST	129	ARG
62	ST	133	VAL
62	ST	139	CYS
62	ST	143	LYS
62	ST	152	ARG
62	ST	153	ARG
62	ST	155	LYS
62	ST	157	TYR
62	ST	158	ARG
63	SU	3	LYS
63	SU	6	THR
63	SU	7	LYS
63	SU	11	ARG
63	SU	15	LYS
63	SU	21	TYR
63	SU	23	SER
63	SU	28	ASP

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Mol	Chain	Res	Type
63	SU	30	GLN
63	SU	38	LYS
63	SU	39	ARG
63	SU	43	ILE
63	SU	44	ILE
63	SU	48	ARG
63	SU	49	LEU
63	SU	50	ARG
63	SU	57	VAL
63	SU	58	THR
63	SU	59	THR
63	SU	61	MET
63	SU	63	ARG
63	SU	66	LYS
63	SU	73	SER
63	SU	74	LEU
63	SU	75	ARG
63	SU	77	GLN
63	SU	78	GLU
63	SU	80	GLU
63	SU	81	ARG
63	SU	82	GLU
63	SU	83	ARG
63	SU	90	LYS
63	SU	91	LYS
63	SU	95	ASP
63	SU	96	VAL
63	SU	102	SER
63	SU	105	THR
63	SU	111	SER
63	SU	119	THR
63	SU	121	LEU
63	SU	122	LYS
64	SV	13	LEU
64	SV	14	LEU
64	SV	16	MET
64	SV	24	LYS
64	SV	31	LEU
64	SV	32	VAL
64	SV	35	LYS
64	SV	37	ILE
64	SV	39	ARG

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Mol	Chain	Res	Type
64	SV	50	ASN
64	SV	51	ILE
64	SV	60	LEU
64	SV	61	THR
64	SV	65	GLU
64	SV	66	ASP
64	SV	68	LEU
64	SV	70	LYS
64	SV	73	GLU
64	SV	80	ILE
64	SV	84	MET
64	SV	85	LEU
64	SV	89	ASN
64	SV	91	PHE
64	SV	95	LYS
64	SV	96	ASP
64	SV	97	MET
64	SV	99	ILE
64	SV	100	LEU
64	SV	103	THR
64	SV	104	ILE
64	SV	113	GLU
64	SV	117	LYS
64	SV	118	THR
64	SV	119	ARG
64	SV	120	CYS
64	SV	121	GLU
64	SV	126	HIS
64	SV	132	VAL
64	SV	133	ARG
64	SV	136	HIS
64	SV	140	THR
65	SW	4	VAL
65	SW	5	THR
65	SW	13	ILE
65	SW	21	LYS
65	SW	23	ARG
65	SW	25	ILE
65	SW	27	LYS
65	SW	28	CYS
65	SW	33	ASP
65	SW	36	LYS

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Mol	Chain	Res	Type
65	SW	37	THR
65	SW	39	VAL
65	SW	40	SER
65	SW	46	ARG
65	SW	49	ASP
65	SW	57	SER
65	SW	59	ILE
65	SW	62	PHE
65	SW	64	ILE
65	SW	65	SER
65	SW	69	SER
65	SW	70	ILE
65	SW	77	ARG
65	SW	82	LEU
65	SW	86	LYS
65	SW	87	THR
65	SW	88	THR
65	SW	92	THR
65	SW	93	LYS
65	SW	94	ARG
65	SW	98	LYS
65	SW	99	VAL
65	SW	103	ILE
65	SW	108	LEU
65	SW	110	GLN
65	SW	111	LYS
65	SW	112	LEU
65	SW	113	LEU
65	SW	117	GLU
65	SW	120	ARG
65	SW	121	HIS
65	SW	125	ASN
65	SW	127	ARG
65	SW	129	MET
65	SW	137	LEU
65	SW	138	GLN
66	SX	28	ILE
66	SX	33	ASP
66	SX	35	LYS
66	SX	37	VAL
66	SX	38	GLU
66	SX	39	ARG

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Mol	Chain	Res	Type
66	SX	43	SER
66	SX	44	ILE
66	SX	45	VAL
66	SX	46	LYS
66	SX	54	SER
66	SX	58	ARG
66	SX	61	VAL
66	SX	62	ARG
66	SX	63	ARG
66	SX	67	THR
66	SX	75	GLU
66	SX	77	THR
66	SX	81	HIS
66	SX	84	GLU
66	SX	91	THR
66	SX	94	VAL
66	SX	100	ASP
66	SX	101	ILE
66	SX	102	SER
66	SX	104	ILE
66	SX	105	LEU
66	SX	106	SER
66	SX	110	VAL
66	SX	111	ILE
66	SX	114	ILE
66	SX	116	VAL
66	SX	118	VAL
66	SX	119	GLU
66	SX	120	VAL
67	SY	5	ASP
67	SY	6	ILE
67	SY	9	LYS
67	SY	11	SER
67	SY	12	SER
67	SY	14	VAL
67	SY	15	VAL
67	SY	16	VAL
67	SY	17	ASP
67	SY	20	ILE
67	SY	23	LYS
67	SY	24	CYS
67	SY	27	THR

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Mol	Chain	Res	Type
67	SY	29	ARG
67	SY	31	ILE
67	SY	34	LYS
67	SY	43	VAL
67	SY	46	VAL
67	SY	49	LYS
67	SY	52	MET
67	SY	53	ILE
67	SY	54	GLU
67	SY	55	ASN
67	SY	57	TYR
67	SY	58	VAL
67	SY	59	THR
67	SY	68	SER
67	SY	74	SER
67	SY	76	PHE
67	SY	77	MET
67	SY	79	LEU
67	SY	81	GLN
67	SY	82	GLU
67	SY	85	LEU
68	Sb	3	GLU
68	Sb	4	ILE
68	Sb	5	THR
68	Sb	9	ARG
68	Sb	11	VAL
68	Sb	12	LEU
68	Sb	14	ASN
68	Sb	16	LEU
68	Sb	17	LEU
68	Sb	20	GLN
68	Sb	24	VAL
68	Sb	31	CYS
68	Sb	32	THR
68	Sb	35	SER
68	Sb	36	LYS
68	Sb	37	GLU
68	Sb	39	ILE
68	Sb	40	LYS
68	Sb	47	LEU
68	Sb	48	LYS
68	Sb	52	GLN

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Mol	Chain	Res	Type
68	Sb	53	LYS
68	Sb	54	ASN
68	Sb	55	ILE
68	Sb	56	VAL
68	Sb	57	LEU
68	Sb	60	PHE
68	Sb	61	LYS
68	Sb	62	THR
68	Sb	63	SER
68	Sb	73	CYS
68	Sb	77	GLN
68	Sb	78	ASN
68	Sb	79	MET
68	Sb	82	LEU
68	Sb	84	LYS
68	Sb	91	LYS
68	Sb	92	ILE
68	Sb	96	LEU
68	Sb	97	ILE
68	Sb	105	ARG
68	Sb	108	LEU
68	Sb	111	LEU
68	Sb	117	LYS
68	Sb	118	LYS
69	Sc	15	VAL
69	Sc	16	ASP
69	Sc	19	THR
69	Sc	20	LEU
69	Sc	23	ASP
69	Sc	24	GLU
69	Sc	29	GLU
69	Sc	35	LYS
69	Sc	36	ASN
69	Sc	38	LYS
69	Sc	39	CYS
69	Sc	40	ILE
69	Sc	41	THR
69	Sc	45	ILE
69	Sc	47	GLU
69	Sc	48	ARG
69	Sc	50	ARG
69	Sc	53	VAL

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Mol	Chain	Res	Type
69	Sc	57	LYS
69	Sc	60	MET
69	Sc	63	LEU
69	Sc	64	VAL
69	Sc	66	SER
69	Sc	71	ILE
69	Sc	72	VAL
69	Sc	75	SER
69	Sc	77	ARG
69	Sc	78	MET
69	Sc	79	THR
69	Sc	82	LYS
69	Sc	83	ASN
69	Sc	84	MET
69	Sc	86	LYS
69	Sc	88	GLU
70	Sd	6	ARG
70	Sd	10	ARG
70	Sd	11	SER
70	Sd	12	LYS
70	Sd	15	CYS
70	Sd	18	THR
70	Sd	20	ILE
70	Sd	21	VAL
70	Sd	28	ARG
70	Sd	30	VAL
70	Sd	33	ASP
70	Sd	34	LYS
70	Sd	35	VAL
70	Sd	36	ILE
70	Sd	37	LYS
70	Sd	40	THR
70	Sd	41	ILE
70	Sd	45	VAL
70	Sd	47	ASN
70	Sd	48	THR
70	Sd	49	ILE
70	Sd	51	ASP
70	Sd	52	ASP
70	Sd	54	LEU
70	Sd	58	VAL
70	Sd	59	ILE

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Mol	Chain	Res	Type
70	Sd	64	ILE
70	Sd	66	LYS
70	Sd	68	TYR
70	Sd	71	VAL
70	Sd	79	ILE
70	Sd	87	ARG
70	Sd	93	LYS
71	Se	46	VAL
71	Se	48	LEU
71	Se	49	LEU
71	Se	54	VAL
71	Se	59	LYS
71	Se	61	LYS
71	Se	63	LYS
71	Se	67	GLN
71	Se	71	SER
71	Se	74	LEU
71	Se	75	GLU
71	Se	76	ILE
71	Se	77	LYS
71	Se	81	CYS
71	Se	83	ASP
71	Se	84	ILE
71	Se	86	VAL
71	Se	87	VAL
71	Se	89	SER
71	Se	92	ASN
71	Se	93	THR
71	Se	97	CYS
71	Se	102	SER
71	Se	103	GLN
71	Se	104	ILE
71	Se	106	ILE
71	Se	108	THR
71	Se	115	THR
71	Se	118	VAL
71	Se	120	ARG
71	Se	121	TYR
71	Se	122	ARG
72	Sg	5	ILE
72	Sg	9	VAL
72	Sg	11	GLU

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Mol	Chain	Res	Type
72	Sg	12	VAL
72	Sg	13	LEU
72	Sg	15	ARG
72	Sg	18	SER
72	Sg	19	ARG
72	Sg	22	ILE
72	Sg	23	THR
72	Sg	24	GLN
72	Sg	25	VAL
72	Sg	26	LYS
72	Sg	28	GLU
72	Sg	31	THR
72	Sg	34	LYS
72	Sg	36	GLN
72	Sg	37	ILE
72	Sg	38	ILE
72	Sg	39	ARG
72	Sg	40	ASN
72	Sg	45	VAL
72	Sg	47	LYS
72	Sg	51	LEU
72	Sg	52	VAL
72	Sg	55	GLU
72	Sg	57	GLU
72	Sg	58	ARG
72	Sg	59	GLU
72	Sg	61	ARG
72	Sg	62	ARG
72	Sg	63	LEU
72	Sg	64	ARG
73	Sh	88	ARG
73	Sh	91	GLU
73	Sh	92	PHE
73	Sh	94	THR
73	Sh	96	ILE
73	Sh	101	GLU
73	Sh	102	CYS
73	Sh	104	ILE
73	Sh	105	CYS
73	Sh	111	VAL
73	Sh	112	TYR
73	Sh	113	ARG

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Mol	Chain	Res	Type
73	Sh	117	LEU
73	Sh	119	ILE
73	Sh	120	CYS
73	Sh	121	ARG
73	Sh	122	ARG
73	Sh	130	LYS
73	Sh	131	ILE
73	Sh	134	VAL
73	Sh	135	LYS
73	Sh	136	LEU
74	Sj	1	ARG
74	Sj	3	HIS
74	Sj	6	LEU
74	Sj	7	THR
74	Sj	11	LYS
74	Sj	12	VAL
74	Sj	13	ARG
74	Sj	14	LYS
74	Sj	15	CYS
74	Sj	16	THR
74	Sj	18	LYS
74	Sj	19	LYS
74	Sj	26	ARG
74	Sj	31	ARG
74	Sj	34	LYS
74	Sj	35	ARG
74	Sj	36	LEU
74	Sj	40	LYS
74	Sj	43	VAL
74	Sj	46	THR
74	Sj	52	ARG
74	Sj	53	ARG
74	Sj	54	LEU
74	Sj	60	LEU
74	Sj	61	ILE
74	Sj	64	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (202) such sidechains are listed below:

Mol	Chain	Res	Type
1	LA	62	GLN
1	LA	73	ASN

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Mol	Chain	Res	Type
1	LA	194	ASN
1	LA	205	ASN
2	LB	42	HIS
2	LB	55	HIS
2	LB	68	HIS
2	LB	69	ASN
2	LB	109	HIS
2	LB	153	HIS
2	LB	187	ASN
2	LB	259	ASN
2	LB	290	ASN
2	LB	313	ASN
2	LB	345	HIS
2	LB	347	ASN
3	LC	14	GLN
3	LC	34	ASN
3	LC	61	HIS
3	LC	123	ASN
3	LC	210	ASN
3	LC	266	GLN
6	LF	17	GLN
6	LF	39	GLN
6	LF	81	HIS
6	LF	142	ASN
6	LF	272	GLN
7	LG	4	ASN
8	LH	63	ASN
8	LH	105	GLN
8	LH	115	ASN
8	LH	154	GLN
8	LH	181	HIS
9	LI	41	GLN
9	LI	43	GLN
9	LI	62	ASN
9	LI	87	HIS
9	LI	93	GLN
9	LI	152	HIS
10	LJ	46	HIS
10	LJ	105	ASN
10	LJ	183	GLN
11	LK	73	ASN
11	LK	163	GLN

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Mol	Chain	Res	Type
11	LK	207	ASN
12	LL	43	GLN
12	LL	63	GLN
13	LM	37	ASN
13	LM	92	GLN
13	LM	95	ASN
13	LM	171	GLN
14	LN	48	GLN
14	LN	60	GLN
14	LN	72	GLN
14	LN	96	GLN
15	LO	117	ASN
15	LO	153	ASN
15	LO	176	ASN
16	LP	69	HIS
16	LP	140	HIS
16	LP	186	GLN
17	LQ	96	GLN
17	LQ	133	HIS
18	LR	30	HIS
18	LR	69	HIS
19	LS	130	ASN
19	LS	146	GLN
20	LT	60	GLN
20	LT	122	ASN
20	LT	154	HIS
20	LT	165	GLN
21	LU	75	GLN
21	LU	95	HIS
22	LV	13	GLN
22	LV	46	ASN
22	LV	92	GLN
23	LW	101	GLN
23	LW	103	ASN
24	LX	46	ASN
25	LY	79	ASN
27	La	87	ASN
28	Lb	66	ASN
28	Lb	120	GLN
29	Lc	6	ASN
29	Lc	53	GLN
30	Ld	11	GLN

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Mol	Chain	Res	Type
30	Ld	50	ASN
31	Le	12	ASN
31	Le	34	GLN
31	Le	85	ASN
32	Lf	54	GLN
32	Lf	97	HIS
33	Lg	24	GLN
34	Lh	11	HIS
34	Lh	51	GLN
34	Lh	62	HIS
35	Li	46	GLN
35	Li	91	ASN
36	Lj	29	HIS
36	Lj	72	ASN
36	Lj	89	ASN
37	Lk	12	HIS
38	Ll	53	ASN
39	Ln	5	ASN
39	Ln	89	HIS
39	Ln	94	ASN
39	Ln	188	ASN
39	Ln	200	ASN
41	Lp	81	GLN
42	Lq	25	GLN
43	Ls	92	ASN
43	Ls	98	HIS
45	SA	47	GLN
45	SA	100	HIS
46	SB	81	GLN
46	SB	125	ASN
46	SB	194	GLN
46	SB	203	ASN
47	SC	28	HIS
47	SC	89	ASN
47	SC	151	GLN
48	SD	40	HIS
48	SD	43	GLN
48	SD	81	ASN
48	SD	99	ASN
48	SD	155	HIS
48	SD	190	ASN
48	SD	194	ASN

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Mol	Chain	Res	Type
48	SD	202	GLN
49	SE	96	HIS
49	SE	188	ASN
49	SE	230	ASN
49	SE	250	ASN
50	SF	65	HIS
50	SF	68	ASN
50	SF	123	GLN
51	SG	19	ASN
51	SG	31	GLN
51	SG	62	ASN
51	SG	65	GLN
51	SG	71	GLN
51	SG	95	ASN
51	SG	204	GLN
51	SG	236	ASN
52	SH	22	GLN
52	SH	74	GLN
52	SH	76	ASN
53	SI	5	HIS
53	SI	61	ASN
53	SI	83	HIS
53	SI	89	GLN
53	SI	134	GLN
54	SJ	56	HIS
54	SJ	101	HIS
54	SJ	113	HIS
56	SL	15	HIS
56	SL	19	ASN
56	SL	47	ASN
57	SM	6	HIS
57	SM	26	ASN
58	SO	31	HIS
58	SO	96	ASN
60	SQ	32	HIS
60	SQ	79	GLN
60	SQ	142	HIS
61	SR	79	HIS
61	SR	128	HIS
62	ST	92	HIS
63	SU	30	GLN
63	SU	51	ASN

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Mol	Chain	Res	Type
64	SV	86	ASN
64	SV	88	ASN
64	SV	89	ASN
64	SV	98	HIS
65	SW	68	HIS
65	SW	91	HIS
65	SW	121	HIS
65	SW	138	GLN
66	SX	78	ASN
66	SX	115	GLN
67	SY	28	ASN
67	SY	40	GLN
67	SY	81	GLN
68	Sb	14	ASN
68	Sb	46	GLN
68	Sb	52	GLN
68	Sb	78	ASN
69	Sc	28	ASN
69	Sc	42	HIS
69	Sc	44	GLN
69	Sc	83	ASN
70	Sd	17	HIS
70	Sd	25	ASN
70	Sd	47	ASN
70	Sd	72	GLN
71	Se	45	ASN
71	Se	60	HIS
71	Se	90	HIS
71	Se	117	GLN
72	Sg	6	ASN
72	Sg	40	ASN
73	Sh	127	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	LD	141/142 (99%)	48 (34%)	4 (2%)
44	Lt	2588/2697 (95%)	988 (38%)	0
5	LE	116/121 (95%)	39 (33%)	4 (3%)
75	St	1453/1454 (99%)	714 (49%)	0
76	u	74/75 (98%)	35 (47%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
77	v	74/75 (98%)	46 (62%)	0
78	y	10/11 (90%)	7 (70%)	0
All	All	4456/4575 (97%)	1877 (42%)	8 (0%)

All (1877) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	LD	6	C
4	LD	9	C
4	LD	10	G
4	LD	14	G
4	LD	20	G
4	LD	21	C
4	LD	22	C
4	LD	24	C
4	LD	25	G
4	LD	27	C
4	LD	28	C
4	LD	29	C
4	LD	31	G
4	LD	33	C
4	LD	35	G
4	LD	39	C
4	LD	40	G
4	LD	52	G
4	LD	59	G
4	LD	60	A
4	LD	64	G
4	LD	70	C
4	LD	72	G
4	LD	73	A
4	LD	75	C
4	LD	76	C
4	LD	80	C
4	LD	81	G
4	LD	85	C
4	LD	86	G
4	LD	87	A
4	LD	88	G
4	LD	89	A
4	LD	104	A
4	LD	105	A

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Mol	Chain	Res	Type
4	LD	106	C
4	LD	108	C
4	LD	110	G
4	LD	111	C
4	LD	112	G
4	LD	117	C
4	LD	118	C
4	LD	124	C
4	LD	126	C
4	LD	133	G
4	LD	135	C
4	LD	138	C
4	LD	140	G
5	LE	3	G
5	LE	4	U
5	LE	7	G
5	LE	11	A
5	LE	12	U
5	LE	22	G
5	LE	23	A
5	LE	30	U
5	LE	32	A
5	LE	33	A
5	LE	38	U
5	LE	39	U
5	LE	42	G
5	LE	44	A
5	LE	50	A
5	LE	51	A
5	LE	54	G
5	LE	55	A
5	LE	56	A
5	LE	59	G
5	LE	63	U
5	LE	64	C
5	LE	65	A
5	LE	78	A
5	LE	79	C
5	LE	83	G
5	LE	85	U
5	LE	86	C
5	LE	87	G

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Mol	Chain	Res	Type
5	LE	95	C
5	LE	96	G
5	LE	98	G
5	LE	99	G
5	LE	102	A
5	LE	110	U
5	LE	111	G
5	LE	113	C
5	LE	114	G
5	LE	115	A
44	Lt	2	G
44	Lt	3	C
44	Lt	4	G
44	Lt	9	U
44	Lt	10	G
44	Lt	24	G
44	Lt	25	A
44	Lt	30	C
44	Lt	39	A
44	Lt	42	A
44	Lt	43	U
44	Lt	48	G
44	Lt	49	U
44	Lt	58	G
44	Lt	59	A
44	Lt	64	A
44	Lt	65	A
44	Lt	66	A
44	Lt	67	C
44	Lt	70	A
44	Lt	71	C
44	Lt	72	C
44	Lt	73	G
44	Lt	74	G
44	Lt	84	C
44	Lt	85	U
44	Lt	86	A
44	Lt	87	G
44	Lt	90	G
44	Lt	100	C
44	Lt	107	A
44	Lt	109	C

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Mol	Chain	Res	Type
44	Lt	117	G
44	Lt	118	A
44	Lt	119	A
44	Lt	120	G
44	Lt	121	G
44	Lt	122	C
44	Lt	123	G
44	Lt	124	C
44	Lt	127	U
44	Lt	128	G
44	Lt	129	U
44	Lt	153	C
44	Lt	158	G
44	Lt	166	G
44	Lt	167	G
44	Lt	168	G
44	Lt	169	C
44	Lt	173	G
44	Lt	176	C
44	Lt	179	G
44	Lt	181	G
44	Lt	185	G
44	Lt	186	C
44	Lt	187	A
44	Lt	190	C
44	Lt	194	G
44	Lt	222	A
44	Lt	224	U
44	Lt	230	U
44	Lt	235	G
44	Lt	238	C
44	Lt	239	G
44	Lt	248	G
44	Lt	249	A
44	Lt	250	A
44	Lt	251	G
44	Lt	256	G
44	Lt	258	G
44	Lt	259	C
44	Lt	263	C
44	Lt	267	C
44	Lt	281	G

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Mol	Chain	Res	Type
44	Lt	289	A
44	Lt	290	C
44	Lt	294	U
44	Lt	295	A
44	Lt	301	C
44	Lt	302	C
44	Lt	303	A
44	Lt	304	A
44	Lt	305	G
44	Lt	314	G
44	Lt	317	A
44	Lt	321	G
44	Lt	322	U
44	Lt	326	A
44	Lt	327	A
44	Lt	328	G
44	Lt	335	C
44	Lt	336	U
44	Lt	339	G
44	Lt	340	G
44	Lt	343	G
44	Lt	349	A
44	Lt	350	A
44	Lt	351	G
44	Lt	352	A
44	Lt	356	G
44	Lt	357	A
44	Lt	366	G
44	Lt	369	C
44	Lt	370	G
44	Lt	372	C
44	Lt	375	C
44	Lt	376	C
44	Lt	377	C
44	Lt	378	G
44	Lt	379	C
44	Lt	384	C
44	Lt	388	U
44	Lt	389	C
44	Lt	397	A
44	Lt	405	A
44	Lt	424	G

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Mol	Chain	Res	Type
44	Lt	425	A
44	Lt	427	C
44	Lt	429	C
44	Lt	430	G
44	Lt	434	G
44	Lt	435	A
44	Lt	436	G
44	Lt	437	C
44	Lt	438	C
44	Lt	443	C
44	Lt	444	G
44	Lt	449	A
44	Lt	454	G
44	Lt	456	G
44	Lt	459	A
44	Lt	460	G
44	Lt	463	G
44	Lt	477	A
44	Lt	479	G
44	Lt	484	U
44	Lt	485	G
44	Lt	486	C
44	Lt	491	G
44	Lt	492	U
44	Lt	493	G
44	Lt	494	C
44	Lt	497	G
44	Lt	500	C
44	Lt	501	C
44	Lt	502	G
44	Lt	503	A
44	Lt	504	G
44	Lt	513	C
44	Lt	515	U
44	Lt	517	G
44	Lt	518	G
44	Lt	520	C
44	Lt	525	A
44	Lt	533	A
44	Lt	534	U
44	Lt	537	A
44	Lt	546	G

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Mol	Chain	Res	Type
44	Lt	547	A
44	Lt	549	G
44	Lt	550	G
44	Lt	554	G
44	Lt	555	G
44	Lt	556	C
44	Lt	561	C
44	Lt	562	G
44	Lt	564	A
44	Lt	566	G
44	Lt	571	G
44	Lt	574	G
44	Lt	575	A
44	Lt	578	C
44	Lt	588	U
44	Lt	591	U
44	Lt	596	C
44	Lt	605	C
44	Lt	611	G
44	Lt	612	G
44	Lt	613	A
44	Lt	624	G
44	Lt	625	G
44	Lt	631	A
44	Lt	632	A
44	Lt	633	G
44	Lt	634	A
44	Lt	637	C
44	Lt	640	C
44	Lt	641	G
44	Lt	642	A
44	Lt	650	G
44	Lt	654	G
44	Lt	656	U
44	Lt	661	G
44	Lt	662	C
44	Lt	666	C
44	Lt	670	A
44	Lt	677	C
44	Lt	678	C
44	Lt	679	A
44	Lt	681	G

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Mol	Chain	Res	Type
44	Lt	688	G
44	Lt	691	G
44	Lt	692	C
44	Lt	694	C
44	Lt	695	C
44	Lt	696	G
44	Lt	699	G
44	Lt	706	C
44	Lt	708	C
44	Lt	709	G
44	Lt	715	C
44	Lt	719	G
44	Lt	720	G
44	Lt	721	C
44	Lt	722	C
44	Lt	723	G
44	Lt	724	G
44	Lt	727	G
44	Lt	728	G
44	Lt	731	C
44	Lt	732	G
44	Lt	734	G
44	Lt	737	G
44	Lt	738	C
44	Lt	741	G
44	Lt	742	C
44	Lt	743	C
44	Lt	747	C
44	Lt	749	C
44	Lt	755	C
44	Lt	756	C
44	Lt	757	C
44	Lt	760	A
44	Lt	764	C
44	Lt	767	A
44	Lt	769	G
44	Lt	770	G
44	Lt	776	G
44	Lt	777	C
44	Lt	785	C
44	Lt	787	G
44	Lt	788	C

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Mol	Chain	Res	Type
44	Lt	789	U
44	Lt	790	G
44	Lt	791	G
44	Lt	794	U
44	Lt	798	C
44	Lt	799	G
44	Lt	802	G
44	Lt	803	C
44	Lt	804	G
44	Lt	805	G
44	Lt	806	G
44	Lt	807	C
44	Lt	808	G
44	Lt	809	A
44	Lt	814	G
44	Lt	821	G
44	Lt	827	G
44	Lt	829	C
44	Lt	832	U
44	Lt	834	C
44	Lt	839	A
44	Lt	841	G
44	Lt	854	G
44	Lt	860	A
44	Lt	861	C
44	Lt	862	G
44	Lt	863	A
44	Lt	864	U
44	Lt	865	C
44	Lt	866	C
44	Lt	869	A
44	Lt	870	C
44	Lt	871	G
44	Lt	873	C
44	Lt	878	C
44	Lt	882	G
44	Lt	888	C
44	Lt	889	G
44	Lt	890	C
44	Lt	891	C
44	Lt	897	C
44	Lt	899	G

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Mol	Chain	Res	Type
44	Lt	900	C
44	Lt	901	G
44	Lt	906	G
44	Lt	907	G
44	Lt	908	C
44	Lt	909	G
44	Lt	919	C
44	Lt	920	C
44	Lt	921	C
44	Lt	922	G
44	Lt	923	A
44	Lt	984	C
44	Lt	985	G
44	Lt	986	A
44	Lt	987	A
44	Lt	990	G
44	Lt	994	G
44	Lt	997	C
44	Lt	998	C
44	Lt	999	G
44	Lt	1001	A
44	Lt	1003	A
44	Lt	1005	U
44	Lt	1006	G
44	Lt	1007	G
44	Lt	1008	A
44	Lt	1009	G
44	Lt	1015	C
44	Lt	1016	G
44	Lt	1018	A
44	Lt	1019	G
44	Lt	1021	C
44	Lt	1024	G
44	Lt	1025	G
44	Lt	1026	A
44	Lt	1028	C
44	Lt	1029	C
44	Lt	1030	G
44	Lt	1031	C
44	Lt	1032	G
44	Lt	1036	G
44	Lt	1038	C

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Mol	Chain	Res	Type
44	Lt	1039	C
44	Lt	1040	G
44	Lt	1044	C
44	Lt	1045	G
44	Lt	1046	C
44	Lt	1047	G
44	Lt	1053	G
44	Lt	1054	G
44	Lt	1055	U
44	Lt	1058	G
44	Lt	1062	C
44	Lt	1073	C
44	Lt	1074	C
44	Lt	1075	G
44	Lt	1076	G
44	Lt	1077	G
44	Lt	1079	G
44	Lt	1080	C
44	Lt	1081	G
44	Lt	1082	A
44	Lt	1087	G
44	Lt	1091	C
44	Lt	1095	G
44	Lt	1096	G
44	Lt	1105	G
44	Lt	1109	G
44	Lt	1117	G
44	Lt	1118	U
44	Lt	1120	C
44	Lt	1122	G
44	Lt	1125	C
44	Lt	1126	U
44	Lt	1134	A
44	Lt	1135	G
44	Lt	1136	U
44	Lt	1138	G
44	Lt	1140	C
44	Lt	1143	U
44	Lt	1144	A
44	Lt	1150	C
44	Lt	1151	G
44	Lt	1152	C

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Mol	Chain	Res	Type
44	Lt	1153	C
44	Lt	1154	C
44	Lt	1159	G
44	Lt	1161	A
44	Lt	1162	C
44	Lt	1165	A
44	Lt	1166	G
44	Lt	1167	G
44	Lt	1168	G
44	Lt	1169	G
44	Lt	1171	A
44	Lt	1172	G
44	Lt	1178	U
44	Lt	1191	G
44	Lt	1192	C
44	Lt	1195	C
44	Lt	1196	U
44	Lt	1198	G
44	Lt	1199	C
44	Lt	1204	G
44	Lt	1207	G
44	Lt	1210	U
44	Lt	1217	U
44	Lt	1220	G
44	Lt	1225	G
44	Lt	1226	G
44	Lt	1230	A
44	Lt	1231	A
44	Lt	1233	A
44	Lt	1236	G
44	Lt	1237	G
44	Lt	1238	G
44	Lt	1239	A
44	Lt	1240	A
44	Lt	1241	G
44	Lt	1242	G
44	Lt	1243	G
44	Lt	1244	G
44	Lt	1249	C
44	Lt	1252	G
44	Lt	1253	C
44	Lt	1256	G

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Mol	Chain	Res	Type
44	Lt	1257	U
44	Lt	1258	C
44	Lt	1260	A
44	Lt	1261	A
44	Lt	1262	C
44	Lt	1264	G
44	Lt	1268	G
44	Lt	1272	G
44	Lt	1273	C
44	Lt	1275	G
44	Lt	1277	G
44	Lt	1278	A
44	Lt	1279	C
44	Lt	1280	U
44	Lt	1282	C
44	Lt	1284	G
44	Lt	1286	A
44	Lt	1290	G
44	Lt	1292	G
44	Lt	1298	C
44	Lt	1299	G
44	Lt	1300	C
44	Lt	1303	A
44	Lt	1306	C
44	Lt	1307	G
44	Lt	1308	C
44	Lt	1309	C
44	Lt	1310	C
44	Lt	1311	G
44	Lt	1317	C
44	Lt	1318	G
44	Lt	1323	C
44	Lt	1324	G
44	Lt	1328	A
44	Lt	1329	C
44	Lt	1331	G
44	Lt	1339	G
44	Lt	1346	G
44	Lt	1347	G
44	Lt	1349	G
44	Lt	1350	C
44	Lt	1355	G

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Mol	Chain	Res	Type
44	Lt	1356	C
44	Lt	1357	C
44	Lt	1361	G
44	Lt	1365	G
44	Lt	1369	C
44	Lt	1375	C
44	Lt	1376	C
44	Lt	1377	C
44	Lt	1379	G
44	Lt	1380	G
44	Lt	1381	A
44	Lt	1382	C
44	Lt	1383	G
44	Lt	1384	C
44	Lt	1386	U
44	Lt	1387	U
44	Lt	1389	C
44	Lt	1392	G
44	Lt	1394	A
44	Lt	1395	G
44	Lt	1400	G
44	Lt	1401	G
44	Lt	1402	G
44	Lt	1406	G
44	Lt	1407	G
44	Lt	1419	G
44	Lt	1423	G
44	Lt	1424	U
44	Lt	1434	C
44	Lt	1435	C
44	Lt	1438	U
44	Lt	1439	G
44	Lt	1440	A
44	Lt	1448	G
44	Lt	1449	G
44	Lt	1451	G
44	Lt	1452	G
44	Lt	1454	G
44	Lt	1455	C
44	Lt	1456	C
44	Lt	1457	G
44	Lt	1461	G

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Mol	Chain	Res	Type
44	Lt	1464	C
44	Lt	1469	U
44	Lt	1470	A
44	Lt	1473	G
44	Lt	1474	A
44	Lt	1476	C
44	Lt	1477	G
44	Lt	1478	C
44	Lt	1479	A
44	Lt	1481	C
44	Lt	1482	A
44	Lt	1484	G
44	Lt	1485	A
44	Lt	1489	C
44	Lt	1490	G
44	Lt	1495	C
44	Lt	1496	A
44	Lt	1498	C
44	Lt	1499	A
44	Lt	1502	C
44	Lt	1509	G
44	Lt	1510	C
44	Lt	1511	G
44	Lt	1512	G
44	Lt	1513	G
44	Lt	1514	A
44	Lt	1515	G
44	Lt	1516	C
44	Lt	1521	G
44	Lt	1524	G
44	Lt	1528	A
44	Lt	1531	G
44	Lt	1533	A
44	Lt	1538	G
44	Lt	1552	U
44	Lt	1558	C
44	Lt	1562	A
44	Lt	1563	A
44	Lt	1567	G
44	Lt	1571	G
44	Lt	1578	A
44	Lt	1579	C

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Mol	Chain	Res	Type
44	Lt	1580	G
44	Lt	1581	G
44	Lt	1582	C
44	Lt	1585	G
44	Lt	1586	C
44	Lt	1587	C
44	Lt	1589	G
44	Lt	1590	G
44	Lt	1592	C
44	Lt	1593	A
44	Lt	1594	G
44	Lt	1596	A
44	Lt	1599	G
44	Lt	1600	G
44	Lt	1601	A
44	Lt	1602	A
44	Lt	1603	C
44	Lt	1604	G
44	Lt	1605	G
44	Lt	1611	G
44	Lt	1615	U
44	Lt	1619	G
44	Lt	1620	A
44	Lt	1624	U
44	Lt	1626	U
44	Lt	1629	U
44	Lt	1633	A
44	Lt	1634	A
44	Lt	1635	C
44	Lt	1641	G
44	Lt	1646	G
44	Lt	1647	A
44	Lt	1648	G
44	Lt	1649	G
44	Lt	1655	A
44	Lt	1656	C
44	Lt	1657	C
44	Lt	1658	C
44	Lt	1664	U
44	Lt	1665	G
44	Lt	1672	C
44	Lt	1673	G

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Mol	Chain	Res	Type
44	Lt	1680	C
44	Lt	1689	G
44	Lt	1690	C
44	Lt	1692	A
44	Lt	1693	C
44	Lt	1694	G
44	Lt	1697	C
44	Lt	1698	G
44	Lt	1702	C
44	Lt	1707	A
44	Lt	1710	C
44	Lt	1712	A
44	Lt	1713	U
44	Lt	1719	G
44	Lt	1720	A
44	Lt	1722	G
44	Lt	1727	G
44	Lt	1728	G
44	Lt	1731	A
44	Lt	1732	A
44	Lt	1740	A
44	Lt	1743	A
44	Lt	1744	A
44	Lt	1745	C
44	Lt	1746	U
44	Lt	1747	A
44	Lt	1748	U
44	Lt	1749	G
44	Lt	1750	A
44	Lt	1751	C
44	Lt	1753	C
44	Lt	1754	U
44	Lt	1755	C
44	Lt	1757	U
44	Lt	1758	A
44	Lt	1760	G
44	Lt	1761	G
44	Lt	1764	G
44	Lt	1767	A
44	Lt	1768	A
44	Lt	1769	A
44	Lt	1772	C

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Mol	Chain	Res	Type
44	Lt	1774	U
44	Lt	1775	C
44	Lt	1783	A
44	Lt	1786	U
44	Lt	1787	U
44	Lt	1789	C
44	Lt	1793	G
44	Lt	1794	U
44	Lt	1795	G
44	Lt	1796	C
44	Lt	1798	U
44	Lt	1801	A
44	Lt	1802	U
44	Lt	1803	G
44	Lt	1807	C
44	Lt	1808	A
44	Lt	1811	G
44	Lt	1814	G
44	Lt	1822	U
44	Lt	1823	G
44	Lt	1824	U
44	Lt	1832	C
44	Lt	1833	G
44	Lt	1835	G
44	Lt	1842	C
44	Lt	1845	G
44	Lt	1846	C
44	Lt	1851	A
44	Lt	1852	G
44	Lt	1859	G
44	Lt	1860	A
44	Lt	1861	A
44	Lt	1862	C
44	Lt	1863	G
44	Lt	1864	G
44	Lt	1865	G
44	Lt	1866	C
44	Lt	1867	G
44	Lt	1868	A
44	Lt	1873	C
44	Lt	1876	C
44	Lt	1879	G

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Mol	Chain	Res	Type
44	Lt	1881	G
44	Lt	1885	C
44	Lt	1886	A
44	Lt	1887	A
44	Lt	1888	G
44	Lt	1889	A
44	Lt	1890	A
44	Lt	1891	G
44	Lt	1892	A
44	Lt	1893	C
44	Lt	1899	U
44	Lt	1902	G
44	Lt	1905	U
44	Lt	1907	A
44	Lt	1910	C
44	Lt	1914	C
44	Lt	1915	C
44	Lt	1922	U
44	Lt	1923	G
44	Lt	1925	G
44	Lt	1926	G
44	Lt	1927	G
44	Lt	1928	G
44	Lt	1930	G
44	Lt	1931	G
44	Lt	1932	G
44	Lt	1934	C
44	Lt	1936	G
44	Lt	1939	G
44	Lt	1940	G
44	Lt	1941	C
44	Lt	1942	G
44	Lt	1943	C
44	Lt	1944	A
44	Lt	1945	G
44	Lt	1946	C
44	Lt	1947	G
44	Lt	1948	C
44	Lt	1949	A
44	Lt	1950	C
44	Lt	1953	G
44	Lt	1954	G

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Mol	Chain	Res	Type
44	Lt	1956	A
44	Lt	1957	G
44	Lt	1958	G
44	Lt	1959	C
44	Lt	1960	C
44	Lt	1961	G
44	Lt	1962	C
44	Lt	1963	G
44	Lt	1964	C
44	Lt	1965	C
44	Lt	1967	C
44	Lt	1968	U
44	Lt	1969	G
44	Lt	1971	G
44	Lt	1972	A
44	Lt	1973	C
44	Lt	1974	A
44	Lt	1975	C
44	Lt	1976	C
44	Lt	1977	C
44	Lt	1978	U
44	Lt	1979	G
44	Lt	1982	G
44	Lt	1984	C
44	Lt	1985	C
44	Lt	1986	G
44	Lt	1988	C
44	Lt	1989	G
44	Lt	1990	C
44	Lt	1991	C
44	Lt	1999	U
44	Lt	2000	C
44	Lt	2004	C
44	Lt	2005	G
44	Lt	2006	G
44	Lt	2008	C
44	Lt	2009	G
44	Lt	2010	C
44	Lt	2012	C
44	Lt	2017	A
44	Lt	2018	C
44	Lt	2022	C

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Mol	Chain	Res	Type
44	Lt	2023	C
44	Lt	2030	G
44	Lt	2031	G
44	Lt	2032	G
44	Lt	2038	G
44	Lt	2048	G
44	Lt	2049	C
44	Lt	2050	G
44	Lt	2051	C
44	Lt	2052	G
44	Lt	2053	C
44	Lt	2059	A
44	Lt	2060	C
44	Lt	2061	A
44	Lt	2065	G
44	Lt	2066	A
44	Lt	2068	C
44	Lt	2072	G
44	Lt	2075	G
44	Lt	2076	U
44	Lt	2077	C
44	Lt	2080	A
44	Lt	2082	G
44	Lt	2084	C
44	Lt	2089	U
44	Lt	2090	C
44	Lt	2092	G
44	Lt	2093	C
44	Lt	2097	G
44	Lt	2098	A
44	Lt	2100	G
44	Lt	2101	G
44	Lt	2104	A
44	Lt	2105	C
44	Lt	2106	C
44	Lt	2107	U
44	Lt	2108	C
44	Lt	2112	C
44	Lt	2113	G
44	Lt	2114	G
44	Lt	2115	A
44	Lt	2116	G

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Mol	Chain	Res	Type
44	Lt	2118	A
44	Lt	2120	A
44	Lt	2124	G
44	Lt	2126	A
44	Lt	2128	A
44	Lt	2129	A
44	Lt	2130	G
44	Lt	2132	C
44	Lt	2134	G
44	Lt	2137	C
44	Lt	2138	G
44	Lt	2140	C
44	Lt	2142	C
44	Lt	2143	G
44	Lt	2144	C
44	Lt	2151	C
44	Lt	2152	G
44	Lt	2154	G
44	Lt	2163	G
44	Lt	2170	A
44	Lt	2171	A
44	Lt	2177	G
44	Lt	2178	G
44	Lt	2184	C
44	Lt	2185	G
44	Lt	2186	A
44	Lt	2200	C
44	Lt	2201	G
44	Lt	2202	G
44	Lt	2203	C
44	Lt	2213	G
44	Lt	2217	G
44	Lt	2218	U
44	Lt	2219	G
44	Lt	2220	G
44	Lt	2221	C
44	Lt	2222	A
44	Lt	2223	G
44	Lt	2224	A
44	Lt	2225	A
44	Lt	2226	A
44	Lt	2230	U

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Mol	Chain	Res	Type
44	Lt	2231	A
44	Lt	2232	C
44	Lt	2233	C
44	Lt	2234	A
44	Lt	2235	C
44	Lt	2237	G
44	Lt	2239	G
44	Lt	2240	A
44	Lt	2242	A
44	Lt	2244	C
44	Lt	2246	G
44	Lt	2247	G
44	Lt	2250	U
44	Lt	2254	G
44	Lt	2255	C
44	Lt	2261	A
44	Lt	2268	G
44	Lt	2270	A
44	Lt	2272	C
44	Lt	2273	G
44	Lt	2276	G
44	Lt	2278	G
44	Lt	2281	U
44	Lt	2284	U
44	Lt	2285	U
44	Lt	2286	G
44	Lt	2290	C
44	Lt	2291	U
44	Lt	2294	G
44	Lt	2298	U
44	Lt	2308	C
44	Lt	2310	A
44	Lt	2311	C
44	Lt	2313	G
44	Lt	2317	G
44	Lt	2321	G
44	Lt	2322	C
44	Lt	2326	G
44	Lt	2334	A
44	Lt	2339	C
44	Lt	2341	G
44	Lt	2348	C

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Mol	Chain	Res	Type
44	Lt	2355	U
44	Lt	2356	C
44	Lt	2357	A
44	Lt	2358	A
44	Lt	2363	U
44	Lt	2364	C
44	Lt	2365	G
44	Lt	2369	G
44	Lt	2372	G
44	Lt	2373	G
44	Lt	2374	G
44	Lt	2376	U
44	Lt	2377	U
44	Lt	2381	C
44	Lt	2383	G
44	Lt	2393	A
44	Lt	2394	G
44	Lt	2400	U
44	Lt	2401	U
44	Lt	2402	U
44	Lt	2405	C
44	Lt	2406	C
44	Lt	2409	A
44	Lt	2411	U
44	Lt	2412	G
44	Lt	2417	C
44	Lt	2421	G
44	Lt	2429	A
44	Lt	2430	C
44	Lt	2436	G
44	Lt	2437	C
44	Lt	2439	A
44	Lt	2441	U
44	Lt	2456	C
44	Lt	2457	G
44	Lt	2464	G
44	Lt	2467	G
44	Lt	2469	C
44	Lt	2471	G
44	Lt	2472	C
44	Lt	2474	C
44	Lt	2476	G

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Mol	Chain	Res	Type
44	Lt	2483	C
44	Lt	2491	G
44	Lt	2495	G
44	Lt	2496	C
44	Lt	2497	G
44	Lt	2503	C
44	Lt	2506	C
44	Lt	2508	G
44	Lt	2509	C
44	Lt	2514	G
44	Lt	2515	G
44	Lt	2516	G
44	Lt	2523	G
44	Lt	2532	G
44	Lt	2533	C
44	Lt	2539	A
44	Lt	2545	C
44	Lt	2546	A
44	Lt	2547	C
44	Lt	2563	G
44	Lt	2567	G
44	Lt	2568	G
44	Lt	2572	C
44	Lt	2573	G
44	Lt	2575	G
44	Lt	2576	C
44	Lt	2577	C
44	Lt	2579	C
44	Lt	2580	A
44	Lt	2581	G
44	Lt	2583	C
44	Lt	2584	C
44	Lt	2585	C
44	Lt	2587	U
44	Lt	2588	G
44	Lt	2591	C
44	Lt	2592	C
44	Lt	2593	G
44	Lt	2594	U
44	Lt	2595	C
44	Lt	2598	C
44	Lt	2602	C

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Mol	Chain	Res	Type
44	Lt	2603	G
44	Lt	2604	G
44	Lt	2605	C
44	Lt	2608	C
44	Lt	2609	C
44	Lt	2610	G
44	Lt	2611	C
44	Lt	2617	G
44	Lt	2618	A
44	Lt	2625	C
44	Lt	2627	G
44	Lt	2628	G
44	Lt	2629	C
44	Lt	2630	G
44	Lt	2632	G
44	Lt	2634	C
44	Lt	2638	C
44	Lt	2643	A
44	Lt	2649	C
44	Lt	2653	G
44	Lt	2656	C
44	Lt	2658	G
44	Lt	2663	C
44	Lt	2668	G
44	Lt	2669	A
44	Lt	2675	G
44	Lt	2679	C
44	Lt	2680	U
44	Lt	2683	A
44	Lt	2684	G
44	Lt	2687	C
44	Lt	2688	G
75	St	2	A
75	St	3	U
75	St	4	C
75	St	11	A
75	St	13	C
75	St	17	C
75	St	18	C
75	St	26	G
75	St	27	A
75	St	31	U

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Mol	Chain	Res	Type
75	St	32	C
75	St	33	U
75	St	34	C
75	St	40	G
75	St	41	G
75	St	42	A
75	St	44	G
75	St	45	A
75	St	46	A
75	St	49	C
75	St	53	C
75	St	56	G
75	St	58	C
75	St	59	C
75	St	60	G
75	St	62	U
75	St	63	C
75	St	64	A
75	St	65	C
75	St	66	C
75	St	67	C
75	St	68	G
75	St	69	G
75	St	70	G
75	St	71	A
75	St	72	C
75	St	73	G
75	St	74	C
75	St	82	G
75	St	84	C
75	St	86	C
75	St	87	A
75	St	88	G
75	St	91	C
75	St	92	A
75	St	98	U
75	St	101	A
75	St	102	C
75	St	103	C
75	St	104	C
75	St	106	C
75	St	109	C

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Mol	Chain	Res	Type
75	St	111	G
75	St	112	C
75	St	113	G
75	St	114	G
75	St	115	U
75	St	117	C
75	St	118	C
75	St	119	U
75	St	121	C
75	St	122	U
75	St	123	A
75	St	124	G
75	St	125	C
75	St	128	G
75	St	129	A
75	St	130	C
75	St	134	G
75	St	135	C
75	St	136	U
75	St	137	G
75	St	138	G
75	St	139	C
75	St	144	C
75	St	150	C
75	St	151	A
75	St	152	A
75	St	153	G
75	St	154	A
75	St	157	U
75	St	158	G
75	St	160	G
75	St	161	C
75	St	162	G
75	St	163	C
75	St	164	A
75	St	165	C
75	St	166	G
75	St	169	C
75	St	170	G
75	St	171	C
75	St	173	C
75	St	174	G

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Mol	Chain	Res	Type
75	St	175	C
75	St	176	C
75	St	178	C
75	St	179	G
75	St	184	C
75	St	186	A
75	St	187	G
75	St	188	C
75	St	189	A
75	St	190	G
75	St	191	C
75	St	192	G
75	St	194	G
75	St	199	A
75	St	201	C
75	St	202	G
75	St	203	A
75	St	204	C
75	St	205	G
75	St	207	C
75	St	208	C
75	St	209	C
75	St	211	C
75	St	214	G
75	St	215	G
75	St	216	G
75	St	219	U
75	St	224	G
75	St	229	C
75	St	231	C
75	St	232	C
75	St	233	C
75	St	235	G
75	St	242	C
75	St	243	G
75	St	250	G
75	St	251	C
75	St	252	G
75	St	254	G
75	St	255	C
75	St	257	G
75	St	258	A

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Mol	Chain	Res	Type
75	St	261	G
75	St	262	C
75	St	264	C
75	St	265	G
75	St	272	G
75	St	274	C
75	St	281	U
75	St	283	A
75	St	286	G
75	St	290	G
75	St	291	A
75	St	293	U
75	St	294	C
75	St	297	G
75	St	298	A
75	St	300	A
75	St	301	G
75	St	303	G
75	St	304	G
75	St	310	C
75	St	311	G
75	St	313	G
75	St	314	A
75	St	315	C
75	St	317	G
75	St	322	C
75	St	326	U
75	St	328	C
75	St	330	A
75	St	331	G
75	St	332	G
75	St	333	A
75	St	335	G
75	St	336	G
75	St	337	C
75	St	338	A
75	St	339	G
75	St	340	C
75	St	341	A
75	St	348	G
75	St	350	A
75	St	351	C

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Mol	Chain	Res	Type
75	St	352	U
75	St	353	U
75	St	354	G
75	St	356	C
75	St	357	C
75	St	358	A
75	St	360	U
75	St	365	G
75	St	366	G
75	St	368	G
75	St	369	C
75	St	372	G
75	St	381	A
75	St	382	C
75	St	383	G
75	St	390	G
75	St	394	G
75	St	395	A
75	St	396	G
75	St	397	C
75	St	398	G
75	St	399	A
75	St	402	C
75	St	404	G
75	St	406	C
75	St	410	C
75	St	411	A
75	St	412	G
75	St	413	C
75	St	417	C
75	St	418	G
75	St	420	C
75	St	421	G
75	St	422	C
75	St	423	G
75	St	424	C
75	St	425	A
75	St	426	G
75	St	429	G
75	St	431	G
75	St	434	C
75	St	435	A

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Mol	Chain	Res	Type
75	St	436	A
75	St	437	G
75	St	438	G
75	St	439	U
75	St	441	U
75	St	442	G
75	St	443	U
75	St	445	C
75	St	446	C
75	St	448	G
75	St	449	C
75	St	454	G
75	St	455	C
75	St	457	G
75	St	458	U
75	St	459	A
75	St	460	A
75	St	461	U
75	St	463	C
75	St	466	G
75	St	471	G
75	St	472	C
75	St	474	A
75	St	475	G
75	St	483	C
75	St	486	C
75	St	487	G
75	St	489	U
75	St	491	C
75	St	494	C
75	St	495	A
75	St	497	U
75	St	498	U
75	St	499	G
75	St	500	A
75	St	501	A
75	St	502	A
75	St	503	C
75	St	504	G
75	St	509	U
75	St	510	A
75	St	515	G

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Mol	Chain	Res	Type
75	St	518	C
75	St	519	C
75	St	520	C
75	St	521	C
75	St	522	G
75	St	524	C
75	St	525	G
75	St	530	G
75	St	534	A
75	St	535	A
75	St	537	C
75	St	542	G
75	St	544	G
75	St	545	C
75	St	550	G
75	St	552	C
75	St	553	A
75	St	554	G
75	St	555	G
75	St	556	C
75	St	557	C
75	St	558	C
75	St	559	G
75	St	560	U
75	St	561	U
75	St	563	G
75	St	567	C
75	St	568	G
75	St	569	C
75	St	570	C
75	St	573	G
75	St	577	G
75	St	578	A
75	St	581	G
75	St	582	C
75	St	584	C
75	St	585	A
75	St	586	G
75	St	588	G
75	St	589	G
75	St	593	C
75	St	594	G

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Mol	Chain	Res	Type
75	St	595	G
75	St	596	C
75	St	597	G
75	St	598	C
75	St	599	G
75	St	600	C
75	St	602	G
75	St	605	G
75	St	606	C
75	St	607	C
75	St	608	G
75	St	609	C
75	St	610	A
75	St	611	G
75	St	612	C
75	St	613	C
75	St	614	C
75	St	616	G
75	St	617	A
75	St	618	G
75	St	619	G
75	St	627	G
75	St	630	G
75	St	640	U
75	St	652	A
75	St	653	C
75	St	657	U
75	St	658	G
75	St	663	A
75	St	667	U
75	St	668	G
75	St	675	C
75	St	676	C
75	St	682	C
75	St	685	C
75	St	686	G
75	St	687	G
75	St	689	C
75	St	691	C
75	St	694	A
75	St	696	G
75	St	698	G

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Mol	Chain	Res	Type
75	St	701	U
75	St	702	G
75	St	703	C
75	St	704	C
75	St	705	A
75	St	706	A
75	St	708	A
75	St	710	C
75	St	713	C
75	St	714	U
75	St	718	U
75	St	719	C
75	St	720	A
75	St	726	G
75	St	727	G
75	St	731	A
75	St	741	G
75	St	742	C
75	St	743	U
75	St	744	A
75	St	746	A
75	St	747	A
75	St	751	G
75	St	752	A
75	St	755	A
75	St	758	C
75	St	759	A
75	St	762	A
75	St	770	C
75	St	775	C
75	St	776	C
75	St	777	G
75	St	779	A
75	St	780	A
75	St	782	C
75	St	783	G
75	St	784	G
75	St	785	U
75	St	786	G
75	St	787	C
75	St	791	C
75	St	793	C

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Mol	Chain	Res	Type
75	St	794	G
75	St	795	C
75	St	796	G
75	St	803	G
75	St	805	G
75	St	807	G
75	St	808	C
75	St	809	G
75	St	810	U
75	St	811	C
75	St	813	C
75	St	814	G
75	St	816	C
75	St	817	G
75	St	820	C
75	St	821	G
75	St	824	C
75	St	829	A
75	St	833	C
75	St	835	G
75	St	836	G
75	St	837	A
75	St	838	G
75	St	840	C
75	St	841	U
75	St	842	C
75	St	843	C
75	St	844	G
75	St	845	G
75	St	846	G
75	St	852	G
75	St	853	G
75	St	855	G
75	St	857	A
75	St	864	C
75	St	882	A
75	St	887	A
75	St	890	G
75	St	892	C
75	St	893	G
75	St	894	G
75	St	898	G

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Mol	Chain	Res	Type
75	St	899	G
75	St	900	U
75	St	902	C
75	St	904	A
75	St	907	A
75	St	908	G
75	St	910	C
75	St	911	G
75	St	913	G
75	St	917	U
75	St	923	G
75	St	926	C
75	St	929	U
75	St	931	U
75	St	932	G
75	St	933	A
75	St	934	C
75	St	938	A
75	St	940	G
75	St	941	C
75	St	943	C
75	St	944	G
75	St	945	C
75	St	949	U
75	St	950	C
75	St	955	G
75	St	958	C
75	St	959	C
75	St	960	G
75	St	961	G
75	St	965	C
75	St	970	A
75	St	971	G
75	St	972	G
75	St	973	A
75	St	974	C
75	St	975	C
75	St	977	A
75	St	984	G
75	St	985	G
75	St	986	C
75	St	987	G

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Mol	Chain	Res	Type
75	St	988	C
75	St	989	G
75	St	990	C
75	St	992	U
75	St	993	U
75	St	995	G
75	St	996	C
75	St	997	G
75	St	998	A
75	St	1000	C
75	St	1001	G
75	St	1005	G
75	St	1006	G
75	St	1007	G
75	St	1008	U
75	St	1010	G
75	St	1015	G
75	St	1016	C
75	St	1017	A
75	St	1018	U
75	St	1020	G
75	St	1022	C
75	St	1027	C
75	St	1028	C
75	St	1029	A
75	St	1032	C
75	St	1033	C
75	St	1034	G
75	St	1039	G
75	St	1042	A
75	St	1043	G
75	St	1047	U
75	St	1048	C
75	St	1049	U
75	St	1052	U
75	St	1054	C
75	St	1055	A
75	St	1056	U
75	St	1057	U
75	St	1063	A
75	St	1067	A
75	St	1068	G

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Mol	Chain	Res	Type
75	St	1072	G
75	St	1074	C
75	St	1076	C
75	St	1077	C
75	St	1078	G
75	St	1079	G
75	St	1080	C
75	St	1083	C
75	St	1085	G
75	St	1087	C
75	St	1088	G
75	St	1089	C
75	St	1090	C
75	St	1091	G
75	St	1094	G
75	St	1098	G
75	St	1099	G
75	St	1100	C
75	St	1101	C
75	St	1103	G
75	St	1104	C
75	St	1105	G
75	St	1106	G
75	St	1109	G
75	St	1110	C
75	St	1112	G
75	St	1113	G
75	St	1114	A
75	St	1115	G
75	St	1117	A
75	St	1121	C
75	St	1122	G
75	St	1123	G
75	St	1124	G
75	St	1127	G
75	St	1128	A
75	St	1131	G
75	St	1132	C
75	St	1133	A
75	St	1134	G
75	St	1135	G
75	St	1138	U

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Mol	Chain	Res	Type
75	St	1139	G
75	St	1141	G
75	St	1142	A
75	St	1150	A
75	St	1151	G
75	St	1152	A
75	St	1153	C
75	St	1157	C
75	St	1160	G
75	St	1163	C
75	St	1164	G
75	St	1165	C
75	St	1166	A
75	St	1175	A
75	St	1177	A
75	St	1178	C
75	St	1179	U
75	St	1180	G
75	St	1183	G
75	St	1184	G
75	St	1185	G
75	St	1187	C
75	St	1188	C
75	St	1189	A
75	St	1190	G
75	St	1192	C
75	St	1193	G
75	St	1194	G
75	St	1195	C
75	St	1198	C
75	St	1202	C
75	St	1204	G
75	St	1208	G
75	St	1210	G
75	St	1211	C
75	St	1212	G
75	St	1213	G
75	St	1214	A
75	St	1215	G
75	St	1222	C
75	St	1224	G
75	St	1225	U

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Mol	Chain	Res	Type
75	St	1227	G
75	St	1228	C
75	St	1230	G
75	St	1232	G
75	St	1233	A
75	St	1235	C
75	St	1236	G
75	St	1237	C
75	St	1238	G
75	St	1242	U
75	St	1246	A
75	St	1247	C
75	St	1248	G
75	St	1249	C
75	St	1251	C
75	St	1256	G
75	St	1257	C
75	St	1261	A
75	St	1262	G
75	St	1264	A
75	St	1265	A
75	St	1266	U
75	St	1267	G
75	St	1268	U
75	St	1269	C
75	St	1270	U
75	St	1271	U
75	St	1272	G
75	St	1273	U
75	St	1278	G
75	St	1283	C
75	St	1285	C
75	St	1289	C
75	St	1293	G
75	St	1295	G
75	St	1296	C
75	St	1297	C
75	St	1301	C
75	St	1302	G
75	St	1304	G
75	St	1305	U
75	St	1306	C

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Mol	Chain	Res	Type
75	St	1310	G
75	St	1319	A
75	St	1321	A
75	St	1322	C
75	St	1323	A
75	St	1324	C
75	St	1325	C
75	St	1326	G
75	St	1333	G
75	St	1334	C
75	St	1335	U
75	St	1339	A
75	St	1345	U
75	St	1346	G
75	St	1348	G
75	St	1349	C
75	St	1350	G
75	St	1351	C
75	St	1352	G
75	St	1355	G
75	St	1356	G
75	St	1359	A
75	St	1360	G
75	St	1362	G
75	St	1363	C
75	St	1365	C
75	St	1367	G
75	St	1368	G
75	St	1369	A
75	St	1371	G
75	St	1372	C
75	St	1373	G
75	St	1374	C
75	St	1375	G
75	St	1379	G
75	St	1380	G
75	St	1381	C
75	St	1384	C
75	St	1391	C
75	St	1392	C
75	St	1394	C
75	St	1398	U

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Mol	Chain	Res	Type
75	St	1399	G
75	St	1400	G
75	St	1401	A
75	St	1402	G
75	St	1403	G
75	St	1405	A
75	St	1410	A
75	St	1411	A
75	St	1412	G
75	St	1415	G
75	St	1417	A
75	St	1421	A
75	St	1422	G
75	St	1423	G
75	St	1424	U
75	St	1425	A
75	St	1428	C
75	St	1430	U
75	St	1434	U
75	St	1435	G
75	St	1437	A
75	St	1438	C
75	St	1444	G
75	St	1446	U
75	St	1447	G
75	St	1448	G
75	St	1449	A
75	St	1450	U
75	St	1451	C
75	St	1452	C
75	St	1453	U
75	St	1454	U
76	u	2	G
76	u	4	A
76	u	5	G
76	u	9	G
76	u	12	G
76	u	14	A
76	u	16	C
76	u	17	G
76	u	18	G
76	u	19	A

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Mol	Chain	Res	Type
76	u	20	A
76	u	21	G
76	u	22	C
76	u	29	G
76	u	30	G
76	u	31	C
76	u	32	C
76	u	37	A
76	u	42	G
76	u	45	G
76	u	46	U
76	u	47	C
76	u	48	G
76	u	49	A
76	u	50	U
76	u	52	G
76	u	54	U
76	u	57	A
76	u	61	C
76	u	64	C
76	u	65	C
76	u	66	U
76	u	70	C
76	u	74	C
76	u	75	A
77	v	2	G
77	v	3	C
77	v	6	A
77	v	7	G
77	v	8	U
77	v	9	G
77	v	11	C
77	v	12	G
77	v	13	C
77	v	14	A
77	v	15	G
77	v	16	C
77	v	17	G
77	v	18	G
77	v	19	A
77	v	20	A
77	v	21	G

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Mol	Chain	Res	Type
77	v	22	C
77	v	25	G
77	v	26	C
77	v	27	U
77	v	30	G
77	v	31	C
77	v	37	A
77	v	40	C
77	v	42	G
77	v	44	G
77	v	45	G
77	v	46	U
77	v	47	C
77	v	48	G
77	v	49	A
77	v	50	U
77	v	52	G
77	v	54	U
77	v	56	G
77	v	57	A
77	v	58	A
77	v	62	A
77	v	63	U
77	v	67	C
77	v	68	U
77	v	69	G
77	v	72	A
77	v	73	C
77	v	74	C
78	y	34	A
78	y	35	U
78	y	36	G
78	y	37	G
78	y	39	G
78	y	40	A
78	y	41	A

All (8) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	LD	39	C
4	LD	73	A

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Mol	Chain	Res	Type
4	LD	85	C
4	LD	88	G
5	LE	63	U
5	LE	85	U
5	LE	110	U
5	LE	114	G

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

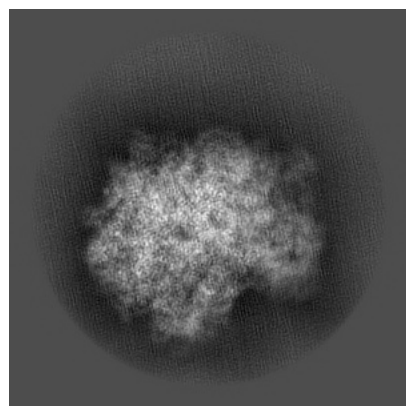
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16235. These allow visual inspection of the internal detail of the map and identification of artifacts.

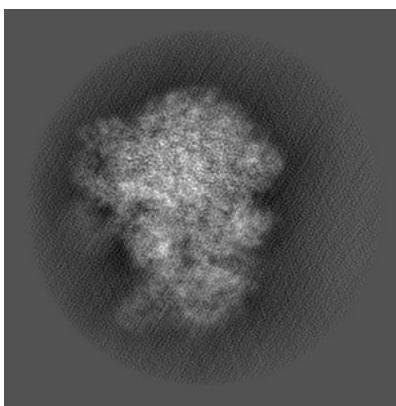
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

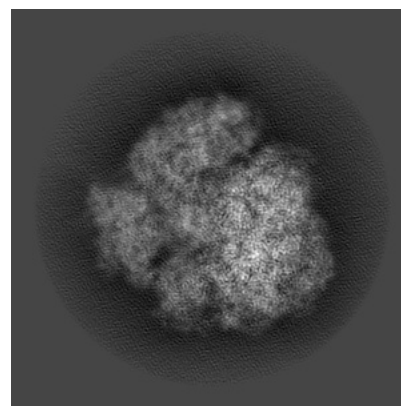
6.1.1 Primary map



X

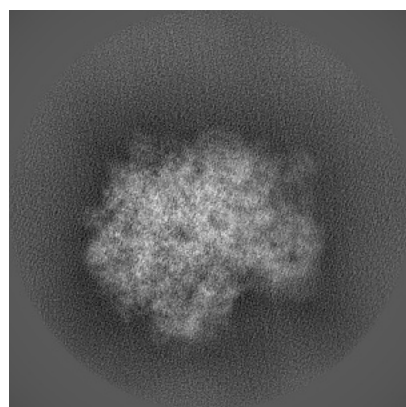


Y

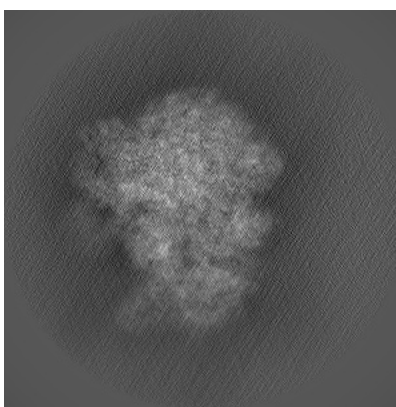


Z

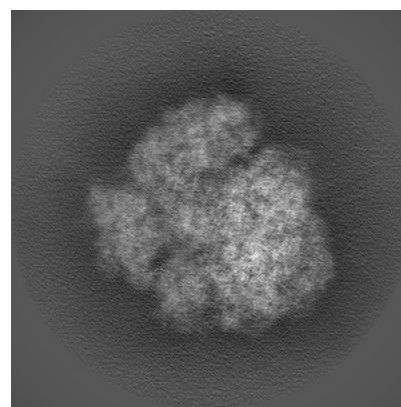
6.1.2 Raw map



X



Y

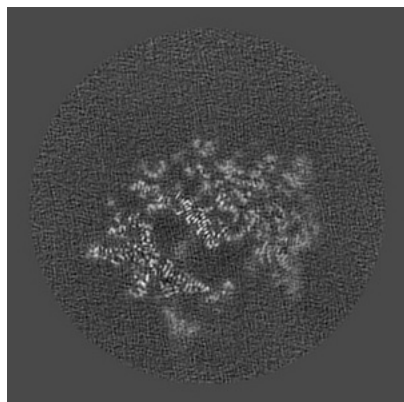


Z

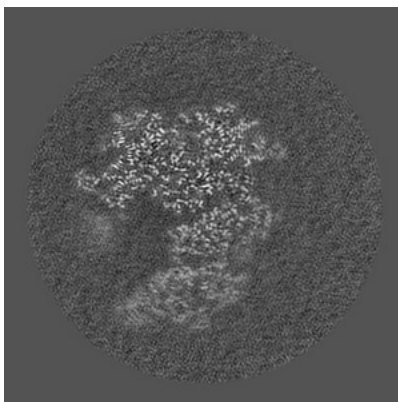
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

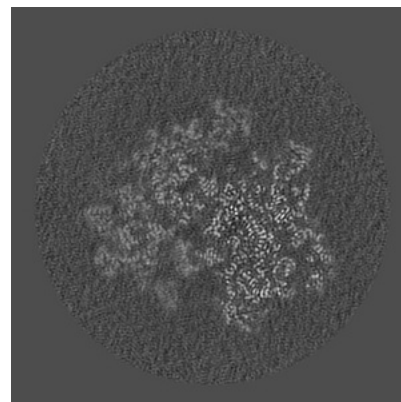
6.2.1 Primary map



X Index: 250

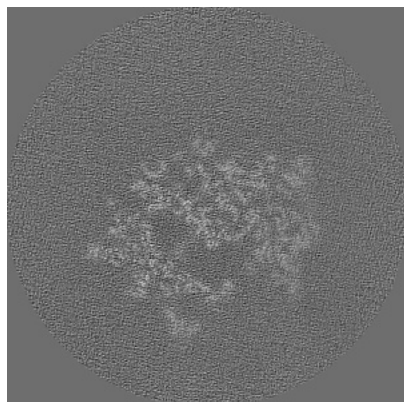


Y Index: 250

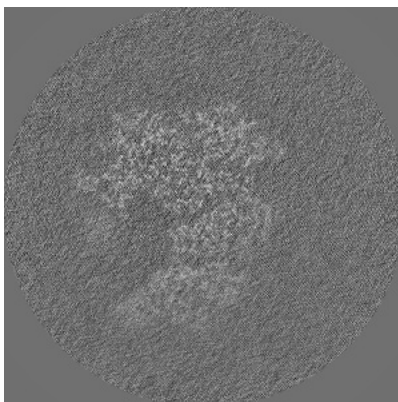


Z Index: 250

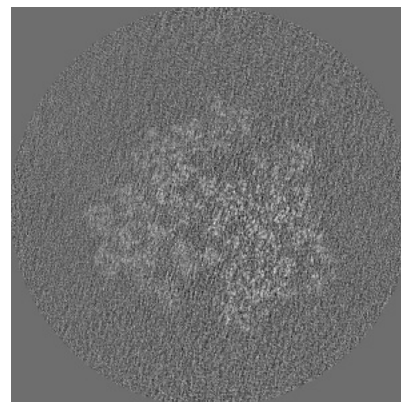
6.2.2 Raw map



X Index: 250



Y Index: 250

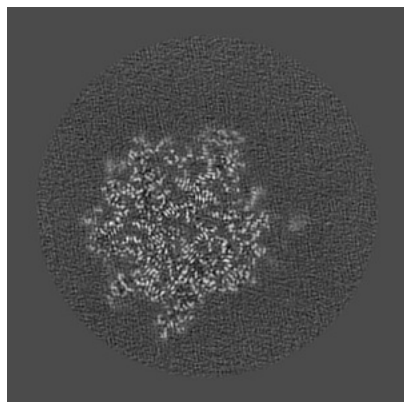


Z Index: 250

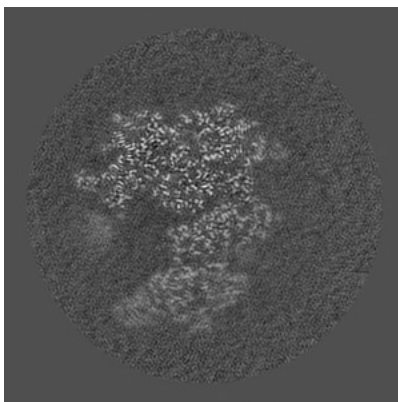
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

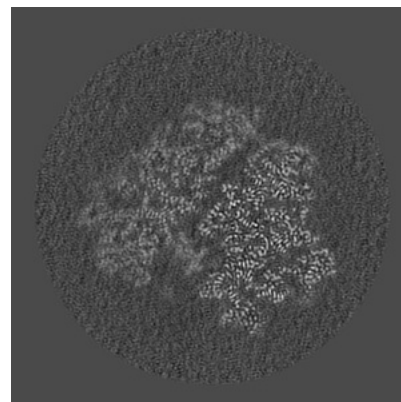
6.3.1 Primary map



X Index: 314

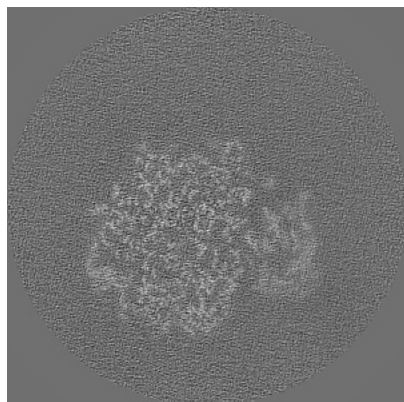


Y Index: 249

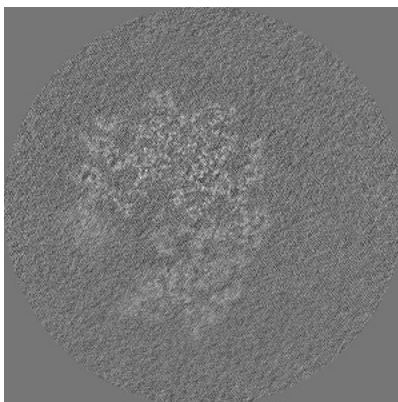


Z Index: 240

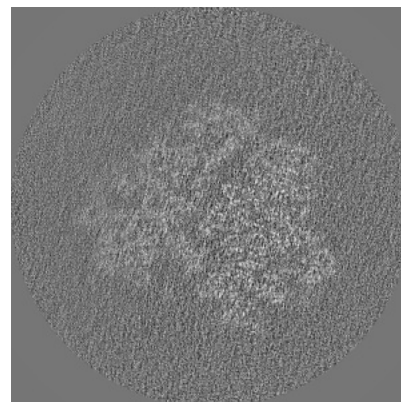
6.3.2 Raw map



X Index: 280



Y Index: 230

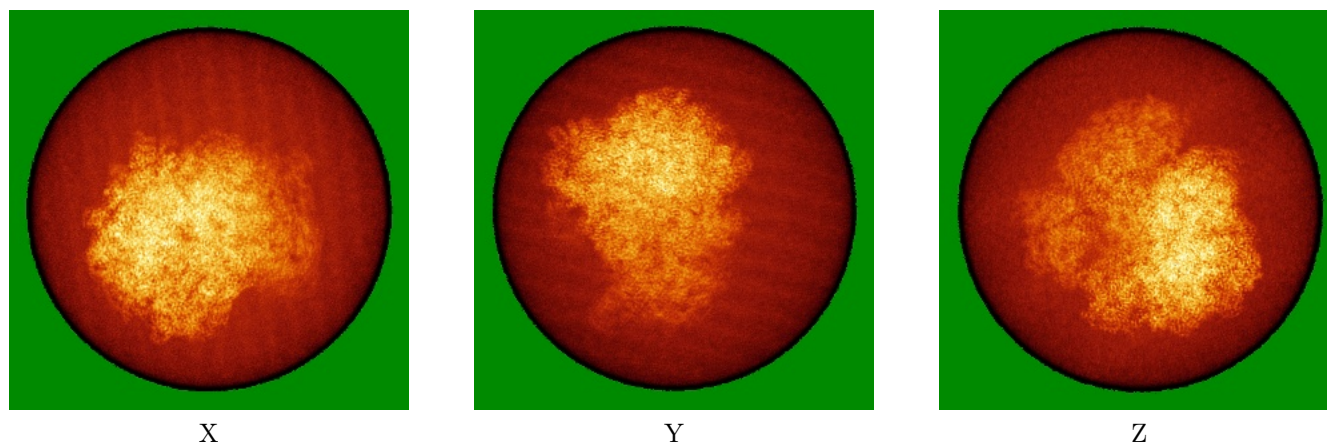


Z Index: 240

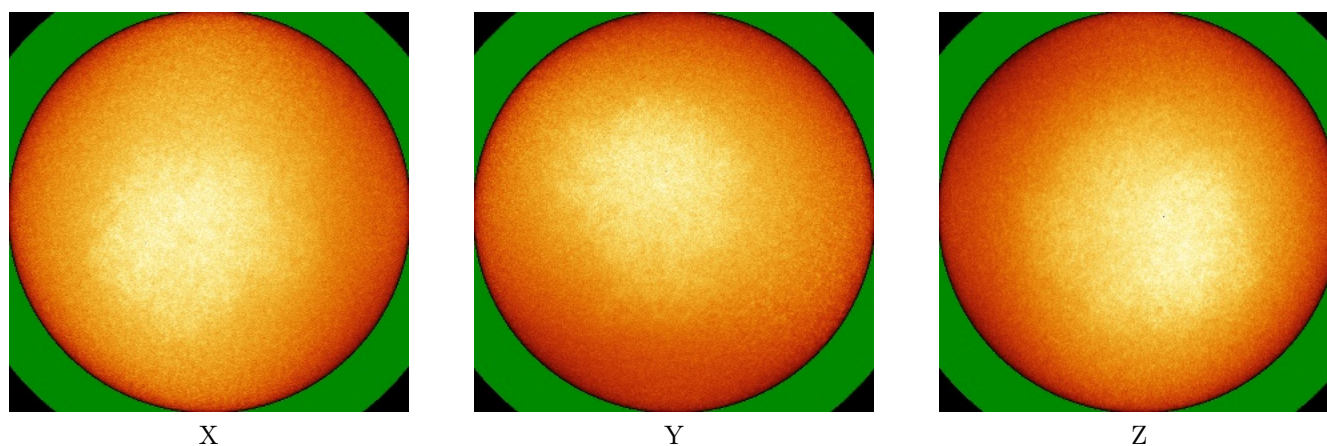
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

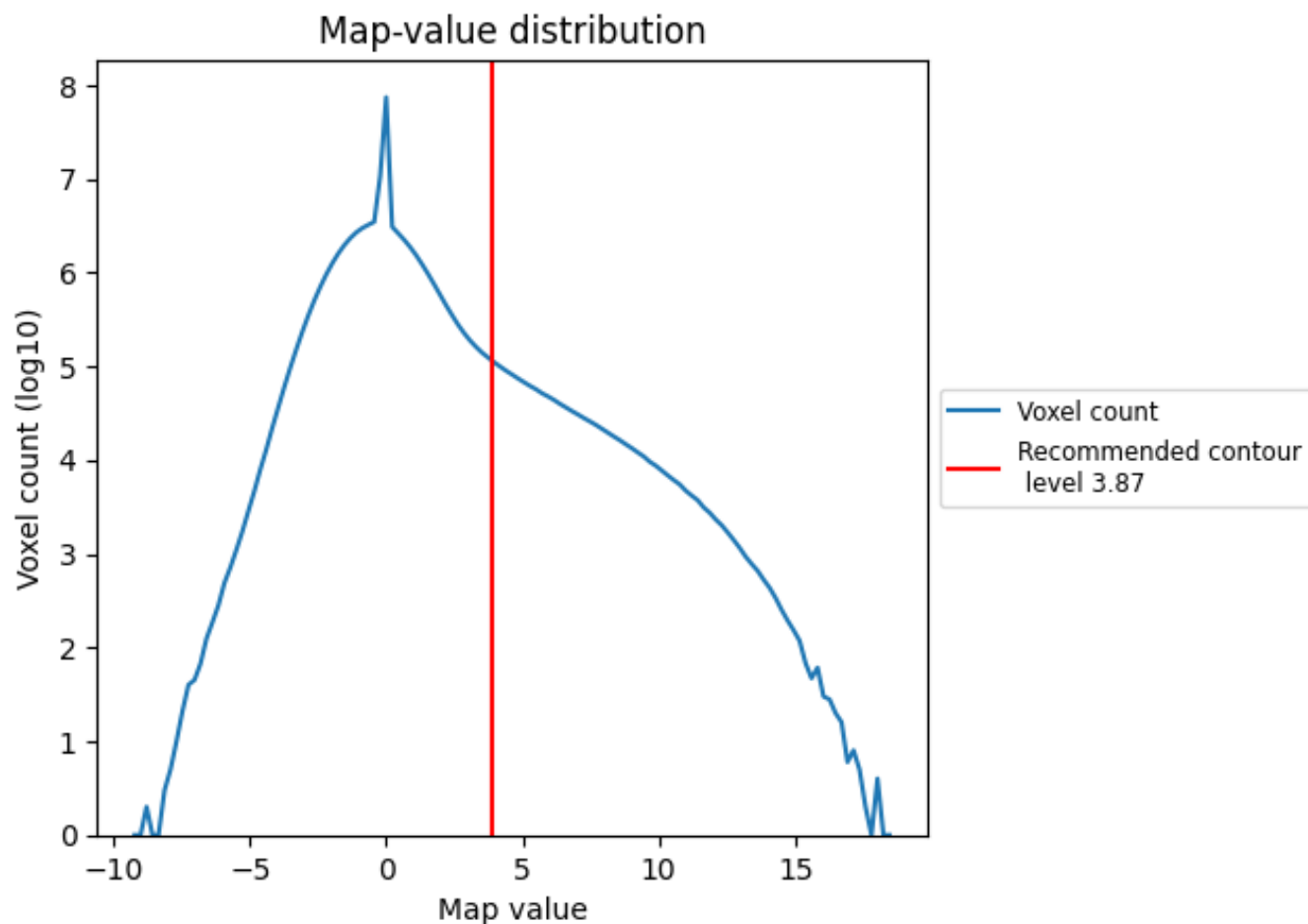
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

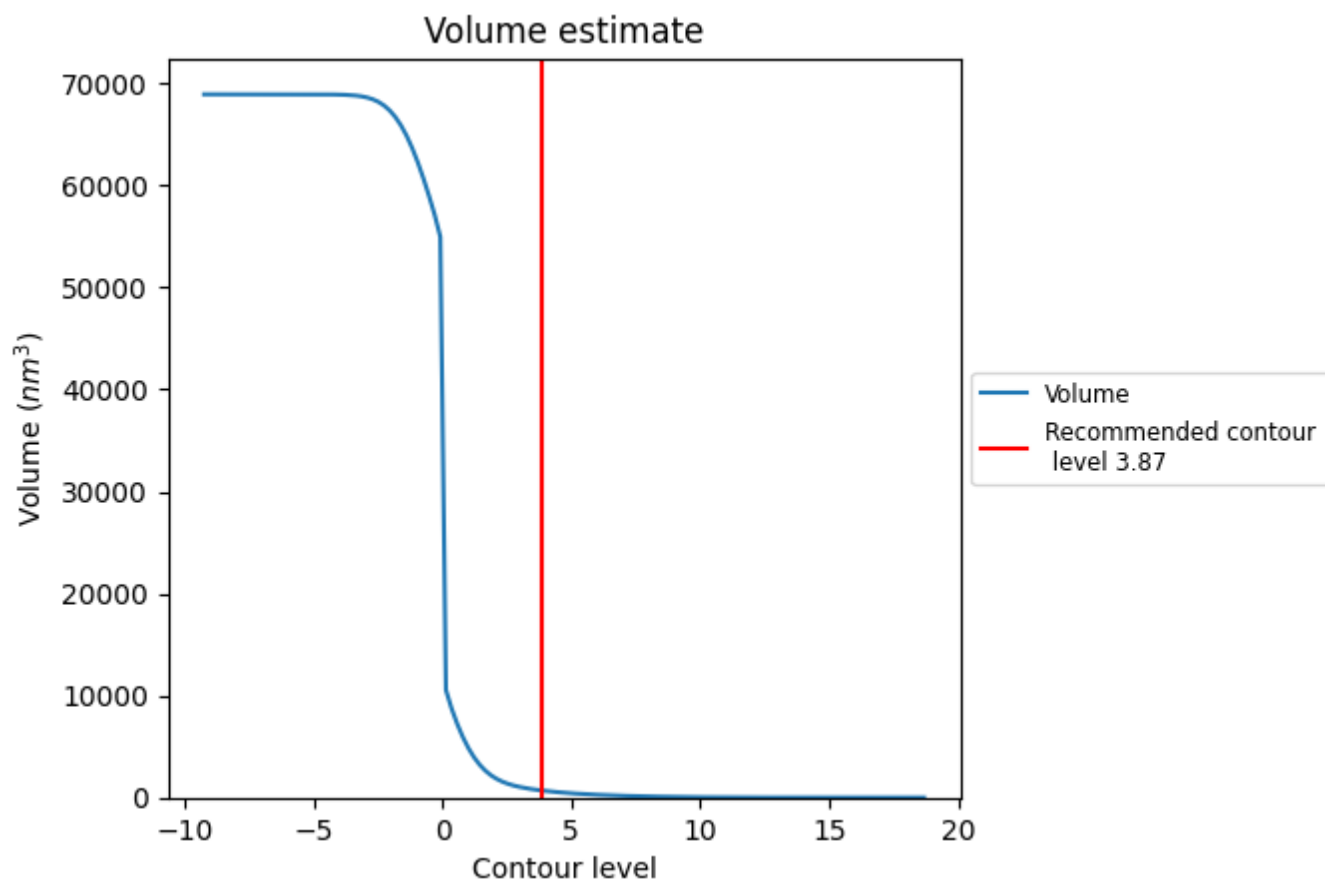
This section contains the results of statistical analysis of the map.

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.

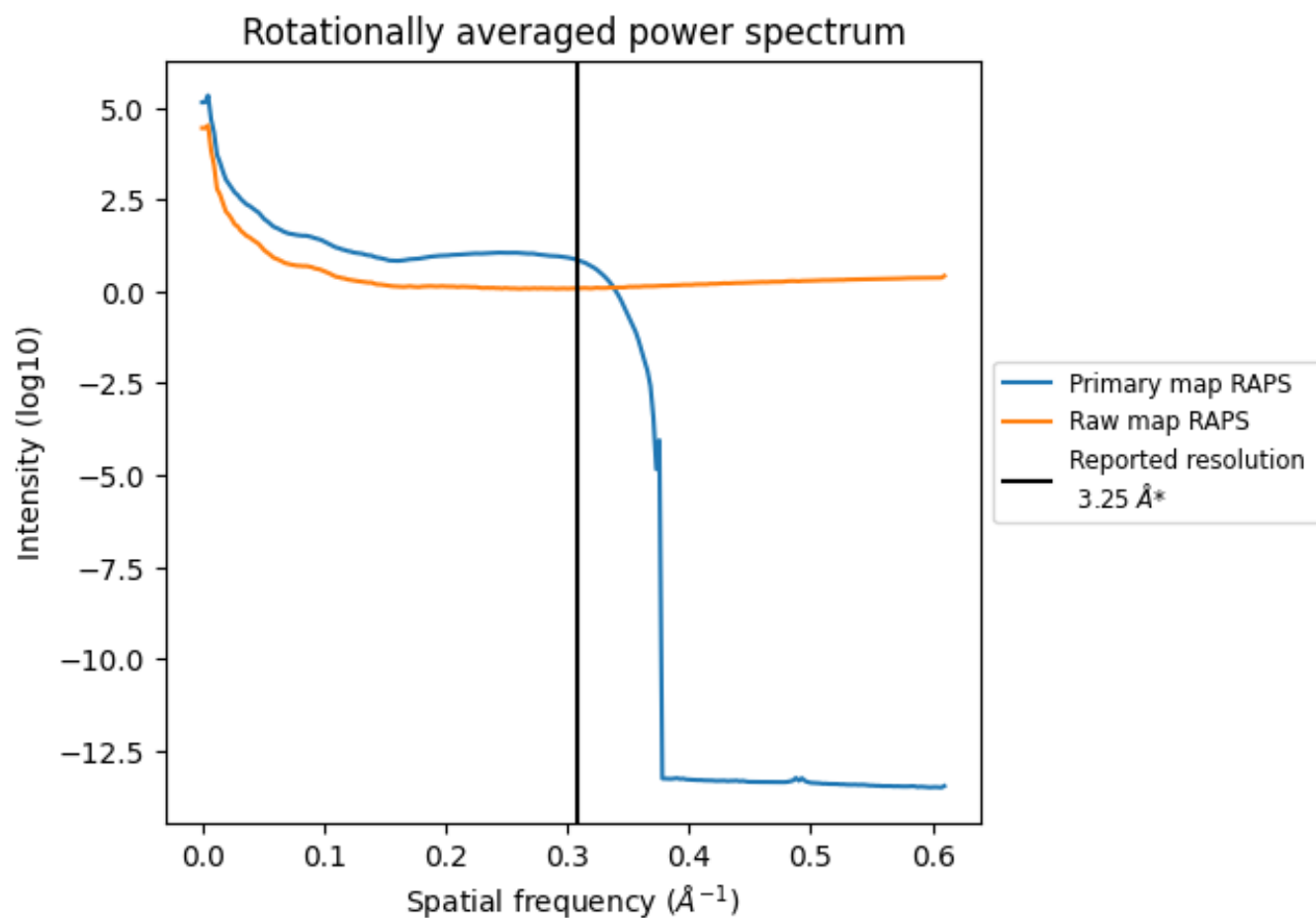
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 689 nm³; this corresponds to an approximate mass of 622 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 ⓘ

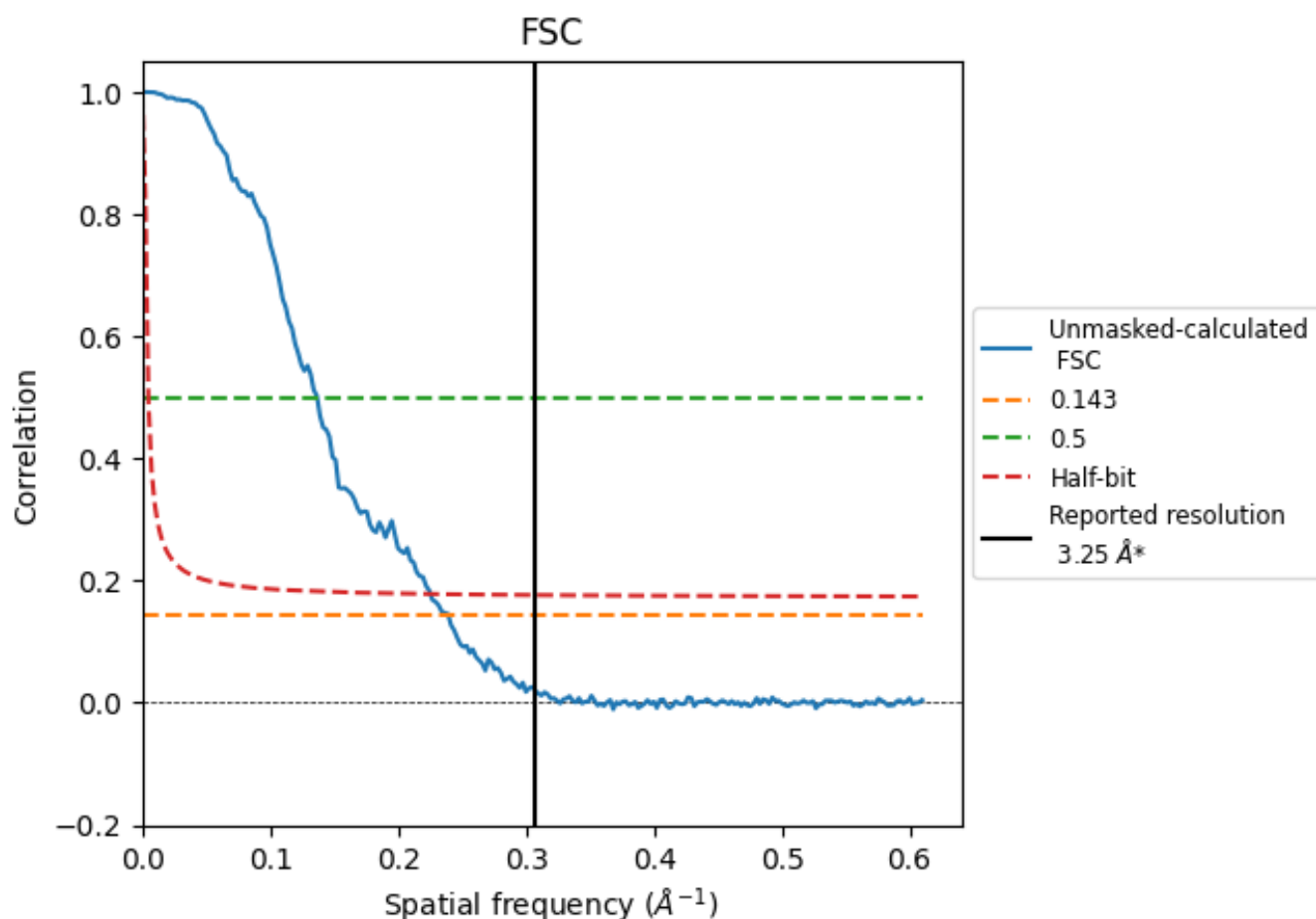


*Reported resolution corresponds to spatial frequency of 0.308 Å⁻¹

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 0.308 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

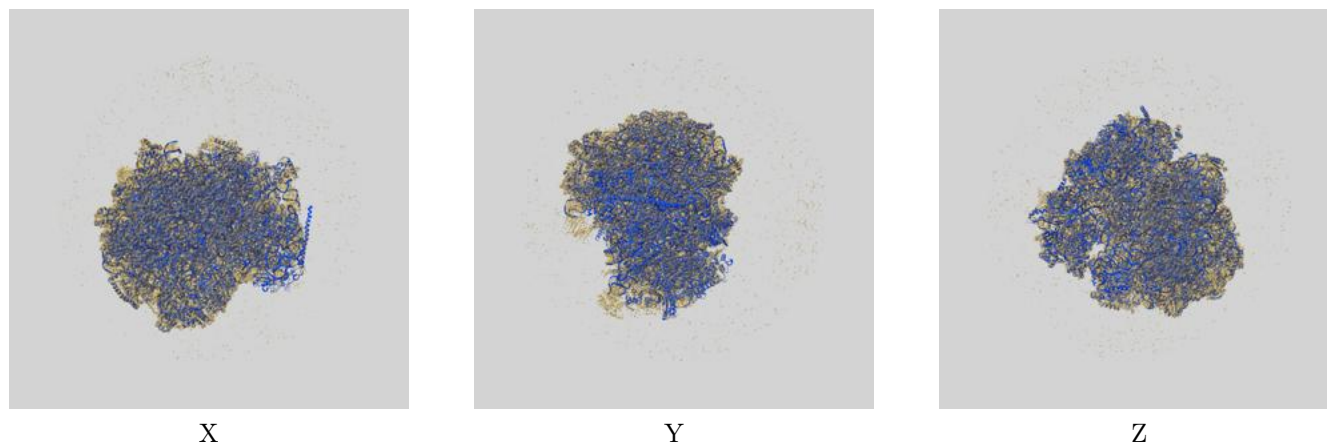
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.25	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.18	7.32	4.44

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.18 differs from the reported value 3.25 by more than 10 %

9 Map-model fit [i](#)

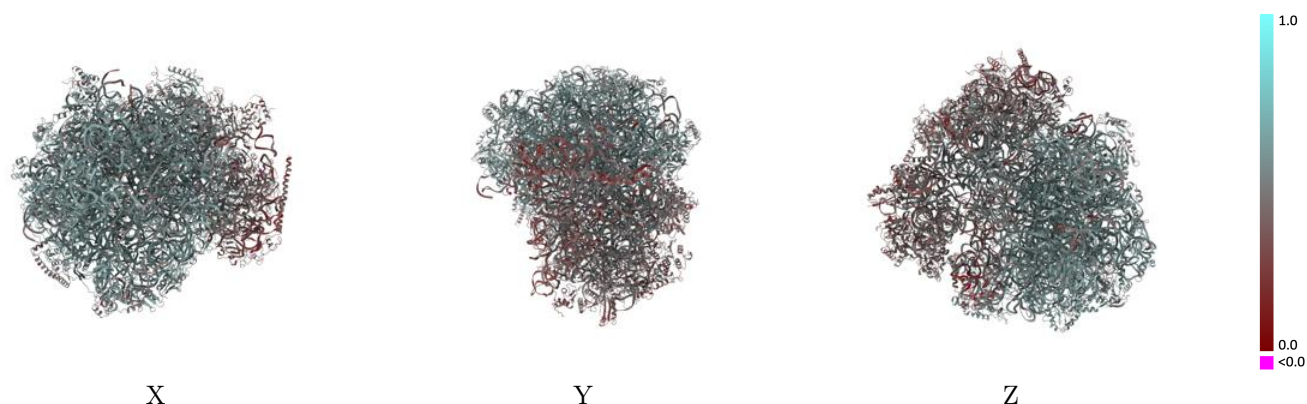
This section contains information regarding the fit between EMDB map EMD-16235 and PDB model 8BTR. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 3.87 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

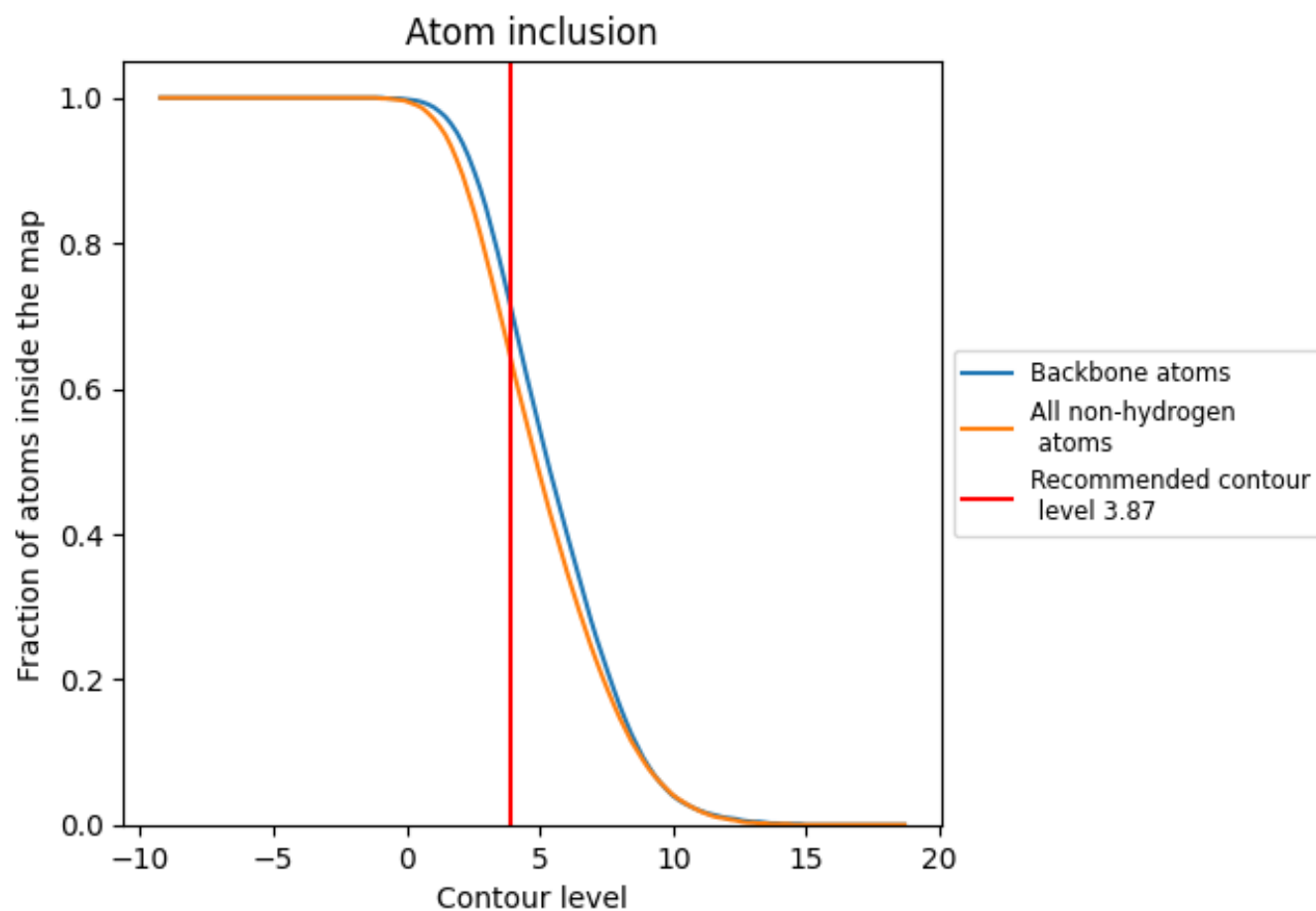


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 65% 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 (3.87) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6470	 0.4990
LA	 0.7210	 0.5800
LB	 0.7110	 0.5580
LC	 0.7320	 0.5590
LD	 0.8410	 0.5500
LE	 0.8710	 0.5560
LF	 0.6150	 0.5260
LG	 0.7380	 0.5760
LH	 0.6450	 0.5370
LI	 0.6250	 0.5280
LJ	 0.6470	 0.5410
LK	 0.6300	 0.5410
LL	 0.6040	 0.5250
LM	 0.7040	 0.5480
LN	 0.6520	 0.5300
LO	 0.7830	 0.5850
LP	 0.6840	 0.5450
LQ	 0.6990	 0.5530
LR	 0.7020	 0.5650
LS	 0.6540	 0.5420
LT	 0.6900	 0.5500
LU	 0.6980	 0.5570
LV	 0.5390	 0.4780
LW	 0.6490	 0.5340
LX	 0.6340	 0.5130
LY	 0.7040	 0.5560
LZ	 0.7270	 0.5530
La	 0.5110	 0.4950
Lb	 0.7760	 0.5760
Lc	 0.7010	 0.5570
Ld	 0.5950	 0.5160
Le	 0.6960	 0.5590
Lf	 0.6960	 0.5550
Lg	 0.7320	 0.5740
Lh	 0.6880	 0.5700



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Chain	Atom inclusion	Q-score
Li	 0.6330	 0.5390
Lj	 0.5930	 0.5140
Lk	 0.7440	 0.5710
Ll	 0.5080	 0.4610
Ln	 0.0950	 0.3020
Lo	 0.5280	 0.5350
Lp	 0.7320	 0.5800
Lq	 0.6890	 0.5510
Ls	 0.7220	 0.5310
Lt	 0.8420	 0.5540
SA	 0.3440	 0.4060
SB	 0.4270	 0.4500
SC	 0.3470	 0.4080
SD	 0.4680	 0.4620
SE	 0.2440	 0.3790
SF	 0.3320	 0.4280
SG	 0.1510	 0.3560
SH	 0.2690	 0.4050
SI	 0.3240	 0.4270
SJ	 0.4460	 0.4630
SK	 0.2910	 0.3820
SL	 0.2540	 0.3360
SM	 0.3240	 0.4390
SO	 0.4120	 0.4790
SP	 0.4130	 0.4530
SQ	 0.5220	 0.4920
SR	 0.3260	 0.4150
ST	 0.2850	 0.3990
SU	 0.1820	 0.3570
SV	 0.3930	 0.4230
SW	 0.3380	 0.4010
SX	 0.2380	 0.3790
SY	 0.3160	 0.4230
Sb	 0.2210	 0.3650
Sc	 0.2910	 0.3920
Sd	 0.5340	 0.4990
Se	 0.2870	 0.4310
Sg	 0.2760	 0.4070
Sh	 0.4190	 0.4250
Sj	 0.2700	 0.4140
St	 0.6090	 0.4320
u	 0.5660	 0.4250

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Chain	Atom inclusion	Q-score
v	 0.2280	 0.3370
y	 0.4940	 0.4370