



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 08:11 PM UTC

PDB ID : 8BSI / pdb_00008bsi
EMDB ID : EMD-16225
Title : Giardia ribosome chimeric hybrid-like GDP+Pi bound state (B1)
Authors : Majumdar, S.; Emmerich, A.G.; Sanyal, S.
Deposited on : 2022-11-25
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

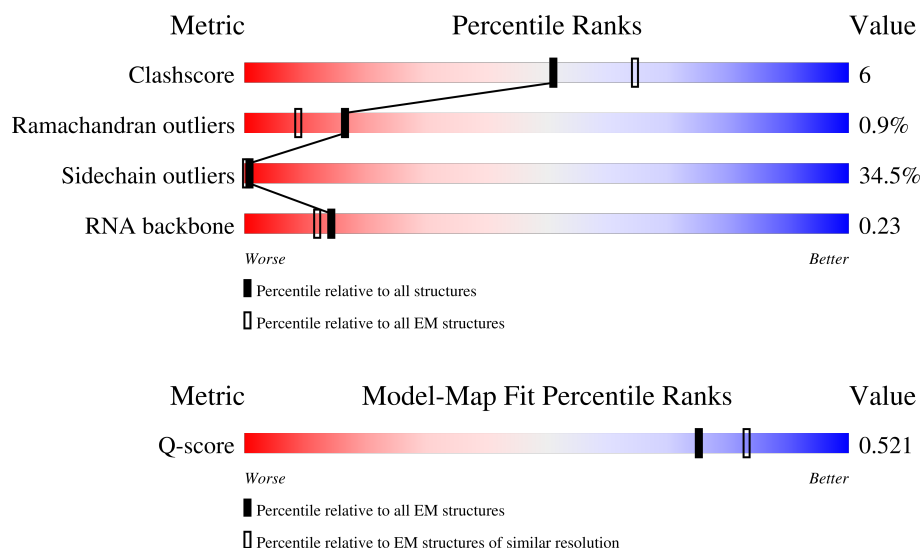
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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.



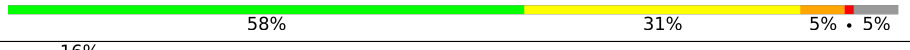
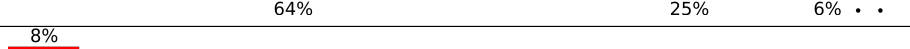
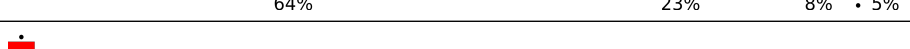
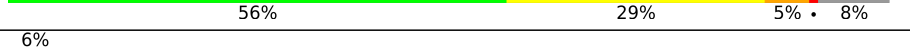
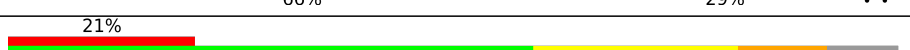
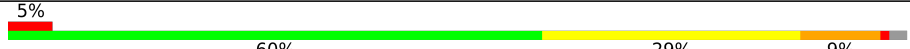
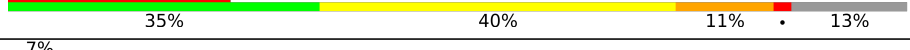
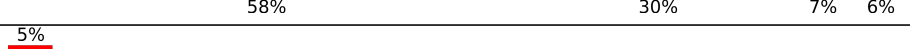
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	
2	LB	379	
3	LC	316	

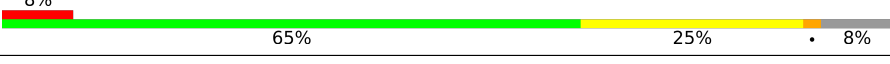
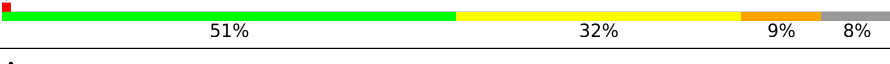
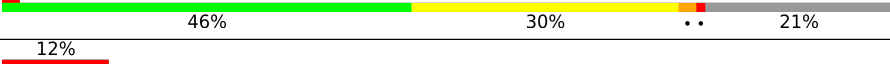
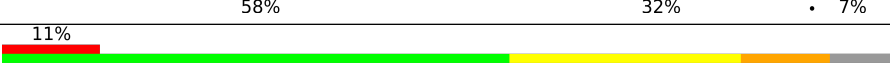
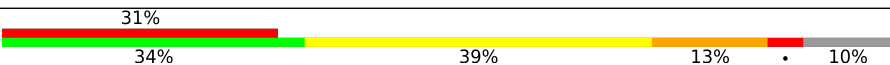
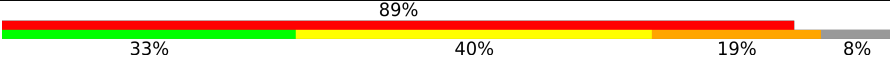
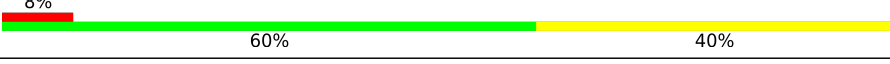
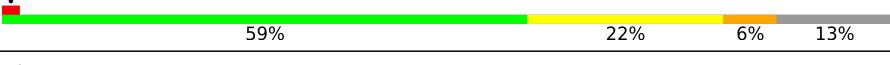
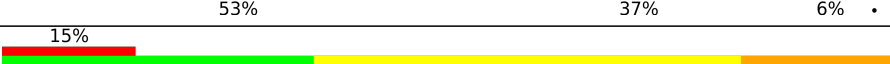
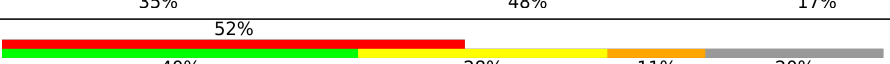
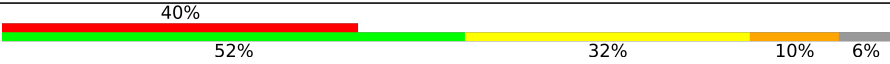
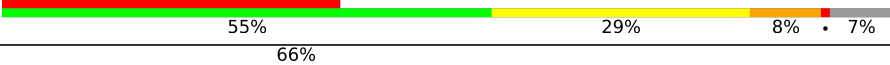
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Mol	Chain	Length	Quality of chain
4	LD	142	
5	LE	121	
6	LF	297	
7	LG	51	
8	LH	235	
9	LI	225	
10	LJ	185	
11	LK	210	
12	LL	173	
13	LM	234	
14	LN	131	
15	LO	204	
16	LP	197	
17	LQ	164	
18	LR	179	
19	LS	196	
20	LT	173	
21	LU	159	
22	LV	124	
23	LW	142	
24	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	Lu	75	
46	SA	245	
47	SB	242	
48	SC	217	
49	SD	248	
50	SE	268	
51	SF	190	
52	SG	248	
53	SH	190	

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Mol	Chain	Length	Quality of chain
54	SI	174	
55	SJ	130	
56	SK	189	
57	SL	134	
58	SM	154	
59	SO	143	
60	SP	154	
61	SQ	145	
62	SR	145	
63	ST	158	
64	SU	137	
65	SV	154	
66	SW	139	
67	SX	126	
68	SY	89	
69	Sb	132	
70	Sc	88	
71	Sd	109	
72	Se	81	
73	Sg	64	
74	Sh	51	
75	Sj	69	
76	St	1454	
77	a	898	
78	y	11	

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 180812 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	245	Total	C	N	O	S	0	0
			1847	1141	377	317	12		

- Molecule 2 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LB	372	Total	C	N	O	S	0	0
			2935	1852	559	503	21		

- Molecule 3 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LC	309	Total	C	N	O	S	0	0
			2412	1516	469	419	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LD	137	Total	C	N	O	P	0	0
			2932	1303	544	948	137		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LE	115	Total	C	N	O	P	0	0
			2457	1096	447	799	115		

- Molecule 6 is a protein called Ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LF	285	Total	C	N	O	S	0	0
			2287	1444	428	407	8		

- Molecule 7 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	LG	49	Total	C	N	O	0	0
			431	275	93	63		

- Molecule 8 is a protein called Ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LH	209	Total	C	N	O	S	0	0
			1694	1079	307	303	5		

- Molecule 9 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LI	180	Total	C	N	O	S	0	0
			1445	921	265	254	5		

- Molecule 10 is a protein called Ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LJ	181	Total	C	N	O	S	0	0
			1427	902	260	255	10		

- Molecule 11 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LK	189	Total	C	N	O	S	0	0
			1552	978	303	264	7		

- Molecule 12 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LL	164	Total	C	N	O	S	0	0
			1321	835	246	235	5		

- Molecule 13 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LM	192	Total	C	N	O	S	0	0
			1539	957	312	264	6		

- Molecule 14 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LN	128	Total	C	N	O	S	0	0
			1006	637	184	179	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	186	Total	C	N	O	S	0	0
			1513	948	297	256	12		

- Molecule 17 is a protein called Ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LQ	151	Total	C	N	O	S	0	0
			1220	773	235	208	4		

- Molecule 18 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LR	177	Total	C	N	O	S	0	0
			1388	860	277	242	9		

- Molecule 19 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LS	181	Total	C	N	O	S	0	0
			1507	927	321	254	5		

- Molecule 20 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LT	169	Total	C	N	O	S	0	0
			1418	896	271	242	9		

- Molecule 21 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LU	153	Total	C	N	O	S	0	0
			1236	772	254	203	7		

- Molecule 22 is a protein called Ribosomal L22e.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LV	108	Total	C	N	O	S	0	0
			887	561	149	175	2		

- Molecule 23 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LW	134	Total	C	N	O	S	0	0
			1023	645	195	178	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	113	Total	C	N	O	S	0	0
			913	588	163	159	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 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	La	122	Total	C	N	O	S	0	0
			976	618	185	168	5		

- 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 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Lc	51	Total	C	N	O	S	0	0
			425	254	97	72	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
			754	475	132	143	4		

- Molecule 31 is a protein called Ribosomal protein L31B.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Le	97	Total	C	N	O		0	0
			795	504	155	136			

- Molecule 32 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lf	125	Total	C	N	O	S	0	0
			1031	655	206	164	6		

- Molecule 33 is a protein called Ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lg	97	Total	C	N	O	S	0	0
			770	492	146	129	3		

- Molecule 34 is a protein called Ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lh	106	Total	C	N	O	S	0	0
			846	522	175	145	4		

- Molecule 35 is a protein called Ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Li	115	Total	C	N	O	S	0	0
			931	590	182	154	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lj	83	Total	C	N	O	S	0	0
			677	430	135	108	4		

- Molecule 37 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lk	86	Total	C	N	O	S	0	0
			697	426	149	115	7		

- Molecule 38 is a protein called Ribosomal L38e.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ll	69	Total	C	N	O	S	0	0
			534	339	92	99	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 60S 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	92	Total	C	N	O	S	0	0
			759	472	158	124	5		

- Molecule 42 is a protein called Ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lq	86	Total	C	N	O	S	0	0
			666	412	135	113	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Ls	45	Total	C	N	O	S	0	0
			374	226	81	61	6		

- 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 RNA chain called E-site tRNA.

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

- Molecule 46 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SA	195	Total	C	N	O	S	0	0
			1556	1001	273	274	8		

- Molecule 47 is a protein called Ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SB	208	Total	C	N	O	S	0	0
			1604	1020	293	286	5		

- Molecule 48 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SC	204	Total	C	N	O	S	0	0
			1614	1018	294	286	16		

- Molecule 49 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SD	223	Total	C	N	O	S	0	0
			1803	1141	333	316	13		

- Molecule 50 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SE	259	Total	C	N	O	S	0	0
			2081	1331	383	355	12		

- Molecule 51 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SF	177	Total	C	N	O	S	0	0
			1382	860	261	252	9		

- Molecule 52 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SG	226	Total	C	N	O	S	0	0
			1785	1120	338	317	10		

- Molecule 53 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SH	184	Total	C	N	O	S	0	0
			1481	948	258	268	7		

- Molecule 54 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SI	163	Total	C	N	O	S	0	0
			1280	804	245	228	3		

- Molecule 55 is a protein called Ribosomal protein S15A.

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

- Molecule 56 is a protein called Ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SK	175	Total	C	N	O	S	0	0
			1416	884	280	246	6		

- Molecule 57 is a protein called Ribosomal protein S10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SL	101	Total	C	N	O	S	0	0
			827	535	139	149	4		

- Molecule 58 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SM	147	Total	C	N	O	S	0	0
			1220	775	239	200	6		

- Molecule 59 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SO	136	Total	C	N	O	S	0	0
			1056	669	209	175	3		

- Molecule 60 is a protein called Ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SP	149	Total	C	N	O	S	0	0
			1187	755	227	200	5		

- Molecule 61 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SQ	124	Total	C	N	O	S	0	0
			911	561	188	159	3		

- Molecule 62 is a protein called Ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SR	112	Total	C	N	O	S	0	0
			912	582	178	144	8		

- Molecule 63 is a protein called Ribosomal protein S16.

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

- Molecule 64 is a protein called Ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SU	66	Total	C	N	O	S	0	0
			526	329	106	89	2		

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 65 is a protein called Ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SV	140	Total	C	N	O	S	0	0
			1113	685	226	196	6		

- Molecule 66 is a protein called Ribosomal protein S19e.

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

- Molecule 67 is a protein called Ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SX	102	Total	C	N	O	S	0	0
			811	516	147	143	5		

- Molecule 68 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SY	82	Total	C	N	O	S	0	0
			615	383	113	113	6		

- Molecule 69 is a protein called Ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sb	118	Total	C	N	O	S	0	0
			941	598	177	160	6		

- Molecule 70 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Sc	71	Total	C	N	O	S	0	0
			561	353	103	99	6		

- Molecule 71 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Sd	98	Total	C	N	O	S	0	0
			796	491	164	134	7		

- Molecule 72 is a protein called Ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Se	80	Total	C	N	O	S	0	0
			629	397	110	116	6		

- Molecule 73 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sg	60	Total	C	N	O	S	0	0
			474	293	91	88	2		

- Molecule 74 is a protein called Ribosomal protein S29A.

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

- Molecule 75 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Sj	64	Total	C	N	O	S	0	0
			525	331	109	84	1		

- Molecule 76 is a RNA chain called Small Subunit rRNA.

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

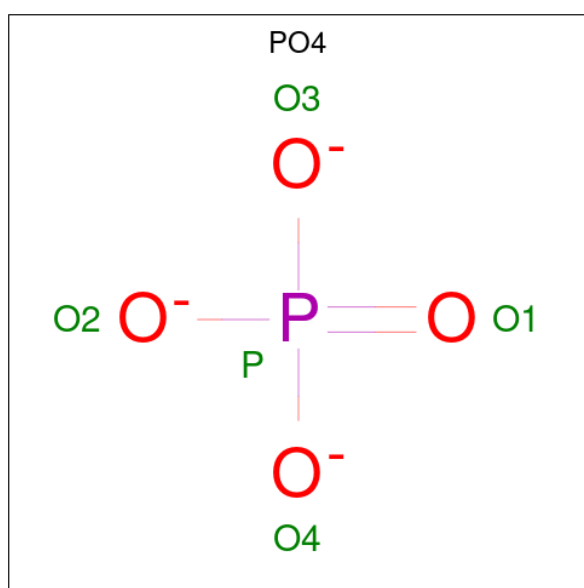
- Molecule 77 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	a	815	Total	C	N	O	S	0	0
			6343	3998	1097	1203	45		

- Molecule 78 is a RNA chain called mRNA.

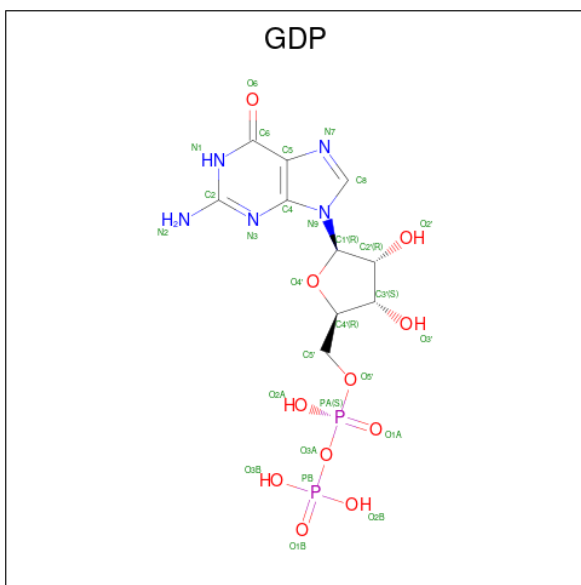
Mol	Chain	Residues	Atoms					AltConf	Trace
78	y	11	Total	C	N	O	P	0	0
			240	108	49	72	11		

- Molecule 79 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
79	a	1	Total	O	P	0
			5	4	1	

- Molecule 80 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$) (labeled as "Ligand of Interest" by depositor).

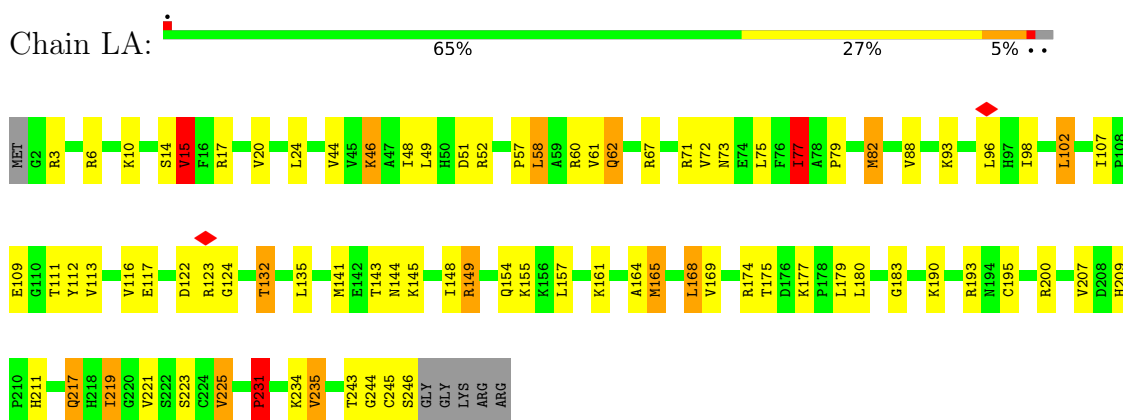


Mol	Chain	Residues	Atoms					AltConf
80	a	1	Total	C	N	O	P	0
			28	10	5	11	2	

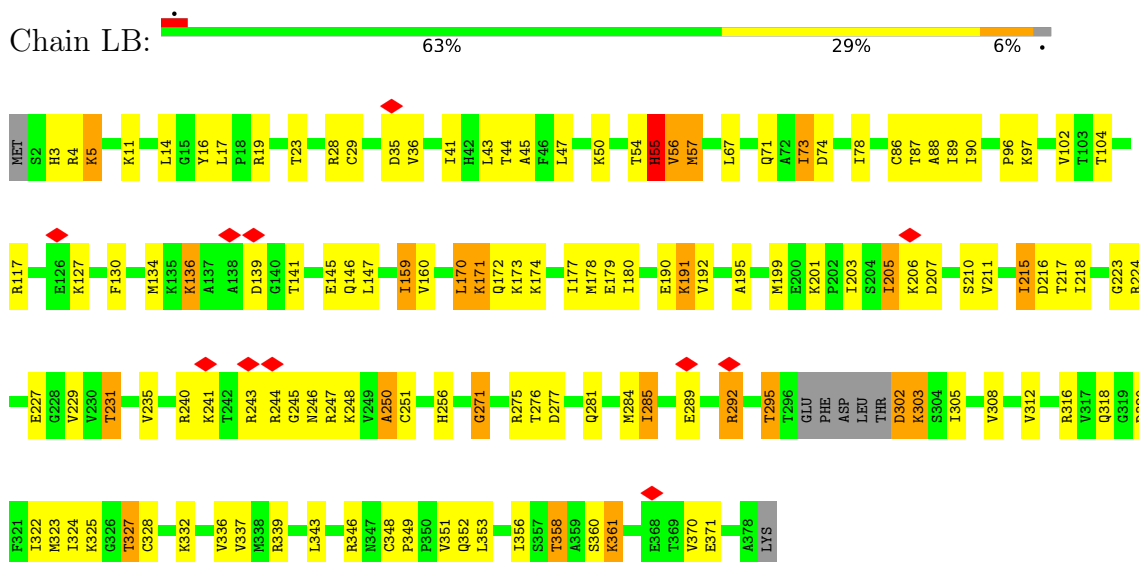
3 Residue-property plots

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

• Molecule 1: Ribosomal protein L2

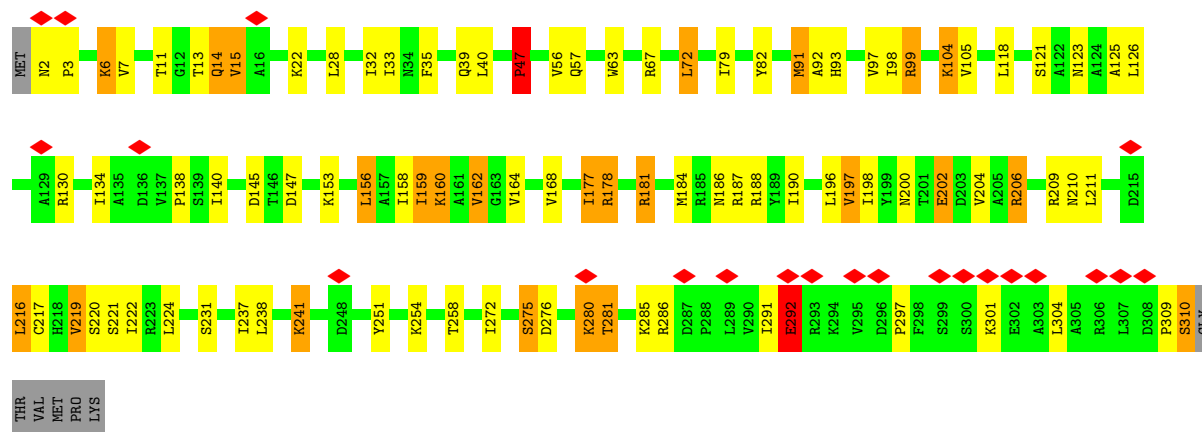


• Molecule 2: Ribosomal protein L3

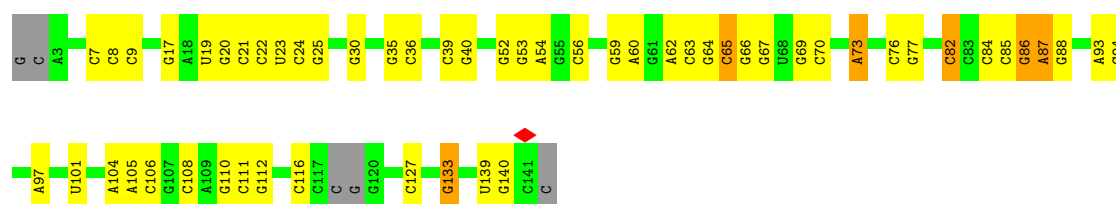


• Molecule 3: Ribosomal protein L4

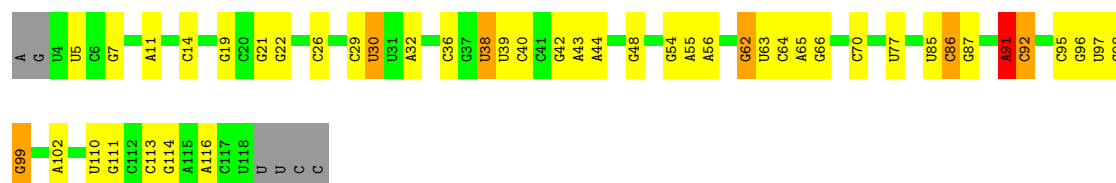




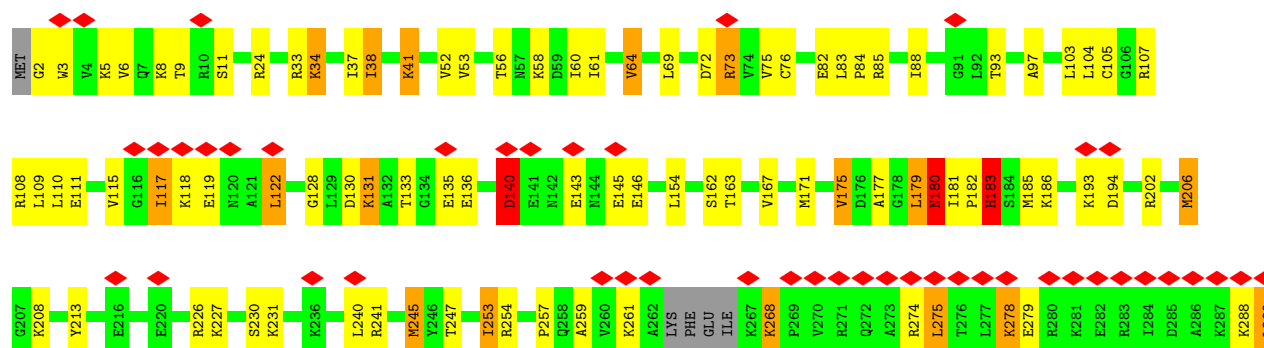
• Molecule 4: 5.8S rRNA

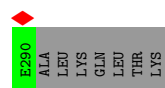


• Molecule 5: 5S rRNA

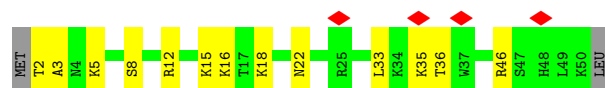
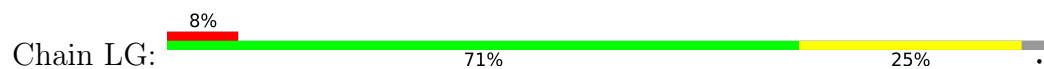


• Molecule 6: Ribosomal protein L5

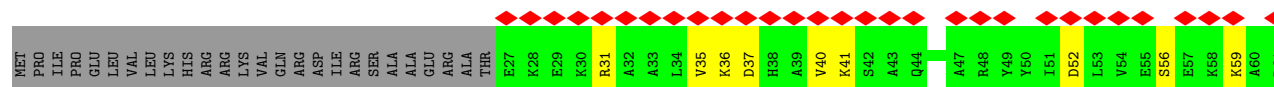




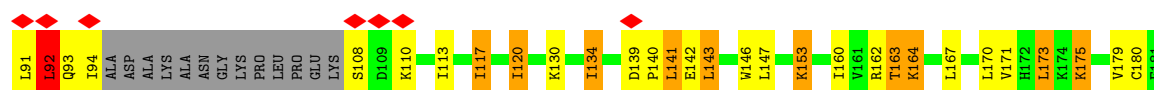
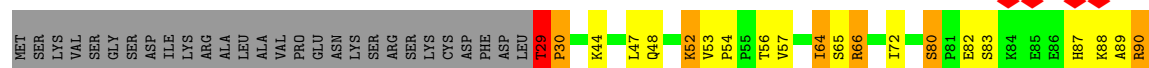
• Molecule 7: Ribosomal protein L39



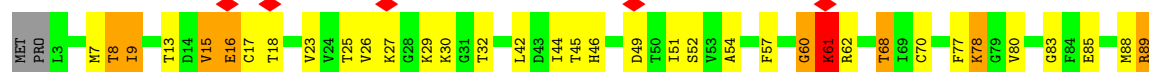
• Molecule 8: Ribosomal protein L7

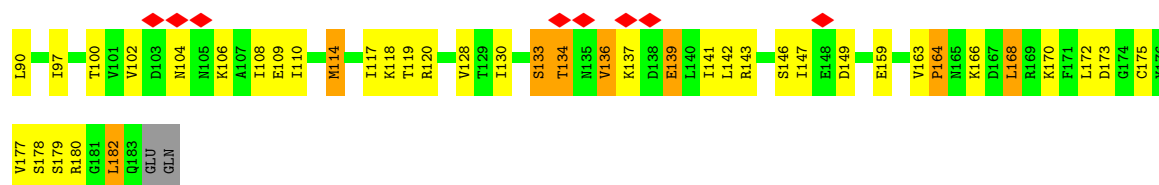


• Molecule 9: 60S ribosomal protein L7a

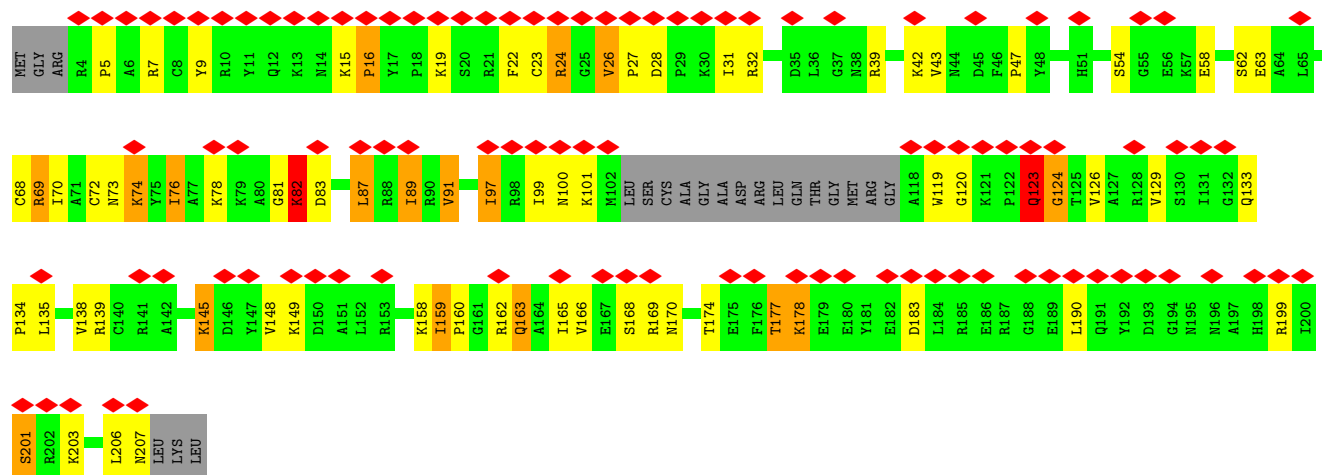


• Molecule 10: Ribosomal protein L6

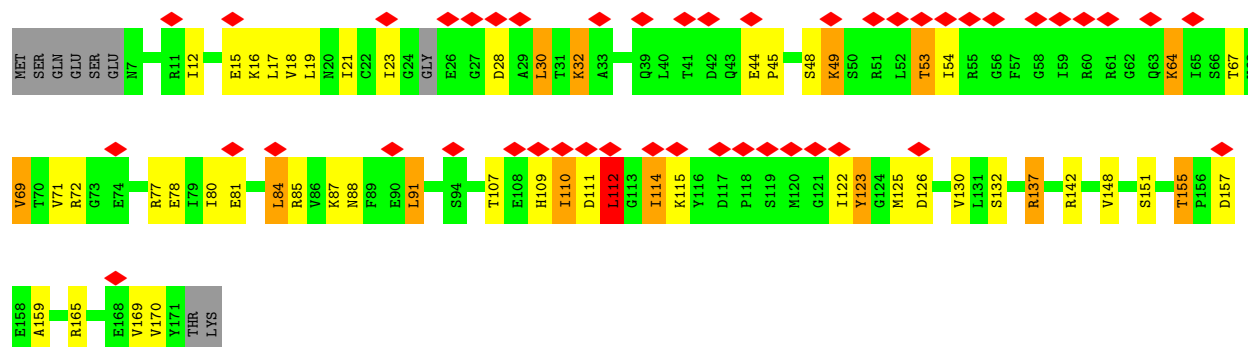




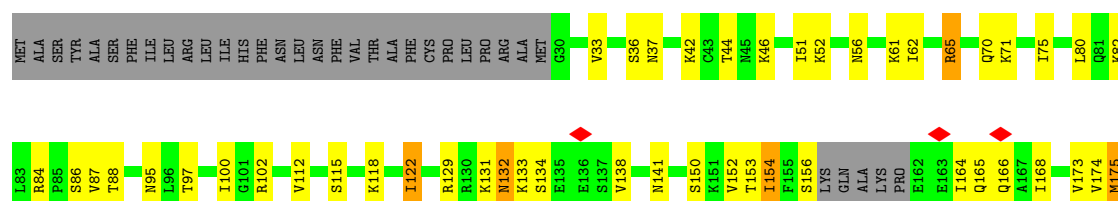
• Molecule 11: Ribosomal protein L10



• Molecule 12: Ribosomal protein L11

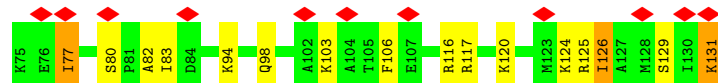


• Molecule 13: 60S ribosomal protein L13

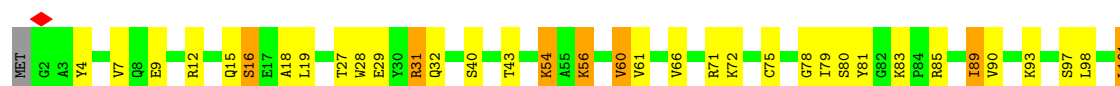




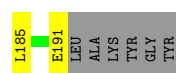
- Molecule 14: Ribosomal protein L14



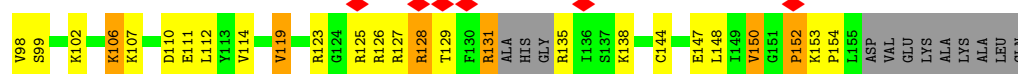
- Molecule 15: Ribosomal protein L15



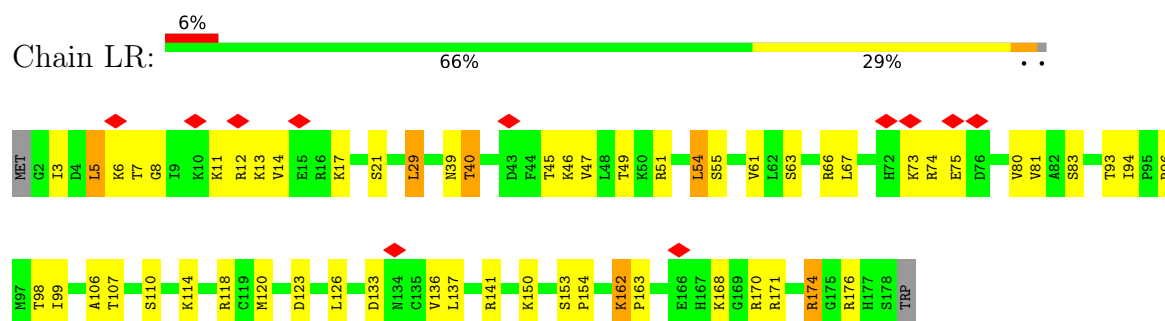
- Molecule 16: Ribosomal protein L13a



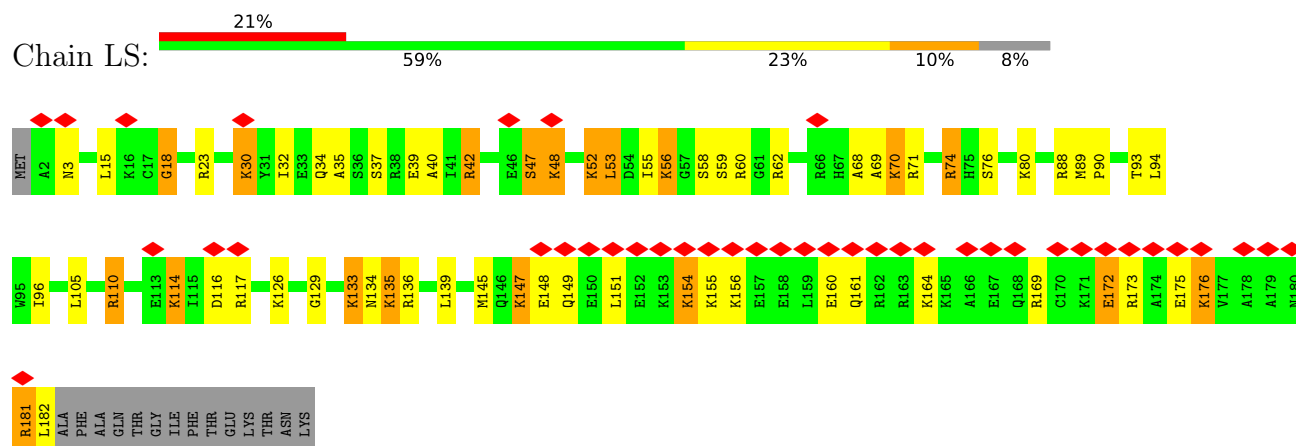
- Molecule 17: Ribosomal protein L17



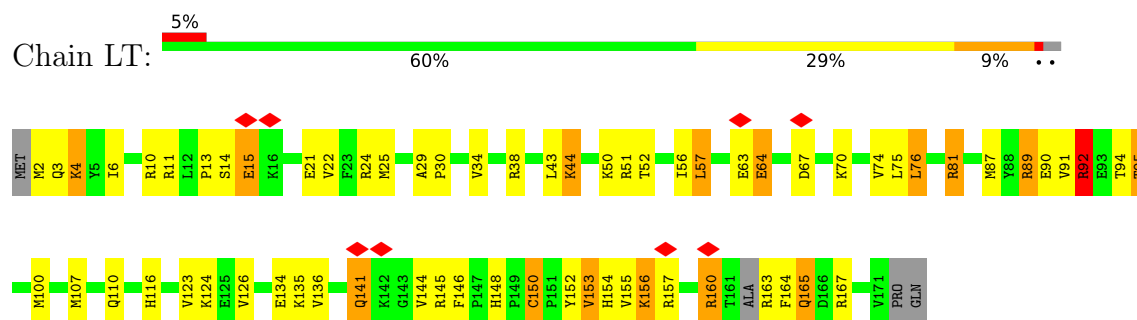
- Molecule 18: Ribosomal protein L18



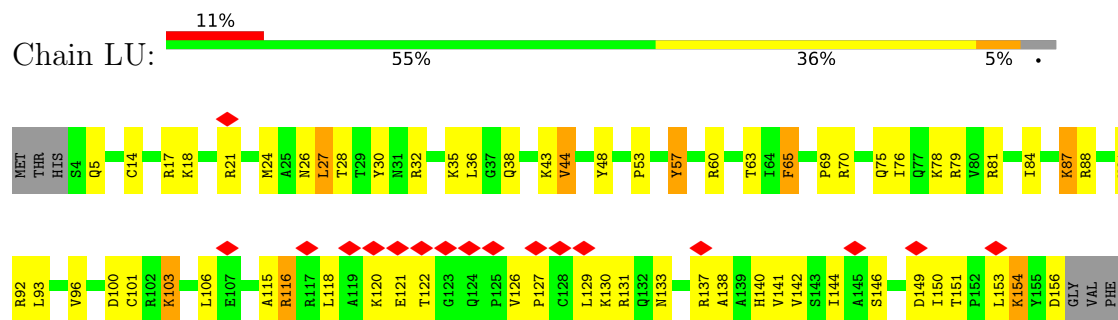
- Molecule 19: Ribosomal protein L19



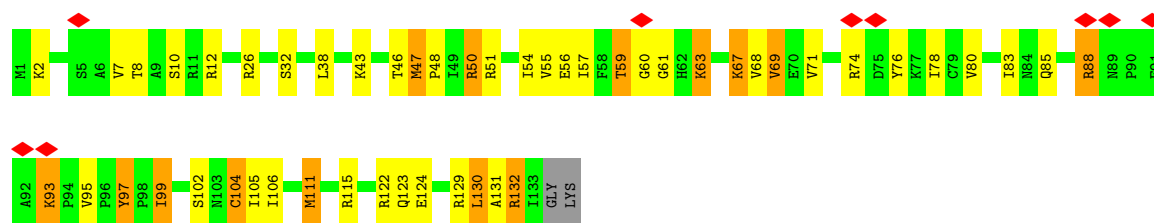
- Molecule 20: 60S ribosomal protein L18a



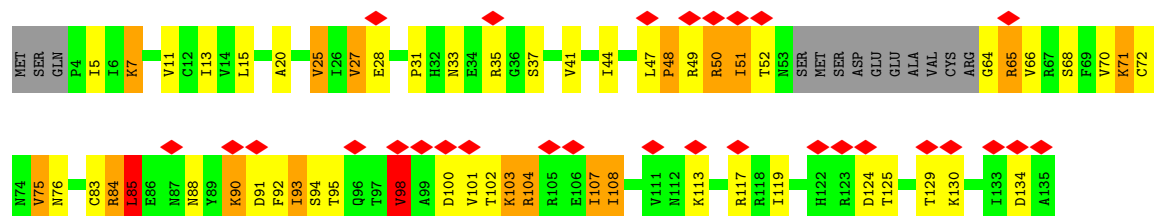
- Molecule 21: Ribosomal protein L21



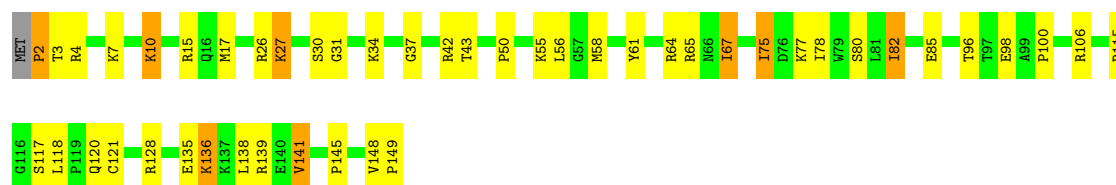
- Molecule 22: Ribosomal L22e



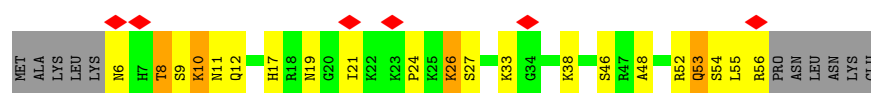
• Molecule 27: 60S ribosomal protein L27



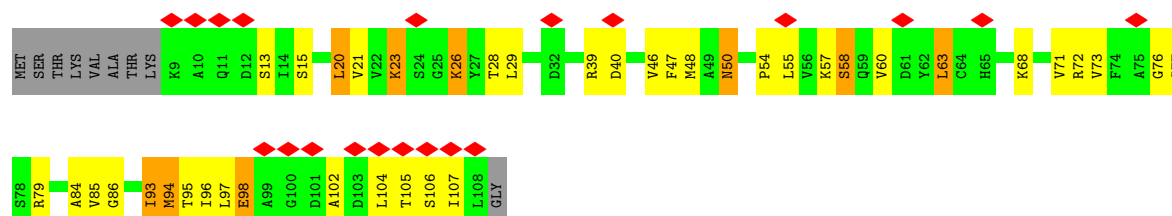
• Molecule 28: Ribosomal protein L27a



• Molecule 29: 60S ribosomal protein L29



• Molecule 30: Ribosomal protein L30

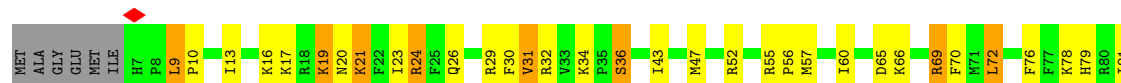


• Molecule 31: Ribosomal protein L31B

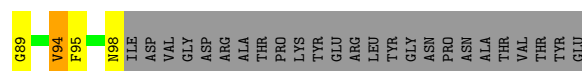
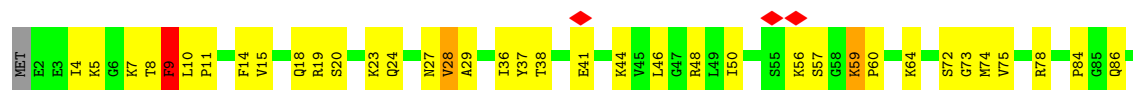


GLU

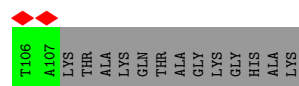
• Molecule 32: Ribosomal protein L32



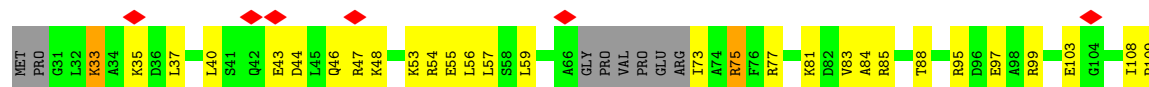
• Molecule 33: Ribosomal protein L35a



• Molecule 34: Ribosomal protein L34



• Molecule 35: Ribosomal protein L29

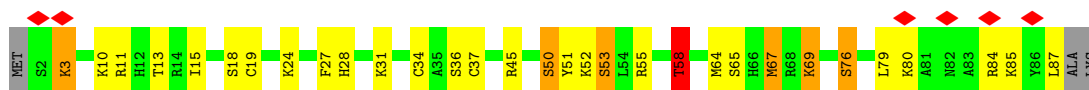




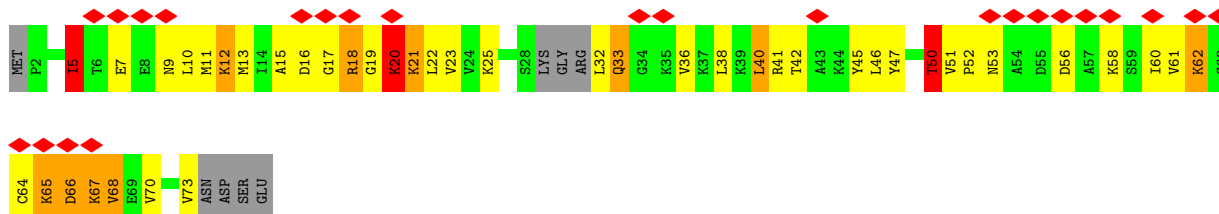
• Molecule 36: Ribosomal protein L36-1



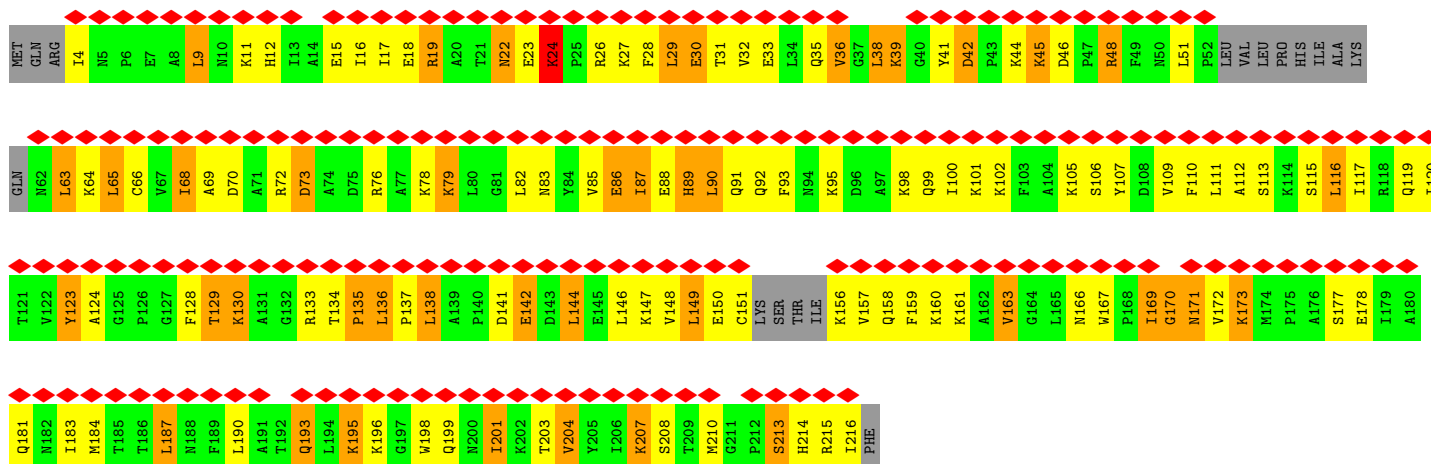
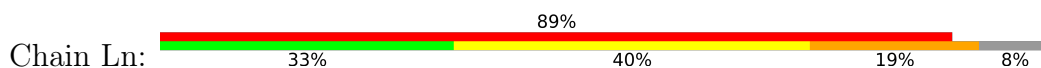
• Molecule 37: Ribosomal protein L37



• Molecule 38: Ribosomal L38e



• Molecule 39: Ribosomal protein L10a



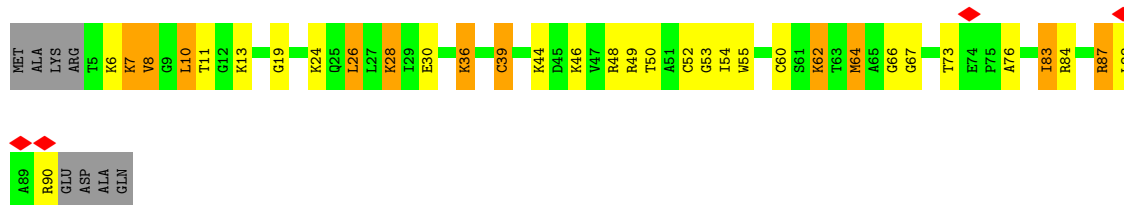
• Molecule 40: 60S ribosomal protein L41



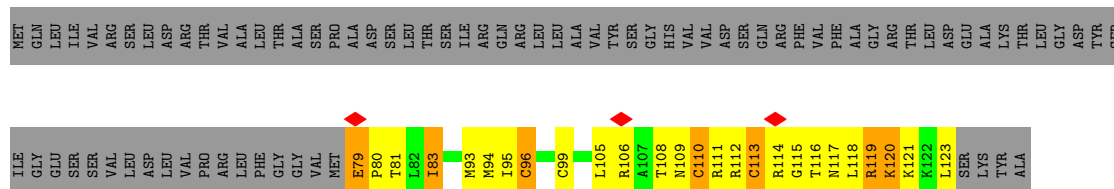
- Molecule 41: Ribosomal protein L44



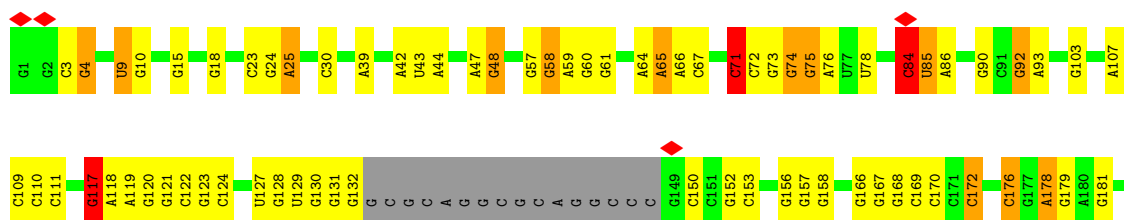
- Molecule 42: Ribosomal protein L37a



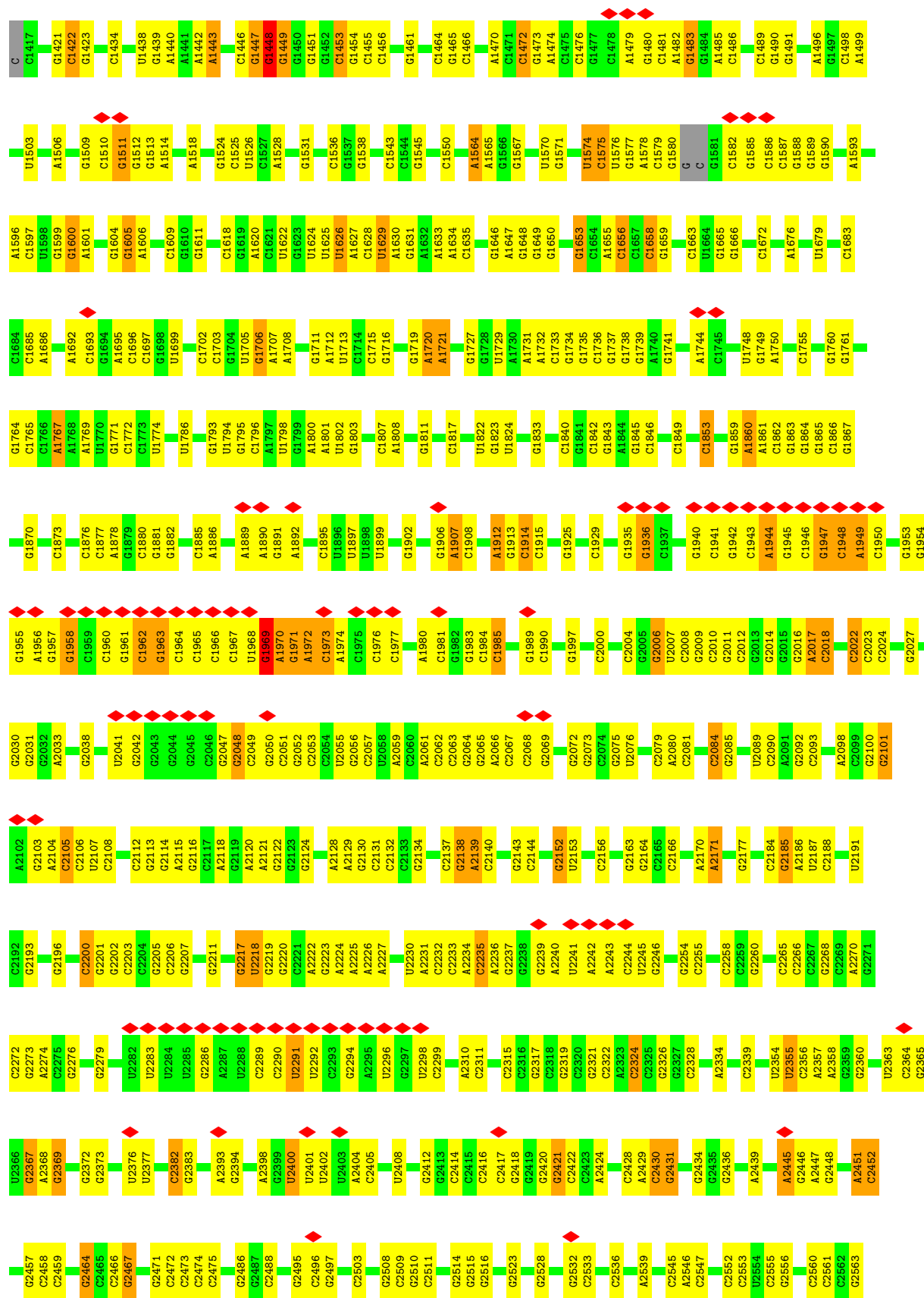
- Molecule 43: Ubiquitin/Ribosomal protein L40e

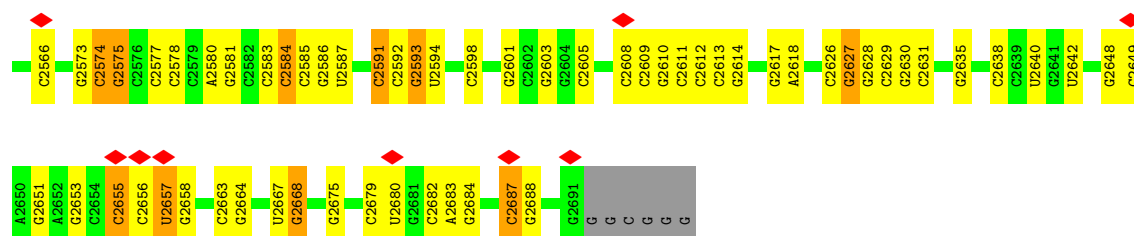


- Molecule 44: Large Subunit rRNA

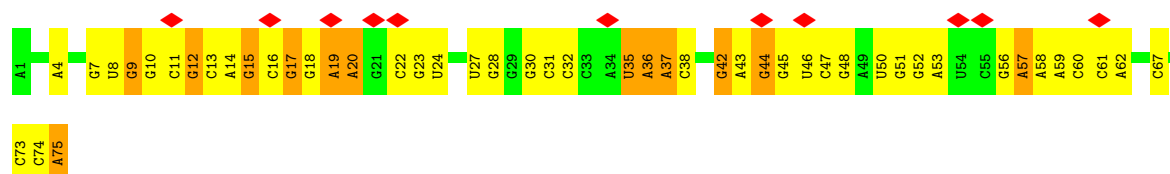




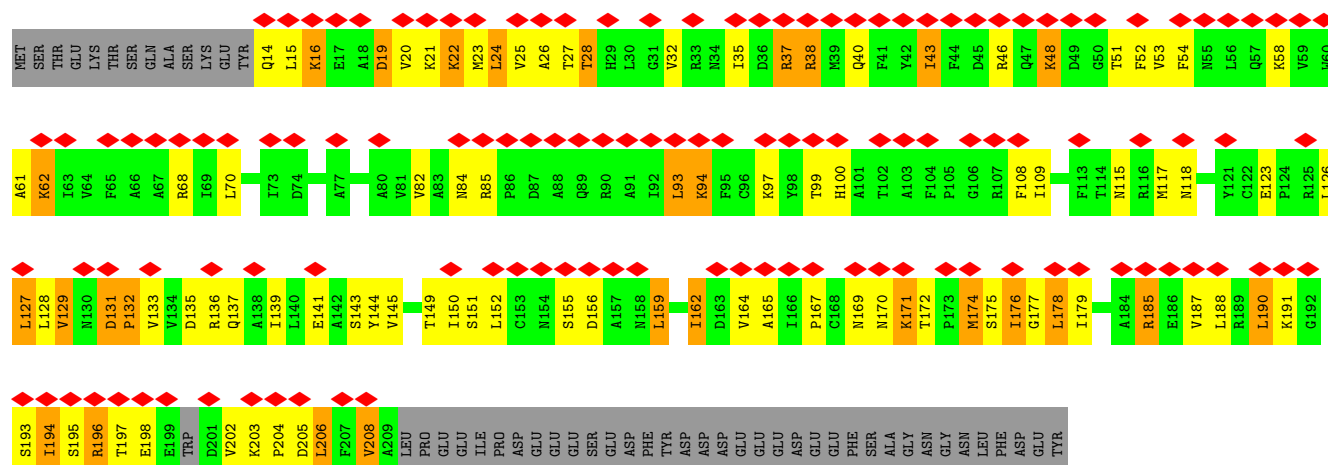




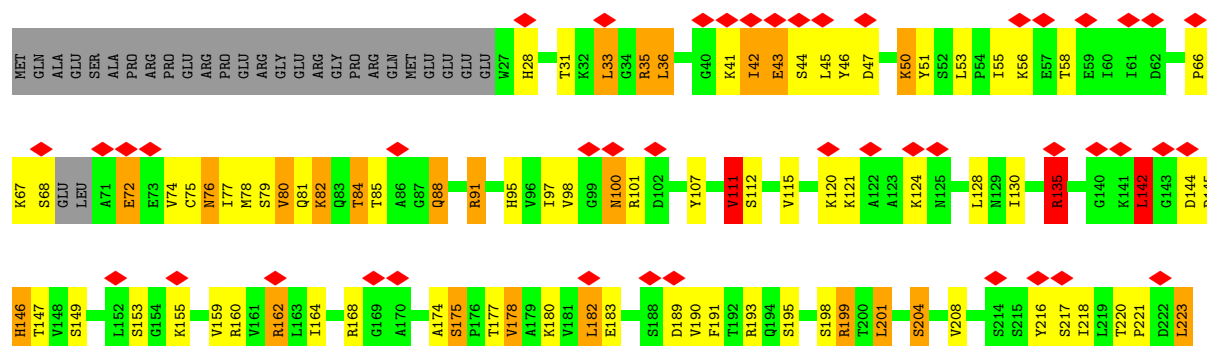
• Molecule 45: E-site tRNA



• Molecule 46: 40S ribosomal protein SA

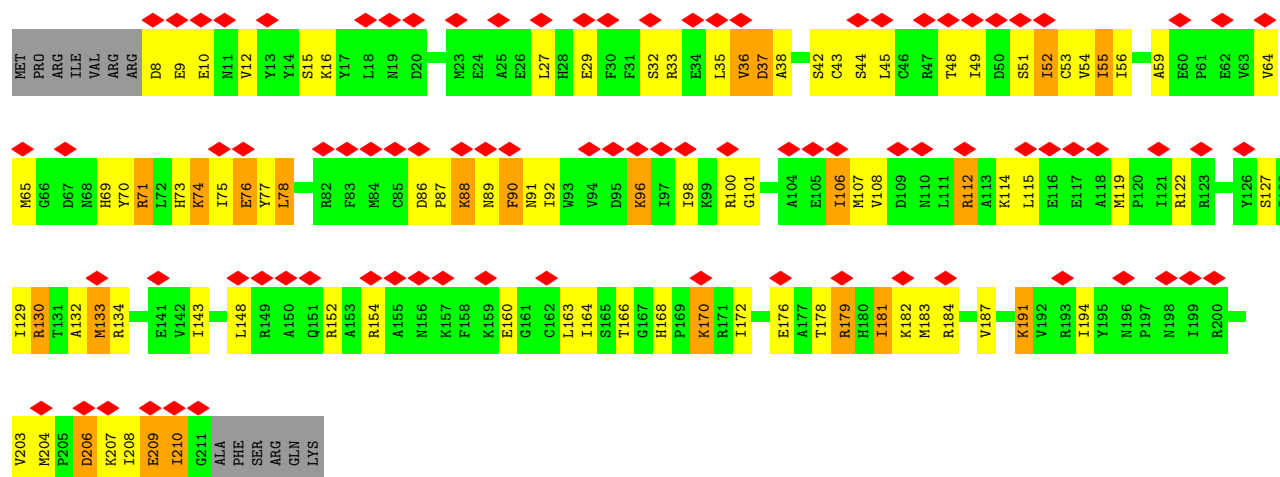


• Molecule 47: Ribosomal protein S2

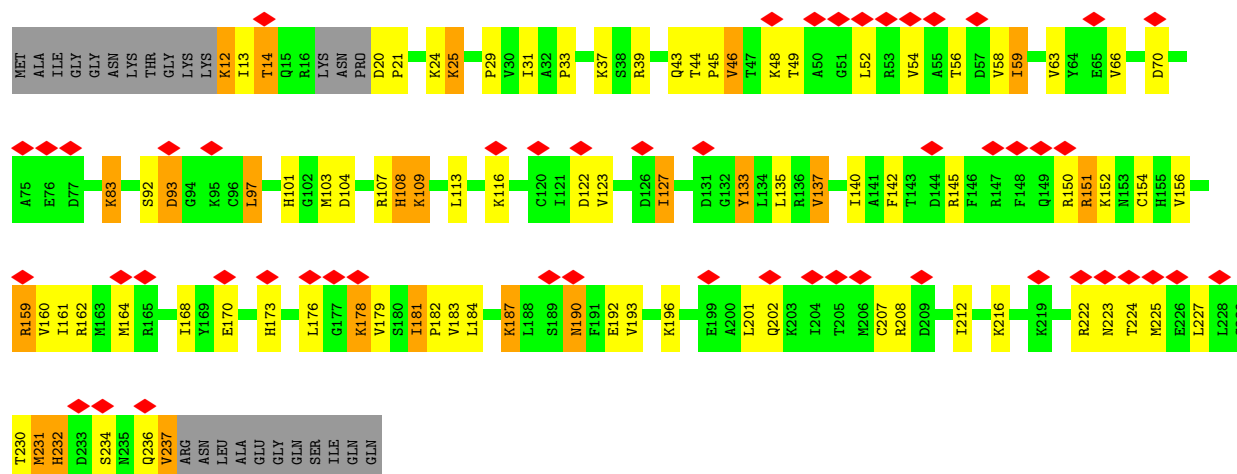




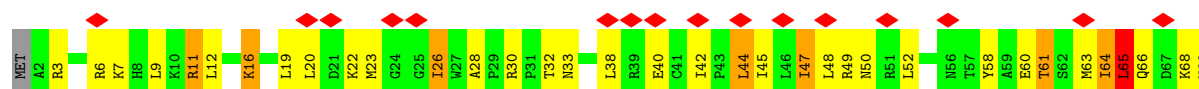
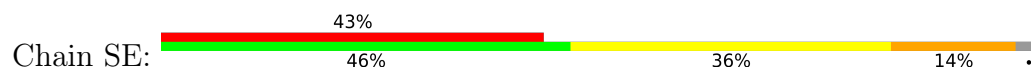
• Molecule 48: Ribosomal protein S3

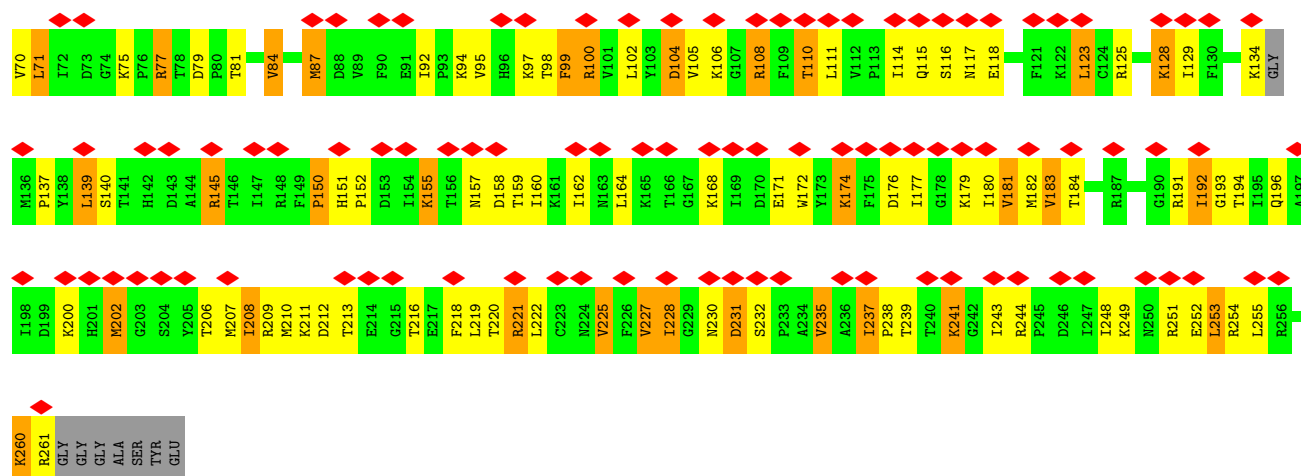


• Molecule 49: 40S ribosomal protein S3a



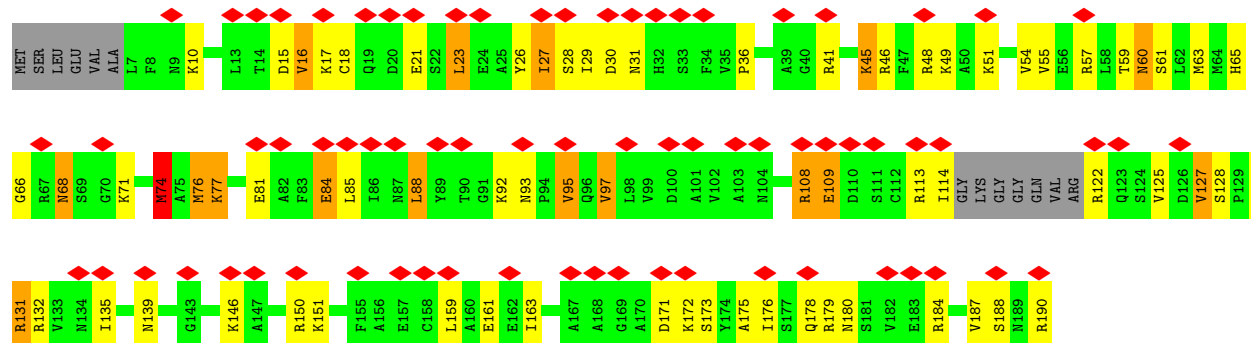
• Molecule 50: 40S ribosomal protein S4





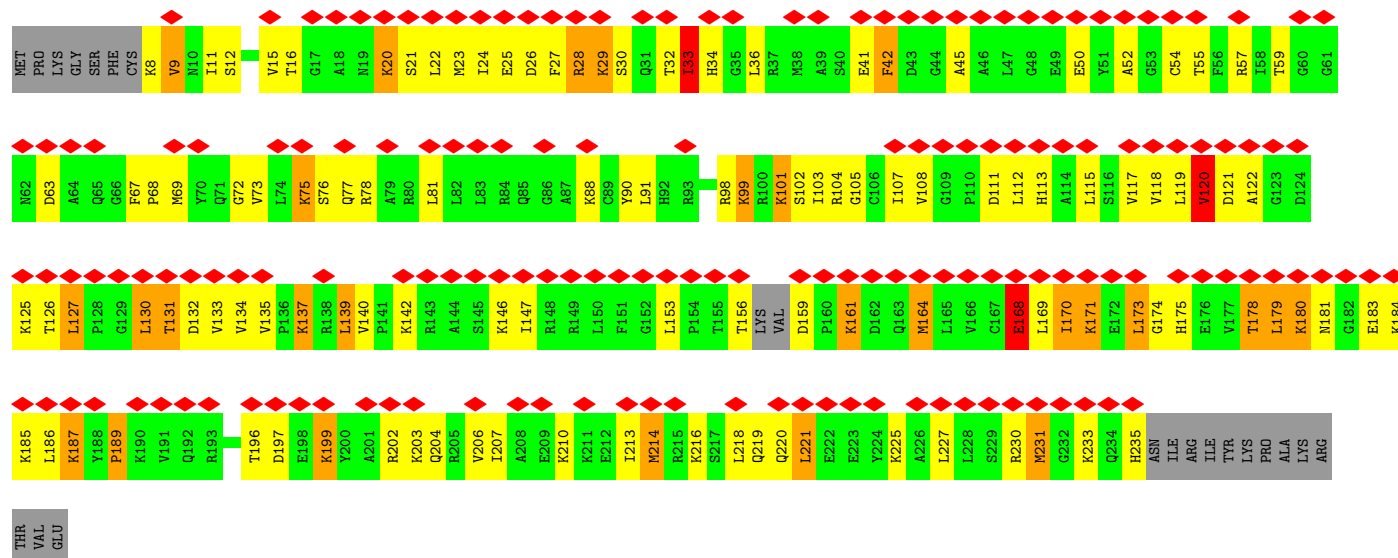
• Molecule 51: Ribosomal protein S5

Chain SF: 38% 55% 29% 8% 7%

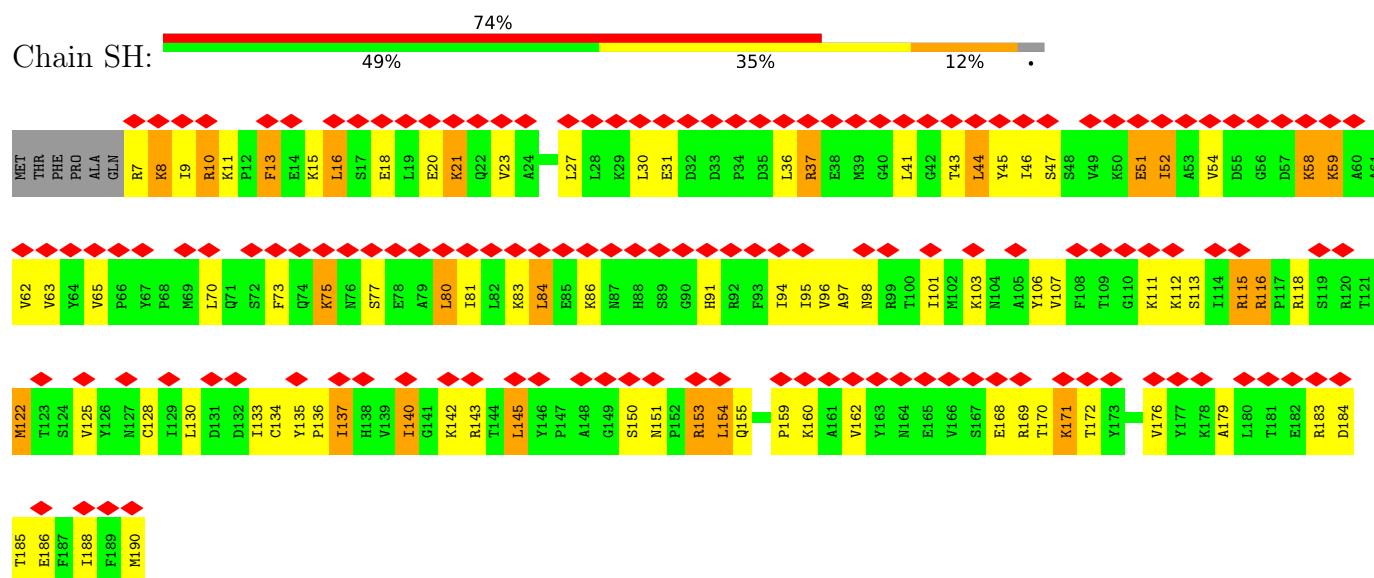


• Molecule 52: 40S ribosomal protein S6

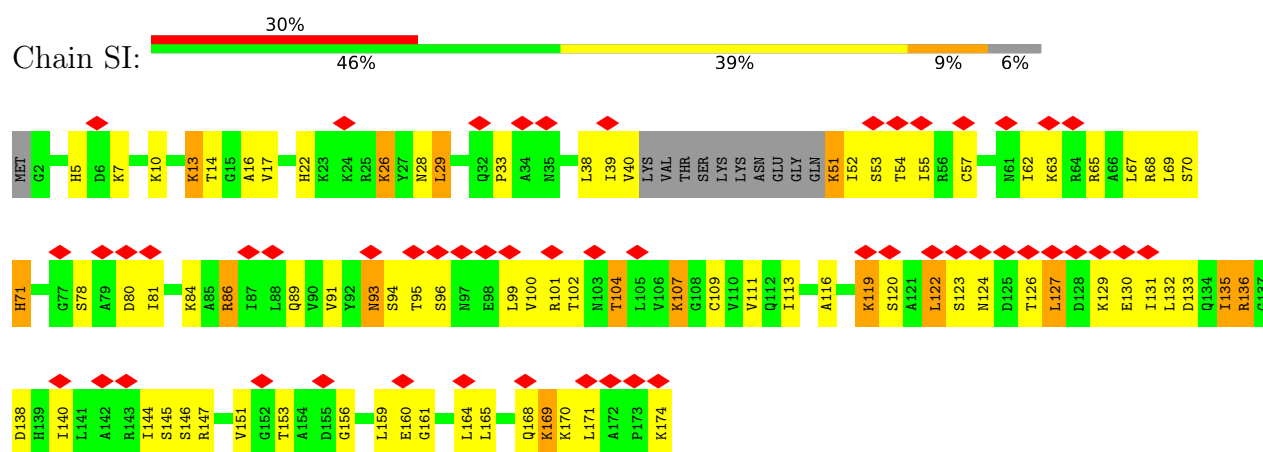
Chain SG: 66% 42% 37% 11% 9%



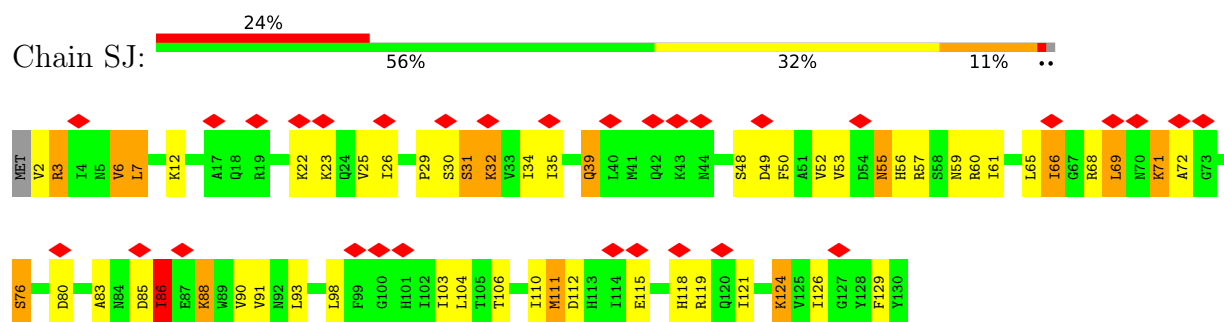
- Molecule 53: 40S ribosomal protein S7



- Molecule 54: 40S ribosomal protein S8

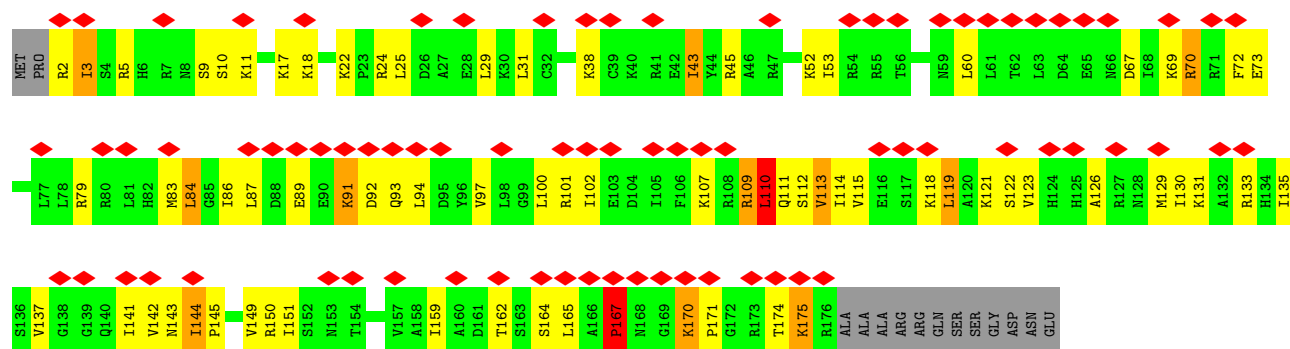


- Molecule 55: Ribosomal protein S15A

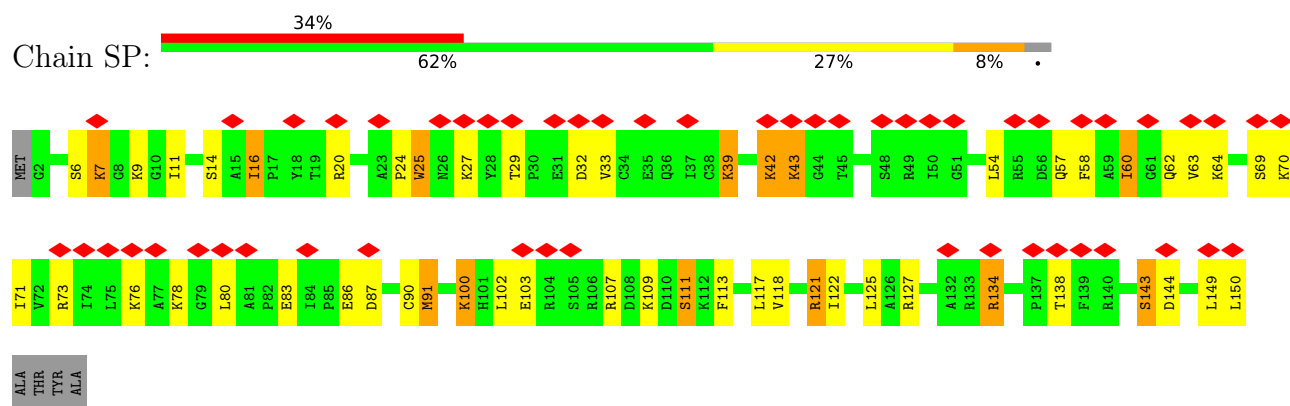


- Molecule 56: Ribosomal protein S9

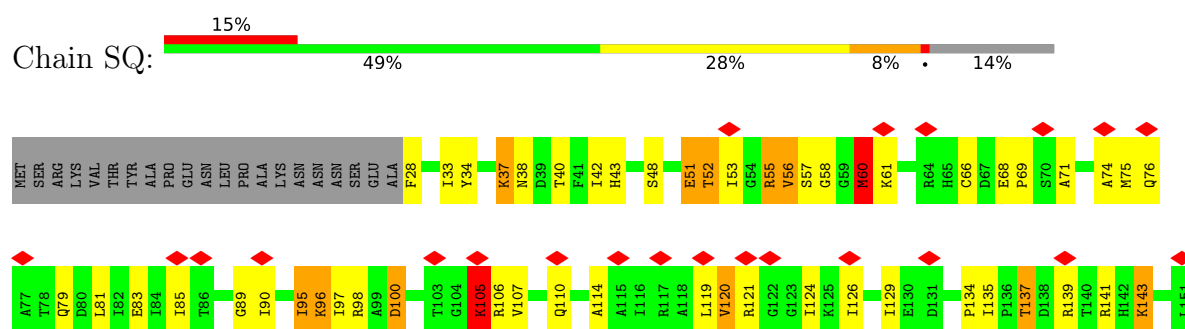




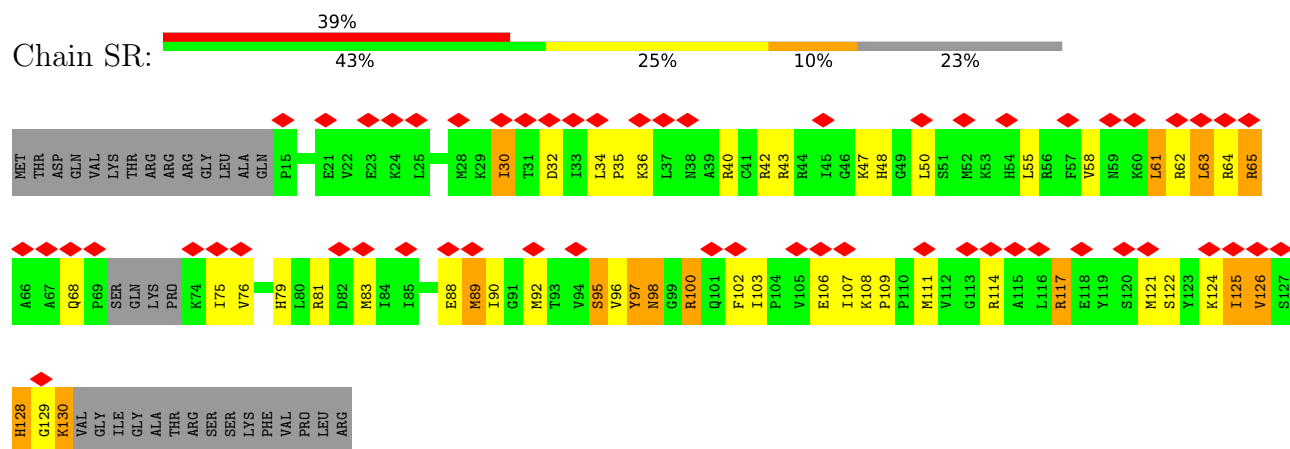
• Molecule 60: Ribosomal protein S13



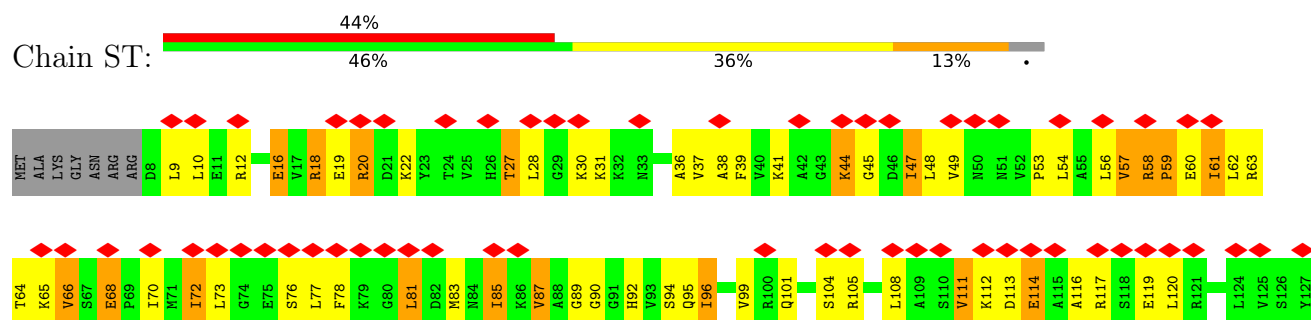
• Molecule 61: Ribosomal protein S14

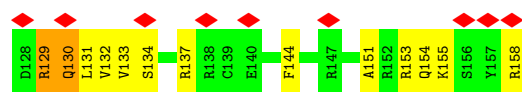


• Molecule 62: Ribosomal protein S15

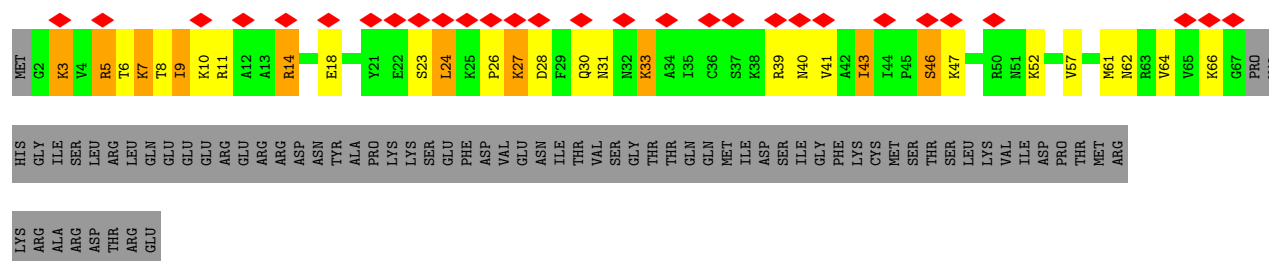
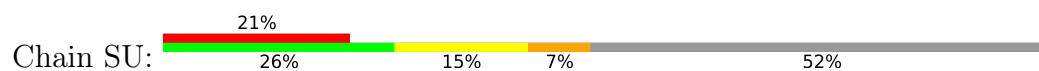


• Molecule 63: Ribosomal protein S16

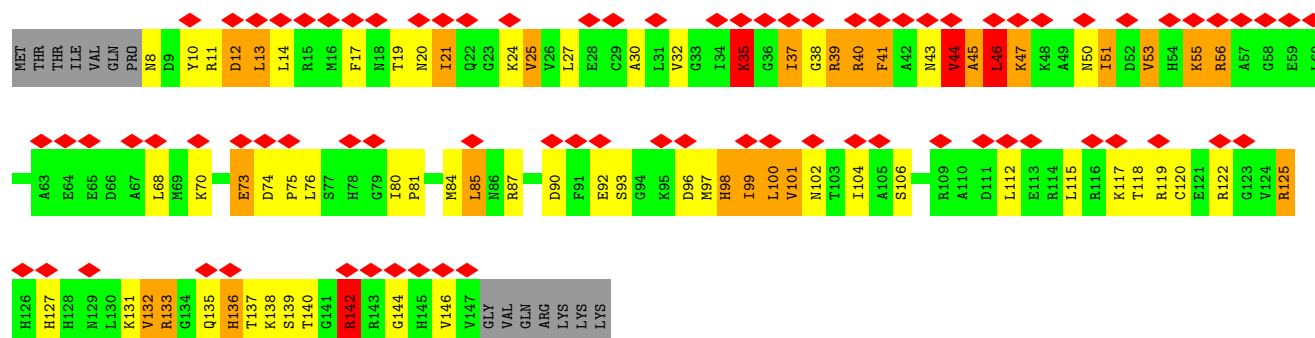




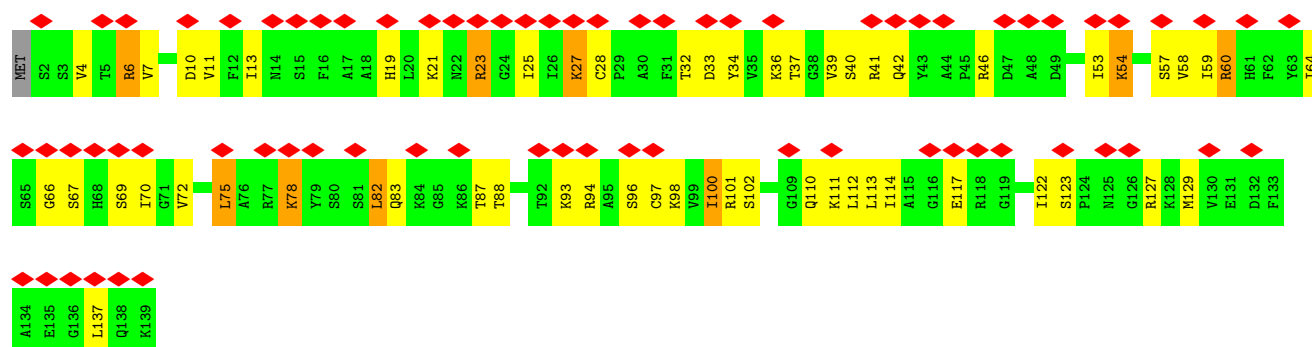
• Molecule 64: Ribosomal protein S17



• Molecule 65: Ribosomal protein S18

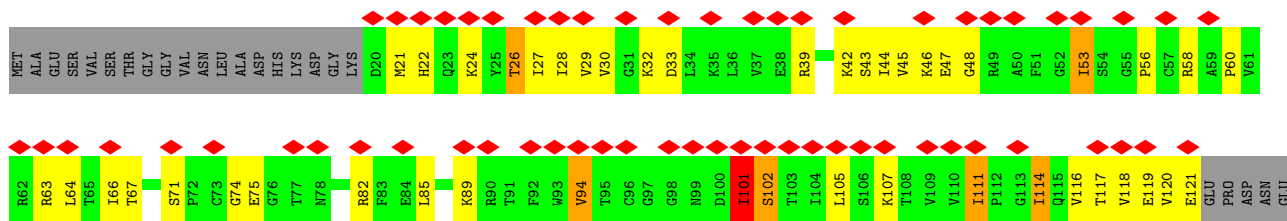


• Molecule 66: Ribosomal protein S19

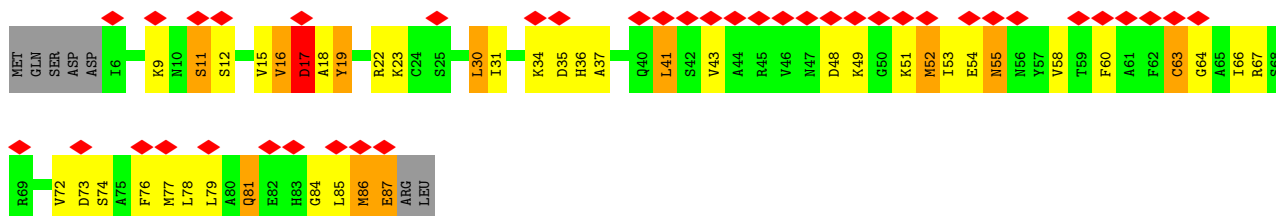
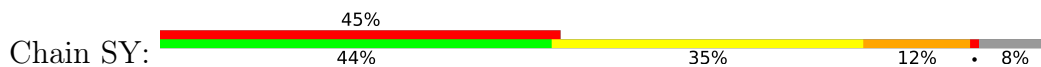


• Molecule 67: Ribosomal protein S20





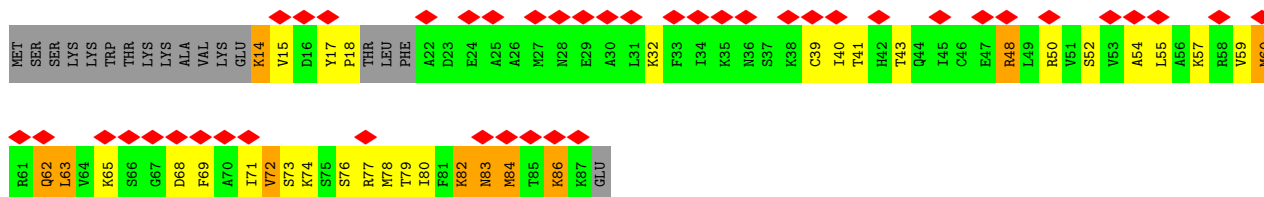
• Molecule 68: 40S ribosomal protein S21



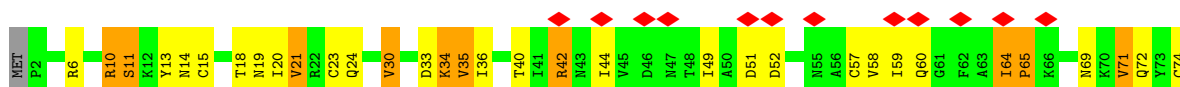
• Molecule 69: Ribosomal protein S24

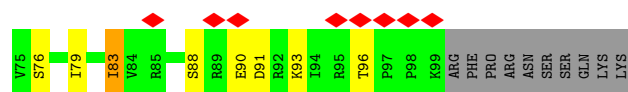


• Molecule 70: 40S ribosomal protein S25

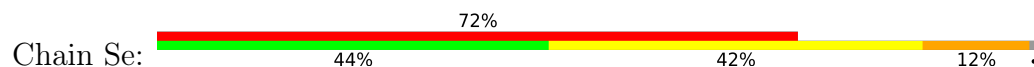


• Molecule 71: 40S ribosomal protein S26

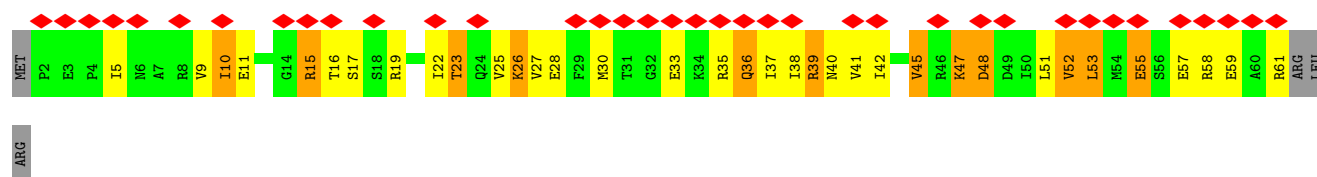




- Molecule 72: Ribosomal protein S27



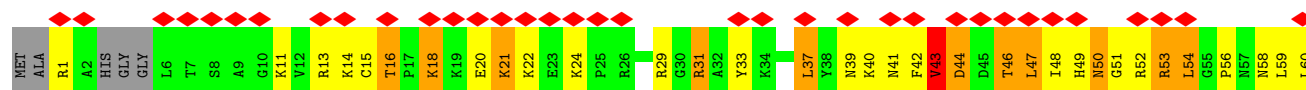
- Molecule 73: Ribosomal protein S28



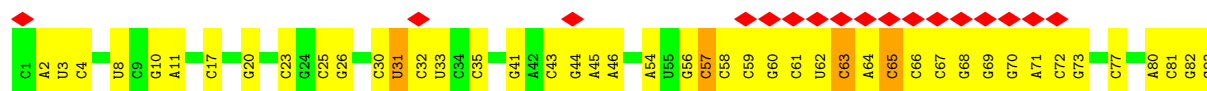
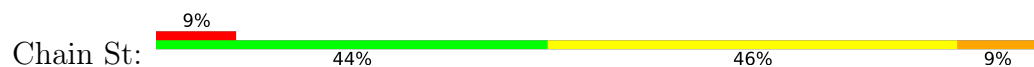
- Molecule 74: Ribosomal protein S29A

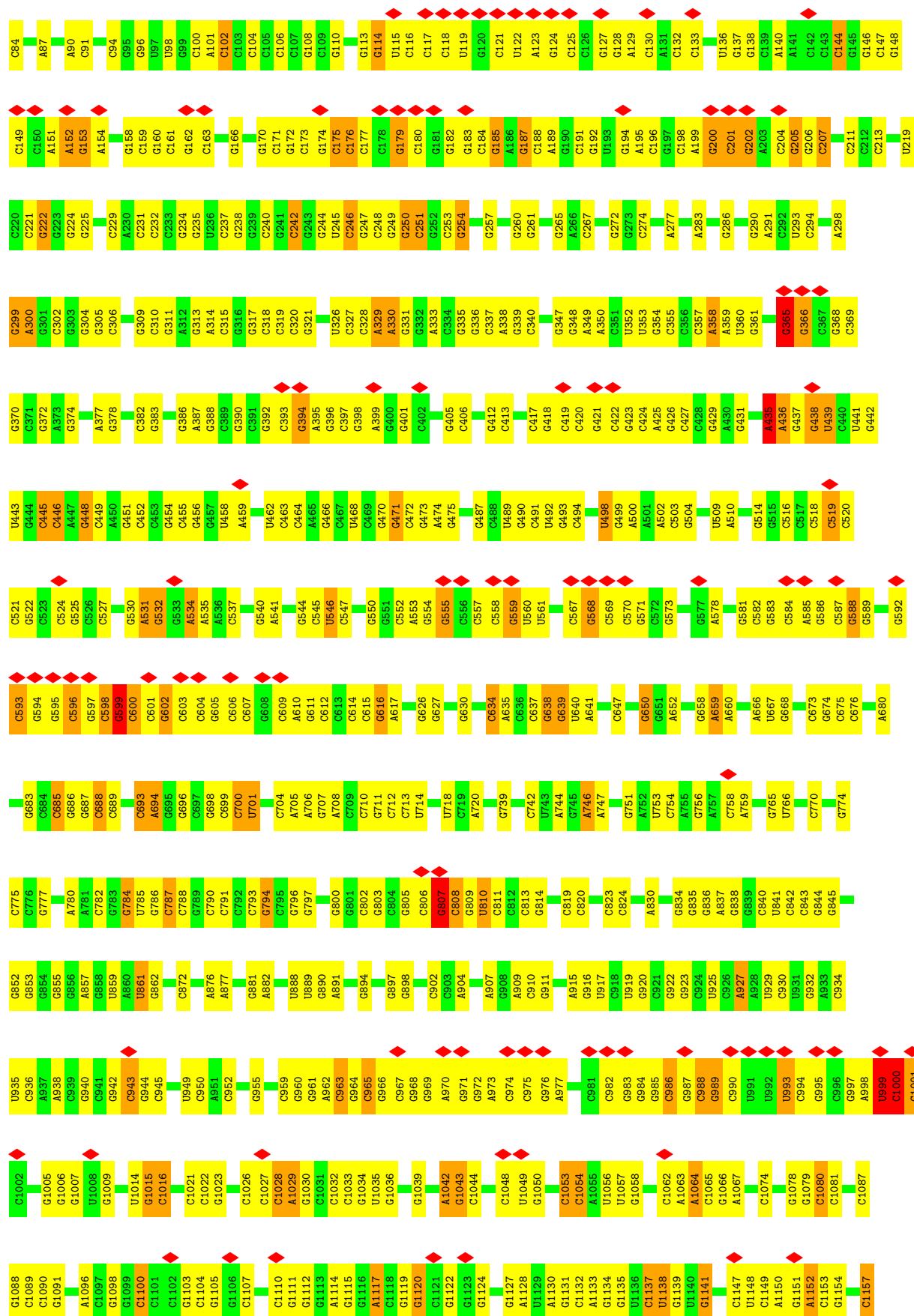


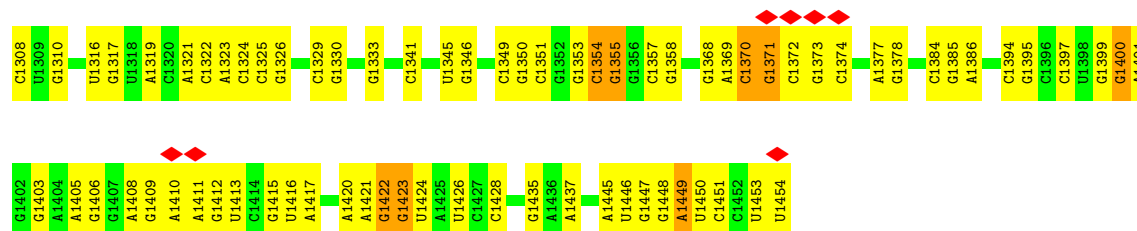
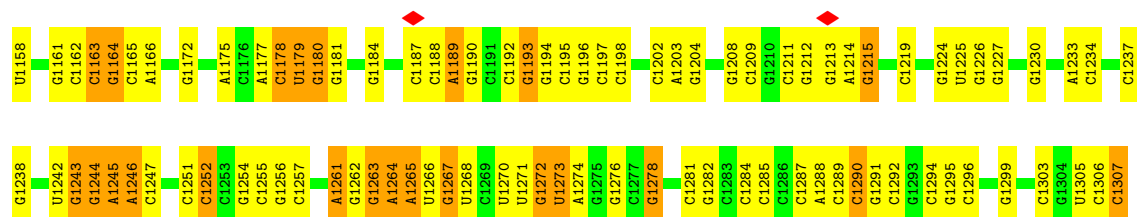
- Molecule 75: 40S ribosomal protein S30



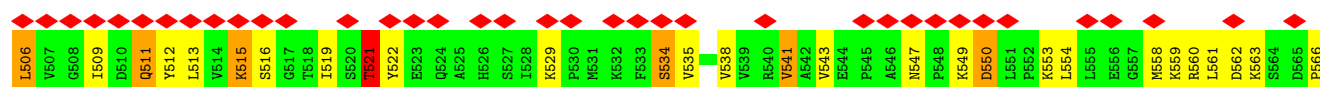
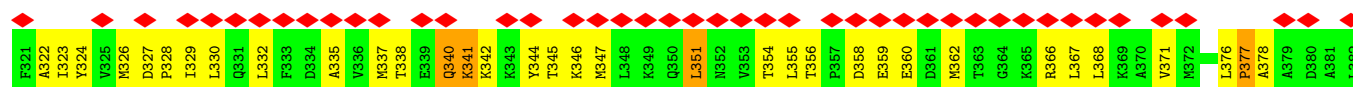
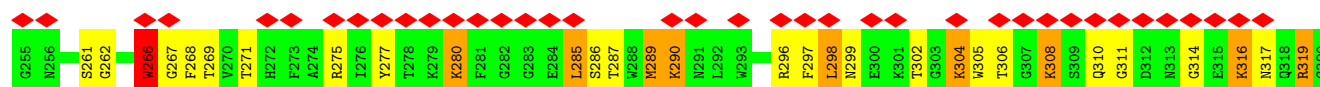
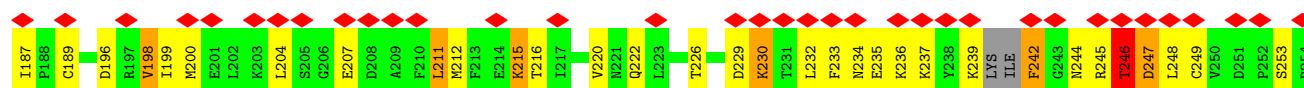
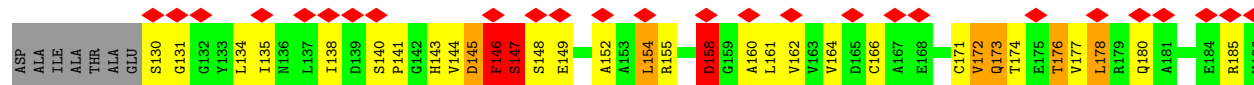
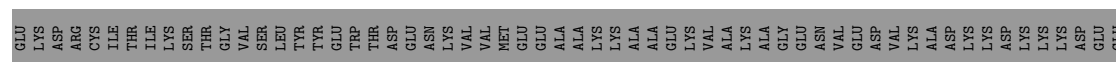
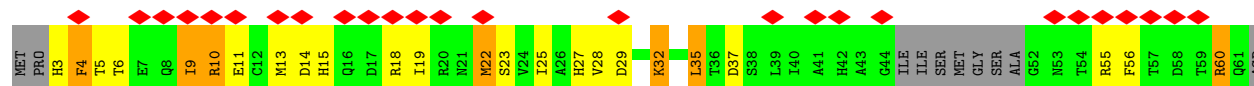
- Molecule 76: Small Subunit rRNA

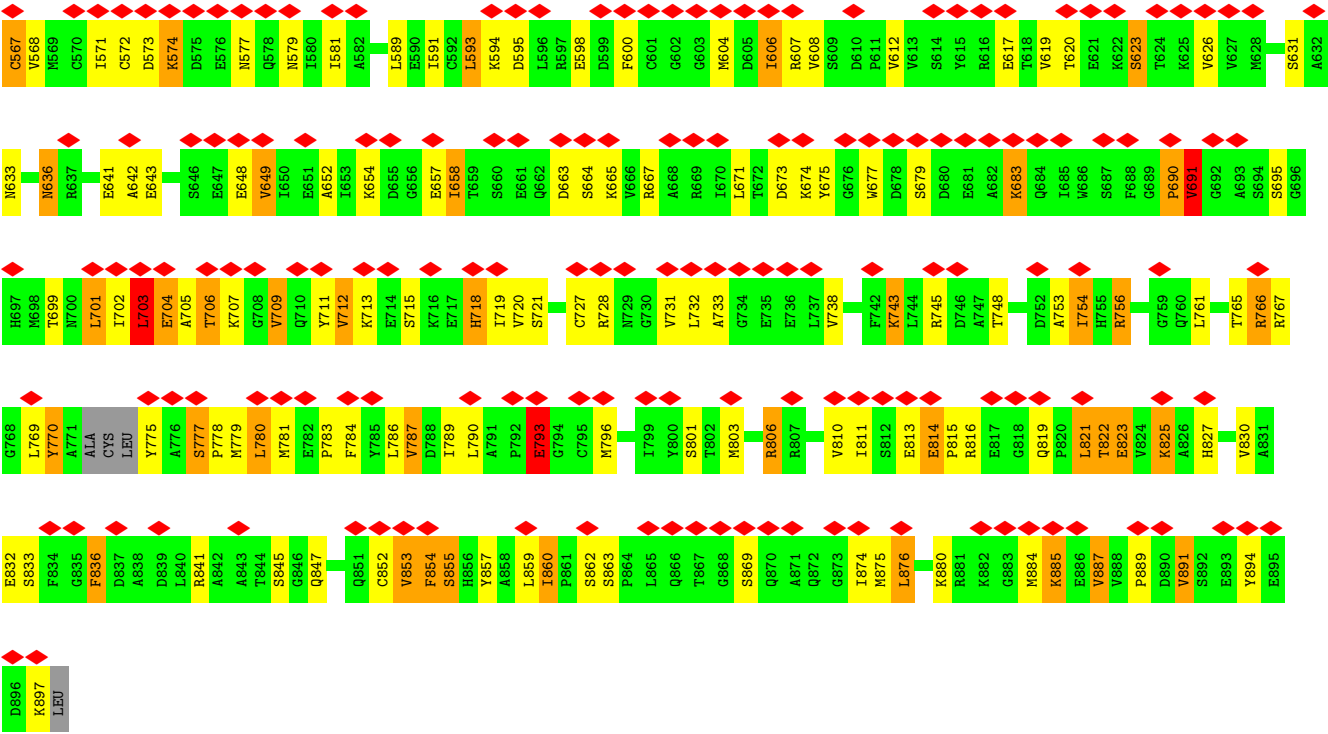




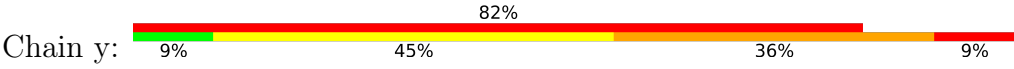


• Molecule 77: Elongation factor 2





● Molecule 78: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35694	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	GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	19.322	Depositor
Minimum map value	-9.629	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.74	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 ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, GDP

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	0.95	0/1880	1.45	9/2528 (0.4%)
2	LB	0.92	0/3004	1.43	19/4055 (0.5%)
3	LC	0.94	0/2463	1.37	13/3342 (0.4%)
4	LD	0.56	0/3274	0.81	1/5104 (0.0%)
5	LE	0.54	0/2747	0.83	3/4281 (0.1%)
6	LF	0.88	0/2328	1.44	12/3122 (0.4%)
7	LG	0.80	0/442	1.39	1/590 (0.2%)
8	LH	0.89	0/1724	1.41	6/2324 (0.3%)
9	LI	0.90	0/1471	1.41	8/1987 (0.4%)
10	LJ	0.92	0/1453	1.45	10/1962 (0.5%)
11	LK	0.89	0/1588	1.40	7/2128 (0.3%)
12	LL	0.89	0/1345	1.38	4/1805 (0.2%)
13	LM	0.90	0/1560	1.39	4/2089 (0.2%)
14	LN	0.88	0/1018	1.42	3/1364 (0.2%)
15	LO	0.89	0/1751	1.38	9/2346 (0.4%)
16	LP	0.91	0/1543	1.38	10/2069 (0.5%)
17	LQ	0.90	0/1244	1.43	4/1662 (0.2%)
18	LR	0.94	1/1409 (0.1%)	1.43	7/1884 (0.4%)
19	LS	0.87	0/1522	1.38	5/2012 (0.2%)
20	LT	0.88	0/1451	1.38	7/1947 (0.4%)
21	LU	0.88	0/1261	1.40	5/1695 (0.3%)
22	LV	0.85	0/903	1.43	7/1216 (0.6%)
23	LW	0.91	0/1043	1.39	1/1406 (0.1%)
24	LX	0.85	0/553	1.43	2/736 (0.3%)
25	LY	0.90	0/933	1.47	9/1262 (0.7%)
26	LZ	0.91	0/1091	1.41	7/1454 (0.5%)
27	La	0.89	0/993	1.45	5/1339 (0.4%)
28	Lb	0.92	0/1231	1.37	4/1647 (0.2%)
29	Lc	0.86	0/432	1.57	6/572 (1.0%)
30	Ld	0.92	0/762	1.44	5/1030 (0.5%)
31	Le	0.90	0/809	1.46	6/1087 (0.6%)
32	Lf	0.88	0/1055	1.39	6/1407 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lg	0.89	0/785	1.48	7/1051 (0.7%)
34	Lh	0.93	0/861	1.43	2/1158 (0.2%)
35	Li	0.84	0/940	1.35	2/1249 (0.2%)
36	Lj	0.85	0/686	1.33	1/909 (0.1%)
37	Lk	0.94	1/713 (0.1%)	1.43	3/945 (0.3%)
38	Ll	0.85	0/537	1.46	7/716 (1.0%)
39	Ln	0.98	0/1621	1.48	12/2183 (0.5%)
40	Lo	0.81	0/229	1.29	0/291
41	Lp	0.86	0/770	1.37	0/1018
42	Lq	0.88	0/675	1.43	3/901 (0.3%)
43	Ls	0.94	0/378	1.55	1/504 (0.2%)
44	Lt	0.57	0/62214	0.84	64/97098 (0.1%)
45	Lu	0.59	0/1795	0.79	0/2798
46	SA	0.92	0/1587	1.47	7/2153 (0.3%)
47	SB	0.92	0/1635	1.43	6/2202 (0.3%)
48	SC	0.92	0/1640	1.38	6/2203 (0.3%)
49	SD	0.86	0/1836	1.43	10/2473 (0.4%)
50	SE	0.95	0/2126	1.42	11/2866 (0.4%)
51	SF	0.90	0/1404	1.48	5/1888 (0.3%)
52	SG	0.91	0/1808	1.42	8/2416 (0.3%)
53	SH	0.92	0/1508	1.36	1/2032 (0.0%)
54	SI	0.92	0/1300	1.40	4/1744 (0.2%)
55	SJ	0.94	0/1048	1.40	4/1412 (0.3%)
56	SK	0.89	0/1435	1.42	6/1919 (0.3%)
57	SL	0.87	0/850	1.41	3/1157 (0.3%)
58	SM	0.91	0/1248	1.31	1/1669 (0.1%)
59	SO	0.88	0/1071	1.39	4/1436 (0.3%)
60	SP	0.88	0/1210	1.38	3/1625 (0.2%)
61	SQ	0.91	0/923	1.47	7/1239 (0.6%)
62	SR	0.89	0/928	1.38	6/1238 (0.5%)
63	ST	0.94	0/1192	1.47	8/1594 (0.5%)
64	SU	0.94	0/530	1.45	2/706 (0.3%)
65	SV	0.92	0/1129	1.53	12/1514 (0.8%)
66	SW	0.93	0/1104	1.42	3/1484 (0.2%)
67	SX	0.91	0/826	1.43	4/1115 (0.4%)
68	SY	0.92	0/623	1.40	0/836
69	Sb	0.87	0/956	1.46	8/1279 (0.6%)
70	Sc	0.89	0/565	1.47	2/750 (0.3%)
71	Sd	0.89	0/809	1.42	2/1088 (0.2%)
72	Se	0.97	0/643	1.44	2/871 (0.2%)
73	Sg	0.93	0/477	1.43	3/638 (0.5%)
74	Sh	0.84	0/417	1.52	6/553 (1.1%)
75	Sj	0.88	0/533	1.52	5/708 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	St	0.58	0/34858	0.84	42/54401 (0.1%)
77	a	0.94	0/6460	1.46	45/8715 (0.5%)
78	y	0.52	0/270	1.15	1/419 (0.2%)
All	All	0.74	2/193436 (0.0%)	1.12	544/282616 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	LR	154	PRO	C-O	-6.37	1.16	1.23
37	Lk	76	SER	N-CA	5.50	1.49	1.46

All (544) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	Lt	1252	G	C2'-C3'-O3'	10.84	129.97	113.70
75	Sj	64	LYS	N-CA-C	-10.48	100.61	113.50
44	Lt	691	G	C2'-C3'-O3'	10.47	129.40	113.70
44	Lt	776	G	C2'-C3'-O3'	9.90	124.35	109.50
76	St	810	U	C2'-C3'-O3'	9.68	124.02	109.50
21	LU	69	PRO	CB-CA-C	-9.55	98.50	111.21
44	Lt	2006	G	C2'-C3'-O3'	9.35	127.72	113.70
44	Lt	1349	G	C2'-C3'-O3'	9.25	127.57	113.70
9	LI	29	THR	CB-CA-C	9.20	129.34	109.10
15	LO	186	PRO	N-CA-C	-9.00	100.59	113.47
25	LY	34	PRO	N-CA-C	9.00	127.97	113.12
44	Lt	2584	C	C2'-C3'-O3'	8.98	122.97	109.50
44	Lt	2591	C	C2'-C3'-O3'	8.74	122.61	109.50
24	LX	33	CYS	CB-CA-C	-8.70	97.16	110.90
49	SD	224	THR	N-CA-C	-8.65	102.64	113.02
59	SO	114	ASP	CA-C-N	-8.59	116.76	122.60
59	SO	114	ASP	C-N-CA	-8.59	116.76	122.60
2	LB	17	LEU	CA-C-O	-8.54	112.92	120.60
2	LB	256	HIS	CA-C-O	-8.49	111.70	119.86
77	a	441	ARG	N-CA-C	-8.46	103.55	114.04
39	Ln	173	LYS	N-CA-C	-8.40	102.05	113.30
70	Sc	72	VAL	N-CA-C	-8.39	104.34	111.56
20	LT	154	HIS	CB-CA-C	8.39	122.33	111.50
33	Lg	84	PRO	CB-CA-C	-8.35	99.99	111.85
76	St	1152	A	C2'-C3'-O3'	8.30	121.95	109.50
7	LG	3	ALA	N-CA-C	-8.22	102.51	112.54
75	Sj	50	ASN	N-CA-C	-8.22	101.41	112.26
76	St	599	G	C2'-C3'-O3'	8.17	125.96	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	Lt	2017	A	C2'-C3'-O3'	8.09	121.64	109.50
66	SW	28	CYS	N-CA-C	8.06	118.87	109.60
76	St	1272	G	C4'-C3'-O3'	8.04	121.46	109.40
44	Lt	2022	C	C2'-C3'-O3'	7.94	125.60	113.70
76	St	330	A	C4'-C3'-O3'	7.92	121.28	109.40
17	LQ	89	VAL	N-CA-C	-7.91	104.76	111.56
76	St	943	C	C4'-C3'-O3'	7.89	121.24	109.40
76	St	435	A	C2'-C3'-O3'	7.86	125.48	113.70
29	Lc	53	GLN	CB-CA-C	-7.83	96.71	109.72
56	SK	111	GLN	N-CA-C	-7.81	102.71	111.14
15	LO	12	ARG	N-CA-C	-7.76	103.61	113.23
76	St	897	G	C2'-C3'-O3'	7.76	125.33	113.70
13	LM	176	PRO	N-CA-C	7.75	124.74	114.27
20	LT	156	LYS	N-CA-C	-7.72	103.12	112.54
76	St	1261	A	C2'-C3'-O3'	7.72	121.08	109.50
77	a	704	GLU	N-CA-C	-7.71	102.96	111.36
48	SC	89	ASN	N-CA-C	-7.68	103.93	113.38
44	Lt	1310	C	N1-C1'-C2'	7.67	123.50	112.00
76	St	1000	C	C2'-C3'-O3'	7.63	125.14	113.70
44	Lt	349	A	C2'-C3'-O3'	-7.58	98.13	109.50
44	Lt	1472	C	C4'-C3'-O3'	7.58	124.37	113.00
76	St	1138	U	C4'-C3'-O3'	7.57	120.75	109.40
76	St	1043	G	C2'-C3'-O3'	7.56	125.04	113.70
44	Lt	2574	C	C2'-C3'-O3'	7.54	125.01	113.70
77	a	149	GLU	CB-CA-C	7.53	123.29	110.79
33	Lg	9	PHE	CA-CB-CG	7.52	121.32	113.80
44	Lt	1135	G	C4'-C3'-O3'	7.45	120.57	109.40
44	Lt	2679	C	C4'-C3'-O3'	7.43	124.15	113.00
44	Lt	1448	G	C2'-C3'-O3'	7.43	124.85	113.70
2	LB	361	LYS	N-CA-C	-7.40	104.25	113.28
61	SQ	60	MET	N-CA-C	-7.40	103.85	113.17
56	SK	3	ILE	N-CA-C	-7.37	104.32	112.80
44	Lt	1472	C	C2'-C3'-O3'	7.36	124.74	113.70
44	Lt	1914	C	C2'-C3'-O3'	7.35	124.72	113.70
8	LH	220	PHE	CA-CB-CG	7.33	121.12	113.80
77	a	234	ASN	N-CA-C	-7.33	103.38	111.36
25	LY	34	PRO	CA-C-O	-7.31	115.75	121.38
44	Lt	71	C	C2'-C3'-O3'	7.31	124.67	113.70
63	ST	131	LEU	N-CA-C	-7.29	103.36	111.82
77	a	709	VAL	N-CA-C	-7.26	103.88	111.58
44	Lt	2627	G	C2'-C3'-O3'	7.25	124.57	113.70
50	SE	26	ILE	N-CA-C	-7.24	104.48	112.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	SD	101	HIS	N-CA-C	-7.21	103.93	114.39
12	LL	112	LEU	N-CA-C	-7.18	102.86	111.69
44	Lt	898	C	C4'-C3'-O3'	7.17	123.75	113.00
18	LR	39	ASN	CB-CA-C	7.12	122.95	110.85
44	Lt	117	G	C4'-C3'-O3'	7.11	123.67	113.00
12	LL	159	ALA	N-CA-C	-7.09	104.25	113.12
33	Lg	86	GLN	N-CA-C	-7.09	104.24	113.17
16	LP	150	VAL	N-CA-C	-7.04	104.11	111.58
44	Lt	2687	C	C2'-C3'-O3'	7.04	120.05	109.50
74	Sh	118	PHE	N-CA-C	-6.99	103.33	112.41
19	LS	47	SER	N-CA-C	-6.98	101.53	110.53
29	Lc	24	PRO	CA-C-O	-6.96	116.02	121.38
44	Lt	326	A	C2'-C3'-O3'	-6.94	99.09	109.50
30	Ld	106	SER	N-CA-C	-6.94	103.10	112.26
11	LK	47	PRO	CB-CA-C	-6.89	102.22	112.55
39	Ln	144	LEU	N-CA-C	-6.88	103.80	111.71
76	St	1193	G	C2'-C3'-O3'	6.87	124.01	113.70
76	St	187	G	C2'-C3'-O3'	6.87	119.80	109.50
62	SR	98	ASN	N-CA-C	-6.86	104.79	113.02
5	LE	91	A	C1'-C2'-O2'	6.85	122.07	111.80
11	LK	160	PRO	CB-CA-C	-6.85	102.10	111.21
54	SI	126	THR	CB-CA-C	6.84	116.61	109.83
73	Sg	19	ARG	N-CA-C	-6.84	103.34	113.61
65	SV	46	LEU	N-CA-C	-6.82	104.86	113.72
52	SG	168	GLU	N-CA-C	-6.80	103.89	111.71
44	Lt	2017	A	C4'-C3'-O3'	6.79	119.59	109.40
53	SH	8	LYS	N-CA-C	-6.76	104.60	112.92
76	St	593	C	C4'-C3'-O3'	6.76	119.54	109.40
44	Lt	1079	G	C2'-C3'-O3'	6.70	119.55	109.50
16	LP	52	LEU	N-CA-C	-6.70	105.24	113.41
66	SW	34	TYR	CB-CA-C	-6.69	98.86	110.17
76	St	588	G	C2'-C3'-O3'	6.69	123.73	113.70
6	LF	140	ASP	CB-CA-C	-6.67	100.41	110.88
76	St	593	C	C2'-C3'-O3'	6.67	119.50	109.50
39	Ln	123	TYR	N-CA-C	6.63	114.22	108.78
3	LC	254	LYS	N-CA-C	-6.61	100.25	110.10
6	LF	128	GLY	CA-C-O	-6.60	117.67	122.23
77	a	854	PHE	CA-C-O	-6.59	113.85	121.10
47	SB	51	TYR	CB-CA-C	6.56	121.82	110.01
18	LR	154	PRO	CB-CA-C	-6.55	103.53	111.46
62	SR	109	PRO	N-CA-C	6.54	118.68	110.70
47	SB	100	ASN	N-CA-C	-6.54	100.15	109.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
74	Sh	122	ARG	N-CA-C	-6.52	105.48	113.50
2	LB	55	HIS	CA-CB-CG	6.51	120.31	113.80
77	a	145	ASP	N-CA-C	-6.51	104.18	111.28
63	ST	16	GLU	N-CA-C	-6.51	104.48	112.88
28	Lb	2	PRO	CA-N-CD	-6.51	102.89	112.00
33	Lg	60	PRO	CB-CA-C	-6.49	103.51	111.11
25	LY	29	VAL	N-CA-C	-6.48	106.47	112.43
25	LY	37	LEU	N-CA-C	6.46	117.98	111.07
61	SQ	105	LYS	CB-CA-C	-6.46	108.45	117.23
76	St	175	C	C2'-C3'-O3'	6.44	119.16	109.50
22	LV	27	ASP	N-CA-C	-6.44	104.34	111.36
76	St	1288	A	C2'-C3'-O3'	-6.43	99.85	109.50
14	LN	116	ARG	N-CA-C	-6.42	105.09	113.12
24	LX	37	CYS	N-CA-C	-6.42	104.29	111.28
31	Le	74	GLY	CA-C-O	-6.42	117.80	122.23
26	LZ	131	ALA	N-CA-C	-6.42	105.75	112.93
2	LB	139	ASP	N-CA-C	-6.41	105.45	113.28
26	LZ	97	TYR	CA-C-O	-6.41	114.58	119.32
67	SX	56	PRO	CB-CA-C	-6.41	104.57	111.56
6	LF	85	ARG	N-CA-C	-6.41	104.39	111.82
74	Sh	120	CYS	CB-CA-C	-6.41	96.54	109.68
76	St	993	U	C2'-C3'-O3'	-6.38	99.93	109.50
20	LT	153	VAL	N-CA-C	-6.38	105.47	112.80
22	LV	47	ASN	N-CA-C	-6.37	103.96	112.94
56	SK	43	ILE	N-CA-C	-6.37	103.37	112.35
37	Lk	58	THR	CB-CA-C	-6.36	97.75	111.11
38	Ll	20	LYS	N-CA-C	-6.36	105.28	114.12
77	a	573	ASP	CA-CB-CG	6.36	118.96	112.60
20	LT	81	ARG	N-CA-C	-6.34	105.03	112.89
55	SJ	86	ILE	N-CA-C	-6.33	103.70	112.50
44	Lt	1511	G	C2'-C3'-O3'	6.33	123.19	113.70
62	SR	79	HIS	N-CA-C	-6.32	104.73	112.88
66	SW	60	ARG	N-CA-C	-6.31	104.64	112.90
6	LF	115	VAL	N-CA-C	-6.28	104.84	113.00
26	LZ	69	VAL	N-CA-C	-6.28	106.08	113.42
2	LB	271	GLY	CA-C-O	-6.27	117.57	122.52
63	ST	39	PHE	CB-CA-C	6.26	120.33	110.19
31	Le	96	THR	CB-CA-C	-6.25	100.47	109.84
33	Lg	84	PRO	N-CA-C	6.25	121.96	113.84
62	SR	35	PRO	CB-CA-C	-6.24	101.78	112.64
11	LK	62	SER	N-CA-C	-6.24	105.16	112.89
46	SA	19	ASP	CB-CA-C	-6.23	97.47	110.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	Ld	97	LEU	CA-C-O	-6.22	114.86	122.64
31	Le	32	ARG	CB-CA-C	-6.21	100.29	110.85
39	Ln	24	LYS	CA-C-O	-6.21	116.18	120.47
71	Sd	65	PRO	CB-CA-C	6.20	118.96	111.46
8	LH	159	VAL	N-CA-C	-6.20	107.21	113.47
2	LB	349	PRO	CB-CA-C	-6.17	103.39	110.92
16	LP	128	PRO	CA-C-O	-6.17	114.63	121.23
1	LA	244	GLY	CA-C-O	-6.16	117.98	122.23
61	SQ	96	LYS	CB-CA-C	-6.16	102.80	111.85
44	Lt	1135	G	C2'-C3'-O3'	6.16	118.74	109.50
69	Sb	87	PRO	CB-CA-C	-6.15	103.52	111.46
11	LK	134	PRO	CB-CA-C	-6.15	103.75	111.56
26	LZ	111	MET	N-CA-C	6.14	118.05	111.36
69	Sb	94	CYS	N-CA-C	-6.12	105.46	113.17
9	LI	163	THR	CB-CA-C	6.12	122.59	110.42
1	LA	219	ILE	N-CA-C	-6.11	104.55	110.72
72	Se	94	PRO	CB-CA-C	-6.10	104.91	111.56
78	y	34	A	C2'-C3'-O3'	6.10	118.65	109.50
15	LO	98	LEU	N-CA-C	-6.08	105.36	112.89
39	Ln	135	PRO	CB-CA-C	6.08	118.98	110.60
25	LY	34	PRO	N-CA-CB	-6.07	98.74	102.81
50	SE	150	PRO	CB-CA-C	-6.07	103.03	110.98
44	Lt	324	A	C2'-C3'-O3'	-6.07	104.60	113.70
76	St	90	A	C4'-C3'-O3'	6.07	118.50	109.40
15	LO	140	PRO	CB-CA-C	-6.06	102.62	112.62
17	LQ	152	PRO	N-CA-C	-6.05	105.12	113.53
22	LV	14	GLY	N-CA-C	6.05	119.99	112.73
76	St	857	A	C2'-C3'-O3'	-6.04	100.45	109.50
77	a	149	GLU	N-CA-C	-6.02	104.72	111.28
2	LB	250	ALA	CA-C-N	-6.02	114.50	122.99
2	LB	250	ALA	C-N-CA	-6.02	114.50	122.99
55	SJ	76	SER	CA-C-O	-6.02	113.77	119.55
31	Le	36	GLU	N-CA-C	-6.02	105.43	112.89
74	Sh	102	CYS	N-CA-CB	6.00	118.90	109.83
44	Lt	459	A	C2'-C3'-O3'	6.00	122.70	113.70
18	LR	162	LYS	CB-CA-C	5.99	117.01	108.68
77	a	173	GLN	CB-CA-C	5.99	122.60	110.38
76	St	1400	G	C2'-C3'-O3'	-5.98	104.73	113.70
3	LC	125	ALA	N-CA-C	-5.97	105.65	113.12
25	LY	95	ARG	CB-CA-C	-5.97	100.75	110.79
32	Lf	10	PRO	N-CA-C	5.97	121.83	113.53
21	LU	48	TYR	CB-CA-C	5.96	119.85	110.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	Lt	1382	C	C2'-C3'-O3'	-5.96	104.75	113.70
28	Lb	31	GLY	CA-C-O	-5.96	118.02	122.37
76	St	365	G	C4'-C3'-O3'	5.96	118.34	109.40
44	Lt	516	G	C2'-C3'-O3'	-5.96	104.77	113.70
35	Li	99	ARG	N-CA-C	-5.92	104.73	111.07
6	LF	183	HIS	CA-CB-CG	5.91	119.71	113.80
77	a	147	SER	CB-CA-C	-5.90	108.57	117.07
27	La	101	VAL	CA-C-O	-5.89	114.93	121.23
44	Lt	590	C	C2'-C3'-O3'	-5.88	104.87	113.70
29	Lc	19	ASN	N-CA-C	-5.88	103.26	110.61
3	LC	251	TYR	CB-CA-C	5.88	120.55	110.79
77	a	158	ASP	N-CA-C	-5.88	107.10	114.56
50	SE	92	ILE	CB-CA-C	5.87	117.93	111.18
60	SP	134	ARG	N-CA-C	-5.87	105.97	113.01
65	SV	47	LYS	N-CA-C	-5.87	104.97	111.36
50	SE	58	TYR	CB-CA-C	-5.86	100.89	110.85
44	Lt	1236	G	C2'-C3'-O3'	5.86	122.49	113.70
76	St	1189	A	C4'-C3'-O3'	-5.86	104.22	113.00
76	St	187	G	C4'-C3'-O3'	5.85	118.17	109.40
16	LP	65	ARG	N-CA-C	-5.84	106.15	113.28
77	a	314	GLY	N-CA-C	-5.83	106.11	115.08
15	LO	43	THR	N-CA-C	-5.82	104.90	112.23
32	Lf	31	VAL	N-CA-C	-5.82	104.84	113.39
37	Lk	51	TYR	N-CA-C	-5.81	105.45	112.54
44	Lt	820	C	C4'-C3'-O3'	5.80	121.71	113.00
51	SF	26	TYR	N-CA-C	5.80	117.61	111.28
3	LC	47	PRO	CB-CA-C	-5.80	104.34	111.64
14	LN	70	THR	N-CA-C	-5.79	105.89	113.12
36	Lj	59	ASP	N-CA-C	5.78	117.25	111.07
3	LC	158	ILE	N-CA-C	-5.78	104.70	111.00
9	LI	167	LEU	N-CA-C	-5.77	104.96	112.23
77	a	377	PRO	N-CA-C	-5.76	105.45	113.81
49	SD	93	ASP	CA-CB-CG	5.75	118.35	112.60
25	LY	55	TRP	N-CA-C	-5.75	104.81	113.89
44	Lt	1308	C	C2'-C3'-O3'	-5.75	105.08	113.70
77	a	573	ASP	CB-CA-C	5.75	118.87	109.90
3	LC	3	PRO	N-CA-C	-5.75	102.18	111.03
30	Ld	40	ASP	N-CA-C	-5.74	106.25	113.72
38	Ll	52	PRO	CA-C-N	-5.74	113.67	122.62
38	Ll	52	PRO	C-N-CA	-5.74	113.67	122.62
37	Lk	76	SER	CB-CA-C	-5.74	108.81	117.07
44	Lt	2200	C	C2'-C3'-O3'	-5.74	105.10	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	LB	55	HIS	CB-CA-C	5.73	121.82	110.42
30	Ld	63	LEU	N-CA-C	-5.73	105.55	112.54
52	SG	180	LYS	N-CA-C	-5.73	106.19	112.72
1	LA	14	SER	CA-C-O	-5.72	114.46	120.58
9	LI	90	ARG	N-CA-C	-5.71	105.80	112.89
44	Lt	1179	U	N1-C1'-C2'	5.71	120.57	112.00
22	LV	13	GLN	CB-CA-C	5.71	121.79	110.42
18	LR	49	THR	N-CA-C	-5.71	104.67	111.69
46	SA	84	ASN	N-CA-C	-5.71	106.19	114.12
75	Sj	43	VAL	CA-C-O	-5.71	116.24	121.72
46	SA	132	PRO	N-CA-C	-5.70	108.75	114.68
48	SC	206	ASP	N-CA-C	-5.70	105.35	112.93
44	Lt	58	G	C2'-C3'-O3'	-5.70	100.96	109.50
77	a	468	PRO	N-CA-C	-5.68	106.14	113.57
65	SV	112	LEU	N-CA-C	-5.67	105.08	112.23
2	LB	44	THR	N-CA-C	5.66	117.53	111.36
44	Lt	84	C	C2'-C3'-O3'	-5.66	101.01	109.50
60	SP	20	ARG	N-CA-C	-5.66	105.58	112.88
76	St	1265	A	C4'-C3'-O3'	-5.65	104.53	113.00
10	LJ	134	THR	N-CA-C	-5.64	105.52	112.90
67	SX	60	PRO	N-CA-C	-5.64	102.35	111.14
65	SV	32	VAL	N-CA-C	-5.63	104.05	111.09
10	LJ	57	PHE	CA-C-O	-5.63	115.75	120.26
47	SB	111	VAL	CA-C-O	-5.63	116.06	121.63
64	SU	26	PRO	N-CA-C	5.63	121.35	113.53
52	SG	189	PRO	N-CA-C	-5.63	102.36	111.14
10	LJ	147	ILE	N-CA-C	-5.62	104.87	111.00
26	LZ	61	GLY	CA-C-O	-5.62	116.20	120.76
65	SV	55	LYS	N-CA-C	-5.62	106.27	113.02
9	LI	30	PRO	CB-CA-C	-5.62	104.01	112.04
44	Lt	2355	U	C4'-C3'-O3'	5.62	117.82	109.40
44	Lt	1536	C	C2'-C3'-O3'	-5.61	105.29	113.70
57	SL	99	PRO	N-CA-C	-5.61	102.39	111.14
52	SG	131	THR	CB-CA-C	5.60	120.37	110.85
44	Lt	2022	C	C4'-C3'-O3'	5.59	121.39	113.00
65	SV	119	ARG	CB-CA-C	5.59	119.96	111.80
12	LL	53	THR	CB-CA-C	-5.58	101.15	110.19
29	Lc	26	LYS	N-CA-C	-5.58	106.30	114.39
77	a	891	VAL	N-CA-C	-5.58	104.12	111.09
1	LA	231	PRO	N-CA-CB	-5.58	97.39	103.25
8	LH	116	LYS	N-CA-C	-5.58	105.60	112.90
16	LP	128	PRO	N-CA-C	-5.58	102.44	111.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	SX	101	ILE	N-CA-CB	5.58	118.12	110.54
50	SE	106	LYS	N-CA-C	-5.57	106.44	113.18
69	Sb	33	TYR	CA-C-N	-5.57	115.51	123.20
69	Sb	33	TYR	C-N-CA	-5.57	115.51	123.20
9	LI	215	GLY	N-CA-C	5.57	120.89	111.04
22	LV	30	LEU	N-CA-C	-5.57	103.56	111.24
35	Li	55	GLU	N-CA-C	-5.56	105.99	112.89
76	St	1043	G	C4'-C3'-C2'	-5.56	97.04	102.60
77	a	847	GLN	N-CA-C	-5.56	106.67	113.50
2	LB	289	GLU	N-CA-C	-5.55	105.23	112.23
1	LA	179	LEU	N-CA-C	-5.55	105.23	111.28
39	Ln	123	TYR	CB-CA-C	-5.55	109.08	117.07
77	a	707	LYS	N-CA-C	-5.54	105.24	111.28
23	LW	47	LYS	N-CA-C	-5.54	98.73	108.20
46	SA	27	THR	N-CA-C	-5.53	106.48	113.23
49	SD	14	THR	N-CA-C	-5.53	105.32	112.68
77	a	266	TRP	CB-CA-C	5.53	119.75	111.89
44	Lt	2011	G	C2'-C3'-O3'	-5.53	105.41	113.70
1	LA	77	ILE	N-CA-C	-5.52	101.92	109.37
46	SA	191	LYS	N-CA-C	-5.52	105.27	111.28
49	SD	70	ASP	N-CA-C	-5.52	104.90	111.69
61	SQ	137	THR	CA-C-O	-5.51	116.03	122.37
69	Sb	82	LEU	N-CA-C	-5.51	105.29	112.23
1	LA	211	HIS	N-CA-C	-5.51	105.28	111.28
50	SE	50	ASN	CA-C-N	-5.51	111.02	121.54
50	SE	50	ASN	C-N-CA	-5.51	111.02	121.54
3	LC	181	ARG	N-CA-C	-5.50	106.34	113.16
44	Lt	2006	G	C4'-C3'-C2'	-5.50	97.10	102.60
16	LP	155	LYS	N-CA-C	-5.50	104.80	112.45
59	SO	107	ARG	CB-CA-C	5.50	120.02	110.72
5	LE	113	C	C4'-C3'-O3'	-5.50	104.75	113.00
50	SE	65	LEU	N-CA-C	-5.50	106.25	113.12
1	LA	79	PRO	N-CA-C	-5.50	102.50	111.68
77	a	222	GLN	N-CA-C	-5.50	104.93	111.69
39	Ln	137	PRO	CB-CA-C	-5.47	104.74	111.64
65	SV	118	THR	CB-CA-C	5.47	121.43	109.99
77	a	246	THR	CB-CA-C	-5.47	102.56	114.10
22	LV	114	ASP	N-CA-C	-5.47	105.22	111.07
39	Ln	170	GLY	CA-C-O	-5.47	117.90	122.33
77	a	266	TRP	CA-CB-CG	5.46	123.98	113.60
76	St	1261	A	C4'-C3'-O3'	5.46	117.59	109.40
39	Ln	169	ILE	N-CA-C	-5.46	104.23	111.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
69	Sb	48	LYS	CB-CA-C	5.46	115.23	109.83
50	SE	52	LEU	N-CA-C	-5.45	106.63	113.28
63	ST	12	ARG	N-CA-C	-5.45	105.36	112.23
73	Sg	10	ILE	N-CA-C	-5.45	107.12	111.81
42	Lq	8	VAL	CA-C-O	-5.45	117.89	122.63
18	LR	114	LYS	N-CA-C	-5.44	105.26	111.14
22	LV	33	ASN	N-CA-C	-5.44	105.43	111.36
9	LI	87	HIS	N-CA-C	-5.44	105.38	112.23
47	SB	43	GLU	CA-C-O	-5.44	115.27	121.58
48	SC	148	LEU	CA-C-O	-5.44	115.78	122.36
50	SE	193	GLY	CA-C-O	-5.44	115.90	121.61
1	LA	193	ARG	CB-CA-C	-5.43	100.52	111.17
73	Sg	48	ASP	CB-CA-C	5.43	120.73	110.35
44	Lt	661	G	C2'-C3'-O3'	-5.42	105.57	113.70
75	Sj	51	GLY	N-CA-C	-5.42	107.62	115.27
2	LB	35	ASP	CA-C-O	-5.42	115.13	120.82
6	LF	8	LYS	CB-CA-C	5.42	120.09	112.07
44	Lt	2627	G	C4'-C3'-O3'	5.42	121.13	113.00
77	a	146	PHE	CA-C-N	-5.42	117.19	123.04
77	a	146	PHE	C-N-CA	-5.42	117.19	123.04
44	Lt	863	A	C4'-C3'-O3'	5.41	117.52	109.40
51	SF	57	ARG	N-CA-C	-5.41	104.93	112.45
72	Se	92	ASN	N-CA-C	-5.41	106.69	113.72
44	Lt	1800	A	C2'-C3'-O3'	-5.41	105.59	113.70
77	a	56	PHE	CA-CB-CG	5.40	119.20	113.80
18	LR	106	ALA	N-CA-C	-5.40	105.47	111.36
33	Lg	89	GLY	N-CA-C	-5.40	107.23	114.25
55	SJ	129	PHE	CA-CB-CG	5.39	119.19	113.80
49	SD	93	ASP	CB-CA-C	5.39	120.02	111.51
59	SO	40	PRO	N-CA-C	-5.39	106.04	113.53
18	LR	5	LEU	N-CA-C	-5.38	105.15	112.26
74	Sh	120	CYS	CA-CB-SG	5.38	126.78	114.40
38	Ll	45	TYR	CB-CA-C	-5.38	98.89	110.45
29	Lc	17	HIS	CB-CA-C	-5.38	102.37	111.02
31	Le	57	ARG	CB-CA-C	5.37	119.39	111.06
38	Ll	5	ILE	CB-CA-C	5.37	117.03	111.23
76	St	568	G	C2'-C3'-O3'	-5.37	105.65	113.70
77	a	242	PHE	CA-CB-CG	5.37	119.17	113.80
2	LB	247	ARG	CB-CA-C	5.35	117.81	111.22
44	Lt	1653	G	C2'-C3'-O3'	-5.35	105.67	113.70
65	SV	56	ARG	CB-CA-C	5.35	120.09	111.36
44	Lt	694	C	C2'-C3'-O3'	5.35	121.72	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	LO	124	ASP	N-CA-C	-5.34	101.33	108.86
57	SL	50	TYR	N-CA-C	-5.33	105.47	111.28
65	SV	142	ARG	CA-C-O	-5.33	115.33	121.47
6	LF	177	ALA	N-CA-C	-5.33	106.00	112.88
13	LM	61	LYS	N-CA-C	-5.33	105.37	111.07
38	LI	42	THR	N-CA-C	-5.33	101.66	109.81
10	LJ	54	ALA	N-CA-C	5.32	117.67	111.02
44	Lt	1625	U	C2'-C3'-O3'	-5.32	105.72	113.70
44	Lt	1880	C	C4'-C3'-O3'	5.32	120.98	113.00
11	LK	123	GLN	CB-CA-C	5.32	118.00	110.24
65	SV	136	HIS	CB-CA-C	5.32	119.10	110.22
11	LK	124	GLY	CA-C-O	-5.32	118.56	122.23
77	a	521	THR	N-CA-C	-5.32	105.56	111.36
52	SG	27	PHE	N-CA-C	-5.31	105.66	111.82
10	LJ	60	GLY	CA-C-N	-5.31	113.89	122.23
10	LJ	60	GLY	C-N-CA	-5.31	113.89	122.23
50	SE	104	ASP	CA-CB-CG	5.31	117.91	112.60
19	LS	18	GLY	CA-C-O	-5.31	116.29	121.76
61	SQ	58	GLY	N-CA-C	-5.30	105.15	111.36
76	St	1152	A	C4'-C3'-O3'	5.30	117.36	109.40
12	LL	155	THR	CA-C-O	-5.30	115.40	120.97
25	LY	37	LEU	CA-C-O	-5.30	115.25	120.82
65	SV	35	LYS	N-CA-C	-5.30	107.18	113.38
3	LC	98	ILE	N-CA-C	-5.30	106.71	112.80
56	SK	109	ARG	CA-C-O	-5.30	114.12	120.10
77	a	793	GLU	N-CA-C	5.30	122.08	110.80
44	Lt	2627	G	C4'-C3'-C2'	-5.29	97.31	102.60
65	SV	115	LEU	N-CA-C	-5.29	105.68	111.82
9	LI	92	LEU	N-CA-C	-5.29	99.53	110.80
76	St	578	A	C2'-C3'-O3'	-5.29	105.76	113.70
46	SA	61	ALA	N-CA-C	-5.29	106.09	112.54
42	Lq	39	CYS	CB-CA-C	-5.28	101.33	109.62
56	SK	167	PRO	N-CA-CB	-5.28	97.71	103.25
21	LU	65	PHE	N-CA-C	-5.28	107.39	113.88
51	SF	23	LEU	N-CA-C	-5.27	106.71	112.72
77	a	753	ALA	N-CA-C	-5.27	106.85	113.28
19	LS	69	ALA	N-CA-C	-5.27	105.13	112.45
77	a	833	SER	N-CA-C	-5.27	105.59	112.23
77	a	141	PRO	CB-CA-C	-5.26	104.09	110.98
29	Lc	21	ILE	CB-CA-C	5.26	119.92	111.29
20	LT	15	GLU	N-CA-C	-5.26	105.60	112.23
48	SC	37	ASP	N-CA-C	-5.26	105.55	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	LQ	35	ILE	N-CA-C	-5.26	106.75	113.22
39	Ln	73	ASP	N-CA-C	-5.26	105.55	111.28
52	SG	25	GLU	CA-C-N	-5.26	115.59	123.00
52	SG	25	GLU	C-N-CA	-5.26	115.59	123.00
61	SQ	100	ASP	N-CA-C	-5.26	105.55	111.28
63	ST	89	GLY	CA-C-O	-5.25	118.03	122.29
21	LU	137	ARG	CA-C-O	-5.25	114.98	120.55
6	LF	97	ALA	N-CA-C	-5.25	105.64	111.36
33	Lg	20	SER	N-CA-C	-5.25	101.43	109.41
43	Ls	113	CYS	N-CA-C	-5.25	99.03	108.58
46	SA	135	ASP	N-CA-C	-5.25	106.64	112.57
67	SX	56	PRO	N-CA-C	5.24	118.73	110.50
44	Lt	1969	G	C4'-C3'-O3'	5.24	120.86	113.00
47	SB	33	LEU	N-CA-C	-5.24	105.65	111.36
76	St	615	C	C2'-C3'-O3'	-5.23	105.85	113.70
27	La	101	VAL	N-CA-C	-5.23	102.84	109.58
47	SB	41	LYS	N-CA-C	-5.23	105.50	111.14
54	SI	168	GLN	N-CA-C	-5.23	105.26	111.69
15	LO	145	ASP	CB-CA-C	-5.23	99.87	110.17
44	Lt	2640	U	C2'-C3'-O3'	-5.22	105.86	113.70
63	ST	129	ARG	CA-C-O	-5.22	115.81	121.87
13	LM	84	ARG	CB-CA-C	5.22	116.72	108.84
3	LC	91	MET	N-CA-C	-5.22	103.14	110.50
11	LK	82	LYS	N-CA-C	-5.22	106.94	113.15
77	a	756	ARG	CB-CA-C	-5.22	103.13	111.17
16	LP	115	VAL	CA-C-O	-5.22	116.71	121.72
6	LF	194	ASP	CA-C-N	-5.21	117.09	121.58
6	LF	194	ASP	C-N-CA	-5.21	117.09	121.58
60	SP	24	PRO	CB-CA-C	-5.21	104.02	112.62
64	SU	33	LYS	N-CA-C	-5.21	106.07	112.90
77	a	425	PRO	CB-CA-C	-5.21	105.02	111.64
49	SD	133	TYR	CB-CA-C	-5.21	101.15	109.75
70	Sc	41	THR	N-CA-C	-5.21	101.44	109.52
51	SF	74	MET	N-CA-C	-5.21	105.66	112.23
17	LQ	154	PRO	N-CA-C	-5.21	104.76	112.26
58	SM	17	PHE	CA-CB-CG	5.20	119.00	113.80
16	LP	104	GLY	CA-C-O	-5.20	117.79	122.57
6	LF	213	TYR	CB-CA-C	-5.20	102.16	110.79
21	LU	57	TYR	CB-CA-C	5.20	121.17	110.31
63	ST	59	PRO	N-CA-C	-5.20	101.76	112.47
3	LC	254	LYS	CB-CA-C	5.19	117.99	109.90
76	St	1043	G	C4'-C3'-O3'	5.19	120.78	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
77	a	816	ARG	N-CA-C	-5.19	101.97	109.59
32	Lf	107	ALA	N-CA-C	-5.18	106.91	113.18
76	St	807	G	C3'-C2'-C1'	-5.18	96.31	101.50
31	Le	5	TYR	CB-CA-C	-5.18	100.76	109.72
74	Sh	125	LYS	N-CA-C	-5.18	106.91	113.18
3	LC	47	PRO	N-CA-C	5.18	119.00	111.03
52	SG	197	ASP	N-CA-C	-5.18	105.71	112.23
63	ST	61	ILE	N-CA-C	-5.18	106.51	112.98
77	a	277	TYR	CB-CA-C	5.17	120.60	110.67
54	SI	70	SER	N-CA-C	5.17	116.73	111.14
76	St	650	G	C4'-C3'-O3'	-5.17	105.24	113.00
27	La	98	VAL	N-CA-CB	5.17	119.76	111.23
76	St	534	A	C4'-C3'-O3'	-5.17	105.25	113.00
69	Sb	37	GLU	N-CA-C	-5.16	105.35	111.69
55	SJ	3	ARG	CB-CA-C	-5.15	103.70	112.00
4	LD	82	C	C4'-C3'-O3'	-5.15	105.28	113.00
20	LT	92	ARG	CB-CA-C	-5.15	102.55	110.78
32	Lf	76	PHE	CA-CB-CG	5.15	118.95	113.80
42	Lq	19	GLY	CA-C-O	-5.15	118.12	122.29
44	Lt	636	U	C2'-C3'-O3'	-5.15	105.98	113.70
44	Lt	1448	G	C4'-C3'-C2'	-5.14	97.46	102.60
51	SF	184	ARG	N-CA-C	-5.14	105.30	112.45
3	LC	82	TYR	CA-C-O	-5.14	115.58	121.54
27	La	75	VAL	N-CA-C	-5.14	104.67	111.09
2	LB	16	TYR	CB-CA-C	5.13	119.39	110.72
76	St	999	U	N1-C1'-C2'	5.13	119.69	112.00
54	SI	104	THR	CB-CA-C	5.12	118.89	109.46
34	Lh	47	GLU	CA-C-O	-5.12	115.90	121.89
10	LJ	7	MET	N-CA-C	-5.11	101.30	109.07
26	LZ	60	GLY	CA-C-N	-5.11	116.71	121.62
26	LZ	60	GLY	C-N-CA	-5.11	116.71	121.62
62	SR	97	TYR	CB-CA-C	-5.11	101.92	109.90
77	a	691	VAL	N-CA-C	-5.11	105.51	110.42
76	St	144	C	C3'-C2'-O2'	5.11	118.36	110.70
44	Lt	1422	C	C4'-C3'-O3'	5.11	120.66	113.00
49	SD	168	ILE	N-CA-C	-5.10	105.44	111.00
10	LJ	57	PHE	CB-CA-C	5.10	114.82	111.20
77	a	391	PRO	N-CA-C	5.10	119.32	111.21
19	LS	3	ASN	CB-CA-C	5.10	119.95	112.09
48	SC	119	MET	CA-C-O	-5.10	116.01	120.60
6	LF	180	ASN	CB-CA-C	5.10	119.22	110.81
16	LP	126	LEU	CB-CA-C	5.10	120.56	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
71	Sd	21	VAL	CA-C-O	-5.10	116.47	121.67
27	La	31	PRO	CB-CA-C	-5.09	105.17	111.64
28	Lb	61	TYR	CB-CA-C	5.09	119.24	110.79
28	Lb	100	PRO	N-CA-C	5.09	118.87	111.03
76	St	1288	A	C3'-C2'-O2'	-5.09	106.97	114.60
38	Ll	50	THR	CB-CA-C	5.08	118.71	110.22
39	Ln	42	ASP	CA-C-O	-5.08	115.82	120.50
14	LN	33	THR	N-CA-C	-5.08	105.74	111.28
32	Lf	19	LYS	N-CA-C	-5.08	106.77	113.12
44	Lt	1079	G	C4'-C3'-O3'	5.07	117.01	109.40
62	SR	126	VAL	CA-C-O	-5.07	115.77	121.05
69	Sb	76	TYR	CB-CA-C	5.07	118.11	109.84
76	St	666	A	C2'-C3'-O3'	5.07	117.11	109.50
49	SD	21	PRO	CB-CA-C	-5.07	104.25	112.62
2	LB	295	THR	CB-CA-C	5.07	118.11	109.80
77	a	391	PRO	CB-CA-C	-5.07	104.74	111.23
2	LB	16	TYR	N-CA-C	-5.07	106.34	112.88
30	Ld	54	PRO	N-CA-C	5.07	120.57	113.53
34	Lh	47	GLU	N-CA-C	-5.07	103.25	110.59
77	a	268	PHE	CA-CB-CG	5.07	118.86	113.80
2	LB	358	THR	N-CA-C	-5.06	105.48	113.02
57	SL	84	GLU	N-CA-C	-5.06	105.76	111.28
2	LB	245	GLY	CA-C-O	-5.06	118.74	122.23
75	Sj	31	ARG	N-CA-C	-5.06	106.37	112.54
3	LC	56	VAL	N-CA-C	-5.06	107.78	112.43
44	Lt	236	A	C2'-C3'-O3'	-5.06	106.11	113.70
8	LH	223	ARG	N-CA-C	-5.05	106.03	113.61
25	LY	35	LYS	N-CA-C	5.05	116.81	110.91
77	a	176	THR	CB-CA-C	5.05	120.54	109.99
10	LJ	83	GLY	CA-C-O	-5.04	117.37	122.56
61	SQ	139	ARG	N-CA-C	5.04	116.73	109.07
16	LP	82	ARG	N-CA-C	-5.03	106.65	112.89
5	LE	38	U	C4'-C3'-O3'	5.03	120.55	113.00
13	LM	132	ASN	CA-C-O	-5.03	115.22	120.55
20	LT	152	TYR	N-CA-C	-5.03	107.12	113.20
48	SC	132	ALA	N-CA-C	-5.03	107.28	113.41
32	Lf	69	ARG	CA-C-O	-5.02	115.54	121.16
15	LO	112	SER	N-CA-C	-5.02	107.21	113.38
15	LO	158	ARG	N-CA-C	-5.02	104.75	111.02
77	a	600	PHE	CA-C-O	-5.02	115.36	121.28
49	SD	29	PRO	N-CA-C	5.01	118.96	111.14
8	LH	137	GLU	N-CA-C	-5.01	105.48	112.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	SK	144	ILE	N-CA-C	5.01	112.51	107.55
39	Ln	46	ASP	CB-CA-C	-5.01	103.32	111.14
8	LH	130	THR	CA-C-O	-5.01	115.25	121.11
77	a	324	TYR	CA-C-N	-5.01	118.02	123.08
77	a	324	TYR	C-N-CA	-5.01	118.02	123.08
77	a	711	TYR	CB-CA-C	5.01	118.36	109.75
10	LJ	61	LYS	N-CA-C	-5.01	107.16	114.12
44	Lt	1074	C	C4'-C3'-O3'	5.01	116.91	109.40
19	LS	68	ALA	N-CA-C	-5.00	107.12	113.18
44	Lt	695	C	C2'-C3'-O3'	-5.00	106.20	113.70
44	Lt	2048	G	C2'-C3'-O3'	-5.00	106.19	113.70
76	St	57	C	C2'-C3'-O3'	-5.00	106.20	113.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	LA	1847	0	1903	26	0
2	LB	2935	0	2973	38	0
3	LC	2412	0	2493	40	0
4	LD	2932	0	1502	11	0
5	LE	2457	0	1246	8	0
6	LF	2287	0	2339	29	0
7	LG	431	0	468	4	0
8	LH	1694	0	1730	28	0
9	LI	1445	0	1522	25	0
10	LJ	1427	0	1473	20	0
11	LK	1552	0	1567	22	0
12	LL	1321	0	1341	15	0
13	LM	1539	0	1625	12	0
14	LN	1006	0	1077	19	0
15	LO	1708	0	1785	19	0
16	LP	1513	0	1546	24	0
17	LQ	1220	0	1260	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	LR	1388	0	1468	9	0
19	LS	1507	0	1614	27	0
20	LT	1418	0	1420	26	0
21	LU	1236	0	1277	20	0
22	LV	887	0	857	23	0
23	LW	1023	0	1063	20	0
24	LX	538	0	547	11	0
25	LY	913	0	959	8	0
26	LZ	1076	0	1140	15	0
27	La	976	0	1015	20	0
28	Lb	1201	0	1233	17	0
29	Lc	425	0	440	4	0
30	Ld	754	0	788	10	0
31	Le	795	0	835	6	0
32	Lf	1031	0	1084	16	0
33	Lg	770	0	805	12	0
34	Lh	846	0	879	13	0
35	Li	931	0	1027	10	0
36	Lj	677	0	735	13	0
37	Lk	697	0	694	12	0
38	Ll	534	0	582	20	0
39	Ln	1592	0	1667	56	0
40	Lo	227	0	272	2	0
41	Lp	759	0	811	9	0
42	Lq	666	0	704	15	0
43	Ls	374	0	387	11	0
44	Lt	55643	0	28280	203	0
45	Lu	1604	0	816	13	0
46	SA	1556	0	1596	42	0
47	SB	1604	0	1653	33	0
48	SC	1614	0	1651	35	0
49	SD	1803	0	1852	27	0
50	SE	2081	0	2170	48	0
51	SF	1382	0	1402	25	0
52	SG	1785	0	1887	43	0
53	SH	1481	0	1544	29	0
54	SI	1280	0	1337	24	0
55	SJ	1031	0	1082	18	0
56	SK	1416	0	1505	19	0
57	SL	827	0	818	26	0
58	SM	1220	0	1249	18	0
59	SO	1056	0	1141	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	SP	1187	0	1260	17	0
61	SQ	911	0	922	24	0
62	SR	912	0	986	18	0
63	ST	1180	0	1250	24	0
64	SU	526	0	582	11	0
65	SV	1113	0	1136	30	0
66	SW	1080	0	1106	15	0
67	SX	811	0	846	13	0
68	SY	615	0	623	20	0
69	Sb	941	0	1001	20	0
70	Sc	561	0	602	20	0
71	Sd	796	0	825	17	0
72	Se	629	0	625	11	0
73	Sg	474	0	503	10	0
74	Sh	409	0	407	12	0
75	Sj	525	0	573	18	0
76	St	31176	0	15856	182	0
77	a	6343	0	6350	128	0
78	y	240	0	120	5	0
79	a	5	0	0	0	0
80	a	28	0	12	0	0
All	All	180812	0	137721	1752	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 6.

All (1752) 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)
44:Lt:1972:A:OP1	44:Lt:1972:A:H4'	1.49	1.12
48:SC:70:TYR:O	48:SC:74:LYS:HG2	1.51	1.10
48:SC:59:ALA:HB2	48:SC:106:ILE:CD1	1.92	0.99
75:Sj:1:ARG:HB3	77:a:718:HIS:HB3	1.48	0.94
58:SM:110:SER:OG	58:SM:112:CYS:SG	2.31	0.87
44:Lt:157:G:H1	44:Lt:172:C:H5	1.19	0.87
48:SC:59:ALA:HB2	48:SC:106:ILE:HD12	1.56	0.87
49:SD:33:PRO:HA	49:SD:232:HIS:HA	1.58	0.84
50:SE:181:VAL:HG12	50:SE:227:VAL:HA	1.61	0.82
23:LW:58:VAL:HG11	23:LW:124:ALA:HB3	1.59	0.82
57:SL:4:ILE:H	76:St:999:U:H1'	1.44	0.82
38:Ll:20:LYS:HG2	38:Ll:40:LEU:HD13	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:SC:59:ALA:HB2	48:SC:106:ILE:HD11	1.61	0.80
3:LC:292:GLU:HG2	8:LH:159:VAL:HG11	1.63	0.80
9:LI:53:VAL:H	9:LI:214:GLY:HA2	1.46	0.80
57:SL:14:ALA:HA	57:SL:91:LEU:HD11	1.63	0.80
54:SI:16:ALA:HB2	76:St:267:C:H5''	1.63	0.79
65:SV:24:LYS:HA	70:Sc:18:PRO:HG3	1.63	0.78
57:SL:65:VAL:HG13	57:SL:83:GLY:HA3	1.66	0.77
58:SM:53:ASP:HB3	58:SM:56:CYS:HB2	1.67	0.77
77:a:235:GLU:HG3	77:a:242:PHE:HA	1.65	0.76
39:Ln:112:ALA:HB2	39:Ln:135:PRO:HB2	1.67	0.76
60:SP:60:ILE:HD11	60:SP:63:VAL:HA	1.69	0.75
11:LK:19:LYS:HB3	11:LK:26:VAL:HG11	1.69	0.73
39:Ln:113:SER:HB3	39:Ln:116:LEU:HB2	1.70	0.73
65:SV:17:PHE:HB3	65:SV:101:VAL:HG11	1.69	0.73
33:Lg:10:LEU:HB3	33:Lg:94:VAL:HG13	1.69	0.73
45:Lu:15:G:H21	45:Lu:19:A:H61	1.36	0.73
38:Ll:15:ALA:HA	38:Ll:20:LYS:HG3	1.70	0.73
76:St:1420:A:H2	76:St:1423:G:H1	1.36	0.72
77:a:862:SER:HB3	77:a:869:SER:HB2	1.71	0.72
57:SL:36:ILE:HB	57:SL:48:PRO:HG3	1.71	0.72
2:LB:159:ILE:HD11	2:LB:195:ALA:HB1	1.73	0.71
39:Ln:27:LYS:HG2	39:Ln:171:ASN:HB3	1.72	0.71
39:Ln:69:ALA:HA	39:Ln:113:SER:HB2	1.72	0.70
71:Sd:23:CYS:HB2	71:Sd:74:CYS:HB3	1.73	0.70
24:LX:7:CYS:SG	24:LX:33:CYS:N	2.61	0.70
44:Lt:1767:A:H2	44:Lt:1774:U:H3	1.37	0.70
50:SE:87:MET:HE1	50:SE:235:VAL:HG11	1.73	0.70
77:a:767:ARG:HG2	77:a:894:TYR:HB3	1.73	0.70
47:SB:80:VAL:HG21	76:St:1042:A:H5''	1.74	0.70
52:SG:45:ALA:HA	52:SG:52:ALA:HA	1.72	0.70
40:Lo:14:LYS:HD2	76:St:859:U:H5''	1.73	0.69
77:a:356:THR:CG2	77:a:358:ASP:OD2	2.40	0.69
23:LW:41:ILE:HD11	23:LW:65:THR:HG23	1.74	0.69
77:a:356:THR:HG22	77:a:358:ASP:OD2	1.91	0.69
18:LR:98:THR:HG23	18:LR:118:ARG:HB3	1.75	0.69
54:SI:14:THR:HG23	76:St:261:G:H1'	1.72	0.69
20:LT:29:ALA:HB1	20:LT:34:VAL:HG13	1.75	0.69
22:LV:13:GLN:HB3	22:LV:71:GLY:HA2	1.75	0.69
69:Sb:20:GLN:HB2	69:Sb:75:ALA:HB3	1.73	0.69
15:LO:89:ILE:HD11	44:Lt:1912:A:H4'	1.75	0.69
71:Sd:44:ILE:HG22	71:Sd:64:ILE:HG22	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:Sj:39:ASN:HA	75:Sj:43:VAL:HG12	1.76	0.68
18:LR:174:ARG:HH11	28:Lb:56:LEU:HD11	1.58	0.68
50:SE:19:LEU:HD11	50:SE:108:ARG:HD2	1.75	0.68
24:LX:45:ARG:HB3	44:Lt:1600:G:H2'	1.75	0.68
76:St:915:A:H2'	76:St:916:G:C8	2.29	0.68
45:Lu:17:G:H21	45:Lu:57:A:H5'	1.59	0.67
10:LJ:9:ILE:HG22	10:LJ:51:ILE:HB	1.76	0.67
52:SG:174:GLY:HA2	76:St:65:C:H3'	1.75	0.67
57:SL:33:VAL:HG23	57:SL:50:TYR:HA	1.77	0.67
51:SF:127:VAL:HG12	51:SF:131:ARG:HB3	1.77	0.67
58:SM:65:ARG:HG3	76:St:100:C:H5'	1.76	0.66
77:a:146:PHE:HB3	77:a:534:SER:HB2	1.77	0.66
27:La:44:ILE:HD11	27:La:47:LEU:HA	1.76	0.66
39:Ln:170:GLY:C	39:Ln:172:VAL:H	2.02	0.66
50:SE:114:ILE:HB	50:SE:118:GLU:HB3	1.78	0.66
59:SO:76:LYS:HB2	76:St:347:G:H5''	1.77	0.66
2:LB:218:ILE:HB	2:LB:337:VAL:HG23	1.78	0.66
46:SA:129:VAL:HG22	46:SA:151:SER:HB2	1.76	0.66
36:Lj:51:ILE:HD11	36:Lj:86:TYR:HB2	1.78	0.66
61:SQ:120:VAL:HG21	71:Sd:52:ASP:HB2	1.77	0.66
44:Lt:1962:C:H2'	44:Lt:1963:G:H4'	1.77	0.66
11:LK:159:ILE:HG13	11:LK:163:GLN:HG3	1.78	0.66
21:LU:44:VAL:HG12	21:LU:53:PRO:HG2	1.78	0.66
51:SF:36:PRO:HB3	51:SF:55:VAL:HG13	1.77	0.66
71:Sd:10:ARG:HB3	71:Sd:34:LYS:HG2	1.77	0.66
77:a:458:LYS:HA	77:a:480:ASN:HA	1.78	0.66
50:SE:192:ILE:HD12	50:SE:237:ILE:HG22	1.76	0.65
63:ST:111:VAL:HG11	63:ST:116:ALA:HB3	1.78	0.65
44:Lt:1311:G:H1	44:Lt:1453:C:H5	1.42	0.65
44:Lt:590:C:H3'	44:Lt:591:U:H4'	1.79	0.65
48:SC:208:ILE:HG22	48:SC:210:ILE:HG12	1.78	0.65
77:a:770:TYR:HA	77:a:777:SER:HB3	1.79	0.65
77:a:425:PRO:HB3	77:a:522:TYR:HB2	1.79	0.65
64:SU:28:ASP:HB3	64:SU:31:ASN:HB3	1.77	0.65
77:a:701:LEU:HD11	77:a:712:VAL:HG11	1.78	0.65
27:La:70:VAL:HG22	27:La:108:ILE:HG13	1.78	0.65
53:SH:134:CYS:HB2	53:SH:137:ILE:HG12	1.78	0.65
16:LP:126:LEU:HD13	16:LP:130:ARG:HB3	1.79	0.64
62:SR:65:ARG:HH21	62:SR:92:MET:HG3	1.61	0.64
11:LK:170:ASN:HA	11:LK:177:THR:HA	1.78	0.64
22:LV:56:VAL:HG13	22:LV:67:ILE:HG23	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:La:98:VAL:HA	27:La:104:ARG:HB2	1.78	0.64
38:Ll:9:ASN:O	38:Ll:13:MET:HG3	1.98	0.64
72:Se:75:GLU:HB3	72:Se:122:ARG:HA	1.79	0.64
76:St:1243:G:H22	76:St:1246:A:H5''	1.63	0.64
77:a:25:ILE:HG12	77:a:160:ALA:HB1	1.79	0.64
39:Ln:138:LEU:HD21	39:Ln:147:LYS:HG3	1.79	0.63
53:SH:16:LEU:HD13	53:SH:20:GLU:HB2	1.79	0.63
30:Ld:50:ASN:HB3	30:Ld:76:GLY:HA2	1.80	0.63
77:a:784:PHE:HB3	77:a:857:TYR:HB3	1.80	0.63
54:SI:122:LEU:HD11	54:SI:136:ARG:HG3	1.81	0.63
65:SV:25:VAL:HB	65:SV:30:ALA:HB2	1.79	0.63
13:LM:95:ASN:HD21	44:Lt:71:C:H4'	1.63	0.63
39:Ln:72:ARG:HH22	39:Ln:76:ARG:HD2	1.62	0.63
47:SB:84:THR:HA	76:St:890:G:H4'	1.81	0.63
46:SA:143:SER:HA	68:SY:67:ARG:HH12	1.64	0.62
77:a:416:ALA:HB2	77:a:425:PRO:HD2	1.81	0.62
53:SH:106:TYR:HA	53:SH:115:ARG:HA	1.81	0.62
8:LH:70:LEU:HD12	21:LU:144:ILE:HG21	1.81	0.62
52:SG:26:ASP:HB2	52:SG:29:LYS:HB2	1.81	0.62
64:SU:24:LEU:HD22	64:SU:57:VAL:HG11	1.82	0.62
70:Sc:60:MET:HA	70:Sc:63:LEU:HB2	1.81	0.62
76:St:1119:G:H4'	76:St:1120:G:H5'	1.82	0.62
50:SE:145:ARG:HG2	76:St:110:G:H4'	1.82	0.62
63:ST:27:THR:HG21	63:ST:105:ARG:HB2	1.80	0.62
30:Ld:29:LEU:HD21	30:Ld:85:VAL:HG11	1.82	0.62
51:SF:97:VAL:HG23	51:SF:163:ILE:HG22	1.81	0.62
67:SX:74:GLY:HA3	76:St:942:G:H5'	1.82	0.62
35:Li:124:LEU:HB3	35:Li:129:LYS:HG3	1.81	0.62
50:SE:99:PHE:HB2	50:SE:111:LEU:HD22	1.80	0.62
56:SK:142:VAL:HG12	56:SK:144:ILE:H	1.62	0.62
51:SF:45:LYS:HD2	51:SF:48:ARG:HG3	1.80	0.62
1:LA:3:ARG:HB2	1:LA:207:VAL:HG22	1.82	0.62
23:LW:14:LYS:HG3	23:LW:130:ARG:HD3	1.82	0.62
44:Lt:533:A:H5''	44:Lt:637:C:H41	1.64	0.62
48:SC:76:GLU:HG3	48:SC:92:ILE:HG13	1.81	0.62
72:Se:96:PHE:HA	72:Se:103:GLN:HA	1.82	0.62
77:a:147:SER:HB3	77:a:567:CYS:HB2	1.82	0.61
2:LB:67:LEU:HD11	23:LW:93:LYS:HB2	1.82	0.61
2:LB:205:ILE:HD12	2:LB:285:ILE:HG23	1.81	0.61
47:SB:162:ARG:HG3	47:SB:193:ARG:HB2	1.80	0.61
51:SF:16:VAL:HG21	51:SF:95:VAL:HG22	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:ST:36:ALA:HB2	63:ST:87:VAL:HG13	1.82	0.61
72:Se:95:VAL:HB	72:Se:105:SER:HB3	1.80	0.61
44:Lt:2156:C:H5'	44:Lt:2185:G:H5''	1.82	0.61
65:SV:37:ILE:HA	76:St:1255:C:H5''	1.82	0.61
10:LJ:16:GLU:HG2	10:LJ:27:LYS:HB3	1.82	0.61
56:SK:67:ASP:H	56:SK:70:ARG:HB3	1.64	0.61
59:SO:28:ARG:HG2	59:SO:32:LEU:HD22	1.83	0.61
44:Lt:1969:G:H2'	44:Lt:1970:A:H2'	1.81	0.61
59:SO:70:VAL:HG11	59:SO:94:ILE:HG21	1.82	0.61
61:SQ:85:ILE:HB	61:SQ:90:ILE:HB	1.81	0.61
8:LH:207:LEU:HB2	44:Lt:879:A:H5''	1.81	0.61
50:SE:137:PRO:HB2	50:SE:150:PRO:HD2	1.80	0.61
54:SI:22:HIS:HB3	76:St:298:A:H5''	1.82	0.61
39:Ln:87:ILE:HA	39:Ln:90:LEU:HB2	1.83	0.61
1:LA:82:MET:HE2	1:LA:88:VAL:HG21	1.82	0.61
2:LB:223:GLY:HA2	2:LB:271:GLY:HA3	1.81	0.61
44:Lt:1972:A:OP1	44:Lt:1972:A:C4'	2.37	0.61
67:SX:45:VAL:HA	67:SX:53:ILE:HG21	1.83	0.61
77:a:623:SER:HB3	77:a:642:ALA:H	1.65	0.61
59:SO:4:THR:HG21	59:SO:12:LYS:HG2	1.82	0.60
77:a:60:ARG:H	77:a:131:GLY:HA3	1.65	0.60
36:Lj:55:ARG:HB2	36:Lj:90:ILE:HG21	1.83	0.60
50:SE:87:MET:HE2	50:SE:123:LEU:HB2	1.83	0.60
74:Sh:102:CYS:HB3	74:Sh:120:CYS:N	2.16	0.60
13:LM:87:VAL:HB	44:Lt:74:G:H5'	1.83	0.60
46:SA:131:ASP:HB2	46:SA:133:VAL:HG23	1.84	0.60
76:St:1000:C:H2'	76:St:1001:G:H8	1.66	0.60
9:LI:29:THR:HB	9:LI:30:PRO:HD3	1.84	0.60
8:LH:98:LEU:HG	8:LH:125:VAL:HG21	1.84	0.60
27:La:98:VAL:HG12	27:La:107:ILE:HD11	1.83	0.60
2:LB:45:ALA:H	2:LB:180:ILE:HG23	1.66	0.60
50:SE:9:LEU:HB2	50:SE:30:ARG:HD3	1.84	0.60
47:SB:175:SER:HB2	76:St:4:C:H4'	1.83	0.60
52:SG:178:THR:HB	52:SG:180:LYS:HG2	1.84	0.60
77:a:417:ILE:HA	77:a:450:SER:HB3	1.83	0.60
47:SB:174:ALA:HB1	47:SB:178:VAL:HG22	1.83	0.59
57:SL:93:LEU:HG	57:SL:97:VAL:HG11	1.84	0.59
2:LB:57:MET:HE2	2:LB:71:GLN:HB3	1.82	0.59
44:Lt:2188:C:H42	45:Lu:75:A:H61	1.50	0.59
67:SX:29:VAL:HG22	67:SX:116:VAL:HG13	1.84	0.59
3:LC:197:VAL:HG13	3:LC:216:LEU:HG	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:LW:58:VAL:HG11	23:LW:124:ALA:CB	2.30	0.59
77:a:158:ASP:HA	77:a:400:ARG:HH12	1.67	0.59
23:LW:84:VAL:HB	23:LW:123:VAL:HG22	1.85	0.59
23:LW:38:LEU:HB3	23:LW:64:ILE:HD13	1.84	0.59
46:SA:62:LYS:HG3	46:SA:167:PRO:HD2	1.83	0.59
47:SB:223:LEU:HD13	68:SY:30:LEU:HD21	1.83	0.59
49:SD:45:PRO:HG2	61:SQ:51:GLU:HB3	1.83	0.59
44:Lt:910:U:H5	44:Lt:995:G:H1	1.49	0.59
46:SA:37:ARG:HG2	76:St:794:G:H5'	1.85	0.59
77:a:27:HIS:HD2	77:a:173:GLN:HB2	1.68	0.59
77:a:703:LEU:HA	77:a:706:THR:HB	1.84	0.59
77:a:789:ILE:HD13	77:a:853:VAL:HG13	1.84	0.59
6:LF:64:VAL:HG21	6:LF:109:LEU:HD22	1.83	0.59
63:ST:105:ARG:HA	63:ST:108:LEU:HD12	1.85	0.59
60:SP:54:LEU:HA	60:SP:58:PHE:HD2	1.67	0.58
65:SV:39:ARG:HG3	65:SV:41:PHE:CD1	2.39	0.58
66:SW:23:ARG:HB3	66:SW:25:ILE:HG13	1.85	0.58
1:LA:117:GLU:HG2	1:LA:124:GLY:H	1.67	0.58
6:LF:136:GLU:HA	6:LF:185:MET:HE3	1.85	0.58
13:LM:86:SER:H	13:LM:141:ASN:HD21	1.51	0.58
19:LS:96:ILE:HD13	44:Lt:1329:C:H5''	1.84	0.58
63:ST:53:PRO:HD3	66:SW:6:ARG:HA	1.84	0.58
61:SQ:34:TYR:HE1	61:SQ:100:ASP:HA	1.68	0.58
41:Lp:14:ARG:HB3	41:Lp:77:CYS:SG	2.42	0.58
73:Sg:39:ARG:HD2	73:Sg:53:LEU:HD22	1.86	0.58
77:a:554:LEU:HD13	77:a:606:ILE:HG21	1.85	0.58
10:LJ:166:LYS:HD2	44:Lt:2324:C:H5''	1.84	0.58
44:Lt:1949:A:H61	44:Lt:1969:G:H21	1.50	0.58
77:a:171:CYS:H	77:a:174:THR:HB	1.69	0.58
23:LW:71:LYS:HB2	23:LW:74:LEU:HD12	1.85	0.58
24:LX:11:SER:HB2	24:LX:54:LYS:HB2	1.85	0.58
29:Lc:48:ALA:HA	29:Lc:53:GLN:HG2	1.86	0.58
17:LQ:29:TYR:HA	17:LQ:119:VAL:HG21	1.83	0.58
1:LA:62:GLN:HG2	1:LA:71:ARG:HB3	1.84	0.58
17:LQ:90:VAL:HG13	17:LQ:148:LEU:HD11	1.84	0.58
52:SG:127:LEU:HD22	52:SG:130:LEU:HB2	1.86	0.58
11:LK:27:PRO:HG3	11:LK:123:GLN:HA	1.86	0.58
44:Lt:1653:G:H1	44:Lt:1658:C:H5	1.51	0.58
70:Sc:72:VAL:HG22	70:Sc:82:LYS:HG2	1.85	0.58
77:a:335:ALA:HA	77:a:338:THR:HG22	1.86	0.57
5:LE:44:A:H5''	12:LL:137:ARG:HH21	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SG:9:VAL:HG13	52:SG:115:LEU:HB3	1.86	0.57
54:SI:161:GLY:HA2	58:SM:22:LEU:HD13	1.85	0.57
59:SO:18:ARG:HD3	76:St:225:G:H5''	1.86	0.57
72:Se:73:PHE:HB2	72:Se:122:ARG:HE	1.70	0.57
1:LA:24:LEU:HB3	1:LA:75:LEU:HD11	1.87	0.57
47:SB:147:THR:HG22	47:SB:189:ASP:HB2	1.85	0.57
77:a:173:GLN:HA	77:a:176:THR:HG22	1.87	0.57
63:ST:73:LEU:HD22	63:ST:120:LEU:HG	1.86	0.57
30:Ld:60:VAL:HG21	30:Ld:93:ILE:HD12	1.86	0.57
32:Lf:72:LEU:HD11	32:Lf:78:LYS:HB2	1.86	0.57
39:Ln:66:CYS:H	39:Ln:110:PHE:HA	1.68	0.57
69:Sb:105:ARG:HH12	69:Sb:108:LEU:HD22	1.70	0.57
76:St:746:A:H2	76:St:766:U:H3	1.53	0.57
76:St:983:G:H22	76:St:986:C:H5''	1.68	0.57
77:a:671:LEU:HA	77:a:675:TYR:HD2	1.69	0.57
28:Lb:75:ILE:HG13	28:Lb:118:LEU:HG	1.86	0.57
61:SQ:43:HIS:CD2	61:SQ:55:ARG:HB2	2.39	0.57
63:ST:114:GLU:HG3	63:ST:116:ALA:H	1.68	0.57
32:Lf:106:SER:HB3	44:Lt:1078:G:H5'	1.87	0.57
44:Lt:1972:A:O2'	44:Lt:1973:C:H2'	2.05	0.57
44:Lt:2445:A:H1'	77:a:172:VAL:HG22	1.85	0.57
77:a:814:GLU:HG2	77:a:823:GLU:HG2	1.87	0.56
45:Lu:35:U:H2'	45:Lu:36:A:C8	2.40	0.56
20:LT:90:GLU:HB3	20:LT:136:VAL:HG21	1.87	0.56
34:Lh:52:ILE:HD13	34:Lh:76:GLY:HA2	1.86	0.56
46:SA:115:ASN:HB3	46:SA:118:ASN:HB2	1.86	0.56
52:SG:20:LYS:HB2	52:SG:130:LEU:HD13	1.86	0.56
76:St:1354:C:H2'	76:St:1355:G:C8	2.40	0.56
77:a:198:VAL:HB	77:a:204:LEU:HD12	1.86	0.56
77:a:452:VAL:HG22	77:a:499:PRO:HA	1.88	0.56
8:LH:173:ILE:HG23	8:LH:178:ASP:HB3	1.88	0.56
44:Lt:47:A:H4'	44:Lt:48:G:H5'	1.86	0.56
70:Sc:69:PHE:HA	70:Sc:83:ASN:HA	1.87	0.56
76:St:439:U:H3	76:St:466:G:H1	1.52	0.56
6:LF:108:ARG:CZ	6:LF:259:ALA:HB2	2.36	0.56
19:LS:117:ARG:HB3	44:Lt:1383:G:H5''	1.87	0.56
47:SB:182:LEU:HG	47:SB:190:VAL:HG11	1.86	0.56
38:Ll:16:ASP:OD1	38:Ll:17:GLY:N	2.39	0.56
39:Ln:207:LYS:HB3	39:Ln:213:SER:HA	1.88	0.56
49:SD:97:LEU:HD22	49:SD:232:HIS:CE1	2.40	0.56
78:y:33:A:H2'	78:y:34:A:H5'	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LB:56:VAL:HG21	2:LB:353:LEU:HD22	1.86	0.56
51:SF:88:LEU:HD21	70:Sc:72:VAL:HG21	1.88	0.56
58:SM:65:ARG:HH21	76:St:102:C:H5	1.54	0.56
77:a:428:LEU:HD11	77:a:504:VAL:HG11	1.87	0.56
17:LQ:11:LEU:HB3	17:LQ:13:VAL:HG13	1.86	0.56
47:SB:164:ILE:HB	47:SB:191:PHE:HB2	1.87	0.56
48:SC:59:ALA:CB	48:SC:106:ILE:CD1	2.75	0.56
57:SL:32:ASN:HB3	57:SL:47:ASN:HB3	1.88	0.56
77:a:426:LEU:HB3	77:a:521:THR:HB	1.88	0.56
2:LB:218:ILE:HG23	2:LB:276:THR:HG22	1.89	0.56
4:LD:73:A:H5''	26:LZ:50:ARG:HB2	1.86	0.56
39:Ln:170:GLY:C	39:Ln:172:VAL:N	2.64	0.56
65:SV:39:ARG:HG3	65:SV:41:PHE:HD1	1.70	0.56
47:SB:42:ILE:HG13	47:SB:235:ILE:HG23	1.88	0.55
76:St:200:G:H21	76:St:207:C:H1'	1.71	0.55
10:LJ:78:LYS:HB3	10:LJ:182:LEU:HD11	1.89	0.55
28:Lb:115:ARG:HA	44:Lt:459:A:H5'	1.87	0.55
45:Lu:19:A:H2'	45:Lu:20:A:H4'	1.86	0.55
46:SA:43:ILE:HG12	46:SA:52:PHE:HB3	1.88	0.55
48:SC:59:ALA:CB	48:SC:106:ILE:HD11	2.34	0.55
50:SE:208:ILE:HD11	50:SE:225:VAL:HG21	1.87	0.55
47:SB:91:ARG:HD2	47:SB:111:VAL:HB	1.88	0.55
53:SH:116:ARG:HH22	76:St:519:C:H5'	1.71	0.55
57:SL:16:LEU:O	57:SL:20:ALA:N	2.37	0.55
65:SV:39:ARG:O	76:St:1254:G:H4'	2.05	0.55
67:SX:48:GLY:HA3	67:SX:53:ILE:HB	1.88	0.55
4:LD:133:G:H1	44:Lt:9:U:H3	1.55	0.55
46:SA:20:VAL:HA	46:SA:24:LEU:HB3	1.88	0.55
55:SJ:86:ILE:O	55:SJ:90:VAL:HG23	2.06	0.55
77:a:433:MET:HG3	77:a:442:PHE:HB3	1.88	0.55
49:SD:182:PRO:HD3	49:SD:227:LEU:HD11	1.88	0.55
57:SL:24:LEU:HD11	57:SL:53:VAL:HG12	1.88	0.55
69:Sb:94:CYS:HB3	69:Sb:96:LEU:HD22	1.87	0.55
76:St:1422:G:H5''	76:St:1423:G:H5'	1.88	0.55
39:Ln:110:PHE:HB3	39:Ln:135:PRO:HB3	1.88	0.55
61:SQ:40:THR:HG21	61:SQ:74:ALA:HB2	1.88	0.55
76:St:498:U:H5''	76:St:784:G:C5	2.41	0.55
20:LT:10:ARG:HG2	20:LT:57:LEU:HD21	1.89	0.55
42:Lq:36:LYS:HG3	42:Lq:48:ARG:HD3	1.88	0.55
52:SG:99:LYS:HG2	52:SG:101:LYS:HE2	1.89	0.55
77:a:461:ILE:HD11	77:a:479:LYS:HB3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Ln:89:HIS:HA	39:Ln:92:GLN:HB2	1.87	0.55
76:St:909:A:H4'	76:St:1299:G:H22	1.72	0.55
76:St:1016:C:N4	78:y:38:A:H4'	2.22	0.55
3:LC:291:ILE:HD12	8:LH:156:ILE:HD12	1.89	0.55
6:LF:109:LEU:HD23	6:LF:179:LEU:HD21	1.88	0.55
36:Lj:19:ARG:O	36:Lj:20:LYS:C	2.50	0.55
38:Ll:5:ILE:HG21	38:Ll:11:MET:HB2	1.88	0.55
58:SM:84:VAL:HG11	58:SM:123:ILE:HG21	1.89	0.55
65:SV:40:ARG:HH21	65:SV:75:PRO:HA	1.72	0.55
19:LS:55:ILE:HB	44:Lt:1357:C:H5''	1.88	0.54
44:Lt:2235:C:H2'	44:Lt:2236:A:C8	2.43	0.54
54:SI:33:PRO:HA	76:St:244:G:H5'	1.89	0.54
78:y:34:A:H1'	78:y:35:U:H4'	1.89	0.54
52:SG:174:GLY:H	76:St:65:C:H5''	1.72	0.54
52:SG:26:ASP:HB3	52:SG:28:ARG:HD2	1.90	0.54
77:a:152:ALA:HB1	77:a:431:SER:HB2	1.88	0.54
9:LI:171:VAL:HG13	9:LI:173:LEU:HB2	1.89	0.54
41:Lp:68:ILE:HD12	41:Lp:91:ILE:HD11	1.89	0.54
1:LA:51:ASP:HB2	1:LA:58:LEU:HD22	1.89	0.54
16:LP:78:ARG:HB2	16:LP:101:VAL:HG21	1.89	0.54
71:Sd:11:SER:H	71:Sd:33:ASP:HB2	1.73	0.54
76:St:975:C:H2'	76:St:976:G:H8	1.73	0.54
77:a:766:ARG:HE	77:a:767:ARG:HG3	1.73	0.54
15:LO:72:LYS:HE3	15:LO:89:ILE:HD12	1.90	0.54
15:LO:104:GLN:HA	15:LO:160:GLU:HG3	1.89	0.54
1:LA:15:VAL:HG22	44:Lt:539:G:H1'	1.90	0.54
53:SH:52:ILE:HG21	53:SH:176:VAL:HG23	1.89	0.54
61:SQ:66:CYS:HB3	76:St:659:A:H5''	1.90	0.54
76:St:201:C:H1'	76:St:202:G:H5'	1.90	0.54
16:LP:168:LYS:HA	16:LP:171:ILE:HG12	1.90	0.53
21:LU:115:ALA:HB1	21:LU:127:PRO:HD2	1.91	0.53
22:LV:13:GLN:HB3	22:LV:71:GLY:CA	2.39	0.53
49:SD:234:SER:HB3	49:SD:237:VAL:HG23	1.90	0.53
55:SJ:31:SER:HB2	76:St:516:C:H5''	1.89	0.53
62:SR:98:ASN:HB2	62:SR:122:SER:HA	1.88	0.53
67:SX:29:VAL:O	67:SX:89:LYS:HA	2.09	0.53
15:LO:16:SER:HB2	36:Lj:41:THR:HB	1.90	0.53
16:LP:52:LEU:HD13	16:LP:142:ILE:HG22	1.90	0.53
36:Lj:51:ILE:HG13	36:Lj:83:LEU:HD12	1.90	0.53
39:Ln:27:LYS:HB3	39:Ln:30:GLU:O	2.08	0.53
50:SE:11:ARG:HA	50:SE:28:ALA:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SH:70:LEU:HD22	53:SH:97:ALA:HB2	1.89	0.53
57:SL:63:ARG:HE	76:St:963:C:H5'	1.72	0.53
48:SC:71:ARG:O	48:SC:75:ILE:HG23	2.08	0.53
52:SG:168:GLU:HB3	52:SG:170:ILE:HG12	1.90	0.53
69:Sb:24:VAL:HG22	69:Sb:73:CYS:SG	2.48	0.53
69:Sb:83:MET:HA	69:Sb:91:LYS:HD3	1.90	0.53
20:LT:22:VAL:HG11	21:LU:144:ILE:HG22	1.90	0.53
22:LV:48:ARG:HD3	22:LV:50:HIS:HB2	1.90	0.53
27:La:25:VAL:HG21	27:La:85:LEU:HD22	1.90	0.53
45:Lu:36:A:H3'	45:Lu:37:A:H5''	1.89	0.53
52:SG:161:LYS:HG3	52:SG:164:MET:HB2	1.89	0.53
65:SV:125:ARG:HD3	65:SV:132:VAL:HG13	1.91	0.53
5:LE:62:G:H5'	6:LF:275:LEU:HD12	1.90	0.53
59:SO:55:ILE:HG21	59:SO:71:ARG:HG2	1.91	0.53
69:Sb:44:ALA:HB2	69:Sb:55:ILE:HD12	1.90	0.53
77:a:362:MET:HB3	77:a:367:LEU:HD13	1.90	0.53
21:LU:53:PRO:HB2	21:LU:57:TYR:HB2	1.90	0.53
52:SG:72:GLY:HA2	76:St:1369:A:H1'	1.90	0.53
70:Sc:18:PRO:HA	70:Sc:52:SER:HB3	1.91	0.53
17:LQ:112:LEU:HB3	17:LQ:150:VAL:HG13	1.91	0.53
37:Lk:52:LYS:HA	37:Lk:55:ARG:HG2	1.90	0.53
44:Lt:243:A:H2'	44:Lt:244:G:C8	2.43	0.53
52:SG:54:CYS:HA	52:SG:122:ALA:HA	1.91	0.53
59:SO:57:ILE:HD11	59:SO:82:THR:HG21	1.90	0.53
63:ST:66:VAL:HG22	63:ST:96:ILE:HG23	1.91	0.53
39:Ln:201:ILE:HD11	39:Ln:204:VAL:HG22	1.91	0.53
54:SI:146:SER:HB2	54:SI:151:VAL:HG21	1.91	0.53
48:SC:35:LEU:HD21	48:SC:64:VAL:HG13	1.90	0.52
59:SO:46:MET:HG3	59:SO:101:LEU:HD23	1.91	0.52
62:SR:81:ARG:HB3	62:SR:117:ARG:HB3	1.90	0.52
34:Lh:64:THR:HB	44:Lt:1310:C:C5	2.45	0.52
52:SG:36:LEU:HD13	52:SG:42:PHE:HB2	1.92	0.52
56:SK:114:ILE:HG21	56:SK:135:ILE:HG12	1.91	0.52
76:St:177:C:H42	76:St:598:C:H42	1.57	0.52
76:St:915:A:H2'	76:St:916:G:H8	1.75	0.52
77:a:498:VAL:HG22	77:a:502:ASN:HD21	1.74	0.52
27:La:11:VAL:HB	27:La:83:CYS:HB3	1.91	0.52
53:SH:154:LEU:HB3	53:SH:185:THR:HG23	1.92	0.52
62:SR:95:SER:HB2	62:SR:102:PHE:HB3	1.92	0.52
77:a:658:ILE:HD12	77:a:671:LEU:HD11	1.90	0.52
11:LK:69:ARG:HB2	11:LK:89:ILE:HD11	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LK:91:VAL:HG11	11:LK:129:VAL:HG12	1.91	0.52
16:LP:137:ARG:O	16:LP:141:GLU:HG2	2.09	0.52
20:LT:157:ARG:HD3	20:LT:160:ARG:HH22	1.75	0.52
50:SE:151:HIS:HD2	50:SE:152:PRO:HD2	1.74	0.52
51:SF:190:ARG:HD2	73:Sg:55:GLU:HB3	1.90	0.52
52:SG:189:PRO:HB3	76:St:63:C:C4	2.44	0.52
52:SG:227:LEU:O	52:SG:231:MET:HB2	2.10	0.52
77:a:338:THR:HG23	77:a:340:GLN:HB2	1.91	0.52
45:Lu:27:U:H2'	45:Lu:28:G:C8	2.45	0.52
46:SA:132:PRO:HB3	46:SA:162:ILE:HD11	1.91	0.52
3:LC:104:LYS:HA	44:Lt:429:C:H5	1.75	0.52
6:LF:182:PRO:HB2	44:Lt:2171:A:H4'	1.92	0.52
44:Lt:84:C:H4'	44:Lt:85:U:H5'	1.92	0.52
49:SD:46:VAL:HG21	49:SD:59:ILE:HD13	1.92	0.52
64:SU:14:ARG:O	64:SU:18:GLU:HG2	2.09	0.52
66:SW:122:ILE:HG12	66:SW:127:ARG:HG2	1.91	0.52
4:LD:65:C:H2'	4:LD:66:G:H8	1.74	0.52
20:LT:30:PRO:HD2	20:LT:34:VAL:HG11	1.92	0.52
67:SX:53:ILE:HA	67:SX:94:VAL:HG13	1.92	0.52
74:Sh:104:ILE:HG12	74:Sh:123:CYS:HB3	1.91	0.52
76:St:320:C:H2'	76:St:321:G:C8	2.45	0.52
33:Lg:9:PHE:HA	33:Lg:95:PHE:HA	1.92	0.52
47:SB:47:ASP:HB3	47:SB:235:ILE:HD11	1.92	0.52
51:SF:84:GLU:HB3	70:Sc:80:ILE:HD13	1.91	0.52
67:SX:43:SER:O	67:SX:47:GLU:HG2	2.10	0.52
77:a:547:ASN:HB2	77:a:550:ASP:HB2	1.91	0.52
8:LH:64:ALA:HB1	8:LH:69:GLN:HB3	1.92	0.52
44:Lt:2138:G:H4'	44:Lt:2139:A:H5''	1.91	0.52
49:SD:49:THR:HG23	49:SD:54:VAL:HA	1.92	0.52
49:SD:113:LEU:HB3	49:SD:142:PHE:CE1	2.44	0.52
3:LC:6:LYS:HE2	3:LC:14:GLN:HE22	1.75	0.51
39:Ln:65:LEU:HD11	39:Ln:148:VAL:HG22	1.92	0.51
47:SB:76:ASN:HB3	47:SB:201:LEU:HD22	1.92	0.51
13:LM:62:ILE:HA	13:LM:65:ARG:HD2	1.92	0.51
22:LV:49:LYS:HA	22:LV:52:VAL:HG13	1.92	0.51
39:Ln:48:ARG:HA	39:Ln:159:PHE:HB2	1.91	0.51
77:a:718:HIS:CD2	77:a:761:LEU:HB3	2.45	0.51
22:LV:24:ALA:HB1	22:LV:28:LEU:HB2	1.92	0.51
49:SD:109:LYS:O	49:SD:113:LEU:HG	2.10	0.51
61:SQ:95:ILE:HG13	61:SQ:126:ILE:HG23	1.92	0.51
76:St:1281:C:H2'	76:St:1282:G:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LJ:172:LEU:HD23	10:LJ:172:LEU:H	1.75	0.51
49:SD:12:LYS:HG2	61:SQ:89:GLY:HA3	1.93	0.51
54:SI:107:LYS:HG2	76:St:242:C:H5'	1.92	0.51
61:SQ:75:MET:O	61:SQ:79:GLN:HG2	2.10	0.51
77:a:10:ARG:HH12	77:a:499:PRO:HD3	1.75	0.51
54:SI:132:LEU:HA	54:SI:135:ILE:HG13	1.92	0.51
76:St:1016:C:C5	78:y:39:U:H2'	2.46	0.51
2:LB:78:ILE:HG12	2:LB:305:ILE:HD11	1.92	0.51
26:LZ:57:ILE:HD13	26:LZ:104:CYS:HB3	1.93	0.51
26:LZ:59:THR:O	26:LZ:63:LYS:HB2	2.11	0.51
37:Lk:28:HIS:HB3	37:Lk:31:LYS:HB2	1.92	0.51
47:SB:46:TYR:CD1	68:SY:19:TYR:HB3	2.46	0.51
55:SJ:6:VAL:HB	55:SJ:34:ILE:HD11	1.92	0.51
72:Se:71:SER:HB3	72:Se:90:HIS:CD2	2.46	0.51
44:Lt:1213:G:H3'	44:Lt:1214:G:H8	1.74	0.51
44:Lt:2382:C:H2'	44:Lt:2383:G:C8	2.46	0.51
48:SC:101:GLY:HA2	48:SC:107:MET:HE3	1.91	0.51
50:SE:128:LYS:H	50:SE:140:SER:HB2	1.76	0.51
53:SH:11:LYS:HG2	53:SH:27:LEU:HB3	1.92	0.51
60:SP:102:LEU:HD21	60:SP:111:SER:HB3	1.93	0.51
65:SV:122:ARG:HA	65:SV:132:VAL:HG11	1.92	0.51
70:Sc:54:ALA:HA	70:Sc:57:LYS:HE3	1.92	0.51
22:LV:91:TYR:HB2	22:LV:94:VAL:HB	1.91	0.51
43:Ls:79:GLU:O	43:Ls:83:ILE:HB	2.11	0.51
50:SE:196:GLN:HG2	50:SE:211:LYS:HB2	1.93	0.51
45:Lu:11:C:H2'	45:Lu:12:G:C8	2.45	0.51
47:SB:142:LEU:HA	68:SY:11:SER:HB3	1.93	0.51
50:SE:183:VAL:HG11	50:SE:220:THR:HG21	1.92	0.51
74:Sh:114:LYS:HG2	76:St:1282:G:H5''	1.93	0.51
76:St:634:C:H2'	76:St:635:A:C8	2.46	0.51
2:LB:14:LEU:HB2	44:Lt:2428:C:H5'	1.93	0.50
6:LF:3:TRP:HB3	44:Lt:751:C:H1'	1.92	0.50
12:LL:84:LEU:HD21	12:LL:91:LEU:HD22	1.93	0.50
19:LS:129:GLY:HA3	44:Lt:558:G:H1'	1.91	0.50
55:SJ:119:ARG:HB2	55:SJ:121:ILE:HG12	1.93	0.50
61:SQ:43:HIS:NE2	61:SQ:52:THR:HB	2.26	0.50
67:SX:102:SER:HA	67:SX:105:LEU:HD12	1.93	0.50
47:SB:159:VAL:HG11	47:SB:204:SER:HA	1.94	0.50
58:SM:71:GLY:HA3	58:SM:84:VAL:HG23	1.93	0.50
77:a:432:LYS:HE2	77:a:434:VAL:HG22	1.92	0.50
27:La:20:ALA:HB3	34:Lh:73:PRO:HD2	1.91	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:SB:146:HIS:H	47:SB:146:HIS:CD2	2.30	0.50
54:SI:124:ASN:HB3	54:SI:127:LEU:HD11	1.94	0.50
63:ST:95:GLN:O	63:ST:99:VAL:HG23	2.11	0.50
6:LF:2:GLY:HA3	44:Lt:729:A:C4	2.46	0.50
27:La:84:ARG:O	27:La:85:LEU:HB2	2.11	0.50
39:Ln:22:ASN:H	44:Lt:1958:G:H5'	1.77	0.50
60:SP:54:LEU:HD23	60:SP:60:ILE:HD13	1.93	0.50
63:ST:59:PRO:HG3	63:ST:92:HIS:HB3	1.94	0.50
76:St:202:G:H4'	76:St:205:G:H1'	1.93	0.50
16:LP:23:GLU:HG3	20:LT:164:PHE:HZ	1.75	0.50
44:Lt:401:A:H5''	44:Lt:1849:C:H5''	1.94	0.50
51:SF:88:LEU:HD23	70:Sc:39:CYS:HB3	1.93	0.50
52:SG:104:ARG:HE	52:SG:105:GLY:H	1.58	0.50
56:SK:110:LEU:HA	56:SK:113:VAL:HB	1.94	0.50
76:St:1080:C:H1'	76:St:1117:A:C4	2.47	0.50
77:a:413:ALA:HB2	77:a:522:TYR:HD1	1.76	0.50
77:a:790:LEU:HD12	77:a:825:LYS:HG2	1.92	0.50
16:LP:12:ILE:HD11	16:LP:126:LEU:HD23	1.93	0.50
49:SD:182:PRO:HA	49:SD:231:MET:SD	2.52	0.50
4:LD:94:C:H5''	37:Lk:76:SER:HB3	1.94	0.50
41:Lp:28:LYS:HD2	44:Lt:2191:U:H1'	1.94	0.50
44:Lt:1362:A:H2'	44:Lt:1363:A:C8	2.46	0.50
44:Lt:1949:A:C8	44:Lt:1949:A:H5''	2.47	0.50
44:Lt:2663:C:H2'	44:Lt:2664:G:C8	2.46	0.50
48:SC:168:HIS:HD2	48:SC:172:ILE:HD11	1.77	0.50
76:St:1197:C:H2'	76:St:1198:C:C6	2.47	0.50
2:LB:227:GLU:HG3	2:LB:231:THR:HB	1.94	0.50
25:LY:92:PRO:HD3	44:Lt:1465:G:H4'	1.94	0.50
32:Lf:90:LEU:O	32:Lf:94:ASN:HB2	2.12	0.50
44:Lt:671:U:H2'	44:Lt:672:G:H8	1.76	0.50
48:SC:130:ARG:HA	48:SC:133:MET:HB2	1.93	0.50
76:St:965:C:H2'	76:St:966:G:C8	2.47	0.50
77:a:703:LEU:HA	77:a:706:THR:CB	2.41	0.50
4:LD:139:U:H5''	9:LI:66:ARG:HD3	1.94	0.49
12:LL:17:LEU:HD22	12:LL:80:ILE:HG13	1.93	0.49
76:St:1329:C:H2'	76:St:1330:G:C8	2.46	0.49
39:Ln:68:ILE:HG23	39:Ln:112:ALA:HA	1.94	0.49
47:SB:178:VAL:HB	47:SB:208:VAL:HG21	1.93	0.49
51:SF:108:ARG:HG2	73:Sg:52:VAL:HG13	1.94	0.49
77:a:267:GLY:H	77:a:378:ALA:HB2	1.77	0.49
60:SP:69:SER:HB3	60:SP:73:ARG:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:St:988:C:H2'	76:St:989:G:C8	2.48	0.49
76:St:1033:C:H2'	76:St:1034:G:C8	2.48	0.49
1:LA:200:ARG:HH12	1:LA:217:GLN:HE22	1.60	0.49
2:LB:215:ILE:HD11	2:LB:324:ILE:HG21	1.95	0.49
43:Ls:110:CYS:SG	43:Ls:113:CYS:N	2.82	0.49
50:SE:64:ILE:HG21	69:Sb:17:LEU:HG	1.95	0.49
76:St:807:G:H1'	76:St:808:C:C6	2.47	0.49
44:Lt:1136:U:H2'	44:Lt:1137:A:H8	1.78	0.49
44:Lt:2055:U:H2'	44:Lt:2056:G:C8	2.46	0.49
46:SA:159:LEU:HD11	46:SA:165:ALA:HB2	1.95	0.49
66:SW:82:LEU:HD11	76:St:1278:G:H5'	1.94	0.49
74:Sh:120:CYS:HB3	74:Sh:123:CYS:H	1.78	0.49
76:St:637:C:H2'	76:St:638:G:C8	2.47	0.49
76:St:1284:C:H1'	76:St:1287:C:H41	1.77	0.49
14:LN:30:ILE:HG21	20:LT:146:PHE:CE2	2.48	0.49
33:Lg:10:LEU:HD12	33:Lg:11:PRO:HD2	1.94	0.49
33:Lg:73:GLY:O	33:Lg:74:MET:C	2.56	0.49
46:SA:143:SER:O	68:SY:37:ALA:HA	2.12	0.49
50:SE:172:TRP:HZ3	50:SE:174:LYS:HG2	1.78	0.49
76:St:358:A:H2'	76:St:359:A:H8	1.78	0.49
2:LB:327:THR:HG21	44:Lt:2464:G:H21	1.78	0.49
19:LS:35:ALA:HB1	19:LS:40:ALA:HB1	1.94	0.49
50:SE:60:GLU:HA	50:SE:63:MET:HE3	1.94	0.49
71:Sd:79:ILE:HD12	76:St:1449:A:H1'	1.93	0.49
77:a:444:ALA:HB3	77:a:506:LEU:HB2	1.94	0.49
56:SK:171:PRO:HA	56:SK:175:LYS:HE3	1.95	0.49
63:ST:151:ALA:HB2	76:St:1274:A:H5''	1.93	0.49
76:St:787:C:H2'	76:St:788:C:C6	2.47	0.49
19:LS:15:LEU:HD22	19:LS:52:LYS:HG2	1.94	0.49
25:LY:46:PRO:HD2	35:Li:109:PRO:HG3	1.95	0.49
44:Lt:1630:A:H8	44:Lt:2398:A:H2	1.60	0.49
49:SD:116:LYS:HG2	76:St:685:C:H5'	1.95	0.49
61:SQ:98:ARG:HD2	61:SQ:134:PRO:HD3	1.95	0.49
63:ST:57:VAL:HG21	63:ST:66:VAL:HG21	1.94	0.49
77:a:311:GLY:HA3	77:a:316:LYS:H	1.77	0.49
3:LC:178:ARG:HH11	3:LC:187:ARG:HB3	1.77	0.49
20:LT:92:ARG:HG2	20:LT:136:VAL:HG13	1.94	0.49
27:La:90:LYS:HB2	27:La:90:LYS:HE3	1.61	0.49
39:Ln:9:LEU:HB3	39:Ln:214:HIS:HB3	1.95	0.49
44:Lt:1935:G:H2'	44:Lt:1936:G:C8	2.48	0.49
65:SV:84:MET:O	65:SV:85:LEU:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SJ:69:LEU:HD11	55:SJ:72:ALA:HB2	1.95	0.48
58:SM:57:PRO:HD2	58:SM:110:SER:HB3	1.94	0.48
65:SV:99:ILE:H	65:SV:99:ILE:HG13	1.51	0.48
72:Se:111:LYS:HG3	76:St:803:G:H5'	1.94	0.48
77:a:322:ALA:O	77:a:327:ASP:HB2	2.13	0.48
3:LC:297:PRO:HG3	8:LH:144:TYR:HB3	1.94	0.48
22:LV:32:LEU:HD23	22:LV:60:VAL:HG13	1.95	0.48
39:Ln:31:THR:HA	39:Ln:171:ASN:HA	1.95	0.48
44:Lt:436:G:N3	44:Lt:436:G:H2'	2.28	0.48
44:Lt:2445:A:C4	77:a:172:VAL:HG13	2.48	0.48
45:Lu:61:C:H2'	45:Lu:62:A:H8	1.78	0.48
56:SK:29:LEU:HB3	75:Sj:42:PHE:HE2	1.78	0.48
65:SV:90:ASP:HB3	65:SV:93:SER:HB3	1.94	0.48
77:a:715:SER:HB3	77:a:718:HIS:CE1	2.48	0.48
8:LH:198:TRP:O	8:LH:199:PRO:C	2.56	0.48
17:LQ:22:LYS:HD3	17:LQ:22:LYS:HA	1.59	0.48
24:LX:52:TRP:H	24:LX:52:TRP:CD1	2.30	0.48
30:Ld:94:MET:HB2	30:Ld:94:MET:HE2	1.77	0.48
62:SR:34:LEU:HG	62:SR:42:ARG:HG2	1.95	0.48
67:SX:111:ILE:HB	67:SX:114:ILE:HG13	1.95	0.48
75:Sj:44:ASP:C	75:Sj:46:THR:H	2.20	0.48
76:St:176:C:H2'	76:St:177:C:C6	2.49	0.48
77:a:185:ARG:HG3	77:a:403:THR:HG21	1.95	0.48
3:LC:15:VAL:HG21	3:LC:145:ASP:HB2	1.95	0.48
3:LC:138:PRO:HD3	3:LC:162:VAL:O	2.12	0.48
44:Lt:1963:G:N3	44:Lt:1963:G:H2'	2.29	0.48
50:SE:33:ASN:HD21	76:St:213:C:H1'	1.79	0.48
59:SO:110:ARG:HE	59:SO:110:ARG:HB3	1.36	0.48
11:LK:24:ARG:HA	11:LK:24:ARG:HD3	1.66	0.48
38:Ll:65:LYS:HB3	38:Ll:65:LYS:HE3	1.50	0.48
46:SA:93:LEU:HD13	46:SA:93:LEU:HA	1.65	0.48
50:SE:212:ASP:HB2	50:SE:218:PHE:HE1	1.79	0.48
65:SV:101:VAL:HG23	65:SV:102:ASN:H	1.78	0.48
77:a:341:LYS:HE3	77:a:341:LYS:HB3	1.73	0.48
77:a:876:LEU:HD11	77:a:887:VAL:HG22	1.96	0.48
2:LB:216:ASP:HB2	2:LB:339:ARG:HG2	1.94	0.48
7:LG:2:THR:HG21	44:Lt:1176:G:O6	2.13	0.48
46:SA:93:LEU:O	46:SA:97:LYS:HG3	2.13	0.48
46:SA:169:ASN:C	46:SA:171:LYS:H	2.21	0.48
54:SI:116:ALA:HA	54:SI:119:LYS:HG2	1.94	0.48
67:SX:26:THR:O	67:SX:118:VAL:HA	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:a:356:THR:HG21	77:a:358:ASP:OD2	2.10	0.48
77:a:393:PRO:O	77:a:397:GLN:HG2	2.13	0.48
15:LO:101:LEU:HD13	15:LO:101:LEU:HA	1.72	0.48
21:LU:18:LYS:HB2	21:LU:21:ARG:HB2	1.96	0.48
41:Lp:21:HIS:HB3	41:Lp:70:LEU:HB3	1.96	0.48
44:Lt:1421:G:H2'	44:Lt:1422:C:C6	2.49	0.48
51:SF:113:ARG:O	51:SF:114:ILE:C	2.57	0.48
53:SH:118:ARG:HD2	53:SH:118:ARG:HA	1.65	0.48
61:SQ:105:LYS:HD2	61:SQ:105:LYS:HA	1.60	0.48
76:St:471:G:H2'	76:St:472:C:C6	2.49	0.48
2:LB:361:LYS:HD2	44:Lt:2467:G:H4'	1.96	0.48
5:LE:21:G:H2'	5:LE:22:G:C8	2.49	0.48
14:LN:11:ARG:HB3	14:LN:27:ILE:HD12	1.96	0.48
44:Lt:1970:A:HO2'	44:Lt:1971:G:H8	1.59	0.48
50:SE:162:ILE:HG22	50:SE:164:LEU:H	1.79	0.48
53:SH:101:ILE:HG21	53:SH:122:MET:HG2	1.94	0.48
55:SJ:55:ASN:HB2	55:SJ:59:ASN:H	1.79	0.48
69:Sb:86:GLU:HG2	69:Sb:87:PRO:HD2	1.95	0.48
74:Sh:135:LYS:O	74:Sh:136:LEU:C	2.57	0.48
20:LT:57:LEU:HD22	21:LU:142:VAL:HG21	1.94	0.48
63:ST:27:THR:CG2	63:ST:105:ARG:HB2	2.44	0.48
76:St:320:C:H2'	76:St:321:G:H8	1.79	0.48
76:St:935:U:H2'	76:St:936:C:C6	2.48	0.48
3:LC:156:LEU:HD13	3:LC:156:LEU:HA	1.71	0.48
14:LN:42:THR:HG22	14:LN:77:ILE:HD13	1.96	0.48
18:LR:171:ARG:HG3	44:Lt:2187:U:H5'	1.96	0.48
19:LS:126:LYS:HA	44:Lt:558:G:H4'	1.96	0.48
30:Ld:23:LYS:HB3	30:Ld:23:LYS:HE3	1.53	0.48
44:Lt:1947:G:H3'	44:Lt:1948:C:H5'	1.96	0.48
46:SA:94:LYS:HD2	46:SA:206:LEU:HB3	1.96	0.48
57:SL:36:ILE:HB	57:SL:48:PRO:CG	2.42	0.48
59:SO:17:ARG:HA	59:SO:17:ARG:HD3	1.43	0.48
61:SQ:137:THR:HG23	76:St:683:G:C5	2.49	0.48
76:St:1178:C:H4'	76:St:1179:U:H5'	1.94	0.48
8:LH:94:VAL:HG13	8:LH:125:VAL:HG23	1.95	0.47
15:LO:186:PRO:HB3	44:Lt:61:G:H21	1.79	0.47
19:LS:18:GLY:HA3	44:Lt:1506:A:H5''	1.96	0.47
19:LS:133:LYS:HE3	19:LS:133:LYS:HB3	1.55	0.47
44:Lt:186:C:H5	44:Lt:1079:G:H2'	1.79	0.47
44:Lt:1685:C:N4	44:Lt:1729:U:H2'	2.29	0.47
45:Lu:14:A:H3'	45:Lu:15:G:H8	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:SC:44:SER:HB3	48:SC:55:ILE:HG23	1.95	0.47
48:SC:52:ILE:HB	48:SC:90:PHE:HD1	1.79	0.47
50:SE:192:ILE:HD11	50:SE:238:PRO:HD2	1.96	0.47
51:SF:63:MET:HE2	51:SF:63:MET:HB2	1.66	0.47
76:St:1394:C:H2'	76:St:1395:G:C8	2.49	0.47
77:a:22:MET:HE1	77:a:161:LEU:HB2	1.95	0.47
1:LA:77:ILE:HG23	1:LA:169:VAL:HG13	1.96	0.47
2:LB:130:PHE:O	2:LB:134:MET:HG2	2.14	0.47
10:LJ:61:LYS:HB3	10:LJ:61:LYS:HE3	1.65	0.47
43:Ls:94:MET:HB3	43:Ls:119:ARG:HB3	1.95	0.47
43:Ls:96:CYS:SG	43:Ls:99:CYS:N	2.79	0.47
44:Lt:716:G:H22	44:Lt:763:U:H4'	1.80	0.47
44:Lt:1720:A:H2'	44:Lt:1721:A:C8	2.49	0.47
48:SC:32:SER:O	48:SC:36:VAL:HB	2.14	0.47
49:SD:127:ILE:HG13	49:SD:135:LEU:HB2	1.96	0.47
52:SG:171:LYS:HE3	52:SG:171:LYS:HB3	1.50	0.47
54:SI:71:HIS:HB3	54:SI:86:ARG:HA	1.96	0.47
60:SP:25:TRP:CD1	60:SP:25:TRP:H	2.30	0.47
71:Sd:14:ASN:HB2	76:St:819:C:H4'	1.96	0.47
77:a:702:ILE:HD12	77:a:704:GLU:HB3	1.95	0.47
20:LT:148:HIS:HD2	20:LT:150:CYS:H	1.62	0.47
25:LY:138:MET:HB2	25:LY:138:MET:HE3	1.82	0.47
30:Ld:48:MET:HE3	30:Ld:48:MET:HB3	1.67	0.47
36:Lj:47:GLU:HB3	36:Lj:83:LEU:HD11	1.96	0.47
39:Ln:41:TYR:HE2	39:Ln:163:VAL:HA	1.78	0.47
44:Lt:1346:G:H2'	44:Lt:1347:G:C8	2.50	0.47
55:SJ:88:LYS:HB2	55:SJ:88:LYS:HE2	1.47	0.47
63:ST:45:GLY:H	63:ST:81:LEU:H	1.62	0.47
76:St:191:C:H2'	76:St:192:G:C8	2.49	0.47
3:LC:35:PHE:O	3:LC:39:GLN:HG2	2.15	0.47
3:LC:72:LEU:HD22	44:Lt:1126:U:H5'	1.95	0.47
9:LI:89:ALA:HA	9:LI:92:LEU:HD22	1.95	0.47
44:Lt:328:G:H1'	44:Lt:351:G:H21	1.78	0.47
46:SA:43:ILE:HA	46:SA:54:PHE:HA	1.97	0.47
58:SM:131:LYS:HB2	76:St:250:G:H3'	1.95	0.47
65:SV:142:ARG:C	65:SV:144:GLY:H	2.23	0.47
76:St:132:C:H41	76:St:149:C:H42	1.62	0.47
76:St:531:A:H3'	76:St:532:G:H8	1.79	0.47
77:a:178:LEU:HD21	77:a:220:VAL:HG13	1.96	0.47
21:LU:17:ARG:HG2	44:Lt:2124:G:H5''	1.96	0.47
44:Lt:2101:G:H2'	44:Lt:2103:G:H22	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SG:119:LEU:HD21	52:SG:122:ALA:HB2	1.97	0.47
55:SJ:83:ALA:HA	55:SJ:86:ILE:HG13	1.96	0.47
76:St:790:C:H2'	76:St:791:C:C6	2.50	0.47
10:LJ:9:ILE:HD12	10:LJ:9:ILE:HA	1.71	0.47
11:LK:81:GLY:C	11:LK:83:ASP:H	2.23	0.47
13:LM:122:ILE:HG22	13:LM:152:VAL:HG21	1.96	0.47
17:LQ:112:LEU:HB3	17:LQ:150:VAL:CG1	2.44	0.47
25:LY:125:LEU:HD22	25:LY:134:VAL:HG21	1.97	0.47
44:Lt:61:G:H22	44:Lt:78:U:H4'	1.79	0.47
54:SI:26:LYS:O	54:SI:29:LEU:HB3	2.14	0.47
60:SP:91:MET:HB3	60:SP:122:ILE:HG12	1.95	0.47
61:SQ:68:GLU:N	61:SQ:69:PRO:HD2	2.30	0.47
62:SR:30:ILE:H	62:SR:30:ILE:HG13	1.32	0.47
69:Sb:27:LEU:H	69:Sb:27:LEU:HG	1.59	0.47
76:St:1016:C:H41	78:y:38:A:H4'	1.79	0.47
3:LC:47:PRO:HB3	3:LC:97:VAL:HG12	1.97	0.47
7:LG:16:LYS:HA	7:LG:16:LYS:HD2	1.65	0.47
19:LS:30:LYS:HA	19:LS:30:LYS:HD3	1.70	0.47
27:La:27:VAL:HG21	27:La:93:ILE:HB	1.96	0.47
28:Lb:37:GLY:O	28:Lb:42:ARG:HA	2.14	0.47
32:Lf:26:GLN:HG2	32:Lf:29:ARG:HD3	1.96	0.47
35:Li:84:ALA:O	35:Li:88:THR:HG23	2.14	0.47
37:Lk:3:LYS:HG3	44:Lt:638:A:H4'	1.97	0.47
37:Lk:58:THR:HG22	44:Lt:23:C:H5''	1.96	0.47
38:Ll:9:ASN:OD1	38:Ll:10:LEU:N	2.48	0.47
39:Ln:45:LYS:HE3	39:Ln:45:LYS:HB2	1.50	0.47
39:Ln:167:TRP:HH2	39:Ln:190:LEU:HD13	1.79	0.47
44:Lt:65:A:N6	44:Lt:75:G:H1'	2.30	0.47
52:SG:63:ASP:HA	52:SG:112:LEU:HA	1.96	0.47
52:SG:161:LYS:CG	52:SG:164:MET:HB2	2.44	0.47
60:SP:39:LYS:HB2	60:SP:39:LYS:HE2	1.53	0.47
61:SQ:60:MET:HB2	61:SQ:60:MET:HE2	1.52	0.47
68:SY:55:ASN:HD22	68:SY:55:ASN:HA	1.54	0.47
76:St:598:C:H2'	76:St:599:G:C8	2.50	0.47
76:St:1263:G:H2'	76:St:1264:A:C8	2.49	0.47
12:LL:32:LYS:HB3	12:LL:123:TYR:OH	2.15	0.47
19:LS:48:LYS:HA	19:LS:48:LYS:HD3	1.59	0.47
20:LT:38:ARG:HD2	20:LT:38:ARG:HA	1.64	0.47
43:Ls:94:MET:HG3	43:Ls:105:LEU:HA	1.95	0.47
44:Lt:25:A:H1'	44:Lt:281:G:H1'	1.97	0.47
49:SD:109:LYS:HA	49:SD:109:LYS:HD3	1.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:SE:61:THR:HG22	50:SE:65:LEU:HD12	1.96	0.47
68:SY:66:ILE:HD12	68:SY:66:ILE:H	1.80	0.47
76:St:710:C:H2'	76:St:711:G:C8	2.50	0.47
77:a:275:ARG:HG2	77:a:285:LEU:HD11	1.97	0.47
3:LC:309:PRO:HB2	8:LH:40:VAL:HG22	1.97	0.47
6:LF:140:ASP:HB3	6:LF:180:ASN:CG	2.40	0.47
9:LI:57:VAL:HG13	9:LI:141:LEU:HD12	1.97	0.47
14:LN:7:VAL:HG11	14:LN:52:LEU:HD21	1.96	0.47
16:LP:58:ARG:HA	16:LP:67:PRO:HD2	1.96	0.47
22:LV:86:PHE:O	22:LV:89:GLN:HG2	2.15	0.47
22:LV:98:LEU:HD22	22:LV:98:LEU:HA	1.74	0.47
26:LZ:130:LEU:HD13	26:LZ:130:LEU:HA	1.77	0.47
44:Lt:1860:A:H1'	44:Lt:2291:U:H5''	1.96	0.47
50:SE:104:ASP:HB3	50:SE:110:THR:HB	1.97	0.47
57:SL:10:LYS:HA	57:SL:10:LYS:HD3	1.47	0.47
58:SM:127:ARG:HD2	76:St:248:C:H4'	1.97	0.47
63:ST:129:ARG:O	63:ST:130:GLN:HB2	2.15	0.47
76:St:445:C:H4'	76:St:446:C:H5''	1.97	0.47
11:LK:9:TYR:OH	11:LK:99:ILE:HG12	2.15	0.47
17:LQ:106:LYS:HB2	17:LQ:106:LYS:HE2	1.61	0.47
25:LY:51:LYS:HB2	25:LY:51:LYS:HE2	1.72	0.47
28:Lb:10:LYS:HE2	28:Lb:10:LYS:HB3	1.66	0.47
32:Lf:83:THR:HG23	32:Lf:86:GLU:H	1.80	0.47
44:Lt:1626:U:H5''	44:Lt:1627:A:H5''	1.97	0.47
46:SA:172:THR:HB	46:SA:175:SER:HB3	1.96	0.47
2:LB:205:ILE:HD11	2:LB:320:ASP:HB3	1.96	0.46
3:LC:159:ILE:HG23	3:LC:164:VAL:HG23	1.96	0.46
9:LI:134:ILE:HG12	9:LI:147:LEU:HD23	1.96	0.46
10:LJ:15:VAL:HG21	10:LJ:77:PHE:CD1	2.50	0.46
11:LK:22:PHE:CZ	44:Lt:761:A:H2'	2.50	0.46
19:LS:70:LYS:HE3	19:LS:70:LYS:HB3	1.69	0.46
20:LT:87:MET:HG3	44:Lt:913:G:H4'	1.96	0.46
21:LU:100:ASP:HB3	21:LU:103:LYS:HB2	1.96	0.46
32:Lf:21:LYS:HE3	32:Lf:21:LYS:HB3	1.59	0.46
39:Ln:48:ARG:H	39:Ln:48:ARG:HG2	1.49	0.46
43:Ls:118:LEU:HD23	43:Ls:118:LEU:HA	1.74	0.46
52:SG:146:LYS:HB2	52:SG:146:LYS:HE3	1.68	0.46
72:Se:65:LEU:HD13	72:Se:65:LEU:HA	1.64	0.46
75:Sj:61:ILE:HG23	75:Sj:65:LEU:HD13	1.97	0.46
9:LI:66:ARG:HD2	9:LI:66:ARG:HA	1.50	0.46
20:LT:107:MET:HE3	20:LT:107:MET:HB3	1.72	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:LV:46:ASN:HB3	22:LV:47:ASN:H	1.35	0.46
33:Lg:19:ARG:HE	33:Lg:19:ARG:HB2	1.40	0.46
38:Ll:20:LYS:HB3	38:Ll:68:VAL:HB	1.97	0.46
39:Ln:76:ARG:HB3	39:Ln:144:LEU:HD21	1.97	0.46
44:Lt:398:C:H2'	44:Lt:399:G:C8	2.49	0.46
46:SA:22:LYS:HA	46:SA:22:LYS:HD3	1.38	0.46
50:SE:66:GLN:HB3	76:St:366:G:N3	2.30	0.46
53:SH:23:VAL:HG13	53:SH:84:LEU:HD11	1.96	0.46
53:SH:58:LYS:H	53:SH:58:LYS:HG3	1.55	0.46
54:SI:51:LYS:HG3	54:SI:67:LEU:HD12	1.96	0.46
55:SJ:111:MET:HE2	55:SJ:111:MET:HB3	1.63	0.46
70:Sc:14:LYS:HB2	70:Sc:14:LYS:HE3	1.39	0.46
77:a:787:VAL:HG22	77:a:854:PHE:HA	1.97	0.46
1:LA:58:LEU:HA	1:LA:58:LEU:HD12	1.66	0.46
2:LB:174:LYS:HD2	44:Lt:2626:C:H5'	1.97	0.46
23:LW:36:LYS:HB2	23:LW:69:ASP:HB2	1.96	0.46
26:LZ:71:VAL:HG22	26:LZ:78:ILE:HG22	1.95	0.46
28:Lb:120:GLN:HA	28:Lb:141:VAL:HG22	1.96	0.46
36:Lj:70:LEU:HD23	36:Lj:70:LEU:HA	1.74	0.46
50:SE:139:LEU:HD23	50:SE:150:PRO:HB3	1.96	0.46
53:SH:54:VAL:HG21	53:SH:172:THR:HG22	1.97	0.46
62:SR:125:ILE:HD12	62:SR:125:ILE:HA	1.68	0.46
75:Sj:37:LEU:HD22	75:Sj:37:LEU:HA	1.70	0.46
77:a:593:LEU:HD13	77:a:593:LEU:HA	1.73	0.46
77:a:821:LEU:H	77:a:821:LEU:HG	1.39	0.46
11:LK:145:LYS:HE2	11:LK:145:LYS:HB2	1.55	0.46
15:LO:154:PRO:HB2	44:Lt:57:G:H5''	1.96	0.46
34:Lh:43:PRO:HB2	34:Lh:52:ILE:HG12	1.97	0.46
39:Ln:129:THR:HA	39:Ln:133:ARG:H	1.80	0.46
44:Lt:760:A:H2'	44:Lt:761:A:C8	2.49	0.46
46:SA:16:LYS:HD2	46:SA:16:LYS:HA	1.64	0.46
47:SB:95:HIS:HB3	47:SB:107:TYR:HE1	1.81	0.46
77:a:230:LYS:O	77:a:244:ASN:HB3	2.15	0.46
1:LA:102:LEU:HD12	1:LA:107:ILE:HG12	1.98	0.46
6:LF:268:LYS:HA	6:LF:268:LYS:HD3	1.67	0.46
10:LJ:89:ARG:HE	10:LJ:139:GLU:HG3	1.81	0.46
26:LZ:2:LYS:HD2	26:LZ:7:VAL:HB	1.97	0.46
31:Le:71:ARG:HD2	31:Le:84:ILE:HD11	1.98	0.46
44:Lt:2555:C:H2'	44:Lt:2556:G:O4'	2.15	0.46
48:SC:45:LEU:HD12	48:SC:45:LEU:HA	1.79	0.46
48:SC:71:ARG:HA	48:SC:74:LYS:CG	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:SC:78:LEU:HD11	57:SL:76:TYR:HB3	1.97	0.46
50:SE:253:LEU:HD13	50:SE:253:LEU:HA	1.76	0.46
51:SF:131:ARG:HE	51:SF:135:ILE:HD11	1.80	0.46
60:SP:7:LYS:HE2	60:SP:7:LYS:HB3	1.67	0.46
63:ST:20:ARG:HE	63:ST:20:ARG:HB2	1.44	0.46
75:Sj:63:GLN:HE21	75:Sj:63:GLN:HB2	1.50	0.46
75:Sj:64:LYS:HB2	75:Sj:64:LYS:HE2	1.47	0.46
77:a:297:PHE:HA	77:a:319:ARG:HA	1.98	0.46
3:LC:210:ASN:HB2	44:Lt:178:A:OP2	2.15	0.46
13:LM:102:ARG:HH12	44:Lt:76:A:H8	1.64	0.46
14:LN:30:ILE:HG21	20:LT:146:PHE:HE2	1.80	0.46
14:LN:52:LEU:HD13	14:LN:52:LEU:HA	1.70	0.46
23:LW:64:ILE:HG12	23:LW:81:ALA:HB2	1.97	0.46
32:Lf:31:VAL:HB	44:Lt:403:C:H5''	1.98	0.46
39:Ln:19:ARG:H	39:Ln:19:ARG:HG3	1.60	0.46
42:Lq:7:LYS:HB3	42:Lq:7:LYS:HE3	1.68	0.46
74:Sh:113:ARG:HE	74:Sh:113:ARG:HB3	1.18	0.46
77:a:683:LYS:HB3	77:a:683:LYS:HE3	1.48	0.46
17:LQ:152:PRO:O	17:LQ:153:LYS:C	2.57	0.46
18:LR:51:ARG:HD3	18:LR:54:LEU:HD22	1.97	0.46
26:LZ:83:ILE:HG22	26:LZ:97:TYR:HB3	1.97	0.46
42:Lq:36:LYS:HE2	42:Lq:36:LYS:HB2	1.71	0.46
44:Lt:1912:A:H3'	44:Lt:1913:G:H8	1.80	0.46
47:SB:135:ARG:HG2	47:SB:145:PRO:HB2	1.96	0.46
59:SO:85:VAL:HG13	59:SO:130:LEU:HD21	1.97	0.46
8:LH:78:VAL:HG21	8:LH:183:ILE:O	2.16	0.46
12:LL:109:HIS:HB2	12:LL:114:ILE:HD12	1.97	0.46
14:LN:68:PRO:O	14:LN:72:GLN:HB3	2.16	0.46
26:LZ:78:ILE:HG13	26:LZ:99:ILE:HG22	1.98	0.46
27:La:15:LEU:HB3	34:Lh:84:ARG:HG2	1.98	0.46
28:Lb:34:LYS:O	44:Lt:93:A:H5''	2.16	0.46
46:SA:94:LYS:HD3	46:SA:97:LYS:HD2	1.98	0.46
47:SB:50:LYS:HB2	47:SB:50:LYS:HE3	1.61	0.46
54:SI:10:LYS:HG3	76:St:251:C:H5''	1.98	0.46
55:SJ:7:LEU:HD13	55:SJ:34:ILE:HG12	1.98	0.46
76:St:1028:C:H1'	76:St:1029:A:H5'	1.97	0.46
12:LL:16:LYS:HE2	12:LL:130:VAL:HG21	1.97	0.46
16:LP:108:CYS:HA	44:Lt:2603:G:H4'	1.98	0.46
19:LS:181:ARG:H	19:LS:181:ARG:HG3	1.67	0.46
38:Ll:33:GLN:HE21	38:Ll:33:GLN:HB2	1.54	0.46
39:Ln:149:LEU:HD13	39:Ln:149:LEU:HA	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:SA:19:ASP:CG	46:SA:23:MET:HB2	2.41	0.46
53:SH:145:LEU:HD11	53:SH:155:GLN:HB2	1.98	0.46
76:St:922:G:H5'	76:St:934:C:H42	1.80	0.46
1:LA:75:LEU:HD23	1:LA:75:LEU:HA	1.79	0.46
14:LN:67:LYS:HB2	14:LN:67:LYS:HE2	1.76	0.46
21:LU:118:LEU:HD12	21:LU:118:LEU:HA	1.75	0.46
22:LV:13:GLN:HB3	22:LV:71:GLY:C	2.41	0.46
27:La:47:LEU:O	27:La:48:PRO:C	2.59	0.46
33:Lg:78:ARG:HH22	44:Lt:875:G:H5''	1.81	0.46
39:Ln:123:TYR:HB3	39:Ln:124:ALA:H	1.47	0.46
39:Ln:130:LYS:HB2	39:Ln:130:LYS:HE2	1.50	0.46
70:Sc:86:LYS:HD2	70:Sc:86:LYS:HA	1.45	0.46
3:LC:93:HIS:HE1	44:Lt:409:G:H5'	1.81	0.45
5:LE:86:C:H2'	5:LE:87:G:C8	2.51	0.45
19:LS:114:LYS:HB3	19:LS:114:LYS:HE3	1.38	0.45
22:LV:49:LYS:HA	22:LV:52:VAL:CG1	2.45	0.45
33:Lg:50:ILE:HG22	33:Lg:94:VAL:HB	1.98	0.45
47:SB:36:LEU:HD23	47:SB:42:ILE:HG12	1.97	0.45
48:SC:71:ARG:HA	48:SC:74:LYS:HG3	1.97	0.45
48:SC:191:LYS:HB3	48:SC:191:LYS:HE3	1.37	0.45
63:ST:44:LYS:HE3	63:ST:44:LYS:HB3	1.73	0.45
66:SW:60:ARG:O	66:SW:64:ILE:HG12	2.16	0.45
76:St:704:C:H2'	76:St:705:A:C8	2.52	0.45
3:LC:7:VAL:HG11	3:LC:241:LYS:HG3	1.98	0.45
3:LC:178:ARG:HE	3:LC:178:ARG:HB2	1.49	0.45
13:LM:141:ASN:HD22	13:LM:141:ASN:HA	1.57	0.45
20:LT:44:LYS:HB3	20:LT:44:LYS:HE3	1.51	0.45
24:LX:48:ARG:HH21	24:LX:59:LEU:HG	1.81	0.45
25:LY:116:LEU:HD13	25:LY:116:LEU:HA	1.72	0.45
35:Li:56:LEU:HD23	35:Li:56:LEU:HA	1.80	0.45
46:SA:203:LYS:HD3	46:SA:205:ASP:HB3	1.97	0.45
49:SD:127:ILE:HG12	49:SD:137:VAL:HG22	1.97	0.45
49:SD:178:LYS:HB3	49:SD:178:LYS:HE3	1.74	0.45
59:SO:107:ARG:HG3	59:SO:112:VAL:HG12	1.98	0.45
61:SQ:134:PRO:HB3	76:St:641:A:H5''	1.97	0.45
66:SW:100:ILE:H	66:SW:100:ILE:HG12	1.46	0.45
72:Se:63:LYS:HE2	72:Se:63:LYS:HB2	1.40	0.45
76:St:200:G:H1	76:St:205:G:H22	1.64	0.45
8:LH:90:VAL:HB	8:LH:95:ARG:HG3	1.97	0.45
10:LJ:133:SER:HB2	10:LJ:136:VAL:H	1.80	0.45
23:LW:115:LYS:HB2	23:LW:115:LYS:HE3	1.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:Ll:5:ILE:HB	38:Ll:47:TYR:HB3	1.98	0.45
39:Ln:195:LYS:HA	39:Ln:195:LYS:HD3	1.38	0.45
51:SF:139:ASN:HB3	51:SF:175:ALA:HA	1.99	0.45
54:Sl:5:HIS:CE1	54:Sl:28:ASN:HA	2.52	0.45
55:SJ:60:ARG:HH21	72:Se:67:GLN:HE21	1.64	0.45
60:SP:100:LYS:HB2	60:SP:100:LYS:HE2	1.46	0.45
74:Sh:120:CYS:HB2	74:Sh:123:CYS:HB2	1.27	0.45
74:Sh:136:LEU:HB3	76:St:1124:G:H21	1.80	0.45
76:St:693:C:H2'	76:St:694:A:C8	2.50	0.45
77:a:289:MET:HE3	77:a:289:MET:HB3	1.62	0.45
77:a:298:LEU:HB2	77:a:305:TRP:CE3	2.51	0.45
77:a:359:GLU:HA	77:a:362:MET:HB2	1.97	0.45
1:LA:225:VAL:HG11	1:LA:234:LYS:HA	1.99	0.45
2:LB:171:LYS:HE3	2:LB:171:LYS:HB3	1.49	0.45
6:LF:104:LEU:HD13	6:LF:253:ILE:HG12	1.99	0.45
6:LF:278:LYS:HA	6:LF:278:LYS:HD3	1.72	0.45
9:LI:139:ASP:HB3	9:LI:140:PRO:HD3	1.99	0.45
10:LJ:60:GLY:HA3	44:Lt:910:U:H5''	1.99	0.45
14:LN:60:GLN:HB3	14:LN:82:ALA:HB1	1.99	0.45
19:LS:134:ASN:HD21	19:LS:136:ARG:HB3	1.81	0.45
23:LW:58:VAL:CG1	23:LW:124:ALA:HB3	2.40	0.45
38:Ll:21:LYS:HE2	38:Ll:21:LYS:HB3	1.57	0.45
46:SA:62:LYS:HA	46:SA:62:LYS:HD3	1.56	0.45
47:SB:101:ARG:HA	47:SB:101:ARG:HD3	1.82	0.45
53:SH:75:LYS:HD2	53:SH:75:LYS:HA	1.56	0.45
54:Sl:10:LYS:HB3	54:Sl:10:LYS:HE3	1.60	0.45
59:SO:107:ARG:HB3	59:SO:110:ARG:HB2	1.98	0.45
61:SQ:105:LYS:HB3	61:SQ:106:ARG:H	1.52	0.45
63:ST:45:GLY:HA2	63:ST:78:PHE:O	2.17	0.45
74:Sh:117:LEU:H	74:Sh:117:LEU:HG	1.53	0.45
76:St:707:G:H2'	76:St:708:A:C8	2.51	0.45
1:LA:96:LEU:HB3	42:Lq:87:ARG:HG3	1.99	0.45
10:LJ:8:THR:HG23	10:LJ:52:SER:HB2	1.98	0.45
11:LK:100:ASN:HA	11:LK:120:GLY:HA2	1.98	0.45
17:LQ:35:ILE:HD12	17:LQ:35:ILE:HA	1.80	0.45
22:LV:30:LEU:HG	22:LV:95:PHE:HE2	1.81	0.45
44:Lt:250:A:O3'	44:Lt:251:G:H4'	2.17	0.45
47:SB:128:LEU:HD23	47:SB:128:LEU:HA	1.77	0.45
53:SH:10:ARG:HA	53:SH:10:ARG:HD3	1.39	0.45
53:SH:171:LYS:HD3	53:SH:171:LYS:HA	1.58	0.45
56:SK:25:LEU:HD13	76:St:471:G:H5''	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SL:73:ARG:HD2	57:SL:73:ARG:HA	1.61	0.45
65:SV:21:ILE:HG22	65:SV:30:ALA:HB1	1.97	0.45
65:SV:24:LYS:HD3	70:Sc:18:PRO:HD3	1.98	0.45
76:St:1022:C:H2'	76:St:1023:G:H8	1.81	0.45
76:St:1033:C:H2'	76:St:1034:G:H8	1.82	0.45
77:a:19:ILE:HA	77:a:134:LEU:HB3	1.99	0.45
77:a:261:SER:HB2	77:a:266:TRP:CD1	2.52	0.45
77:a:652:ALA:HB1	77:a:657:GLU:HB2	1.98	0.45
2:LB:3:HIS:HD2	2:LB:5:LYS:HA	1.82	0.45
9:LI:80:SER:HB2	9:LI:170:LEU:O	2.17	0.45
12:LL:64:LYS:H	12:LL:64:LYS:HG3	1.46	0.45
17:LQ:3:LYS:HD2	17:LQ:3:LYS:HA	1.44	0.45
19:LS:88:ARG:HG2	44:Lt:1496:A:H5'	1.99	0.45
26:LZ:67:LYS:HB2	26:LZ:67:LYS:HE2	1.51	0.45
32:Lf:95:LYS:HD2	32:Lf:95:LYS:HA	1.55	0.45
34:Lh:84:ARG:HE	34:Lh:84:ARG:HB3	1.32	0.45
42:Lq:62:LYS:HB2	42:Lq:62:LYS:HE2	1.35	0.45
44:Lt:2430:C:H2'	44:Lt:2431:G:C8	2.52	0.45
48:SC:53:CYS:HA	48:SC:91:ASN:O	2.16	0.45
52:SG:33:ILE:HA	52:SG:36:LEU:HD12	1.98	0.45
59:SO:32:LEU:HD12	59:SO:32:LEU:HA	1.79	0.45
59:SO:80:LYS:HB3	59:SO:80:LYS:HE2	1.50	0.45
76:St:140:A:H1'	76:St:329:A:C8	2.51	0.45
76:St:200:G:H5''	76:St:201:C:C5	2.52	0.45
6:LF:202:ARG:O	6:LF:206:MET:HB2	2.17	0.45
44:Lt:740:U:H2'	44:Lt:741:G:C8	2.51	0.45
44:Lt:1362:A:N6	44:Lt:1413:G:H2'	2.32	0.45
44:Lt:2188:C:H42	45:Lu:75:A:N6	2.13	0.45
44:Lt:2458:C:H2'	44:Lt:2459:C:C6	2.51	0.45
48:SC:38:ALA:HB1	48:SC:64:VAL:HG22	1.98	0.45
50:SE:241:LYS:HB3	50:SE:241:LYS:HE2	1.70	0.45
61:SQ:143:LYS:HB2	61:SQ:143:LYS:HE2	1.45	0.45
76:St:601:C:H2'	76:St:602:G:O4'	2.17	0.45
77:a:280:LYS:HA	77:a:280:LYS:HD3	1.69	0.45
9:LI:64:ILE:HA	9:LI:64:ILE:HD12	1.59	0.45
9:LI:164:LYS:HD2	9:LI:175:LYS:HG3	1.99	0.45
12:LL:32:LYS:HB2	12:LL:32:LYS:HE2	1.57	0.45
21:LU:116:ARG:HD3	21:LU:116:ARG:HA	1.69	0.45
34:Lh:63:LEU:HD12	34:Lh:63:LEU:HA	1.79	0.45
44:Lt:538:U:H2'	44:Lt:539:G:C8	2.52	0.45
50:SE:251:ARG:HB2	56:SK:72:PHE:HE2	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SL:4:ILE:HG21	57:SL:56:ILE:HD11	1.98	0.45
57:SL:20:ALA:HB2	57:SL:99:PRO:HB3	1.99	0.45
59:SO:101:LEU:HD23	59:SO:123:ILE:HD11	1.98	0.45
60:SP:42:LYS:HA	60:SP:42:LYS:HD3	1.72	0.45
64:SU:39:ARG:HB3	64:SU:40:ASN:H	1.64	0.45
66:SW:137:LEU:HD12	66:SW:137:LEU:HA	1.76	0.45
77:a:783:PRO:HD2	77:a:860:ILE:HB	1.98	0.45
3:LC:123:ASN:HB3	3:LC:126:LEU:HB2	1.98	0.45
11:LK:76:ILE:H	11:LK:76:ILE:HG12	1.65	0.45
16:LP:45:ARG:HE	16:LP:45:ARG:HB2	1.33	0.45
16:LP:118:PRO:HG2	20:LT:165:GLN:OE1	2.17	0.45
22:LV:55:LYS:HD2	22:LV:72:TYR:HB2	1.99	0.45
26:LZ:47:MET:SD	26:LZ:48:PRO:HD2	2.57	0.45
34:Lh:56:PRO:HG2	34:Lh:63:LEU:HD11	1.99	0.45
38:Ll:5:ILE:HD13	38:Ll:5:ILE:HA	1.73	0.45
44:Lt:2105:C:H2'	44:Lt:2106:C:H6	1.82	0.45
65:SV:44:VAL:C	65:SV:46:LEU:H	2.25	0.45
71:Sd:24:GLN:HG3	71:Sd:71:VAL:HG12	1.98	0.45
71:Sd:30:VAL:HG22	71:Sd:35:VAL:HG12	1.98	0.45
76:St:1307:C:H2'	76:St:1308:C:C6	2.52	0.45
77:a:32:LYS:HE3	77:a:32:LYS:HB3	1.52	0.45
77:a:148:SER:HB3	77:a:566:PRO:CG	2.47	0.45
5:LE:91:A:HO2'	5:LE:92:C:H6	1.65	0.45
13:LM:118:LYS:HA	13:LM:118:LYS:HD3	1.79	0.45
27:La:33:ASN:HB2	27:La:35:ARG:HG2	1.99	0.45
39:Ln:79:LYS:HD2	39:Ln:79:LYS:HA	1.82	0.45
39:Ln:147:LYS:HA	39:Ln:150:GLU:HG2	1.98	0.45
41:Lp:84:LYS:HB2	41:Lp:84:LYS:HE2	1.32	0.45
44:Lt:117:G:H1'	44:Lt:119:A:N6	2.31	0.45
44:Lt:1446:C:H2'	44:Lt:1447:G:H8	1.82	0.45
46:SA:139:ILE:HG23	46:SA:149:THR:HG21	1.98	0.45
49:SD:161:ILE:HA	49:SD:164:MET:HE3	1.99	0.45
51:SF:128:SER:HB2	73:Sg:45:VAL:HG13	1.99	0.45
56:SK:91:LYS:H	56:SK:91:LYS:HG2	1.35	0.45
60:SP:113:PHE:CE2	60:SP:117:LEU:HD11	2.52	0.45
60:SP:118:VAL:HA	60:SP:121:ARG:HE	1.82	0.45
69:Sb:19:ARG:HB3	69:Sb:76:TYR:CD1	2.52	0.45
76:St:673:C:H2'	76:St:674:G:C8	2.52	0.45
76:St:1370:C:H2'	76:St:1371:G:O4'	2.17	0.45
8:LH:100:LEU:HD22	44:Lt:812:G:H1'	1.98	0.44
12:LL:49:LYS:HA	12:LL:64:LYS:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LN:131:LYS:HA	14:LN:131:LYS:HD3	1.54	0.44
22:LV:48:ARG:HH22	44:Lt:2657:U:H4'	1.82	0.44
32:Lf:111:LYS:HB2	32:Lf:111:LYS:HE2	1.81	0.44
37:Lk:27:PHE:HA	37:Lk:34:CYS:HA	2.00	0.44
37:Lk:69:LYS:HB2	37:Lk:69:LYS:HE3	1.74	0.44
39:Ln:24:LYS:HB3	39:Ln:29:LEU:HA	1.99	0.44
39:Ln:87:ILE:H	39:Ln:87:ILE:HG13	1.40	0.44
44:Lt:328:G:H1'	44:Lt:351:G:N2	2.32	0.44
44:Lt:700:U:H2'	44:Lt:701:U:C6	2.53	0.44
46:SA:196:ARG:HE	68:SY:51:LYS:H	1.65	0.44
50:SE:100:ARG:HE	50:SE:100:ARG:HB2	1.53	0.44
62:SR:100:ARG:HG2	76:St:927:A:C5	2.51	0.44
63:ST:18:ARG:H	63:ST:18:ARG:HG3	1.57	0.44
64:SU:9:ILE:HG21	64:SU:52:LYS:HB3	1.99	0.44
66:SW:82:LEU:HD13	76:St:1215:G:H4'	1.99	0.44
71:Sd:88:SER:HA	76:St:1316:U:H5'	1.99	0.44
72:Se:52:ASP:HB3	72:Se:55:GLU:HB2	1.99	0.44
76:St:1015:G:H4'	76:St:1016:C:H5''	1.98	0.44
8:LH:170:LYS:H	8:LH:170:LYS:HG2	1.41	0.44
19:LS:154:LYS:HA	19:LS:154:LYS:HD2	1.33	0.44
21:LU:21:ARG:HE	21:LU:21:ARG:HB3	1.55	0.44
44:Lt:2084:C:H2'	44:Lt:2085:G:C8	2.52	0.44
46:SA:174:MET:HE2	46:SA:174:MET:HB2	1.56	0.44
46:SA:190:LEU:O	68:SY:52:MET:HA	2.18	0.44
50:SE:44:LEU:HD13	50:SE:84:VAL:HG21	1.98	0.44
50:SE:260:LYS:HB3	50:SE:260:LYS:HE3	1.53	0.44
54:SI:169:LYS:HE3	54:SI:169:LYS:HB2	1.40	0.44
71:Sd:83:ILE:H	71:Sd:83:ILE:HG12	1.65	0.44
76:St:436:A:H1'	76:St:470:G:H1'	1.99	0.44
6:LF:41:LYS:HD2	6:LF:41:LYS:HA	1.61	0.44
14:LN:31:LEU:N	14:LN:31:LEU:HD23	2.32	0.44
15:LO:151:ILE:HD13	15:LO:151:ILE:HA	1.70	0.44
20:LT:64:GLU:HB2	20:LT:95:THR:HG22	1.99	0.44
23:LW:21:LEU:HD11	23:LW:103:ASN:HB3	2.00	0.44
25:LY:118:LEU:H	25:LY:118:LEU:HG	1.57	0.44
39:Ln:9:LEU:HD12	39:Ln:214:HIS:HD2	1.82	0.44
39:Ln:65:LEU:HB2	39:Ln:111:LEU:HB2	2.00	0.44
44:Lt:917:G:H1	44:Lt:988:U:H3	1.65	0.44
44:Lt:2217:G:H2'	44:Lt:2218:U:C6	2.51	0.44
52:SG:139:LEU:HB3	76:St:63:C:C4	2.52	0.44
58:SM:16:ILE:HG21	58:SM:30:LEU:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SV:12:ASP:HB2	65:SV:13:LEU:H	1.63	0.44
77:a:478:ILE:H	77:a:478:ILE:HG13	1.51	0.44
77:a:787:VAL:HG13	77:a:853:VAL:HG12	1.98	0.44
1:LA:111:THR:HG23	42:Lq:83:ILE:HD11	2.00	0.44
2:LB:250:ALA:HB1	44:Lt:2369:G:N3	2.33	0.44
3:LC:91:MET:HE2	3:LC:91:MET:HB3	1.80	0.44
3:LC:92:ALA:HB1	44:Lt:520:C:H5''	1.99	0.44
3:LC:200:ASN:HB2	3:LC:219:VAL:CG2	2.47	0.44
6:LF:275:LEU:HB3	6:LF:279:GLU:HB2	2.00	0.44
11:LK:74:LYS:HE3	11:LK:74:LYS:HB3	1.68	0.44
11:LK:119:TRP:HZ3	44:Lt:836:G:H5''	1.82	0.44
21:LU:154:LYS:HB3	21:LU:154:LYS:HE2	1.48	0.44
36:Lj:55:ARG:HG2	36:Lj:56:MET:HG3	2.00	0.44
39:Ln:187:LEU:HD23	39:Ln:187:LEU:HA	1.72	0.44
44:Lt:1109:G:H2'	44:Lt:1110:G:C8	2.53	0.44
48:SC:77:TYR:CD2	57:SL:19:ASN:HA	2.52	0.44
49:SD:151:ARG:HE	49:SD:151:ARG:HB3	1.49	0.44
49:SD:231:MET:HB2	49:SD:231:MET:HE2	1.38	0.44
52:SG:180:LYS:HD2	52:SG:180:LYS:HA	1.74	0.44
58:SM:132:THR:HG22	76:St:238:G:OP1	2.18	0.44
63:ST:58:ARG:HD2	63:ST:58:ARG:HA	1.65	0.44
65:SV:40:ARG:HB3	65:SV:98:HIS:CD2	2.53	0.44
66:SW:58:VAL:HG22	66:SW:75:LEU:HD11	1.99	0.44
72:Se:48:LEU:C	72:Se:50:TYR:H	2.26	0.44
77:a:211:LEU:HD12	77:a:211:LEU:HA	1.85	0.44
12:LL:15:GLU:HG3	12:LL:72:ARG:HH21	1.82	0.44
31:Le:91:PHE:HA	31:Le:94:LEU:HD12	2.00	0.44
34:Lh:65:ARG:HE	44:Lt:1311:G:H5'	1.83	0.44
39:Ln:35:GLN:HG2	39:Ln:166:ASN:CG	2.42	0.44
44:Lt:176:C:H4'	44:Lt:178:A:N7	2.32	0.44
44:Lt:596:C:H42	44:Lt:2404:A:H5''	1.82	0.44
44:Lt:2055:U:H2'	44:Lt:2056:G:H8	1.83	0.44
58:SM:127:ARG:O	58:SM:128:PRO:C	2.59	0.44
65:SV:47:LYS:HA	65:SV:51:ILE:O	2.17	0.44
69:Sb:23:VAL:HG22	69:Sb:72:PHE:HD2	1.83	0.44
75:Sj:54:LEU:HD13	75:Sj:58:ASN:HD22	1.83	0.44
6:LF:38:ILE:HD13	21:LU:30:TYR:HB3	2.00	0.44
6:LF:179:LEU:HD22	6:LF:179:LEU:HA	1.84	0.44
11:LK:178:LYS:HE3	11:LK:178:LYS:HB2	1.60	0.44
13:LM:82:LYS:HB3	13:LM:82:LYS:HE3	1.82	0.44
15:LO:28:TRP:HA	15:LO:31:ARG:HH21	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LP:34:ARG:HA	16:LP:104:GLY:H	1.82	0.44
25:LY:61:LEU:HD22	25:LY:89:ALA:HB2	1.99	0.44
33:Lg:14:PHE:CE1	33:Lg:29:ALA:HB1	2.53	0.44
39:Ln:65:LEU:HA	39:Ln:109:VAL:O	2.17	0.44
39:Ln:90:LEU:O	39:Ln:93:PHE:HB2	2.18	0.44
43:Ls:113:CYS:SG	43:Ls:116:THR:HB	2.58	0.44
49:SD:187:LYS:HA	49:SD:187:LYS:HD3	1.74	0.44
50:SE:239:THR:HG21	76:St:559:G:H5'	1.99	0.44
53:SH:140:ILE:HG13	53:SH:159:PRO:HD3	1.99	0.44
70:Sc:62:GLN:HA	70:Sc:65:LYS:HB3	1.99	0.44
2:LB:41:ILE:HD11	2:LB:191:LYS:HA	1.99	0.44
6:LF:289:LEU:HA	6:LF:289:LEU:HD22	1.65	0.44
8:LH:233:ARG:HE	8:LH:233:ARG:HB2	1.41	0.44
12:LL:45:PRO:HA	12:LL:69:VAL:HG13	1.99	0.44
14:LN:117:ARG:HH12	44:Lt:2593:G:H21	1.65	0.44
16:LP:181:LYS:HA	16:LP:181:LYS:HD2	1.51	0.44
17:LQ:82:TRP:O	44:Lt:1840:C:H5''	2.18	0.44
45:Lu:42:G:H2'	45:Lu:43:A:C8	2.52	0.44
46:SA:46:ARG:HH12	76:St:813:C:H5'	1.82	0.44
57:SL:33:VAL:CG2	57:SL:50:TYR:HA	2.44	0.44
61:SQ:71:ALA:HB1	61:SQ:114:ALA:HB2	2.00	0.44
65:SV:38:GLY:HA3	65:SV:100:LEU:HA	1.99	0.44
76:St:392:G:H1'	76:St:394:G:C2	2.53	0.44
27:La:51:ILE:HD12	27:La:51:ILE:HA	1.81	0.44
39:Ln:38:LEU:HD22	39:Ln:38:LEU:HA	1.85	0.44
39:Ln:166:ASN:HB3	44:Lt:1953:G:H1'	1.99	0.44
44:Lt:1150:C:H2'	44:Lt:1151:G:C8	2.53	0.44
46:SA:37:ARG:HD3	46:SA:37:ARG:HA	1.56	0.44
48:SC:77:TYR:CD2	48:SC:87:PRO:HG2	2.53	0.44
65:SV:81:PRO:HD2	65:SV:84:MET:HB2	2.00	0.44
67:SX:64:LEU:HB2	67:SX:85:LEU:HB3	2.00	0.44
69:Sb:91:LYS:HB2	69:Sb:91:LYS:HE2	1.50	0.44
76:St:72:C:H2'	76:St:73:G:O4'	2.18	0.44
76:St:318:C:H2'	76:St:319:C:C6	2.52	0.44
76:St:700:C:H2'	76:St:701:U:C6	2.52	0.44
76:St:876:A:H2'	76:St:877:A:C8	2.53	0.44
76:St:1000:C:H2'	76:St:1001:G:C8	2.51	0.44
2:LB:4:ARG:O	2:LB:5:LYS:HB2	2.17	0.44
3:LC:177:ILE:HG23	3:LC:188:ARG:HG3	2.00	0.44
19:LS:176:LYS:HD2	19:LS:176:LYS:HA	1.67	0.44
26:LZ:26:ARG:HG3	26:LZ:76:TYR:CZ	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:La:49:ARG:HG2	27:La:50:ARG:H	1.82	0.44
27:La:103:LYS:HB2	27:La:103:LYS:HE3	1.72	0.44
39:Ln:142:GLU:H	39:Ln:142:GLU:HG2	1.51	0.44
44:Lt:326:A:H1'	44:Lt:327:A:H5''	2.00	0.44
44:Lt:1574:U:H2'	44:Lt:1575:C:O4'	2.17	0.44
44:Lt:2451:A:H2'	44:Lt:2452:C:C6	2.53	0.44
54:SI:151:VAL:HG23	54:SI:153:THR:HG22	1.99	0.44
66:SW:23:ARG:HA	66:SW:23:ARG:HD3	1.63	0.44
68:SY:30:LEU:HD12	68:SY:30:LEU:HA	1.80	0.44
69:Sb:110:ASN:HB3	69:Sb:114:ARG:HH21	1.81	0.44
77:a:397:GLN:HB3	77:a:417:ILE:HG12	2.00	0.44
77:a:649:VAL:HG21	77:a:677:TRP:HE1	1.83	0.44
10:LJ:68:THR:HB	44:Lt:2528:G:O2'	2.18	0.43
11:LK:5:PRO:HB2	11:LK:7:ARG:HG2	2.00	0.43
13:LM:122:ILE:HG23	13:LM:154:ILE:HD11	2.00	0.43
18:LR:29:LEU:HD13	18:LR:29:LEU:HA	1.73	0.43
28:Lb:136:LYS:HE3	28:Lb:136:LYS:HB3	1.36	0.43
44:Lt:243:A:H2'	44:Lt:244:G:H8	1.83	0.43
44:Lt:1629:U:H1'	44:Lt:2400:U:H5''	1.99	0.43
51:SF:88:LEU:HD21	70:Sc:82:LYS:HB3	2.00	0.43
68:SY:78:LEU:HD12	68:SY:78:LEU:HA	1.78	0.43
69:Sb:10:LYS:HB2	69:Sb:10:LYS:HE3	1.62	0.43
73:Sg:35:ARG:HA	73:Sg:35:ARG:HD3	1.71	0.43
22:LV:45:ILE:H	22:LV:52:VAL:HG12	1.83	0.43
44:Lt:84:C:H1'	44:Lt:85:U:C6	2.53	0.43
44:Lt:1853:C:H5'	44:Lt:2408:U:H4'	2.00	0.43
49:SD:13:ILE:HG21	49:SD:25:LYS:HB2	1.99	0.43
51:SF:132:ARG:HE	51:SF:132:ARG:HB3	1.57	0.43
52:SG:137:LYS:HB3	76:St:149:C:H4'	1.99	0.43
62:SR:100:ARG:HE	62:SR:100:ARG:HB2	1.45	0.43
68:SY:16:VAL:O	68:SY:17:ASP:C	2.60	0.43
75:Sj:18:LYS:H	75:Sj:18:LYS:HG3	1.43	0.43
1:LA:168:LEU:HD21	42:Lq:76:ALA:HA	2.00	0.43
9:LI:117:ILE:H	9:LI:117:ILE:HG13	1.48	0.43
24:LX:42:LYS:HB3	24:LX:42:LYS:HE3	1.33	0.43
26:LZ:130:LEU:C	26:LZ:132:ARG:H	2.26	0.43
33:Lg:19:ARG:HB3	33:Lg:24:GLN:HG3	2.01	0.43
38:Ll:62:LYS:HB3	38:Ll:62:LYS:HE2	1.39	0.43
39:Ln:9:LEU:H	39:Ln:9:LEU:HD22	1.82	0.43
48:SC:88:LYS:HB2	48:SC:88:LYS:HE2	1.58	0.43
52:SG:69:MET:HE1	52:SG:108:VAL:HG12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SJ:35:ILE:HG23	55:SJ:50:PHE:HE2	1.83	0.43
57:SL:12:VAL:HG22	57:SL:36:ILE:HD12	1.99	0.43
62:SR:61:LEU:HD22	62:SR:61:LEU:HA	1.86	0.43
65:SV:53:VAL:HG21	66:SW:46:ARG:HD2	1.99	0.43
71:Sd:24:GLN:HG2	71:Sd:72:GLN:O	2.19	0.43
2:LB:292:ARG:HA	2:LB:302:ASP:O	2.18	0.43
15:LO:164:LEU:HD21	44:Lt:61:G:H5''	1.99	0.43
19:LS:105:LEU:HD22	19:LS:135:LYS:HG2	2.00	0.43
44:Lt:455:C:C5	44:Lt:456:G:H1'	2.53	0.43
44:Lt:1605:G:N3	44:Lt:1605:G:H5'	2.33	0.43
48:SC:170:LYS:HB3	48:SC:170:LYS:HE3	1.34	0.43
55:SJ:39:GLN:HG3	55:SJ:50:PHE:HZ	1.83	0.43
57:SL:60:LEU:HD23	57:SL:60:LEU:HA	1.88	0.43
76:St:1180:G:H2'	76:St:1181:G:C8	2.54	0.43
3:LC:40:LEU:HD23	3:LC:40:LEU:HA	1.87	0.43
3:LC:202:GLU:HB3	3:LC:204:VAL:HG13	2.00	0.43
5:LE:99:G:P	20:LT:52:THR:HG21	2.59	0.43
14:LN:126:ILE:HD13	14:LN:126:ILE:HA	1.80	0.43
20:LT:10:ARG:NH1	20:LT:13:PRO:HD3	2.34	0.43
31:Le:99:LYS:HE2	31:Le:99:LYS:HB2	1.42	0.43
39:Ln:86:GLU:HB2	39:Ln:87:ILE:H	1.50	0.43
44:Lt:567:C:H2'	44:Lt:568:C:C6	2.53	0.43
44:Lt:2667:U:H4'	44:Lt:2668:G:H5'	1.99	0.43
46:SA:177:GLY:HA3	46:SA:208:VAL:HG12	2.01	0.43
47:SB:146:HIS:H	47:SB:146:HIS:HD2	1.64	0.43
63:ST:90:GLY:HA2	76:St:1296:C:H5''	2.01	0.43
68:SY:63:CYS:SG	68:SY:64:GLY:N	2.92	0.43
69:Sb:102:PRO:HB2	69:Sb:103:VAL:H	1.52	0.43
76:St:559:G:N3	76:St:559:G:H2'	2.33	0.43
76:St:1157:C:H2'	76:St:1158:U:C6	2.52	0.43
77:a:401:VAL:HG11	77:a:418:ARG:HB2	2.00	0.43
1:LA:165:MET:HB2	1:LA:165:MET:HE2	1.70	0.43
14:LN:117:ARG:HH22	44:Lt:2593:G:H21	1.66	0.43
23:LW:52:ARG:HE	23:LW:52:ARG:HB2	1.30	0.43
28:Lb:3:THR:HG21	44:Lt:1116:G:H2'	2.00	0.43
43:Ls:99:CYS:HB3	43:Ls:113:CYS:HB3	1.68	0.43
46:SA:48:LYS:H	46:SA:48:LYS:HG2	1.43	0.43
50:SE:16:LYS:HD2	50:SE:16:LYS:HA	1.76	0.43
50:SE:251:ARG:HB2	56:SK:72:PHE:CE2	2.53	0.43
56:SK:114:ILE:HA	56:SK:119:LEU:HD12	2.00	0.43
57:SL:22:LEU:HD21	57:SL:24:LEU:HG	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:SO:40:PRO:HG2	59:SO:120:PHE:HZ	1.83	0.43
76:St:152:A:H3'	76:St:153:G:H5''	2.00	0.43
76:St:438:G:H5''	76:St:438:G:N3	2.33	0.43
77:a:4:PHE:HD2	77:a:4:PHE:HA	1.69	0.43
77:a:619:VAL:HA	77:a:780:LEU:O	2.19	0.43
6:LF:34:LYS:HA	21:LU:27:LEU:HD21	2.00	0.43
8:LH:161:ASN:HA	8:LH:164:ILE:HD12	2.00	0.43
9:LI:196:LEU:HD23	9:LI:196:LEU:HA	1.80	0.43
15:LO:78:GLY:HA2	15:LO:89:ILE:HD13	2.00	0.43
15:LO:185:ARG:HA	15:LO:185:ARG:HD3	1.68	0.43
32:Lf:30:PHE:HB3	32:Lf:32:ARG:HG2	2.00	0.43
36:Lj:55:ARG:HE	36:Lj:90:ILE:HG12	1.83	0.43
44:Lt:1935:G:H21	44:Lt:1985:C:H5	1.65	0.43
46:SA:171:LYS:HD2	46:SA:171:LYS:HA	1.88	0.43
47:SB:199:ARG:HE	47:SB:199:ARG:HB3	1.14	0.43
52:SG:231:MET:HE2	52:SG:231:MET:HB3	1.90	0.43
53:SH:13:PHE:HD2	53:SH:13:PHE:HA	1.74	0.43
60:SP:43:LYS:HA	60:SP:43:LYS:HD2	1.72	0.43
68:SY:9:LYS:HA	68:SY:15:VAL:HA	1.99	0.43
70:Sc:62:GLN:H	70:Sc:62:GLN:HG2	1.49	0.43
75:Sj:47:LEU:HG	75:Sj:65:LEU:HD11	2.01	0.43
76:St:200:G:H5''	76:St:201:C:H5	1.83	0.43
76:St:1164:G:N3	76:St:1164:G:H2'	2.34	0.43
76:St:1202:C:H2'	76:St:1203:A:C8	2.54	0.43
77:a:290:LYS:HE3	77:a:290:LYS:HB3	1.79	0.43
4:LD:65:C:H5''	35:Li:81:LYS:HD2	1.99	0.43
10:LJ:88:MET:HB3	10:LJ:175:CYS:SG	2.58	0.43
12:LL:112:LEU:HD12	12:LL:112:LEU:HA	1.75	0.43
13:LM:184:ILE:HG13	28:Lb:82:ILE:HG23	2.01	0.43
23:LW:23:VAL:HG13	23:LW:54:PRO:HB2	2.01	0.43
24:LX:44:LYS:HE2	24:LX:44:LYS:HB2	1.36	0.43
31:Le:25:PRO:HD3	31:Le:59:ILE:HG13	2.00	0.43
41:Lp:93:ARG:H	41:Lp:93:ARG:HG3	1.43	0.43
44:Lt:2016:G:H4'	44:Lt:2018:C:C2	2.54	0.43
45:Lu:9:G:H21	45:Lu:44:G:H3'	1.83	0.43
46:SA:144:TYR:O	68:SY:36:HIS:HB3	2.19	0.43
54:SI:57:CYS:HB3	76:St:246:C:H5'	2.00	0.43
55:SJ:71:LYS:HE3	55:SJ:71:LYS:HB2	1.92	0.43
65:SV:44:VAL:HB	65:SV:45:ALA:H	1.56	0.43
77:a:351:LEU:HD22	77:a:351:LEU:HA	1.90	0.43
1:LA:209:HIS:CE1	1:LA:235:VAL:HG11	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:LC:280:LYS:HE3	3:LC:280:LYS:HB3	1.34	0.43
3:LC:281:THR:HG23	18:LR:40:THR:HG21	2.01	0.43
8:LH:175:CYS:SG	8:LH:178:ASP:HB2	2.59	0.43
16:LP:6:ILE:HB	16:LP:32:LEU:HD12	2.00	0.43
16:LP:130:ARG:HA	16:LP:130:ARG:HD3	1.65	0.43
19:LS:42:ARG:HE	19:LS:42:ARG:HB2	1.40	0.43
30:Ld:26:LYS:H	30:Ld:26:LYS:HG2	1.65	0.43
39:Ln:63:LEU:H	39:Ln:63:LEU:HG	1.59	0.43
40:Lo:2:ARG:HD2	40:Lo:2:ARG:HA	1.87	0.43
47:SB:31:THR:O	47:SB:35:ARG:HG2	2.19	0.43
53:SH:44:LEU:HD12	53:SH:44:LEU:HA	1.79	0.43
69:Sb:14:ASN:N	69:Sb:14:ASN:OD1	2.52	0.43
73:Sg:47:LYS:HE2	73:Sg:47:LYS:HB3	1.70	0.43
2:LB:211:VAL:HG22	2:LB:284:MET:HA	2.01	0.43
3:LC:99:ARG:HA	44:Lt:412:A:H5'	2.01	0.43
3:LC:206:ARG:H	3:LC:206:ARG:HG2	1.43	0.43
8:LH:68:ASN:HD22	8:LH:68:ASN:HA	1.55	0.43
11:LK:27:PRO:HG3	11:LK:124:GLY:H	1.83	0.43
16:LP:54:LYS:HB3	16:LP:54:LYS:HE2	1.71	0.43
19:LS:56:LYS:HE3	19:LS:56:LYS:HB3	1.68	0.43
21:LU:65:PHE:CE2	21:LU:88:ARG:HB3	2.54	0.43
34:Lh:96:ASN:O	34:Lh:100:ARG:HB2	2.19	0.43
35:Li:75:ARG:HD2	35:Li:75:ARG:HA	1.58	0.43
38:Ll:65:LYS:HB2	38:Ll:66:ASP:H	1.59	0.43
44:Lt:1483:G:H8	44:Lt:1483:G:H5'	1.84	0.43
46:SA:169:ASN:C	46:SA:171:LYS:N	2.77	0.43
47:SB:35:ARG:HG2	47:SB:35:ARG:H	1.60	0.43
50:SE:202:MET:HG3	76:St:185:G:O4'	2.19	0.43
53:SH:51:GLU:H	53:SH:51:GLU:HG2	1.29	0.43
64:SU:7:LYS:HD2	64:SU:7:LYS:HA	1.36	0.43
66:SW:54:LYS:HE2	66:SW:54:LYS:HB3	1.80	0.43
75:Sj:16:THR:HG21	76:St:464:C:H1'	2.01	0.43
75:Sj:61:ILE:HD12	75:Sj:61:ILE:HA	1.74	0.43
77:a:885:LYS:HD2	77:a:885:LYS:HA	1.61	0.43
6:LF:73:ARG:HE	6:LF:73:ARG:HB2	1.59	0.42
9:LI:52:LYS:HB3	9:LI:52:LYS:HE3	1.62	0.42
11:LK:82:LYS:HB2	11:LK:82:LYS:HE3	1.49	0.42
15:LO:56:LYS:HB3	15:LO:56:LYS:HE2	1.60	0.42
15:LO:60:VAL:HG22	15:LO:134:LEU:HB2	1.99	0.42
16:LP:32:LEU:HB2	16:LP:101:VAL:HG12	2.01	0.42
18:LR:163:PRO:HG3	28:Lb:50:PRO:HG2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LS:110:ARG:HE	19:LS:110:ARG:HB3	1.29	0.42
20:LT:25:MET:HE2	20:LT:25:MET:HB3	1.80	0.42
20:LT:141:GLN:H	20:LT:141:GLN:HG2	1.50	0.42
26:LZ:93:LYS:H	26:LZ:93:LYS:HG2	1.51	0.42
27:La:65:ARG:H	27:La:65:ARG:HG3	1.53	0.42
38:Ll:12:LYS:HD2	38:Ll:12:LYS:HA	1.64	0.42
44:Lt:1442:A:H2'	44:Lt:1443:A:C8	2.54	0.42
44:Lt:1877:C:H2'	44:Lt:1878:A:C8	2.54	0.42
50:SE:44:LEU:HA	50:SE:47:ILE:HG13	2.01	0.42
75:Sj:48:ILE:HD11	75:Sj:56:PRO:HA	2.00	0.42
77:a:11:GLU:O	77:a:14:ASP:HB2	2.19	0.42
77:a:308:LYS:HA	77:a:308:LYS:HD3	1.72	0.42
77:a:574:LYS:HD2	77:a:574:LYS:HA	1.41	0.42
77:a:690:PRO:HB2	77:a:691:VAL:H	1.56	0.42
2:LB:292:ARG:H	2:LB:292:ARG:HG3	1.64	0.42
9:LI:143:LEU:HD22	9:LI:143:LEU:HA	1.88	0.42
23:LW:22:PRO:HB3	23:LW:55:LYS:HD3	2.00	0.42
27:La:7:LYS:HA	27:La:7:LYS:HD3	1.69	0.42
32:Lf:101:ILE:HG22	32:Lf:105:VAL:HG11	2.00	0.42
38:Ll:18:ARG:HB2	38:Ll:19:GLY:H	1.41	0.42
44:Lt:235:G:H22	44:Lt:256:G:H21	1.67	0.42
50:SE:221:ARG:HH21	76:St:531:A:H2'	1.83	0.42
52:SG:179:LEU:HD12	52:SG:179:LEU:HA	1.73	0.42
56:SK:84:LEU:HB3	56:SK:86:ILE:HG13	2.00	0.42
58:SM:90:HIS:CD2	76:St:222:G:H5''	2.54	0.42
65:SV:70:LYS:O	65:SV:73:GLU:HG3	2.19	0.42
74:Sh:103:ARG:HD2	74:Sh:119:ILE:HG12	2.01	0.42
76:St:179:G:H22	76:St:596:C:H3'	1.84	0.42
76:St:1053:C:H2'	76:St:1054:C:H3'	2.01	0.42
76:St:1078:G:H2'	76:St:1079:G:C8	2.54	0.42
76:St:1251:C:H2'	76:St:1252:C:C6	2.54	0.42
77:a:174:THR:HA	77:a:177:VAL:HG22	2.00	0.42
77:a:458:LYS:HB3	77:a:458:LYS:HE2	1.81	0.42
77:a:732:LEU:HD21	77:a:781:MET:HE2	2.01	0.42
77:a:733:ALA:HB2	77:a:875:MET:HG2	2.01	0.42
77:a:780:LEU:HD13	77:a:780:LEU:HA	1.73	0.42
2:LB:89:ILE:HD12	2:LB:147:LEU:HD21	2.01	0.42
3:LC:33:ILE:HG23	3:LC:224:LEU:HD11	2.01	0.42
3:LC:118:LEU:HD23	3:LC:118:LEU:HA	1.80	0.42
28:Lb:149:PRO:HA	36:Lj:9:LYS:O	2.19	0.42
37:Lk:55:ARG:HD2	44:Lt:305:G:N7	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Lt:224:U:H2'	44:Lt:225:A:C8	2.54	0.42
46:SA:170:ASN:HA	46:SA:176:ILE:HG12	2.02	0.42
49:SD:159:ARG:HE	49:SD:159:ARG:HB3	1.68	0.42
52:SG:72:GLY:O	76:St:1377:A:H1'	2.20	0.42
55:SJ:25:VAL:HG12	55:SJ:65:LEU:HD11	2.01	0.42
60:SP:16:ILE:HG12	76:St:616:G:H5''	2.01	0.42
66:SW:25:ILE:HG23	66:SW:110:GLN:HG2	2.01	0.42
75:Sj:53:ARG:HD2	75:Sj:53:ARG:HA	1.76	0.42
76:St:1290:C:H2'	76:St:1291:G:C8	2.54	0.42
77:a:154:LEU:HD12	77:a:154:LEU:HA	1.74	0.42
77:a:789:ILE:HG12	77:a:836:PHE:HZ	1.84	0.42
2:LB:67:LEU:HG	23:LW:93:LYS:HD3	2.01	0.42
4:LD:139:U:H3	44:Lt:4:G:H1	1.68	0.42
6:LF:154:LEU:HB3	44:Lt:2170:A:H2	1.84	0.42
8:LH:31:ARG:HD2	8:LH:31:ARG:HA	1.70	0.42
9:LI:146:TRP:CD1	9:LI:146:TRP:H	2.34	0.42
26:LZ:88:ARG:HE	26:LZ:88:ARG:HB3	1.47	0.42
29:Lc:9:SER:HA	29:Lc:12:GLN:HG2	2.02	0.42
35:Li:33:LYS:HB3	35:Li:33:LYS:HE3	1.64	0.42
42:Lq:49:ARG:HG3	42:Lq:55:TRP:CE2	2.54	0.42
50:SE:228:ILE:HD12	50:SE:228:ILE:HA	1.92	0.42
52:SG:75:LYS:O	52:SG:105:GLY:HA3	2.19	0.42
53:SH:153:ARG:HE	53:SH:153:ARG:HB3	1.50	0.42
56:SK:52:LYS:HA	56:SK:52:LYS:HD3	1.87	0.42
62:SR:50:LEU:HB3	62:SR:55:LEU:HG	2.02	0.42
67:SX:74:GLY:HA3	76:St:942:G:C5'	2.49	0.42
69:Sb:4:ILE:HG22	69:Sb:28:HIS:HB3	2.01	0.42
74:Sh:135:LYS:HB3	74:Sh:135:LYS:HE2	1.46	0.42
76:St:1420:A:H2	76:St:1423:G:N1	2.12	0.42
77:a:178:LEU:HD13	77:a:178:LEU:HA	1.75	0.42
77:a:246:THR:HB	77:a:247:ASP:H	1.69	0.42
77:a:299:ASN:HD21	77:a:304:LYS:HE2	1.84	0.42
7:LG:33:LEU:HD21	44:Lt:302:C:C4	2.54	0.42
15:LO:54:LYS:HE3	15:LO:54:LYS:HB3	1.42	0.42
32:Lf:47:MET:HE1	32:Lf:55:ARG:HB2	2.00	0.42
33:Lg:59:LYS:HB2	33:Lg:59:LYS:HE3	1.61	0.42
38:Ll:36:VAL:O	38:Ll:50:THR:HA	2.19	0.42
39:Ln:112:ALA:H	39:Ln:136:LEU:N	2.17	0.42
42:Lq:10:LEU:HD11	42:Lq:30:GLU:HB3	2.00	0.42
42:Lq:67:GLY:HA3	42:Lq:73:THR:HG23	2.00	0.42
44:Lt:1051:C:H2'	44:Lt:1052:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:SA:28:THR:HA	46:SA:169:ASN:HB2	2.02	0.42
50:SE:71:LEU:HD13	50:SE:71:LEU:HA	1.91	0.42
50:SE:94:LYS:HB2	69:Sb:16:LEU:HD23	2.01	0.42
55:SJ:66:ILE:H	55:SJ:66:ILE:HG12	1.65	0.42
56:SK:114:ILE:HD11	56:SK:126:ALA:HB1	2.02	0.42
58:SM:98:TYR:O	59:SO:8:TYR:HA	2.20	0.42
70:Sc:82:LYS:HB2	70:Sc:82:LYS:HE2	1.53	0.42
76:St:638:G:H2'	76:St:639:G:C8	2.55	0.42
3:LC:206:ARG:HA	3:LC:209:ARG:HD3	2.01	0.42
10:LJ:26:VAL:HG12	10:LJ:80:VAL:HG21	2.01	0.42
10:LJ:114:MET:HE3	10:LJ:114:MET:HB3	1.75	0.42
10:LJ:168:LEU:HD13	10:LJ:168:LEU:HA	1.89	0.42
19:LS:53:LEU:HD12	19:LS:53:LEU:HA	1.86	0.42
19:LS:172:GLU:O	19:LS:175:GLU:HG3	2.19	0.42
23:LW:139:GLU:H	23:LW:139:GLU:HG3	1.55	0.42
41:Lp:17:LYS:HB3	41:Lp:17:LYS:HE3	1.40	0.42
44:Lt:452:G:H21	44:Lt:455:C:H5	1.66	0.42
47:SB:226:LYS:HB2	47:SB:226:LYS:HE2	1.29	0.42
48:SC:179:ARG:HA	48:SC:179:ARG:HD3	1.72	0.42
50:SE:155:LYS:HA	50:SE:155:LYS:HD3	1.43	0.42
54:SI:99:LEU:HA	54:SI:102:THR:HG22	2.02	0.42
57:SL:45:LEU:HD13	57:SL:45:LEU:HA	1.72	0.42
8:LH:81:VAL:HG11	8:LH:122:LEU:HD21	2.02	0.42
47:SB:221:PRO:HA	47:SB:224:TRP:CE2	2.55	0.42
48:SC:209:GLU:H	48:SC:209:GLU:HG2	1.53	0.42
51:SF:109:GLU:HG3	51:SF:125:VAL:O	2.19	0.42
59:SO:138:ARG:HE	59:SO:138:ARG:HB3	1.52	0.42
62:SR:108:LYS:HB3	62:SR:108:LYS:HE3	1.83	0.42
62:SR:130:LYS:HD3	62:SR:130:LYS:HA	1.56	0.42
64:SU:27:LYS:HD3	64:SU:62:ASN:HD21	1.85	0.42
76:St:1281:C:H2'	76:St:1282:G:H8	1.83	0.42
77:a:215:LYS:HD3	77:a:215:LYS:HA	1.52	0.42
2:LB:170:LEU:HD13	2:LB:170:LEU:HA	1.81	0.42
6:LF:111:GLU:HG3	6:LF:257:PRO:HG3	2.00	0.42
9:LI:189:LYS:N	9:LI:190:PRO:HD2	2.35	0.42
16:LP:185:LEU:HD23	16:LP:185:LEU:HA	1.89	0.42
22:LV:18:PHE:HD1	22:LV:103:GLU:HA	1.84	0.42
28:Lb:118:LEU:HD23	28:Lb:118:LEU:HA	1.90	0.42
44:Lt:751:C:H2'	44:Lt:752:G:C8	2.54	0.42
44:Lt:1448:G:H2'	44:Lt:1449:G:C8	2.55	0.42
51:SF:74:MET:HA	51:SF:77:LYS:HE2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SG:214:MET:HE3	52:SG:214:MET:HB3	1.70	0.42
57:SL:17:TYR:HB2	57:SL:87:ILE:HG21	2.02	0.42
64:SU:27:LYS:HB3	76:St:1100:C:H5''	2.02	0.42
68:SY:60:PHE:HD2	68:SY:76:PHE:HE2	1.68	0.42
74:Sh:95:HIS:H	76:St:1157:C:H5''	1.84	0.42
76:St:1316:U:H2'	76:St:1317:G:C8	2.55	0.42
77:a:743:LYS:HB3	77:a:743:LYS:HE2	1.68	0.42
1:LA:157:LEU:HD23	1:LA:157:LEU:HA	1.86	0.42
2:LB:56:VAL:O	2:LB:73:ILE:HA	2.20	0.42
2:LB:136:LYS:HE3	2:LB:136:LYS:HB3	1.77	0.42
4:LD:65:C:O2'	35:Li:88:THR:HG21	2.19	0.42
6:LF:108:ARG:HA	6:LF:257:PRO:HB2	2.01	0.42
9:LI:153:LYS:HE2	9:LI:153:LYS:HB2	1.62	0.42
12:LL:30:LEU:HA	12:LL:30:LEU:HD13	1.75	0.42
22:LV:32:LEU:HD23	22:LV:60:VAL:CG1	2.50	0.42
41:Lp:88:ARG:HD2	41:Lp:88:ARG:HA	1.87	0.42
43:Ls:95:ILE:HG21	44:Lt:2319:G:H4'	2.02	0.42
44:Lt:2235:C:H2'	44:Lt:2236:A:H8	1.84	0.42
49:SD:83:LYS:HE3	49:SD:83:LYS:HB2	1.35	0.42
60:SP:33:VAL:HG11	60:SP:60:ILE:HG21	2.01	0.42
61:SQ:56:VAL:HG22	61:SQ:60:MET:HE1	2.02	0.42
65:SV:20:ASN:HD22	65:SV:20:ASN:HA	1.69	0.42
73:Sg:26:LYS:HD3	73:Sg:26:LYS:HA	1.80	0.42
76:St:113:G:H3'	76:St:114:G:C5'	2.50	0.42
76:St:1015:G:N7	76:St:1137:C:H5'	2.34	0.42
76:St:1267:G:H2'	76:St:1268:U:C6	2.54	0.42
1:LA:57:PRO:HB3	42:Lq:54:ILE:HG13	2.00	0.42
1:LA:149:ARG:HE	1:LA:149:ARG:HB3	1.70	0.42
8:LH:120:ASN:O	8:LH:124:ILE:HG13	2.20	0.42
19:LS:90:PRO:HB2	19:LS:93:THR:HG23	2.02	0.42
22:LV:97:VAL:HG13	22:LV:107:LEU:HD23	2.01	0.42
28:Lb:135:GLU:HG3	28:Lb:145:PRO:HG2	2.01	0.42
37:Lk:67:MET:HE3	37:Lk:67:MET:HB3	1.62	0.42
44:Lt:1283:G:H2'	44:Lt:1284:G:O4'	2.19	0.42
44:Lt:1655:A:H2'	44:Lt:1656:C:O4'	2.20	0.42
46:SA:26:ALA:HB2	46:SA:178:LEU:HD13	2.02	0.42
52:SG:171:LYS:HA	52:SG:184:LYS:HA	2.02	0.42
59:SO:124:LYS:HB3	59:SO:124:LYS:HE3	1.74	0.42
63:ST:38:ALA:HA	63:ST:85:ILE:HA	2.02	0.42
65:SV:35:LYS:HB2	65:SV:101:VAL:HG12	2.02	0.42
69:Sb:9:ARG:HH22	76:St:555:G:H2'	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Sc:60:MET:HB3	70:Sc:60:MET:HE2	1.64	0.42
76:St:1357:C:H2'	76:St:1358:G:O4'	2.20	0.42
3:LC:196:LEU:HD23	3:LC:237:ILE:HG12	2.01	0.41
5:LE:30:U:H3	5:LE:48:G:H1	1.67	0.41
10:LJ:146:SER:HB3	10:LJ:149:ASP:HB2	2.01	0.41
14:LN:46:LYS:HB3	14:LN:46:LYS:HE2	1.52	0.41
14:LN:74:LYS:HA	14:LN:77:ILE:HG22	2.02	0.41
24:LX:28:ARG:HA	24:LX:28:ARG:HD2	1.84	0.41
34:Lh:63:LEU:O	34:Lh:67:GLN:HB2	2.20	0.41
36:Lj:72:ASN:HB3	36:Lj:75:ARG:HB2	2.01	0.41
38:Ll:67:LYS:HB3	38:Ll:67:LYS:HE3	1.47	0.41
44:Lt:61:G:N2	44:Lt:78:U:H4'	2.35	0.41
44:Lt:986:A:H4'	44:Lt:987:A:H4'	2.01	0.41
44:Lt:1181:C:H2'	44:Lt:1182:G:C8	2.54	0.41
47:SB:88:GLN:H	47:SB:88:GLN:HG2	1.22	0.41
50:SE:237:ILE:H	50:SE:237:ILE:HG13	1.53	0.41
51:SF:76:MET:HE3	51:SF:76:MET:HB2	1.57	0.41
52:SG:173:LEU:HD23	52:SG:187:LYS:HZ1	1.85	0.41
71:Sd:57:CYS:HB3	71:Sd:59:ILE:HG22	2.02	0.41
75:Sj:21:LYS:HE2	75:Sj:21:LYS:HB3	1.38	0.41
76:St:919:U:H2'	76:St:920:G:C8	2.55	0.41
77:a:196:ASP:HB3	77:a:266:TRP:HE1	1.85	0.41
6:LF:175:VAL:HG11	6:LF:183:HIS:HE1	1.85	0.41
8:LH:142:LEU:HA	8:LH:142:LEU:HD23	1.81	0.41
11:LK:87:LEU:HD12	11:LK:138:VAL:HG22	2.02	0.41
14:LN:106:PHE:CZ	33:Lg:94:VAL:HG22	2.55	0.41
16:LP:165:TYR:HB2	44:Lt:2575:G:H1'	2.02	0.41
22:LV:16:ILE:H	22:LV:16:ILE:HG13	1.49	0.41
44:Lt:688:G:H2'	44:Lt:689:C:C6	2.56	0.41
48:SC:96:LYS:HE2	48:SC:96:LYS:HB3	1.65	0.41
52:SG:90:TYR:CZ	52:SG:99:LYS:HB3	2.54	0.41
54:SI:93:ASN:HB2	54:SI:100:VAL:HG22	2.02	0.41
57:SL:24:LEU:HD23	57:SL:24:LEU:HA	1.91	0.41
61:SQ:37:LYS:HB2	61:SQ:37:LYS:HE3	1.36	0.41
62:SR:111:MET:HE3	62:SR:111:MET:HB3	1.91	0.41
64:SU:3:LYS:HD2	76:St:1120:G:H1'	2.02	0.41
68:SY:41:LEU:H	68:SY:41:LEU:HG	1.57	0.41
71:Sd:34:LYS:HB3	71:Sd:34:LYS:HE3	1.58	0.41
76:St:58:C:H5''	76:St:365:G:C8	2.55	0.41
76:St:1141:G:N3	76:St:1141:G:H2'	2.34	0.41
77:a:417:ILE:HG13	77:a:449:PHE:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:LC:72:LEU:CD2	44:Lt:1126:U:H5'	2.50	0.41
6:LF:88:ILE:HG23	6:LF:245:MET:HE3	2.02	0.41
16:LP:113:LYS:H	16:LP:113:LYS:HG3	1.62	0.41
37:Lk:50:SER:HB3	37:Lk:53:SER:HB3	2.02	0.41
39:Ln:33:GLU:HB2	39:Ln:207:LYS:HG3	2.03	0.41
39:Ln:36:VAL:HG13	39:Ln:204:VAL:HG13	2.02	0.41
53:SH:21:LYS:H	53:SH:21:LYS:HG3	1.69	0.41
65:SV:135:GLN:HE21	76:St:1163:C:H1'	1.85	0.41
70:Sc:18:PRO:C	70:Sc:55:LEU:HB2	2.46	0.41
77:a:397:GLN:HG2	77:a:397:GLN:H	1.57	0.41
6:LF:83:LEU:N	6:LF:84:PRO:HD2	2.35	0.41
8:LH:133:GLU:H	8:LH:133:GLU:HG3	1.69	0.41
9:LI:53:VAL:HA	9:LI:54:PRO:HD3	1.90	0.41
9:LI:184:VAL:HG12	9:LI:189:LYS:HG2	2.02	0.41
10:LJ:163:VAL:HA	10:LJ:164:PRO:HD3	1.94	0.41
13:LM:181:LYS:HE3	13:LM:181:LYS:HB3	1.47	0.41
16:LP:55:MET:HG2	16:LP:69:HIS:HB3	2.03	0.41
16:LP:173:LYS:HE3	16:LP:173:LYS:HB3	1.36	0.41
23:LW:80:PRO:HG2	23:LW:110:PRO:HD3	2.02	0.41
28:Lb:27:LYS:H	28:Lb:27:LYS:HG2	1.54	0.41
32:Lf:9:LEU:H	32:Lf:9:LEU:HG	1.42	0.41
35:Li:77:ARG:H	35:Li:77:ARG:HG3	1.59	0.41
44:Lt:240:U:H2'	44:Lt:241:G:C8	2.55	0.41
46:SA:127:LEU:HD23	46:SA:127:LEU:HA	1.83	0.41
51:SF:27:ILE:H	51:SF:27:ILE:HG12	1.51	0.41
51:SF:60:ASN:HD22	51:SF:60:ASN:HA	1.58	0.41
52:SG:67:PHE:HA	52:SG:68:PRO:HD3	1.83	0.41
53:SH:86:LYS:HA	53:SH:86:LYS:HD3	1.83	0.41
56:SK:109:ARG:O	56:SK:110:LEU:HB3	2.21	0.41
61:SQ:61:LYS:HE3	61:SQ:61:LYS:HB3	1.79	0.41
75:Sj:1:ARG:HH12	77:a:756:ARG:HH21	1.68	0.41
76:St:160:G:O5'	76:St:160:G:H8	2.04	0.41
1:LA:217:GLN:HE21	1:LA:217:GLN:HB3	1.63	0.41
2:LB:206:LYS:HB2	2:LB:206:LYS:HE2	1.88	0.41
11:LK:19:LYS:HA	11:LK:23:CYS:HB3	2.02	0.41
20:LT:3:GLN:O	20:LT:4:LYS:HB3	2.20	0.41
27:La:71:LYS:HZ3	44:Lt:1303:A:H5''	1.85	0.41
33:Lg:18:GLN:HB2	33:Lg:28:VAL:HG22	2.02	0.41
37:Lk:52:LYS:HE3	37:Lk:52:LYS:HB2	1.88	0.41
39:Ln:35:GLN:NE2	39:Ln:166:ASN:HB2	2.36	0.41
42:Lq:28:LYS:HE3	42:Lq:28:LYS:HB3	1.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Lt:778:C:H42	44:Lt:804:G:H1	1.67	0.41
48:SC:209:GLU:HG3	64:SU:43:ILE:HD12	2.02	0.41
50:SE:128:LYS:HE2	50:SE:128:LYS:HB3	1.68	0.41
66:SW:78:LYS:H	66:SW:78:LYS:HG2	1.65	0.41
77:a:485:ILE:HG22	77:a:494:GLN:HG3	2.03	0.41
77:a:705:ALA:O	77:a:709:VAL:N	2.54	0.41
3:LC:310:SER:HB3	8:LH:40:VAL:HA	2.01	0.41
11:LK:97:ILE:HD13	11:LK:97:ILE:HA	1.76	0.41
21:LU:129:LEU:HB2	44:Lt:808:G:H8	1.85	0.41
23:LW:30:ALA:O	23:LW:119:ILE:HA	2.21	0.41
44:Lt:92:G:H2'	44:Lt:93:A:C8	2.55	0.41
44:Lt:829:C:H2'	44:Lt:830:C:C6	2.55	0.41
46:SA:38:ARG:HB3	46:SA:159:LEU:HD23	2.03	0.41
56:SK:83:MET:HG3	56:SK:150:ARG:HD3	2.02	0.41
56:SK:130:ILE:HD13	56:SK:145:PRO:HA	2.03	0.41
63:ST:68:GLU:O	63:ST:72:ILE:HG23	2.21	0.41
68:SY:84:GLY:O	68:SY:85:LEU:C	2.64	0.41
69:Sb:84:LYS:HE3	69:Sb:84:LYS:HB2	1.78	0.41
73:Sg:15:ARG:HE	73:Sg:23:THR:HG23	1.86	0.41
76:St:299:G:H2'	76:St:300:A:C8	2.55	0.41
76:St:347:G:N2	76:St:349:A:H3'	2.35	0.41
8:LH:112:MET:HB3	8:LH:112:MET:HE2	1.76	0.41
21:LU:81:ARG:HD2	21:LU:81:ARG:HA	1.86	0.41
26:LZ:132:ARG:HD3	26:LZ:132:ARG:HA	1.74	0.41
31:Le:99:LYS:H	31:Le:99:LYS:HG3	1.59	0.41
32:Lf:69:ARG:O	32:Lf:70:PHE:HB2	2.20	0.41
38:Ll:20:LYS:O	38:Ll:21:LYS:C	2.63	0.41
39:Ln:35:GLN:HE21	39:Ln:166:ASN:HB2	1.85	0.41
44:Lt:1213:G:H3'	44:Lt:1214:G:C8	2.54	0.41
44:Lt:1705:U:H2'	44:Lt:1706:G:C8	2.55	0.41
44:Lt:2121:A:H2'	44:Lt:2122:G:C8	2.55	0.41
44:Lt:2367:G:H5'	44:Lt:2369:G:C8	2.55	0.41
44:Lt:2613:C:H2'	44:Lt:2614:G:C8	2.56	0.41
44:Lt:2655:C:H2'	44:Lt:2656:C:C6	2.56	0.41
47:SB:82:LYS:HE3	47:SB:82:LYS:HB3	1.74	0.41
48:SC:73:HIS:HB3	57:SL:101:PRO:HB3	2.02	0.41
48:SC:112:ARG:HG3	48:SC:181:ILE:HB	2.03	0.41
49:SD:187:LYS:HA	49:SD:190:ASN:HD22	1.84	0.41
51:SF:74:MET:HE1	76:St:1179:U:H1'	2.02	0.41
53:SH:59:LYS:O	53:SH:91:HIS:HA	2.21	0.41
56:SK:83:MET:O	56:SK:151:ILE:HG12	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:SR:63:LEU:HD22	62:SR:63:LEU:HA	1.84	0.41
62:SR:128:HIS:HB3	62:SR:129:GLY:H	1.36	0.41
77:a:19:ILE:O	77:a:393:PRO:HD2	2.21	0.41
77:a:731:VAL:HG21	77:a:778:PRO:HD3	2.02	0.41
1:LA:46:LYS:HB3	1:LA:46:LYS:HE2	1.80	0.41
1:LA:183:GLY:HA3	44:Lt:613:A:OP1	2.21	0.41
2:LB:147:LEU:HD23	2:LB:147:LEU:HA	1.79	0.41
3:LC:160:LYS:HE2	3:LC:160:LYS:HB2	1.82	0.41
6:LF:131:LYS:HD2	6:LF:131:LYS:HA	1.56	0.41
12:LL:110:ILE:H	12:LL:110:ILE:HG13	1.40	0.41
14:LN:21:LYS:HB3	14:LN:21:LYS:HE3	1.96	0.41
15:LO:155:VAL:HG13	44:Lt:60:G:H5''	2.02	0.41
17:LQ:94:LEU:O	17:LQ:98:VAL:HG23	2.21	0.41
24:LX:62:LYS:HA	24:LX:62:LYS:HD3	1.88	0.41
44:Lt:792:C:H2'	44:Lt:793:C:H2'	2.01	0.41
44:Lt:1961:G:N3	44:Lt:1961:G:H2'	2.35	0.41
44:Lt:2131:C:H2'	44:Lt:2132:C:C6	2.55	0.41
51:SF:66:GLY:C	51:SF:68:ASN:N	2.78	0.41
52:SG:221:LEU:HA	52:SG:221:LEU:HD13	1.81	0.41
59:SO:88:ASP:HA	76:St:448:G:H4'	2.01	0.41
60:SP:42:LYS:HZ2	60:SP:42:LYS:HG2	1.82	0.41
66:SW:114:ILE:HD12	66:SW:114:ILE:HA	1.84	0.41
76:St:1064:A:H2'	76:St:1065:C:C6	2.55	0.41
77:a:815:PRO:HA	77:a:822:THR:HB	2.02	0.41
1:LA:132:THR:HG21	44:Lt:1666:G:OP1	2.21	0.41
3:LC:272:ILE:O	3:LC:275:SER:HB3	2.20	0.41
4:LD:65:C:H2'	4:LD:66:G:C8	2.55	0.41
5:LE:95:C:H4'	20:LT:116:HIS:HB3	2.02	0.41
7:LG:12:ARG:HE	7:LG:12:ARG:HB3	1.47	0.41
16:LP:48:LYS:HB3	16:LP:48:LYS:HE2	1.66	0.41
17:LQ:64:LYS:HD3	44:Lt:1134:A:H5''	2.02	0.41
18:LR:46:LYS:HE3	18:LR:46:LYS:HB3	1.63	0.41
18:LR:67:LEU:HD13	18:LR:99:ILE:HD13	2.03	0.41
19:LS:74:ARG:HD3	19:LS:74:ARG:HA	1.68	0.41
19:LS:147:LYS:HE3	19:LS:147:LYS:HB3	1.66	0.41
20:LT:81:ARG:HE	20:LT:81:ARG:HB3	1.60	0.41
22:LV:12:GLU:O	22:LV:13:GLN:HB2	2.20	0.41
24:LX:57:ARG:O	24:LX:62:LYS:N	2.54	0.41
27:La:49:ARG:HG3	27:La:64:GLY:N	2.36	0.41
28:Lb:64:ARG:HB2	28:Lb:67:ILE:HB	2.03	0.41
29:Lc:8:THR:HG23	29:Lc:10:LYS:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Ld:84:ALA:C	30:Ld:86:GLY:N	2.78	0.41
38:Ll:67:LYS:H	38:Ll:67:LYS:HG2	1.59	0.41
44:Lt:624:G:H4'	44:Lt:625:G:H5'	2.01	0.41
44:Lt:822:C:H2'	44:Lt:823:G:C8	2.56	0.41
44:Lt:1564:A:H3'	44:Lt:1565:A:H8	1.85	0.41
46:SA:185:ARG:NH1	46:SA:194:ILE:HG21	2.36	0.41
46:SA:194:ILE:HD12	46:SA:194:ILE:HA	1.77	0.41
48:SC:65:MET:HE3	48:SC:69:HIS:CE1	2.56	0.41
50:SE:94:LYS:HA	50:SE:94:LYS:HD3	1.84	0.41
51:SF:88:LEU:CD2	70:Sc:72:VAL:HG21	2.50	0.41
54:Sl:13:LYS:HE3	54:Sl:13:LYS:HB2	1.43	0.41
57:SL:88:ARG:O	57:SL:92:ASP:N	2.54	0.41
58:SM:77:LYS:HB2	58:SM:77:LYS:HE2	1.78	0.41
58:SM:87:ASP:HB3	58:SM:151:PHE:CZ	2.56	0.41
67:SX:101:ILE:HG13	67:SX:102:SER:N	2.35	0.41
70:Sc:48:ARG:HA	70:Sc:48:ARG:HD2	1.57	0.41
76:St:30:C:H2'	76:St:31:U:O4'	2.20	0.41
76:St:546:U:H2'	76:St:547:C:H6	1.86	0.41
76:St:861:U:H2'	76:St:862:G:C8	2.55	0.41
76:St:1244:G:H2'	76:St:1245:A:C8	2.55	0.41
77:a:35:LEU:HD13	77:a:262:GLY:HA2	2.02	0.41
77:a:245:ARG:HA	77:a:245:ARG:HD3	1.63	0.41
77:a:376:LEU:O	77:a:377:PRO:C	2.64	0.41
1:LA:116:VAL:HG13	1:LA:164:ALA:HB2	2.03	0.41
2:LB:55:HIS:HB3	44:Lt:2467:G:H1'	2.02	0.41
16:LP:118:PRO:HA	16:LP:121:MET:HG3	2.03	0.41
17:LQ:131:ARG:HE	17:LQ:131:ARG:HB3	1.69	0.41
29:Lc:55:LEU:HD12	29:Lc:55:LEU:HA	1.80	0.41
34:Lh:5:ARG:H	34:Lh:5:ARG:HG2	1.62	0.41
42:Lq:26:LEU:HA	42:Lq:26:LEU:HD13	1.74	0.41
43:Ls:109:ASN:HB3	43:Ls:115:GLY:HA2	2.03	0.41
44:Lt:2560:C:H2'	44:Lt:2561:C:C6	2.56	0.41
53:SH:52:ILE:HD13	53:SH:179:ALA:HB2	2.03	0.41
62:SR:90:ILE:HA	62:SR:107:ILE:HG22	2.01	0.41
65:SV:13:LEU:H	65:SV:13:LEU:HG	1.39	0.41
76:St:472:C:H2'	76:St:473:G:O4'	2.21	0.41
76:St:599:G:C2	76:St:600:C:H1'	2.56	0.41
4:LD:7:C:H2'	4:LD:8:C:O4'	2.21	0.40
6:LF:107:ARG:HD2	6:LF:254:ARG:HG3	2.03	0.40
9:LI:92:LEU:HA	9:LI:92:LEU:HD12	1.74	0.40
20:LT:76:LEU:HD21	20:LT:89:ARG:HG3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:LX:58:LEU:HD22	24:LX:64:MET:HB3	2.02	0.40
31:Le:40:LYS:HD3	31:Le:40:LYS:HA	1.92	0.40
32:Lf:24:ARG:HB2	32:Lf:36:SER:O	2.21	0.40
37:Lk:3:LYS:HE2	37:Lk:3:LYS:HB3	1.56	0.40
39:Ln:159:PHE:CE2	39:Ln:193:GLN:HB3	2.56	0.40
44:Lt:1711:G:H2'	44:Lt:1712:A:C8	2.56	0.40
49:SD:133:TYR:CD1	49:SD:181:ILE:HG13	2.56	0.40
50:SE:3:ARG:HB3	76:St:80:A:H1'	2.03	0.40
52:SG:196:THR:H	52:SG:199:LYS:HB3	1.87	0.40
54:SI:145:SER:OG	54:SI:156:GLY:HA2	2.20	0.40
56:SK:60:LEU:HB3	56:SK:94:LEU:HD13	2.02	0.40
59:SO:133:LEU:HD13	59:SO:133:LEU:HA	1.77	0.40
61:SQ:95:ILE:HG13	61:SQ:126:ILE:CG2	2.51	0.40
76:St:1080:C:H2'	76:St:1081:C:C6	2.56	0.40
76:St:1273:U:H2'	76:St:1274:A:H8	1.86	0.40
76:St:1384:C:H2'	76:St:1385:G:O4'	2.20	0.40
77:a:9:ILE:O	77:a:13:MET:HG2	2.22	0.40
77:a:477:PHE:HB3	77:a:512:TYR:CZ	2.55	0.40
2:LB:88:ALA:HB3	2:LB:160:VAL:HB	2.03	0.40
17:LQ:79:LYS:HE3	17:LQ:79:LYS:HB2	1.99	0.40
36:Lj:70:LEU:HD11	36:Lj:79:LYS:HE3	2.02	0.40
36:Lj:79:LYS:HD3	36:Lj:79:LYS:HA	1.70	0.40
39:Ln:66:CYS:HB2	39:Ln:107:TYR:CB	2.51	0.40
43:Ls:112:ARG:O	43:Ls:114:ARG:N	2.53	0.40
44:Lt:1384:C:H4'	44:Lt:1397:G:H4'	2.03	0.40
44:Lt:1545:G:N3	44:Lt:1609:C:H2'	2.36	0.40
44:Lt:2445:A:C8	77:a:845:SER:HB3	2.55	0.40
53:SH:37:ARG:HA	53:SH:37:ARG:HD2	1.31	0.40
73:Sg:28:GLU:HA	73:Sg:36:GLN:HA	2.03	0.40
76:St:435:A:H2'	76:St:436:A:C8	2.56	0.40
77:a:229:ASP:HB2	77:a:245:ARG:HB2	2.03	0.40
77:a:511:GLN:H	77:a:511:GLN:HG3	1.55	0.40
77:a:754:ILE:HD12	77:a:754:ILE:HA	1.61	0.40
2:LB:160:VAL:HG22	2:LB:179:GLU:HG2	2.03	0.40
3:LC:304:LEU:HD23	3:LC:304:LEU:HA	1.92	0.40
6:LF:117:ILE:HA	6:LF:117:ILE:HD12	1.80	0.40
8:LH:102:ARG:HB3	8:LH:199:PRO:HG3	2.04	0.40
9:LI:54:PRO:HG2	15:LO:18:ALA:HA	2.04	0.40
9:LI:120:ILE:HD12	9:LI:120:ILE:HA	1.87	0.40
15:LO:28:TRP:O	15:LO:32:GLN:HG2	2.21	0.40
22:LV:26:LYS:HD3	22:LV:26:LYS:HA	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Ld:20:LEU:HD12	30:Ld:20:LEU:HA	1.78	0.40
30:Ld:58:SER:HB2	34:Lh:92:LEU:HD13	2.03	0.40
39:Ln:39:LYS:HB3	39:Ln:39:LYS:HE3	1.93	0.40
42:Lq:53:GLY:HA2	42:Lq:66:GLY:O	2.21	0.40
42:Lq:64:MET:H	42:Lq:64:MET:HG2	1.70	0.40
47:SB:72:GLU:HA	47:SB:98:VAL:HA	2.03	0.40
49:SD:108:HIS:CG	71:Sd:65:PRO:HB2	2.56	0.40
50:SE:230:ASN:HB3	50:SE:231:ASP:H	1.73	0.40
52:SG:101:LYS:HE3	52:SG:101:LYS:HB2	1.64	0.40
52:SG:120:VAL:HB	52:SG:121:ASP:H	1.72	0.40
52:SG:170:ILE:HG13	52:SG:187:LYS:HD2	2.03	0.40
53:SH:80:LEU:HD13	53:SH:80:LEU:HA	1.84	0.40
53:SH:135:TYR:N	53:SH:136:PRO:HD2	2.36	0.40
58:SM:85:ARG:HA	58:SM:104:HIS:HD2	1.86	0.40
59:SO:7:LEU:HD23	59:SO:7:LEU:HA	1.80	0.40
59:SO:137:LYS:HZ3	76:St:30:C:H4'	1.85	0.40
73:Sg:55:GLU:H	73:Sg:55:GLU:HG2	1.52	0.40
76:St:253:C:H2'	76:St:254:G:C8	2.56	0.40
76:St:392:G:H2'	76:St:393:C:C6	2.57	0.40
77:a:541:VAL:HB	77:a:589:LEU:HD21	2.02	0.40
77:a:636:ASN:ND2	77:a:756:ARG:HG2	2.37	0.40
4:LD:86:G:H4'	4:LD:87:A:H5'	2.04	0.40
8:LH:119:LEU:HD23	8:LH:119:LEU:HA	1.94	0.40
12:LL:91:LEU:HD12	12:LL:91:LEU:HA	1.79	0.40
21:LU:78:LYS:HD3	21:LU:87:LYS:HE3	2.03	0.40
44:Lt:2421:G:H2'	44:Lt:2422:C:C6	2.57	0.40
46:SA:203:LYS:HG2	46:SA:204:PRO:HD2	2.02	0.40
48:SC:166:THR:HG23	76:St:1127:G:H1'	2.03	0.40
55:SJ:32:LYS:HE2	55:SJ:32:LYS:HB3	1.52	0.40
59:SO:130:LEU:HD12	59:SO:130:LEU:HA	1.79	0.40
68:SY:81:GLN:HA	68:SY:87:GLU:C	2.46	0.40
71:Sd:13:TYR:CE1	76:St:688:C:H1'	2.57	0.40
75:Sj:59:LEU:HD12	75:Sj:59:LEU:HA	1.94	0.40
77:a:147:SER:HB2	77:a:148:SER:H	1.49	0.40
2:LB:78:ILE:HG13	2:LB:323:MET:HG3	2.02	0.40
3:LC:178:ARG:NH1	3:LC:187:ARG:HB3	2.37	0.40
9:LI:44:LYS:O	9:LI:48:GLN:HG3	2.22	0.40
10:LJ:106:LYS:HE2	10:LJ:106:LYS:HB2	1.74	0.40
14:LN:64:ILE:CD1	14:LN:73:LEU:HD12	2.52	0.40
15:LO:4:TYR:HD1	15:LO:4:TYR:HA	1.79	0.40
17:LQ:21:VAL:HG11	17:LQ:89:VAL:HG11	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LQ:35:ILE:HG13	17:LQ:43:ALA:HB1	2.04	0.40
17:LQ:128:ARG:H	17:LQ:128:ARG:HG2	1.77	0.40
21:LU:87:LYS:NZ	44:Lt:2152:G:H22	2.20	0.40
28:Lb:118:LEU:HD12	28:Lb:138:LEU:HA	2.03	0.40
32:Lf:66:LYS:HB2	32:Lf:66:LYS:HE2	1.92	0.40
35:Li:115:ARG:H	35:Li:115:ARG:HG3	1.38	0.40
41:Lp:15:GLU:HB3	41:Lp:17:LYS:HG2	2.02	0.40
44:Lt:1907:A:H2'	44:Lt:1908:C:C6	2.57	0.40
44:Lt:1944:A:H2'	44:Lt:1945:G:O4'	2.22	0.40
49:SD:223:ASN:C	49:SD:225:MET:H	2.30	0.40
52:SG:127:LEU:HB3	52:SG:130:LEU:H	1.86	0.40
55:SJ:124:LYS:HB3	55:SJ:124:LYS:HE3	1.80	0.40
62:SR:89:MET:HB3	62:SR:89:MET:HE2	1.58	0.40
63:ST:47:ILE:HG22	63:ST:85:ILE:HD11	2.04	0.40
64:SU:5:ARG:HB3	64:SU:10:LYS:HG3	2.03	0.40
68:SY:86:MET:HE3	68:SY:86:MET:HB3	1.68	0.40
71:Sd:42:ARG:HA	71:Sd:42:ARG:HD2	1.53	0.40
77:a:806:ARG:HG3	77:a:836:PHE:HB2	2.03	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	243/251 (97%)	232 (96%)	9 (4%)	2 (1%)	16	44
2	LB	368/379 (97%)	347 (94%)	18 (5%)	3 (1%)	16	44
3	LC	307/316 (97%)	294 (96%)	12 (4%)	1 (0%)	36	65
6	LF	281/297 (95%)	262 (93%)	18 (6%)	1 (0%)	30	59
7	LG	47/51 (92%)	46 (98%)	1 (2%)	0	100	100
8	LH	207/235 (88%)	204 (99%)	1 (0%)	2 (1%)	12	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	LI	176/225 (78%)	162 (92%)	12 (7%)	2 (1%)	11	38
10	LJ	179/185 (97%)	164 (92%)	13 (7%)	2 (1%)	11	38
11	LK	185/210 (88%)	178 (96%)	5 (3%)	2 (1%)	11	38
12	LL	160/173 (92%)	156 (98%)	4 (2%)	0	100	100
13	LM	188/234 (80%)	178 (95%)	7 (4%)	3 (2%)	7	29
14	LN	126/131 (96%)	118 (94%)	7 (6%)	1 (1%)	16	44
15	LO	201/204 (98%)	193 (96%)	6 (3%)	2 (1%)	12	40
16	LP	184/197 (93%)	176 (96%)	5 (3%)	3 (2%)	7	29
17	LQ	147/164 (90%)	139 (95%)	8 (5%)	0	100	100
18	LR	175/179 (98%)	166 (95%)	8 (5%)	1 (1%)	21	50
19	LS	179/196 (91%)	174 (97%)	5 (3%)	0	100	100
20	LT	165/173 (95%)	158 (96%)	6 (4%)	1 (1%)	21	50
21	LU	151/159 (95%)	138 (91%)	12 (8%)	1 (1%)	18	47
22	LV	106/124 (86%)	93 (88%)	11 (10%)	2 (2%)	6	26
23	LW	132/142 (93%)	130 (98%)	2 (2%)	0	100	100
24	LX	61/189 (32%)	58 (95%)	2 (3%)	1 (2%)	7	29
25	LY	111/141 (79%)	105 (95%)	4 (4%)	2 (2%)	6	26
26	LZ	131/135 (97%)	128 (98%)	3 (2%)	0	100	100
27	La	118/135 (87%)	104 (88%)	12 (10%)	2 (2%)	7	28
28	Lb	146/149 (98%)	139 (95%)	6 (4%)	1 (1%)	18	47
29	Lc	49/62 (79%)	44 (90%)	5 (10%)	0	100	100
30	Ld	98/109 (90%)	94 (96%)	1 (1%)	3 (3%)	3	18
31	Le	95/106 (90%)	90 (95%)	5 (5%)	0	100	100
32	Lf	123/136 (90%)	115 (94%)	6 (5%)	2 (2%)	7	29
33	Lg	95/123 (77%)	91 (96%)	4 (4%)	0	100	100
34	Lh	104/120 (87%)	94 (90%)	9 (9%)	1 (1%)	12	40
35	Li	111/124 (90%)	107 (96%)	4 (4%)	0	100	100
36	Lj	79/90 (88%)	76 (96%)	2 (2%)	1 (1%)	9	33
37	Lk	84/89 (94%)	79 (94%)	5 (6%)	0	100	100
38	Ll	65/77 (84%)	61 (94%)	3 (5%)	1 (2%)	8	30
39	Ln	194/217 (89%)	177 (91%)	16 (8%)	1 (0%)	24	54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	Lo	23/25 (92%)	23 (100%)	0	0	100	100
41	Lp	90/106 (85%)	87 (97%)	3 (3%)	0	100	100
42	Lq	84/94 (89%)	81 (96%)	2 (2%)	1 (1%)	10	35
43	Ls	43/127 (34%)	37 (86%)	3 (7%)	3 (7%)	1	6
46	SA	191/245 (78%)	178 (93%)	12 (6%)	1 (0%)	24	54
47	SB	202/242 (84%)	191 (95%)	7 (4%)	4 (2%)	6	25
48	SC	202/217 (93%)	190 (94%)	11 (5%)	1 (0%)	24	54
49	SD	219/248 (88%)	210 (96%)	9 (4%)	0	100	100
50	SE	255/268 (95%)	234 (92%)	19 (8%)	2 (1%)	16	44
51	SF	173/190 (91%)	167 (96%)	5 (3%)	1 (1%)	21	50
52	SG	222/248 (90%)	207 (93%)	13 (6%)	2 (1%)	14	42
53	SH	182/190 (96%)	166 (91%)	15 (8%)	1 (0%)	24	54
54	SI	159/174 (91%)	152 (96%)	6 (4%)	1 (1%)	21	50
55	SJ	127/130 (98%)	117 (92%)	9 (7%)	1 (1%)	16	44
56	SK	173/189 (92%)	164 (95%)	6 (4%)	3 (2%)	7	28
57	SL	99/134 (74%)	97 (98%)	2 (2%)	0	100	100
58	SM	143/154 (93%)	134 (94%)	7 (5%)	2 (1%)	9	31
59	SO	134/143 (94%)	131 (98%)	3 (2%)	0	100	100
60	SP	147/154 (96%)	142 (97%)	4 (3%)	1 (1%)	18	47
61	SQ	122/145 (84%)	112 (92%)	8 (7%)	2 (2%)	7	29
62	SR	108/145 (74%)	102 (94%)	5 (5%)	1 (1%)	14	42
63	ST	149/158 (94%)	135 (91%)	13 (9%)	1 (1%)	18	47
64	SU	64/137 (47%)	59 (92%)	4 (6%)	1 (2%)	7	29
65	SV	138/154 (90%)	112 (81%)	21 (15%)	5 (4%)	2	16
66	SW	136/139 (98%)	126 (93%)	8 (6%)	2 (2%)	8	30
67	SX	100/126 (79%)	100 (100%)	0	0	100	100
68	SY	80/89 (90%)	74 (92%)	4 (5%)	2 (2%)	4	21
69	Sb	116/132 (88%)	104 (90%)	9 (8%)	3 (3%)	4	21
70	Sc	67/88 (76%)	63 (94%)	3 (4%)	1 (2%)	8	30
71	Sd	96/109 (88%)	91 (95%)	5 (5%)	0	100	100
72	Se	78/81 (96%)	70 (90%)	7 (9%)	1 (1%)	9	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	Sg	58/64 (91%)	53 (91%)	5 (9%)	0	100	100
74	Sh	47/51 (92%)	45 (96%)	2 (4%)	0	100	100
75	Sj	60/69 (87%)	55 (92%)	5 (8%)	0	100	100
77	a	805/898 (90%)	748 (93%)	45 (6%)	12 (2%)	8	30
All	All	10663/12090 (88%)	10027 (94%)	537 (5%)	99 (1%)	16	42

All (99) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	LA	15	VAL
1	LA	231	PRO
2	LB	303	LYS
34	Lh	6	VAL
42	Lq	6	LYS
60	SP	143	SER
61	SQ	38	ASN
65	SV	44	VAL
65	SV	133	ARG
68	SY	17	ASP
68	SY	18	ALA
69	Sb	35	SER
70	Sc	84	MET
77	a	690	PRO
77	a	793	GLU
6	LF	122	LEU
8	LH	207	LEU
9	LI	184	VAL
16	LP	181	LYS
25	LY	49	PRO
27	La	85	LEU
30	Ld	77	SER
30	Ld	98	GLU
47	SB	135	ARG
50	SE	77	ARG
51	SF	65	HIS
52	SG	33	ILE
53	SH	150	SER
58	SM	28	ARG
65	SV	45	ALA
66	SW	66	GLY
69	Sb	102	PRO

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Mol	Chain	Res	Type
72	Se	121	TYR
77	a	534	SER
77	a	535	VAL
77	a	855	SER
77	a	887	VAL
15	LO	81	TYR
16	LP	126	LEU
21	LU	138	ALA
22	LV	13	GLN
32	Lf	56	PRO
32	Lf	92	MET
43	Ls	80	PRO
43	Ls	120	LYS
43	Ls	121	LYS
47	SB	44	SER
54	SI	138	ASP
56	SK	110	LEU
56	SK	167	PRO
58	SM	53	ASP
62	SR	75	ILE
65	SV	101	VAL
77	a	249	CYS
77	a	515	LYS
77	a	889	PRO
2	LB	36	VAL
2	LB	55	HIS
3	LC	292	GLU
8	LH	102	ARG
9	LI	163	THR
10	LJ	137	LYS
14	LN	5	ARG
16	LP	129	GLU
20	LT	4	LYS
24	LX	27	SER
28	Lb	15	ARG
39	Ln	22	ASN
46	SA	109	ILE
47	SB	142	LEU
48	SC	210	ILE
50	SE	244	ARG
56	SK	170	LYS
10	LJ	164	PRO

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Mol	Chain	Res	Type
13	LM	168	ILE
13	LM	175	MET
25	LY	38	VAL
27	La	48	PRO
36	Lj	58	LYS
52	SG	120	VAL
61	SQ	124	ILE
64	SU	46	SER
65	SV	85	LEU
66	SW	27	LYS
77	a	703	LEU
11	LK	201	SER
13	LM	177	VAL
30	Ld	102	ALA
38	Ll	7	GLU
63	ST	130	GLN
77	a	499	PRO
18	LR	8	GLY
22	LV	20	VAL
77	a	777	SER
11	LK	16	PRO
15	LO	185	ARG
47	SB	66	PRO
55	SJ	29	PRO
69	Sb	103	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	LA	188/192 (98%)	132 (70%)	56 (30%)	0	1
2	LB	306/313 (98%)	221 (72%)	85 (28%)	0	1
3	LC	257/263 (98%)	198 (77%)	59 (23%)	1	2
6	LF	231/242 (96%)	163 (71%)	68 (29%)	0	1
7	LG	46/48 (96%)	38 (83%)	8 (17%)	2	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	LH	181/204 (89%)	138 (76%)	43 (24%)	1	2
9	LI	161/198 (81%)	117 (73%)	44 (27%)	0	1
10	LJ	160/164 (98%)	105 (66%)	55 (34%)	0	0
11	LK	162/177 (92%)	109 (67%)	53 (33%)	0	0
12	LL	141/149 (95%)	96 (68%)	45 (32%)	0	0
13	LM	163/197 (83%)	113 (69%)	50 (31%)	0	0
14	LN	108/111 (97%)	73 (68%)	35 (32%)	0	0
15	LO	174/175 (99%)	128 (74%)	46 (26%)	0	1
16	LP	156/165 (94%)	106 (68%)	50 (32%)	0	0
17	LQ	130/139 (94%)	86 (66%)	44 (34%)	0	0
18	LR	153/155 (99%)	109 (71%)	44 (29%)	0	1
19	LS	155/167 (93%)	109 (70%)	46 (30%)	0	1
20	LT	151/154 (98%)	108 (72%)	43 (28%)	0	1
21	LU	128/133 (96%)	84 (66%)	44 (34%)	0	0
22	LV	96/110 (87%)	53 (55%)	43 (45%)	0	0
23	LW	108/114 (95%)	76 (70%)	32 (30%)	0	1
24	LX	61/174 (35%)	40 (66%)	21 (34%)	0	0
25	LY	102/123 (83%)	77 (76%)	25 (24%)	1	2
26	LZ	114/115 (99%)	77 (68%)	37 (32%)	0	0
27	La	107/119 (90%)	64 (60%)	43 (40%)	0	0
28	Lb	126/127 (99%)	97 (77%)	29 (23%)	1	2
29	Lc	47/57 (82%)	35 (74%)	12 (26%)	0	1
30	Ld	85/92 (92%)	57 (67%)	28 (33%)	0	0
31	Le	85/92 (92%)	69 (81%)	16 (19%)	1	6
32	Lf	111/120 (92%)	76 (68%)	35 (32%)	0	0
33	Lg	81/103 (79%)	57 (70%)	24 (30%)	0	1
34	Lh	91/100 (91%)	69 (76%)	22 (24%)	1	2
35	Li	99/107 (92%)	66 (67%)	33 (33%)	0	0
36	Lj	71/78 (91%)	47 (66%)	24 (34%)	0	0
37	Lk	72/74 (97%)	49 (68%)	23 (32%)	0	0
38	Ll	61/68 (90%)	32 (52%)	29 (48%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	Ln	173/189 (92%)	79 (46%)	94 (54%)	0	0
40	Lo	22/22 (100%)	14 (64%)	8 (36%)	0	0
41	Lp	82/93 (88%)	59 (72%)	23 (28%)	0	1
42	Lq	67/73 (92%)	45 (67%)	22 (33%)	0	0
43	Ls	41/110 (37%)	28 (68%)	13 (32%)	0	0
46	SA	170/217 (78%)	106 (62%)	64 (38%)	0	0
47	SB	172/201 (86%)	101 (59%)	71 (41%)	0	0
48	SC	170/182 (93%)	107 (63%)	63 (37%)	0	0
49	SD	201/220 (91%)	135 (67%)	66 (33%)	0	0
50	SE	228/232 (98%)	130 (57%)	98 (43%)	0	0
51	SF	148/157 (94%)	94 (64%)	54 (36%)	0	0
52	SG	193/213 (91%)	100 (52%)	93 (48%)	0	0
53	SH	165/170 (97%)	97 (59%)	68 (41%)	0	0
54	SI	138/148 (93%)	80 (58%)	58 (42%)	0	0
55	SJ	114/115 (99%)	72 (63%)	42 (37%)	0	0
56	SK	154/164 (94%)	100 (65%)	54 (35%)	0	0
57	SL	90/119 (76%)	55 (61%)	35 (39%)	0	0
58	SM	131/136 (96%)	91 (70%)	40 (30%)	0	0
59	SO	108/114 (95%)	65 (60%)	43 (40%)	0	0
60	SP	125/130 (96%)	84 (67%)	41 (33%)	0	0
61	SQ	86/113 (76%)	58 (67%)	28 (33%)	0	0
62	SR	100/128 (78%)	68 (68%)	32 (32%)	0	0
63	ST	125/130 (96%)	69 (55%)	56 (45%)	0	0
64	SU	58/124 (47%)	38 (66%)	20 (34%)	0	0
65	SV	118/131 (90%)	67 (57%)	51 (43%)	0	0
66	SW	114/115 (99%)	68 (60%)	46 (40%)	0	0
67	SX	91/110 (83%)	60 (66%)	31 (34%)	0	0
68	SY	65/72 (90%)	36 (55%)	29 (45%)	0	0
69	Sb	103/113 (91%)	54 (52%)	49 (48%)	0	0
70	Sc	63/79 (80%)	39 (62%)	24 (38%)	0	0
71	Sd	92/103 (89%)	65 (71%)	27 (29%)	0	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	Se	72/73 (99%)	38 (53%)	34 (47%)	0	0
73	Sg	53/57 (93%)	21 (40%)	32 (60%)	0	0
74	Sh	43/45 (96%)	22 (51%)	21 (49%)	0	0
75	Sj	56/58 (97%)	25 (45%)	31 (55%)	0	0
77	a	697/765 (91%)	442 (63%)	255 (37%)	0	0
All	All	9296/10340 (90%)	6086 (66%)	3210 (34%)	1	0

All (3210) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	LA	6	ARG
1	LA	10	LYS
1	LA	15	VAL
1	LA	17	ARG
1	LA	20	VAL
1	LA	44	VAL
1	LA	46	LYS
1	LA	48	ILE
1	LA	49	LEU
1	LA	52	ARG
1	LA	58	LEU
1	LA	60	ARG
1	LA	61	VAL
1	LA	62	GLN
1	LA	67	ARG
1	LA	72	VAL
1	LA	73	ASN
1	LA	77	ILE
1	LA	82	MET
1	LA	93	LYS
1	LA	98	ILE
1	LA	102	LEU
1	LA	109	GLU
1	LA	112	TYR
1	LA	113	VAL
1	LA	122	ASP
1	LA	123	ARG
1	LA	132	THR
1	LA	135	LEU
1	LA	141	MET

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Mol	Chain	Res	Type
1	LA	143	THR
1	LA	144	ASN
1	LA	145	LYS
1	LA	148	ILE
1	LA	149	ARG
1	LA	154	GLN
1	LA	155	LYS
1	LA	161	LYS
1	LA	165	MET
1	LA	168	LEU
1	LA	174	ARG
1	LA	175	THR
1	LA	177	LYS
1	LA	180	LEU
1	LA	190	LYS
1	LA	195	CYS
1	LA	217	GLN
1	LA	219	ILE
1	LA	221	VAL
1	LA	223	SER
1	LA	225	VAL
1	LA	231	PRO
1	LA	235	VAL
1	LA	243	THR
1	LA	245	CYS
1	LA	246	SER
2	LB	5	LYS
2	LB	11	LYS
2	LB	19	ARG
2	LB	23	THR
2	LB	28	ARG
2	LB	29	CYS
2	LB	43	LEU
2	LB	47	LEU
2	LB	50	LYS
2	LB	54	THR
2	LB	55	HIS
2	LB	56	VAL
2	LB	57	MET
2	LB	73	ILE
2	LB	74	ASP
2	LB	86	CYS

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Mol	Chain	Res	Type
2	LB	87	THR
2	LB	90	ILE
2	LB	96	PRO
2	LB	97	LYS
2	LB	102	VAL
2	LB	104	THR
2	LB	117	ARG
2	LB	127	LYS
2	LB	136	LYS
2	LB	141	THR
2	LB	145	GLU
2	LB	146	GLN
2	LB	159	ILE
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	190	GLU
2	LB	191	LYS
2	LB	192	VAL
2	LB	199	MET
2	LB	201	LYS
2	LB	203	ILE
2	LB	205	ILE
2	LB	207	ASP
2	LB	210	SER
2	LB	215	ILE
2	LB	217	THR
2	LB	224	ARG
2	LB	229	VAL
2	LB	231	THR
2	LB	235	VAL
2	LB	240	ARG
2	LB	241	LYS
2	LB	243	ARG
2	LB	244	ARG
2	LB	246	ASN
2	LB	248	LYS
2	LB	251	CYS
2	LB	275	ARG

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Mol	Chain	Res	Type
2	LB	277	ASP
2	LB	281	GLN
2	LB	285	ILE
2	LB	292	ARG
2	LB	295	THR
2	LB	302	ASP
2	LB	303	LYS
2	LB	308	VAL
2	LB	312	VAL
2	LB	316	ARG
2	LB	318	GLN
2	LB	322	ILE
2	LB	325	LYS
2	LB	327	THR
2	LB	328	CYS
2	LB	332	LYS
2	LB	336	VAL
2	LB	343	LEU
2	LB	346	ARG
2	LB	348	CYS
2	LB	351	VAL
2	LB	352	GLN
2	LB	356	ILE
2	LB	358	THR
2	LB	360	SER
2	LB	370	VAL
2	LB	371	GLU
3	LC	2	ASN
3	LC	6	LYS
3	LC	11	THR
3	LC	13	THR
3	LC	14	GLN
3	LC	15	VAL
3	LC	22	LYS
3	LC	28	LEU
3	LC	32	ILE
3	LC	47	PRO
3	LC	57	GLN
3	LC	63	TRP
3	LC	67	ARG
3	LC	72	LEU
3	LC	79	ILE

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Mol	Chain	Res	Type
3	LC	99	ARG
3	LC	104	LYS
3	LC	105	VAL
3	LC	121	SER
3	LC	130	ARG
3	LC	134	ILE
3	LC	140	ILE
3	LC	147	ASP
3	LC	153	LYS
3	LC	156	LEU
3	LC	159	ILE
3	LC	160	LYS
3	LC	162	VAL
3	LC	168	VAL
3	LC	177	ILE
3	LC	178	ARG
3	LC	181	ARG
3	LC	184	MET
3	LC	186	ASN
3	LC	190	ILE
3	LC	197	VAL
3	LC	198	ILE
3	LC	202	GLU
3	LC	206	ARG
3	LC	211	LEU
3	LC	216	LEU
3	LC	217	CYS
3	LC	219	VAL
3	LC	220	SER
3	LC	221	SER
3	LC	222	ILE
3	LC	231	SER
3	LC	238	LEU
3	LC	241	LYS
3	LC	258	THR
3	LC	275	SER
3	LC	276	ASP
3	LC	280	LYS
3	LC	281	THR
3	LC	285	LYS
3	LC	286	ARG
3	LC	292	GLU

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Mol	Chain	Res	Type
3	LC	301	LYS
3	LC	310	SER
6	LF	5	LYS
6	LF	6	VAL
6	LF	9	THR
6	LF	11	SER
6	LF	24	ARG
6	LF	33	ARG
6	LF	34	LYS
6	LF	37	ILE
6	LF	38	ILE
6	LF	41	LYS
6	LF	52	VAL
6	LF	53	VAL
6	LF	56	THR
6	LF	58	LYS
6	LF	60	ILE
6	LF	61	ILE
6	LF	64	VAL
6	LF	69	LEU
6	LF	72	ASP
6	LF	73	ARG
6	LF	75	VAL
6	LF	76	CYS
6	LF	82	GLU
6	LF	93	THR
6	LF	103	LEU
6	LF	105	CYS
6	LF	110	LEU
6	LF	117	ILE
6	LF	118	LYS
6	LF	119	GLU
6	LF	122	LEU
6	LF	130	ASP
6	LF	131	LYS
6	LF	133	THR
6	LF	135	GLU
6	LF	140	ASP
6	LF	143	GLU
6	LF	145	GLU
6	LF	146	GLU
6	LF	162	SER

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Mol	Chain	Res	Type
6	LF	163	THR
6	LF	167	VAL
6	LF	171	MET
6	LF	175	VAL
6	LF	179	LEU
6	LF	180	ASN
6	LF	181	ILE
6	LF	183	HIS
6	LF	186	LYS
6	LF	193	LYS
6	LF	206	MET
6	LF	208	LYS
6	LF	226	ARG
6	LF	227	LYS
6	LF	230	SER
6	LF	231	LYS
6	LF	240	LEU
6	LF	241	ARG
6	LF	245	MET
6	LF	247	THR
6	LF	253	ILE
6	LF	261	LYS
6	LF	268	LYS
6	LF	274	ARG
6	LF	275	LEU
6	LF	278	LYS
6	LF	288	LYS
6	LF	289	LEU
7	LG	5	LYS
7	LG	8	SER
7	LG	15	LYS
7	LG	18	LYS
7	LG	22	ASN
7	LG	35	LYS
7	LG	36	THR
7	LG	46	ARG
8	LH	35	VAL
8	LH	36	LYS
8	LH	37	ASP
8	LH	41	LYS
8	LH	52	ASP
8	LH	56	SER

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Mol	Chain	Res	Type
8	LH	59	LYS
8	LH	63	ASN
8	LH	65	LEU
8	LH	68	ASN
8	LH	70	LEU
8	LH	77	LYS
8	LH	82	VAL
8	LH	84	ILE
8	LH	90	VAL
8	LH	101	LEU
8	LH	102	ARG
8	LH	116	LYS
8	LH	125	VAL
8	LH	126	ASP
8	LH	127	HIS
8	LH	133	GLU
8	LH	136	VAL
8	LH	138	THR
8	LH	142	LEU
8	LH	145	LYS
8	LH	154	GLN
8	LH	165	ASP
8	LH	170	LYS
8	LH	174	LEU
8	LH	180	VAL
8	LH	182	GLU
8	LH	183	ILE
8	LH	186	CYS
8	LH	188	SER
8	LH	189	SER
8	LH	202	LEU
8	LH	210	LYS
8	LH	219	ASP
8	LH	220	PHE
8	LH	225	LYS
8	LH	229	GLU
8	LH	233	ARG
9	LI	29	THR
9	LI	47	LEU
9	LI	52	LYS
9	LI	56	THR
9	LI	64	ILE

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Mol	Chain	Res	Type
9	LI	65	SER
9	LI	66	ARG
9	LI	72	ILE
9	LI	80	SER
9	LI	82	GLU
9	LI	83	SER
9	LI	88	LYS
9	LI	90	ARG
9	LI	91	LEU
9	LI	92	LEU
9	LI	93	GLN
9	LI	94	ILE
9	LI	108	SER
9	LI	110	LYS
9	LI	113	ILE
9	LI	117	ILE
9	LI	120	ILE
9	LI	130	LYS
9	LI	134	ILE
9	LI	141	LEU
9	LI	142	GLU
9	LI	143	LEU
9	LI	153	LYS
9	LI	160	ILE
9	LI	162	ARG
9	LI	164	LYS
9	LI	173	LEU
9	LI	175	LYS
9	LI	179	VAL
9	LI	180	CYS
9	LI	182	THR
9	LI	183	ASP
9	LI	187	GLU
9	LI	191	THR
9	LI	199	VAL
9	LI	207	LYS
9	LI	209	MET
9	LI	210	LYS
9	LI	217	ARG
10	LJ	8	THR
10	LJ	9	ILE
10	LJ	13	THR

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Mol	Chain	Res	Type
10	LJ	15	VAL
10	LJ	16	GLU
10	LJ	17	CYS
10	LJ	18	THR
10	LJ	23	VAL
10	LJ	25	THR
10	LJ	29	LYS
10	LJ	30	LYS
10	LJ	32	THR
10	LJ	42	LEU
10	LJ	44	ILE
10	LJ	45	THR
10	LJ	46	HIS
10	LJ	49	ASP
10	LJ	61	LYS
10	LJ	62	ARG
10	LJ	68	THR
10	LJ	70	CYS
10	LJ	78	LYS
10	LJ	85	GLU
10	LJ	89	ARG
10	LJ	90	LEU
10	LJ	97	ILE
10	LJ	100	THR
10	LJ	102	VAL
10	LJ	104	ASN
10	LJ	108	ILE
10	LJ	109	GLU
10	LJ	110	ILE
10	LJ	114	MET
10	LJ	117	ILE
10	LJ	118	LYS
10	LJ	119	THR
10	LJ	120	ARG
10	LJ	128	VAL
10	LJ	130	ILE
10	LJ	133	SER
10	LJ	134	THR
10	LJ	136	VAL
10	LJ	139	GLU
10	LJ	141	ILE
10	LJ	142	LEU

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Mol	Chain	Res	Type
10	LJ	143	ARG
10	LJ	159	GLU
10	LJ	168	LEU
10	LJ	170	LYS
10	LJ	173	ASP
10	LJ	177	VAL
10	LJ	178	SER
10	LJ	179	SER
10	LJ	180	ARG
10	LJ	182	LEU
11	LK	15	LYS
11	LK	16	PRO
11	LK	24	ARG
11	LK	26	VAL
11	LK	28	ASP
11	LK	31	ILE
11	LK	32	ARG
11	LK	39	ARG
11	LK	42	LYS
11	LK	43	VAL
11	LK	54	SER
11	LK	58	GLU
11	LK	63	GLU
11	LK	68	CYS
11	LK	69	ARG
11	LK	70	ILE
11	LK	72	CYS
11	LK	73	ASN
11	LK	74	LYS
11	LK	76	ILE
11	LK	78	LYS
11	LK	82	LYS
11	LK	87	LEU
11	LK	89	ILE
11	LK	91	VAL
11	LK	97	ILE
11	LK	101	LYS
11	LK	123	GLN
11	LK	126	VAL
11	LK	133	GLN
11	LK	135	LEU
11	LK	139	ARG

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Mol	Chain	Res	Type
11	LK	145	LYS
11	LK	148	VAL
11	LK	149	LYS
11	LK	158	LYS
11	LK	159	ILE
11	LK	162	ARG
11	LK	163	GLN
11	LK	165	ILE
11	LK	166	VAL
11	LK	168	SER
11	LK	169	ARG
11	LK	174	THR
11	LK	177	THR
11	LK	178	LYS
11	LK	183	ASP
11	LK	190	LEU
11	LK	199	ARG
11	LK	201	SER
11	LK	203	LYS
11	LK	206	LEU
11	LK	207	ASN
12	LL	12	ILE
12	LL	18	VAL
12	LL	19	LEU
12	LL	21	ILE
12	LL	23	ILE
12	LL	28	ASP
12	LL	30	LEU
12	LL	32	LYS
12	LL	44	GLU
12	LL	48	SER
12	LL	49	LYS
12	LL	53	THR
12	LL	54	ILE
12	LL	64	LYS
12	LL	67	THR
12	LL	69	VAL
12	LL	71	VAL
12	LL	77	ARG
12	LL	78	GLU
12	LL	81	GLU
12	LL	84	LEU

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Mol	Chain	Res	Type
12	LL	85	ARG
12	LL	87	LYS
12	LL	88	ASN
12	LL	91	LEU
12	LL	107	THR
12	LL	110	ILE
12	LL	111	ASP
12	LL	112	LEU
12	LL	114	ILE
12	LL	115	LYS
12	LL	122	ILE
12	LL	123	TYR
12	LL	125	MET
12	LL	126	ASP
12	LL	132	SER
12	LL	137	ARG
12	LL	142	ARG
12	LL	148	VAL
12	LL	151	SER
12	LL	155	THR
12	LL	157	ASP
12	LL	165	ARG
12	LL	169	VAL
12	LL	170	VAL
13	LM	33	VAL
13	LM	36	SER
13	LM	37	ASN
13	LM	42	LYS
13	LM	44	THR
13	LM	46	LYS
13	LM	51	ILE
13	LM	52	LYS
13	LM	56	ASN
13	LM	65	ARG
13	LM	70	GLN
13	LM	71	LYS
13	LM	75	ILE
13	LM	80	LEU
13	LM	88	THR
13	LM	97	THR
13	LM	100	ILE
13	LM	112	VAL

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Mol	Chain	Res	Type
13	LM	115	SER
13	LM	122	ILE
13	LM	129	ARG
13	LM	131	LYS
13	LM	132	ASN
13	LM	133	LYS
13	LM	134	SER
13	LM	138	VAL
13	LM	150	SER
13	LM	153	THR
13	LM	154	ILE
13	LM	156	SER
13	LM	164	ILE
13	LM	165	GLN
13	LM	166	GLN
13	LM	173	VAL
13	LM	174	VAL
13	LM	175	MET
13	LM	181	LYS
13	LM	183	VAL
13	LM	185	THR
13	LM	186	THR
13	LM	189	ILE
13	LM	193	LYS
13	LM	194	LYS
13	LM	196	VAL
13	LM	198	GLU
13	LM	199	ASN
13	LM	211	ARG
13	LM	218	LYS
13	LM	223	ARG
13	LM	224	GLU
14	LN	13	VAL
14	LN	15	LEU
14	LN	21	LYS
14	LN	23	LYS
14	LN	26	VAL
14	LN	29	ASP
14	LN	31	LEU
14	LN	32	SER
14	LN	36	VAL
14	LN	38	ILE

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Mol	Chain	Res	Type
14	LN	43	THR
14	LN	46	LYS
14	LN	47	ARG
14	LN	51	SER
14	LN	52	LEU
14	LN	53	ARG
14	LN	56	MET
14	LN	58	THR
14	LN	59	ASP
14	LN	61	VAL
14	LN	62	ILE
14	LN	64	ILE
14	LN	65	SER
14	LN	77	ILE
14	LN	80	SER
14	LN	83	ILE
14	LN	94	LYS
14	LN	98	GLN
14	LN	103	LYS
14	LN	120	LYS
14	LN	124	LYS
14	LN	125	ARG
14	LN	126	ILE
14	LN	129	SER
14	LN	131	LYS
15	LO	7	VAL
15	LO	9	GLU
15	LO	15	GLN
15	LO	16	SER
15	LO	19	LEU
15	LO	27	THR
15	LO	29	GLU
15	LO	31	ARG
15	LO	40	SER
15	LO	54	LYS
15	LO	56	LYS
15	LO	60	VAL
15	LO	61	VAL
15	LO	66	VAL
15	LO	71	ARG
15	LO	75	CYS
15	LO	79	ILE

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Mol	Chain	Res	Type
15	LO	80	SER
15	LO	83	LYS
15	LO	85	ARG
15	LO	89	ILE
15	LO	90	VAL
15	LO	93	LYS
15	LO	97	SER
15	LO	101	LEU
15	LO	104	GLN
15	LO	110	LEU
15	LO	112	SER
15	LO	117	ASN
15	LO	118	SER
15	LO	131	GLU
15	LO	135	ILE
15	LO	149	ASN
15	LO	151	ILE
15	LO	153	ASN
15	LO	157	LYS
15	LO	159	ARG
15	LO	176	ASN
15	LO	177	LYS
15	LO	179	ILE
15	LO	184	LEU
15	LO	185	ARG
15	LO	187	SER
15	LO	197	THR
15	LO	200	LEU
15	LO	204	ARG
16	LP	16	LEU
16	LP	20	VAL
16	LP	29	GLU
16	LP	30	VAL
16	LP	32	LEU
16	LP	36	GLU
16	LP	40	ILE
16	LP	45	ARG
16	LP	48	LYS
16	LP	52	LEU
16	LP	53	LYS
16	LP	54	LYS
16	LP	64	LEU

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Mol	Chain	Res	Type
16	LP	85	ILE
16	LP	89	THR
16	LP	93	SER
16	LP	96	MET
16	LP	97	SER
16	LP	100	ARG
16	LP	101	VAL
16	LP	103	ASP
16	LP	105	ILE
16	LP	108	CYS
16	LP	109	CYS
16	LP	111	ARG
16	LP	113	LYS
16	LP	116	VAL
16	LP	117	CYS
16	LP	119	SER
16	LP	126	LEU
16	LP	127	ARG
16	LP	129	GLU
16	LP	130	ARG
16	LP	132	ARG
16	LP	134	GLU
16	LP	149	ASP
16	LP	150	VAL
16	LP	155	LYS
16	LP	156	ARG
16	LP	157	ARG
16	LP	160	GLU
16	LP	161	CYS
16	LP	167	ASP
16	LP	168	LYS
16	LP	169	ILE
16	LP	173	LYS
16	LP	180	GLU
16	LP	181	LYS
16	LP	184	GLU
16	LP	191	GLU
17	LQ	3	LYS
17	LQ	9	ASP
17	LQ	11	LEU
17	LQ	12	LEU
17	LQ	15	LYS

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Mol	Chain	Res	Type
17	LQ	17	ARG
17	LQ	18	ARG
17	LQ	22	LYS
17	LQ	24	SER
17	LQ	35	ILE
17	LQ	36	LYS
17	LQ	40	VAL
17	LQ	41	LYS
17	LQ	51	LEU
17	LQ	54	LYS
17	LQ	57	VAL
17	LQ	61	LYS
17	LQ	68	ARG
17	LQ	73	ARG
17	LQ	77	THR
17	LQ	78	ASP
17	LQ	87	VAL
17	LQ	89	VAL
17	LQ	91	LYS
17	LQ	99	SER
17	LQ	102	LYS
17	LQ	106	LYS
17	LQ	107	LYS
17	LQ	110	ASP
17	LQ	111	GLU
17	LQ	114	VAL
17	LQ	119	VAL
17	LQ	123	ARG
17	LQ	125	ARG
17	LQ	126	ARG
17	LQ	127	ARG
17	LQ	128	ARG
17	LQ	129	THR
17	LQ	131	ARG
17	LQ	135	ARG
17	LQ	138	LYS
17	LQ	144	CYS
17	LQ	147	GLU
17	LQ	150	VAL
18	LR	3	ILE
18	LR	5	LEU
18	LR	6	LYS

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Mol	Chain	Res	Type
18	LR	7	THR
18	LR	11	LYS
18	LR	12	ARG
18	LR	13	LYS
18	LR	14	VAL
18	LR	17	LYS
18	LR	21	SER
18	LR	29	LEU
18	LR	40	THR
18	LR	45	THR
18	LR	47	VAL
18	LR	54	LEU
18	LR	55	SER
18	LR	61	VAL
18	LR	63	SER
18	LR	66	ARG
18	LR	73	LYS
18	LR	74	ARG
18	LR	75	GLU
18	LR	80	VAL
18	LR	81	VAL
18	LR	83	SER
18	LR	93	THR
18	LR	94	ILE
18	LR	96	ARG
18	LR	107	THR
18	LR	110	SER
18	LR	120	MET
18	LR	123	ASP
18	LR	126	LEU
18	LR	133	ASP
18	LR	136	VAL
18	LR	137	LEU
18	LR	141	ARG
18	LR	150	LYS
18	LR	153	SER
18	LR	162	LYS
18	LR	168	LYS
18	LR	170	ARG
18	LR	174	ARG
18	LR	176	ARG
19	LS	23	ARG

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Mol	Chain	Res	Type
19	LS	30	LYS
19	LS	32	ILE
19	LS	34	GLN
19	LS	37	SER
19	LS	39	GLU
19	LS	42	ARG
19	LS	47	SER
19	LS	48	LYS
19	LS	52	LYS
19	LS	53	LEU
19	LS	56	LYS
19	LS	58	SER
19	LS	59	SER
19	LS	60	ARG
19	LS	62	ARG
19	LS	70	LYS
19	LS	71	ARG
19	LS	74	ARG
19	LS	76	SER
19	LS	80	LYS
19	LS	89	MET
19	LS	94	LEU
19	LS	110	ARG
19	LS	114	LYS
19	LS	116	ASP
19	LS	133	LYS
19	LS	135	LYS
19	LS	139	LEU
19	LS	145	MET
19	LS	147	LYS
19	LS	148	GLU
19	LS	149	GLN
19	LS	151	LEU
19	LS	154	LYS
19	LS	155	LYS
19	LS	156	LYS
19	LS	160	GLU
19	LS	161	GLN
19	LS	164	LYS
19	LS	169	ARG
19	LS	172	GLU
19	LS	173	ARG

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Mol	Chain	Res	Type
19	LS	176	LYS
19	LS	181	ARG
19	LS	182	LEU
20	LT	2	MET
20	LT	6	ILE
20	LT	11	ARG
20	LT	14	SER
20	LT	15	GLU
20	LT	21	GLU
20	LT	24	ARG
20	LT	43	LEU
20	LT	44	LYS
20	LT	50	LYS
20	LT	51	ARG
20	LT	56	ILE
20	LT	57	LEU
20	LT	63	GLU
20	LT	64	GLU
20	LT	67	ASP
20	LT	70	LYS
20	LT	74	VAL
20	LT	75	LEU
20	LT	76	LEU
20	LT	89	ARG
20	LT	91	VAL
20	LT	92	ARG
20	LT	94	THR
20	LT	95	THR
20	LT	100	MET
20	LT	110	GLN
20	LT	123	VAL
20	LT	124	LYS
20	LT	126	VAL
20	LT	134	GLU
20	LT	135	LYS
20	LT	141	GLN
20	LT	144	VAL
20	LT	145	ARG
20	LT	150	CYS
20	LT	153	VAL
20	LT	155	VAL
20	LT	156	LYS

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Mol	Chain	Res	Type
20	LT	160	ARG
20	LT	163	ARG
20	LT	165	GLN
20	LT	167	ARG
21	LU	5	GLN
21	LU	14	CYS
21	LU	24	MET
21	LU	26	ASN
21	LU	27	LEU
21	LU	28	THR
21	LU	32	ARG
21	LU	35	LYS
21	LU	36	LEU
21	LU	38	GLN
21	LU	43	LYS
21	LU	44	VAL
21	LU	60	ARG
21	LU	63	THR
21	LU	70	ARG
21	LU	75	GLN
21	LU	76	ILE
21	LU	79	ARG
21	LU	84	ILE
21	LU	87	LYS
21	LU	91	VAL
21	LU	92	ARG
21	LU	93	LEU
21	LU	96	VAL
21	LU	101	CYS
21	LU	103	LYS
21	LU	106	LEU
21	LU	116	ARG
21	LU	120	LYS
21	LU	121	GLU
21	LU	122	THR
21	LU	126	VAL
21	LU	130	LYS
21	LU	131	ARG
21	LU	133	ASN
21	LU	140	HIS
21	LU	141	VAL
21	LU	146	SER

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Mol	Chain	Res	Type
21	LU	149	ASP
21	LU	150	ILE
21	LU	151	THR
21	LU	153	LEU
21	LU	154	LYS
21	LU	156	ASP
22	LV	11	LYS
22	LV	15	ASN
22	LV	16	ILE
22	LV	17	ARG
22	LV	20	VAL
22	LV	21	ASP
22	LV	23	SER
22	LV	26	LYS
22	LV	27	ASP
22	LV	30	LEU
22	LV	31	ASN
22	LV	40	ARG
22	LV	44	LYS
22	LV	45	ILE
22	LV	46	ASN
22	LV	54	GLU
22	LV	55	LYS
22	LV	59	SER
22	LV	61	GLU
22	LV	63	ASP
22	LV	65	LEU
22	LV	67	ILE
22	LV	69	THR
22	LV	70	THR
22	LV	73	GLU
22	LV	87	LEU
22	LV	89	GLN
22	LV	91	TYR
22	LV	92	GLN
22	LV	94	VAL
22	LV	96	ARG
22	LV	97	VAL
22	LV	98	LEU
22	LV	100	THR
22	LV	102	LYS
22	LV	104	THR

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Mol	Chain	Res	Type
22	LV	106	THR
22	LV	108	LYS
22	LV	110	TYR
22	LV	112	ILE
22	LV	113	GLU
22	LV	115	ASP
22	LV	118	GLU
23	LW	15	PHE
23	LW	18	SER
23	LW	27	ILE
23	LW	31	ASP
23	LW	37	SER
23	LW	38	LEU
23	LW	39	ASN
23	LW	44	LYS
23	LW	47	LYS
23	LW	52	ARG
23	LW	55	LYS
23	LW	61	MET
23	LW	65	THR
23	LW	69	ASP
23	LW	76	ARG
23	LW	77	LYS
23	LW	79	THR
23	LW	82	VAL
23	LW	88	LYS
23	LW	92	ARG
23	LW	93	LYS
23	LW	98	ILE
23	LW	108	ILE
23	LW	114	LEU
23	LW	115	LYS
23	LW	117	SER
23	LW	120	THR
23	LW	123	VAL
23	LW	125	LYS
23	LW	139	GLU
23	LW	140	CYS
23	LW	142	HIS
24	LX	3	ARG
24	LX	4	ILE
24	LX	5	GLU

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Mol	Chain	Res	Type
24	LX	6	HIS
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	42	LYS
24	LX	43	MET
24	LX	44	LYS
24	LX	50	VAL
24	LX	54	LYS
24	LX	56	TYR
24	LX	59	LEU
24	LX	64	MET
25	LY	35	LYS
25	LY	44	LEU
25	LY	48	ASN
25	LY	50	ILE
25	LY	51	LYS
25	LY	52	LYS
25	LY	56	ASP
25	LY	66	ILE
25	LY	70	GLU
25	LY	73	THR
25	LY	75	ILE
25	LY	76	GLU
25	LY	77	LYS
25	LY	80	THR
25	LY	83	PHE
25	LY	87	ARG
25	LY	95	ARG
25	LY	96	LYS
25	LY	105	LYS
25	LY	108	ARG
25	LY	113	ILE
25	LY	116	LEU
25	LY	118	LEU
25	LY	128	ASP

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Mol	Chain	Res	Type
25	LY	132	MET
26	LZ	8	THR
26	LZ	10	SER
26	LZ	12	ARG
26	LZ	32	SER
26	LZ	38	LEU
26	LZ	43	LYS
26	LZ	46	THR
26	LZ	47	MET
26	LZ	50	ARG
26	LZ	51	ARG
26	LZ	54	ILE
26	LZ	55	VAL
26	LZ	56	GLU
26	LZ	59	THR
26	LZ	63	LYS
26	LZ	67	LYS
26	LZ	68	VAL
26	LZ	69	VAL
26	LZ	74	ARG
26	LZ	80	VAL
26	LZ	85	GLN
26	LZ	88	ARG
26	LZ	93	LYS
26	LZ	95	VAL
26	LZ	99	ILE
26	LZ	102	SER
26	LZ	104	CYS
26	LZ	105	ILE
26	LZ	106	ILE
26	LZ	111	MET
26	LZ	115	ARG
26	LZ	122	ARG
26	LZ	123	GLN
26	LZ	124	GLU
26	LZ	129	ARG
26	LZ	130	LEU
26	LZ	132	ARG
27	La	5	ILE
27	La	7	LYS
27	La	13	ILE
27	La	25	VAL

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Mol	Chain	Res	Type
27	La	27	VAL
27	La	28	GLU
27	La	37	SER
27	La	41	VAL
27	La	50	ARG
27	La	51	ILE
27	La	52	THR
27	La	65	ARG
27	La	66	VAL
27	La	68	SER
27	La	71	LYS
27	La	72	CYS
27	La	73	MET
27	La	75	VAL
27	La	76	ASN
27	La	84	ARG
27	La	85	LEU
27	La	88	ASN
27	La	90	LYS
27	La	91	ASP
27	La	92	PHE
27	La	93	ILE
27	La	94	SER
27	La	95	THR
27	La	98	VAL
27	La	100	ASP
27	La	102	THR
27	La	103	LYS
27	La	104	ARG
27	La	107	ILE
27	La	108	ILE
27	La	113	LYS
27	La	117	ARG
27	La	119	ILE
27	La	124	ASP
27	La	125	THR
27	La	129	THR
27	La	130	LYS
27	La	134	ASP
28	Lb	2	PRO
28	Lb	4	ARG
28	Lb	7	LYS

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Mol	Chain	Res	Type
28	Lb	10	LYS
28	Lb	17	MET
28	Lb	26	ARG
28	Lb	27	LYS
28	Lb	30	SER
28	Lb	43	THR
28	Lb	55	LYS
28	Lb	58	MET
28	Lb	65	ARG
28	Lb	67	ILE
28	Lb	75	ILE
28	Lb	77	LYS
28	Lb	78	ILE
28	Lb	80	SER
28	Lb	82	ILE
28	Lb	85	GLU
28	Lb	96	THR
28	Lb	98	GLU
28	Lb	106	ARG
28	Lb	117	SER
28	Lb	121	CYS
28	Lb	128	ARG
28	Lb	136	LYS
28	Lb	139	ARG
28	Lb	141	VAL
28	Lb	148	VAL
29	Lc	6	ASN
29	Lc	8	THR
29	Lc	10	LYS
29	Lc	11	ASN
29	Lc	26	LYS
29	Lc	27	SER
29	Lc	33	LYS
29	Lc	38	LYS
29	Lc	46	SER
29	Lc	52	ARG
29	Lc	54	SER
29	Lc	56	ARG
30	Ld	13	SER
30	Ld	15	SER
30	Ld	20	LEU
30	Ld	21	VAL

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Mol	Chain	Res	Type
30	Ld	23	LYS
30	Ld	26	LYS
30	Ld	28	THR
30	Ld	39	ARG
30	Ld	46	VAL
30	Ld	47	PHE
30	Ld	50	ASN
30	Ld	55	LEU
30	Ld	57	LYS
30	Ld	58	SER
30	Ld	63	LEU
30	Ld	68	LYS
30	Ld	71	VAL
30	Ld	72	ARG
30	Ld	73	VAL
30	Ld	79	ARG
30	Ld	93	ILE
30	Ld	94	MET
30	Ld	95	THR
30	Ld	96	ILE
30	Ld	98	GLU
30	Ld	104	LEU
30	Ld	105	THR
30	Ld	107	ILE
31	Le	4	VAL
31	Le	8	THR
31	Le	16	ARG
31	Le	22	LYS
31	Le	26	ILE
31	Le	45	ARG
31	Le	63	PRO
31	Le	72	LEU
31	Le	75	ASP
31	Le	77	GLU
31	Le	83	VAL
31	Le	84	ILE
31	Le	86	LYS
31	Le	92	LYS
31	Le	95	THR
31	Le	99	LYS
32	Lf	9	LEU
32	Lf	13	ILE

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Mol	Chain	Res	Type
32	Lf	16	LYS
32	Lf	17	LYS
32	Lf	19	LYS
32	Lf	20	ASN
32	Lf	21	LYS
32	Lf	23	ILE
32	Lf	24	ARG
32	Lf	34	LYS
32	Lf	36	SER
32	Lf	43	ILE
32	Lf	52	ARG
32	Lf	57	MET
32	Lf	60	ILE
32	Lf	65	ASP
32	Lf	72	LEU
32	Lf	79	HIS
32	Lf	81	ILE
32	Lf	82	SER
32	Lf	85	HIS
32	Lf	88	LYS
32	Lf	90	LEU
32	Lf	91	PHE
32	Lf	95	LYS
32	Lf	96	THR
32	Lf	97	HIS
32	Lf	100	GLN
32	Lf	101	ILE
32	Lf	105	VAL
32	Lf	109	SER
32	Lf	110	ARG
32	Lf	118	LYS
32	Lf	119	LYS
32	Lf	122	VAL
33	Lg	4	ILE
33	Lg	5	LYS
33	Lg	7	LYS
33	Lg	8	THR
33	Lg	9	PHE
33	Lg	15	VAL
33	Lg	23	LYS
33	Lg	27	ASN
33	Lg	28	VAL

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Mol	Chain	Res	Type
33	Lg	36	ILE
33	Lg	37	TYR
33	Lg	38	THR
33	Lg	41	GLU
33	Lg	44	LYS
33	Lg	46	LEU
33	Lg	48	ARG
33	Lg	56	LYS
33	Lg	57	SER
33	Lg	59	LYS
33	Lg	64	LYS
33	Lg	72	SER
33	Lg	75	VAL
33	Lg	94	VAL
33	Lg	98	ASN
34	Lh	5	ARG
34	Lh	6	VAL
34	Lh	9	ARG
34	Lh	15	ARG
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	34	LEU
34	Lh	35	ARG
34	Lh	36	VAL
34	Lh	37	LYS
34	Lh	52	ILE
34	Lh	63	LEU
34	Lh	65	ARG
34	Lh	71	SER
34	Lh	77	LYS
34	Lh	84	ARG
34	Lh	100	ARG
34	Lh	102	ILE
35	Li	33	LYS
35	Li	35	LYS
35	Li	37	LEU
35	Li	40	LEU
35	Li	43	GLU

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Mol	Chain	Res	Type
35	Li	44	ASP
35	Li	46	GLN
35	Li	47	ARG
35	Li	48	LYS
35	Li	53	LYS
35	Li	54	ARG
35	Li	57	LEU
35	Li	59	LEU
35	Li	73	ILE
35	Li	75	ARG
35	Li	83	VAL
35	Li	85	ARG
35	Li	95	ARG
35	Li	97	GLU
35	Li	103	GLU
35	Li	108	ILE
35	Li	115	ARG
35	Li	123	GLN
35	Li	126	GLU
35	Li	127	LYS
35	Li	132	LEU
35	Li	134	SER
35	Li	135	LYS
35	Li	136	LEU
35	Li	137	MET
35	Li	147	LYS
35	Li	150	VAL
35	Li	151	LYS
36	Lj	8	LEU
36	Lj	9	LYS
36	Lj	10	LYS
36	Lj	16	ARG
36	Lj	18	VAL
36	Lj	19	ARG
36	Lj	20	LYS
36	Lj	27	LYS
36	Lj	30	GLN
36	Lj	35	SER
36	Lj	36	ILE
36	Lj	43	MET
36	Lj	51	ILE
36	Lj	55	ARG

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Mol	Chain	Res	Type
36	Lj	56	MET
36	Lj	58	LYS
36	Lj	60	ARG
36	Lj	68	LYS
36	Lj	69	ARG
36	Lj	74	LYS
36	Lj	79	LYS
36	Lj	80	ARG
36	Lj	88	ARG
36	Lj	90	ILE
37	Lk	3	LYS
37	Lk	10	LYS
37	Lk	11	ARG
37	Lk	13	THR
37	Lk	15	ILE
37	Lk	18	SER
37	Lk	19	CYS
37	Lk	24	LYS
37	Lk	36	SER
37	Lk	37	CYS
37	Lk	45	ARG
37	Lk	50	SER
37	Lk	53	SER
37	Lk	58	THR
37	Lk	64	MET
37	Lk	65	SER
37	Lk	67	MET
37	Lk	69	LYS
37	Lk	79	LEU
37	Lk	80	LYS
37	Lk	84	ARG
37	Lk	85	LYS
37	Lk	87	LEU
38	Ll	5	ILE
38	Ll	12	LYS
38	Ll	18	ARG
38	Ll	20	LYS
38	Ll	21	LYS
38	Ll	22	LEU
38	Ll	23	VAL
38	Ll	25	LYS
38	Ll	32	LEU

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Mol	Chain	Res	Type
38	Ll	33	GLN
38	Ll	38	LEU
38	Ll	40	LEU
38	Ll	41	ARG
38	Ll	46	LEU
38	Ll	50	THR
38	Ll	51	VAL
38	Ll	53	ASN
38	Ll	56	ASP
38	Ll	58	LYS
38	Ll	60	ILE
38	Ll	61	VAL
38	Ll	62	LYS
38	Ll	64	CYS
38	Ll	65	LYS
38	Ll	66	ASP
38	Ll	67	LYS
38	Ll	68	VAL
38	Ll	70	VAL
38	Ll	73	VAL
39	Ln	4	ILE
39	Ln	9	LEU
39	Ln	11	LYS
39	Ln	12	HIS
39	Ln	15	GLU
39	Ln	16	ILE
39	Ln	17	ILE
39	Ln	18	GLU
39	Ln	19	ARG
39	Ln	23	GLU
39	Ln	24	LYS
39	Ln	26	ARG
39	Ln	28	PHE
39	Ln	29	LEU
39	Ln	30	GLU
39	Ln	32	VAL
39	Ln	36	VAL
39	Ln	38	LEU
39	Ln	39	LYS
39	Ln	42	ASP
39	Ln	44	LYS
39	Ln	45	LYS

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Mol	Chain	Res	Type
39	Ln	48	ARG
39	Ln	51	LEU
39	Ln	63	LEU
39	Ln	64	LYS
39	Ln	65	LEU
39	Ln	68	ILE
39	Ln	70	ASP
39	Ln	73	ASP
39	Ln	78	LYS
39	Ln	79	LYS
39	Ln	82	LEU
39	Ln	83	ASN
39	Ln	85	VAL
39	Ln	86	GLU
39	Ln	87	ILE
39	Ln	88	GLU
39	Ln	89	HIS
39	Ln	90	LEU
39	Ln	91	GLN
39	Ln	95	LYS
39	Ln	98	LYS
39	Ln	99	GLN
39	Ln	100	ILE
39	Ln	101	LYS
39	Ln	102	LYS
39	Ln	105	LYS
39	Ln	106	SER
39	Ln	115	SER
39	Ln	116	LEU
39	Ln	117	ILE
39	Ln	119	GLN
39	Ln	120	ILE
39	Ln	128	PHE
39	Ln	129	THR
39	Ln	130	LYS
39	Ln	134	THR
39	Ln	136	LEU
39	Ln	138	LEU
39	Ln	141	ASP
39	Ln	142	GLU
39	Ln	146	LEU
39	Ln	149	LEU

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Mol	Chain	Res	Type
39	Ln	151	CYS
39	Ln	156	LYS
39	Ln	157	VAL
39	Ln	158	GLN
39	Ln	160	LYS
39	Ln	161	LYS
39	Ln	163	VAL
39	Ln	169	ILE
39	Ln	171	ASN
39	Ln	173	LYS
39	Ln	177	SER
39	Ln	178	GLU
39	Ln	181	GLN
39	Ln	183	ILE
39	Ln	184	MET
39	Ln	187	LEU
39	Ln	193	GLN
39	Ln	195	LYS
39	Ln	196	LYS
39	Ln	198	TRP
39	Ln	199	GLN
39	Ln	201	ILE
39	Ln	203	THR
39	Ln	204	VAL
39	Ln	207	LYS
39	Ln	208	SER
39	Ln	210	MET
39	Ln	213	SER
39	Ln	215	ARG
39	Ln	216	ILE
40	Lo	8	LYS
40	Lo	13	LEU
40	Lo	16	LYS
40	Lo	18	ARG
40	Lo	20	MET
40	Lo	21	LYS
40	Lo	24	SER
40	Lo	25	LYS
41	Lp	2	VAL
41	Lp	12	CYS
41	Lp	14	ARG
41	Lp	15	GLU

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Mol	Chain	Res	Type
41	Lp	17	LYS
41	Lp	19	THR
41	Lp	20	VAL
41	Lp	24	SER
41	Lp	25	LEU
41	Lp	36	GLN
41	Lp	55	ILE
41	Lp	61	LYS
41	Lp	63	THR
41	Lp	67	VAL
41	Lp	74	SER
41	Lp	76	LYS
41	Lp	79	THR
41	Lp	82	VAL
41	Lp	84	LYS
41	Lp	85	ARG
41	Lp	91	ILE
41	Lp	92	SER
41	Lp	93	ARG
42	Lq	7	LYS
42	Lq	8	VAL
42	Lq	10	LEU
42	Lq	11	THR
42	Lq	13	LYS
42	Lq	24	LYS
42	Lq	26	LEU
42	Lq	28	LYS
42	Lq	36	LYS
42	Lq	39	CYS
42	Lq	44	LYS
42	Lq	46	LYS
42	Lq	50	THR
42	Lq	52	CYS
42	Lq	60	CYS
42	Lq	62	LYS
42	Lq	64	MET
42	Lq	83	ILE
42	Lq	84	ARG
42	Lq	87	ARG
42	Lq	88	LEU
42	Lq	90	ARG
43	Ls	79	GLU

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Mol	Chain	Res	Type
43	Ls	81	THR
43	Ls	83	ILE
43	Ls	93	MET
43	Ls	96	CYS
43	Ls	106	ARG
43	Ls	108	THR
43	Ls	110	CYS
43	Ls	111	ARG
43	Ls	117	ASN
43	Ls	119	ARG
43	Ls	120	LYS
43	Ls	123	LEU
46	SA	14	GLN
46	SA	15	LEU
46	SA	16	LYS
46	SA	21	LYS
46	SA	22	LYS
46	SA	24	LEU
46	SA	25	VAL
46	SA	28	THR
46	SA	32	VAL
46	SA	35	ILE
46	SA	37	ARG
46	SA	38	ARG
46	SA	40	GLN
46	SA	43	ILE
46	SA	48	LYS
46	SA	51	THR
46	SA	53	VAL
46	SA	58	LYS
46	SA	62	LYS
46	SA	68	ARG
46	SA	70	LEU
46	SA	82	VAL
46	SA	85	ARG
46	SA	93	LEU
46	SA	94	LYS
46	SA	99	THR
46	SA	100	HIS
46	SA	108	PHE
46	SA	117	MET
46	SA	123	GLU

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Mol	Chain	Res	Type
46	SA	126	LEU
46	SA	127	LEU
46	SA	128	LEU
46	SA	129	VAL
46	SA	131	ASP
46	SA	136	ARG
46	SA	137	GLN
46	SA	141	GLU
46	SA	145	VAL
46	SA	150	ILE
46	SA	152	LEU
46	SA	155	SER
46	SA	156	ASP
46	SA	159	LEU
46	SA	162	ILE
46	SA	164	VAL
46	SA	171	LYS
46	SA	174	MET
46	SA	176	ILE
46	SA	178	LEU
46	SA	179	ILE
46	SA	185	ARG
46	SA	187	VAL
46	SA	188	LEU
46	SA	190	LEU
46	SA	193	SER
46	SA	194	ILE
46	SA	195	SER
46	SA	196	ARG
46	SA	197	THR
46	SA	198	GLU
46	SA	202	VAL
46	SA	206	LEU
46	SA	208	VAL
47	SB	28	HIS
47	SB	33	LEU
47	SB	35	ARG
47	SB	36	LEU
47	SB	42	ILE
47	SB	43	GLU
47	SB	45	LEU
47	SB	50	LYS

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Mol	Chain	Res	Type
47	SB	53	LEU
47	SB	55	ILE
47	SB	56	LYS
47	SB	58	THR
47	SB	67	LYS
47	SB	68	SER
47	SB	72	GLU
47	SB	74	VAL
47	SB	75	CYS
47	SB	76	ASN
47	SB	77	ILE
47	SB	78	MET
47	SB	79	SER
47	SB	80	VAL
47	SB	81	GLN
47	SB	82	LYS
47	SB	84	THR
47	SB	85	THR
47	SB	88	GLN
47	SB	91	ARG
47	SB	97	ILE
47	SB	100	ASN
47	SB	111	VAL
47	SB	112	SER
47	SB	115	VAL
47	SB	120	LYS
47	SB	121	LYS
47	SB	124	LYS
47	SB	130	ILE
47	SB	135	ARG
47	SB	142	LEU
47	SB	144	ASP
47	SB	146	HIS
47	SB	149	SER
47	SB	153	SER
47	SB	155	LYS
47	SB	160	ARG
47	SB	162	ARG
47	SB	168	ARG
47	SB	175	SER
47	SB	177	THR
47	SB	178	VAL

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Mol	Chain	Res	Type
47	SB	180	LYS
47	SB	182	LEU
47	SB	183	GLU
47	SB	195	SER
47	SB	198	SER
47	SB	199	ARG
47	SB	201	LEU
47	SB	204	SER
47	SB	216	TYR
47	SB	217	SER
47	SB	218	ILE
47	SB	220	THR
47	SB	223	LEU
47	SB	226	LYS
47	SB	227	GLU
47	SB	232	VAL
47	SB	233	GLN
47	SB	235	ILE
47	SB	236	ARG
47	SB	237	THR
47	SB	238	MET
48	SC	8	ASP
48	SC	9	GLU
48	SC	10	GLU
48	SC	12	VAL
48	SC	15	SER
48	SC	16	LYS
48	SC	27	LEU
48	SC	29	GLU
48	SC	33	ARG
48	SC	36	VAL
48	SC	37	ASP
48	SC	42	SER
48	SC	43	CYS
48	SC	48	THR
48	SC	49	ILE
48	SC	51	SER
48	SC	52	ILE
48	SC	54	VAL
48	SC	55	ILE
48	SC	56	ILE
48	SC	71	ARG

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Mol	Chain	Res	Type
48	SC	74	LYS
48	SC	76	GLU
48	SC	78	LEU
48	SC	86	ASP
48	SC	88	LYS
48	SC	90	PHE
48	SC	96	LYS
48	SC	98	ILE
48	SC	100	ARG
48	SC	106	ILE
48	SC	108	VAL
48	SC	112	ARG
48	SC	114	LYS
48	SC	115	LEU
48	SC	122	ARG
48	SC	127	SER
48	SC	129	ILE
48	SC	130	ARG
48	SC	133	MET
48	SC	134	ARG
48	SC	143	ILE
48	SC	152	ARG
48	SC	154	ARG
48	SC	160	GLU
48	SC	163	LEU
48	SC	164	ILE
48	SC	170	LYS
48	SC	176	GLU
48	SC	178	THR
48	SC	179	ARG
48	SC	181	ILE
48	SC	182	LYS
48	SC	183	MET
48	SC	184	ARG
48	SC	187	VAL
48	SC	191	LYS
48	SC	194	ILE
48	SC	203	VAL
48	SC	204	MET
48	SC	206	ASP
48	SC	207	LYS
48	SC	209	GLU

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Mol	Chain	Res	Type
49	SD	12	LYS
49	SD	14	THR
49	SD	20	ASP
49	SD	24	LYS
49	SD	25	LYS
49	SD	31	ILE
49	SD	37	LYS
49	SD	39	ARG
49	SD	43	GLN
49	SD	44	THR
49	SD	46	VAL
49	SD	48	LYS
49	SD	52	LEU
49	SD	56	THR
49	SD	58	VAL
49	SD	59	ILE
49	SD	63	VAL
49	SD	66	VAL
49	SD	83	LYS
49	SD	92	SER
49	SD	93	ASP
49	SD	97	LEU
49	SD	103	MET
49	SD	104	ASP
49	SD	107	ARG
49	SD	108	HIS
49	SD	109	LYS
49	SD	122	ASP
49	SD	123	VAL
49	SD	127	ILE
49	SD	137	VAL
49	SD	140	ILE
49	SD	145	ARG
49	SD	150	ARG
49	SD	151	ARG
49	SD	152	LYS
49	SD	154	CYS
49	SD	156	VAL
49	SD	159	ARG
49	SD	160	VAL
49	SD	162	ARG
49	SD	170	GLU

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Mol	Chain	Res	Type
49	SD	173	HIS
49	SD	176	LEU
49	SD	178	LYS
49	SD	179	VAL
49	SD	181	ILE
49	SD	183	VAL
49	SD	184	LEU
49	SD	187	LYS
49	SD	190	ASN
49	SD	192	GLU
49	SD	193	VAL
49	SD	196	LYS
49	SD	201	LEU
49	SD	202	GLN
49	SD	207	CYS
49	SD	208	ARG
49	SD	212	ILE
49	SD	216	LYS
49	SD	222	ARG
49	SD	230	THR
49	SD	231	MET
49	SD	232	HIS
49	SD	236	GLN
49	SD	237	VAL
50	SE	6	ARG
50	SE	7	LYS
50	SE	11	ARG
50	SE	12	LEU
50	SE	16	LYS
50	SE	20	LEU
50	SE	22	LYS
50	SE	23	MET
50	SE	26	ILE
50	SE	32	THR
50	SE	38	LEU
50	SE	40	GLU
50	SE	42	ILE
50	SE	44	LEU
50	SE	45	ILE
50	SE	47	ILE
50	SE	48	LEU
50	SE	49	ARG

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Mol	Chain	Res	Type
50	SE	61	THR
50	SE	64	ILE
50	SE	65	LEU
50	SE	68	LYS
50	SE	69	ASN
50	SE	70	VAL
50	SE	71	LEU
50	SE	75	LYS
50	SE	77	ARG
50	SE	79	ASP
50	SE	81	THR
50	SE	84	VAL
50	SE	87	MET
50	SE	95	VAL
50	SE	97	LYS
50	SE	98	THR
50	SE	99	PHE
50	SE	100	ARG
50	SE	102	LEU
50	SE	105	VAL
50	SE	108	ARG
50	SE	110	THR
50	SE	115	GLN
50	SE	116	SER
50	SE	117	ASN
50	SE	123	LEU
50	SE	125	ARG
50	SE	128	LYS
50	SE	129	ILE
50	SE	134	LYS
50	SE	139	LEU
50	SE	145	ARG
50	SE	155	LYS
50	SE	157	ASN
50	SE	158	ASP
50	SE	159	THR
50	SE	160	ILE
50	SE	168	LYS
50	SE	171	GLU
50	SE	174	LYS
50	SE	176	ASP
50	SE	177	ILE

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Mol	Chain	Res	Type
50	SE	179	LYS
50	SE	180	ILE
50	SE	181	VAL
50	SE	182	MET
50	SE	183	VAL
50	SE	184	THR
50	SE	191	ARG
50	SE	192	ILE
50	SE	194	THR
50	SE	200	LYS
50	SE	202	MET
50	SE	206	THR
50	SE	207	MET
50	SE	208	ILE
50	SE	209	ARG
50	SE	210	MET
50	SE	213	THR
50	SE	216	THR
50	SE	219	LEU
50	SE	221	ARG
50	SE	222	LEU
50	SE	225	VAL
50	SE	227	VAL
50	SE	228	ILE
50	SE	231	ASP
50	SE	232	SER
50	SE	235	VAL
50	SE	237	ILE
50	SE	241	LYS
50	SE	243	ILE
50	SE	248	ILE
50	SE	249	LYS
50	SE	252	GLU
50	SE	253	LEU
50	SE	254	ARG
50	SE	255	LEU
50	SE	260	LYS
50	SE	261	ARG
51	SF	10	LYS
51	SF	15	ASP
51	SF	16	VAL
51	SF	17	LYS

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Mol	Chain	Res	Type
51	SF	18	CYS
51	SF	21	GLU
51	SF	23	LEU
51	SF	27	ILE
51	SF	28	SER
51	SF	29	ILE
51	SF	30	ASP
51	SF	31	ASN
51	SF	41	ARG
51	SF	45	LYS
51	SF	46	ARG
51	SF	49	LYS
51	SF	51	LYS
51	SF	54	VAL
51	SF	59	THR
51	SF	60	ASN
51	SF	61	SER
51	SF	68	ASN
51	SF	71	LYS
51	SF	74	MET
51	SF	76	MET
51	SF	77	LYS
51	SF	81	GLU
51	SF	84	GLU
51	SF	85	LEU
51	SF	88	LEU
51	SF	92	LYS
51	SF	93	ASN
51	SF	95	VAL
51	SF	97	VAL
51	SF	108	ARG
51	SF	109	GLU
51	SF	122	ARG
51	SF	127	VAL
51	SF	130	LEU
51	SF	131	ARG
51	SF	146	LYS
51	SF	150	ARG
51	SF	151	LYS
51	SF	159	LEU
51	SF	161	GLU
51	SF	171	ASP

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Mol	Chain	Res	Type
51	SF	172	LYS
51	SF	173	SER
51	SF	176	ILE
51	SF	178	GLN
51	SF	179	ARG
51	SF	180	ASN
51	SF	187	VAL
51	SF	188	SER
52	SG	8	LYS
52	SG	9	VAL
52	SG	11	ILE
52	SG	12	SER
52	SG	15	VAL
52	SG	16	THR
52	SG	20	LYS
52	SG	21	SER
52	SG	22	LEU
52	SG	23	MET
52	SG	24	ILE
52	SG	28	ARG
52	SG	29	LYS
52	SG	30	SER
52	SG	32	THR
52	SG	33	ILE
52	SG	34	HIS
52	SG	41	GLU
52	SG	42	PHE
52	SG	50	GLU
52	SG	55	THR
52	SG	57	ARG
52	SG	59	THR
52	SG	73	VAL
52	SG	75	LYS
52	SG	76	SER
52	SG	77	GLN
52	SG	78	ARG
52	SG	81	LEU
52	SG	88	LYS
52	SG	91	LEU
52	SG	98	ARG
52	SG	99	LYS
52	SG	101	LYS

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Mol	Chain	Res	Type
52	SG	102	SER
52	SG	103	ILE
52	SG	107	ILE
52	SG	111	ASP
52	SG	113	HIS
52	SG	117	VAL
52	SG	118	VAL
52	SG	120	VAL
52	SG	125	LYS
52	SG	126	THR
52	SG	127	LEU
52	SG	130	LEU
52	SG	131	THR
52	SG	132	ASP
52	SG	133	VAL
52	SG	134	VAL
52	SG	135	VAL
52	SG	137	LYS
52	SG	139	LEU
52	SG	140	VAL
52	SG	142	LYS
52	SG	147	ILE
52	SG	153	LEU
52	SG	156	THR
52	SG	159	ASP
52	SG	161	LYS
52	SG	164	MET
52	SG	168	GLU
52	SG	169	LEU
52	SG	170	ILE
52	SG	171	LYS
52	SG	173	LEU
52	SG	175	HIS
52	SG	178	THR
52	SG	179	LEU
52	SG	181	ASN
52	SG	183	GLU
52	SG	185	LYS
52	SG	186	LEU
52	SG	187	LYS
52	SG	199	LYS
52	SG	202	ARG

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Mol	Chain	Res	Type
52	SG	203	LYS
52	SG	204	GLN
52	SG	206	VAL
52	SG	207	ILE
52	SG	210	LYS
52	SG	213	ILE
52	SG	214	MET
52	SG	216	LYS
52	SG	218	LEU
52	SG	219	GLN
52	SG	220	GLN
52	SG	221	LEU
52	SG	225	LYS
52	SG	230	ARG
52	SG	231	MET
52	SG	233	LYS
52	SG	235	HIS
53	SH	7	ARG
53	SH	8	LYS
53	SH	9	ILE
53	SH	10	ARG
53	SH	13	PHE
53	SH	15	LYS
53	SH	16	LEU
53	SH	18	GLU
53	SH	21	LYS
53	SH	30	LEU
53	SH	31	GLU
53	SH	36	LEU
53	SH	37	ARG
53	SH	41	LEU
53	SH	43	THR
53	SH	44	LEU
53	SH	45	TYR
53	SH	46	ILE
53	SH	47	SER
53	SH	51	GLU
53	SH	52	ILE
53	SH	58	LYS
53	SH	59	LYS
53	SH	62	VAL
53	SH	63	VAL

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Mol	Chain	Res	Type
53	SH	65	VAL
53	SH	73	PHE
53	SH	75	LYS
53	SH	77	SER
53	SH	80	LEU
53	SH	81	ILE
53	SH	83	LYS
53	SH	84	LEU
53	SH	94	ILE
53	SH	95	ILE
53	SH	96	VAL
53	SH	98	ASN
53	SH	103	LYS
53	SH	107	VAL
53	SH	111	LYS
53	SH	112	LYS
53	SH	113	SER
53	SH	115	ARG
53	SH	116	ARG
53	SH	122	MET
53	SH	125	VAL
53	SH	128	CYS
53	SH	130	LEU
53	SH	133	ILE
53	SH	137	ILE
53	SH	140	ILE
53	SH	142	LYS
53	SH	143	ARG
53	SH	145	LEU
53	SH	151	ASN
53	SH	153	ARG
53	SH	154	LEU
53	SH	160	LYS
53	SH	162	VAL
53	SH	168	GLU
53	SH	169	ARG
53	SH	170	THR
53	SH	171	LYS
53	SH	183	ARG
53	SH	184	ASP
53	SH	186	GLU
53	SH	188	ILE

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Mol	Chain	Res	Type
53	SH	190	MET
54	SI	7	LYS
54	SI	13	LYS
54	SI	17	VAL
54	SI	26	LYS
54	SI	29	LEU
54	SI	38	LEU
54	SI	39	ILE
54	SI	40	VAL
54	SI	51	LYS
54	SI	52	ILE
54	SI	53	SER
54	SI	54	THR
54	SI	55	ILE
54	SI	62	ILE
54	SI	63	LYS
54	SI	65	ARG
54	SI	68	ARG
54	SI	69	LEU
54	SI	71	HIS
54	SI	78	SER
54	SI	80	ASP
54	SI	81	ILE
54	SI	84	LYS
54	SI	86	ARG
54	SI	89	GLN
54	SI	91	VAL
54	SI	93	ASN
54	SI	94	SER
54	SI	95	THR
54	SI	96	SER
54	SI	101	ARG
54	SI	104	THR
54	SI	107	LYS
54	SI	109	CYS
54	SI	111	VAL
54	SI	113	ILE
54	SI	119	LYS
54	SI	120	SER
54	SI	122	LEU
54	SI	123	SER
54	SI	127	LEU

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Mol	Chain	Res	Type
54	SI	129	LYS
54	SI	130	GLU
54	SI	131	ILE
54	SI	133	ASP
54	SI	135	ILE
54	SI	136	ARG
54	SI	140	ILE
54	SI	144	ILE
54	SI	147	ARG
54	SI	159	LEU
54	SI	160	GLU
54	SI	164	LEU
54	SI	165	LEU
54	SI	169	LYS
54	SI	170	LYS
54	SI	171	LEU
54	SI	174	LYS
55	SJ	2	VAL
55	SJ	3	ARG
55	SJ	6	VAL
55	SJ	7	LEU
55	SJ	12	LYS
55	SJ	22	LYS
55	SJ	23	LYS
55	SJ	26	ILE
55	SJ	30	SER
55	SJ	31	SER
55	SJ	32	LYS
55	SJ	39	GLN
55	SJ	48	SER
55	SJ	49	ASP
55	SJ	52	VAL
55	SJ	53	VAL
55	SJ	55	ASN
55	SJ	56	HIS
55	SJ	57	ARG
55	SJ	61	ILE
55	SJ	66	ILE
55	SJ	68	ARG
55	SJ	69	LEU
55	SJ	71	LYS
55	SJ	76	SER

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Mol	Chain	Res	Type
55	SJ	80	ASP
55	SJ	85	ASP
55	SJ	86	ILE
55	SJ	88	LYS
55	SJ	91	VAL
55	SJ	93	LEU
55	SJ	98	LEU
55	SJ	103	ILE
55	SJ	104	LEU
55	SJ	106	THR
55	SJ	110	ILE
55	SJ	111	MET
55	SJ	112	ASP
55	SJ	115	GLU
55	SJ	118	HIS
55	SJ	124	LYS
55	SJ	126	ILE
56	SK	2	ARG
56	SK	3	ILE
56	SK	5	ARG
56	SK	9	SER
56	SK	10	SER
56	SK	11	LYS
56	SK	17	LYS
56	SK	18	LYS
56	SK	22	LYS
56	SK	24	ARG
56	SK	31	LEU
56	SK	38	LYS
56	SK	43	ILE
56	SK	45	ARG
56	SK	53	ILE
56	SK	69	LYS
56	SK	70	ARG
56	SK	73	GLU
56	SK	79	ARG
56	SK	84	LEU
56	SK	87	LEU
56	SK	89	GLU
56	SK	91	LYS
56	SK	92	ASP
56	SK	93	GLN

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Mol	Chain	Res	Type
56	SK	97	VAL
56	SK	100	LEU
56	SK	101	ARG
56	SK	102	ILE
56	SK	107	LYS
56	SK	110	LEU
56	SK	112	SER
56	SK	113	VAL
56	SK	115	VAL
56	SK	118	LYS
56	SK	119	LEU
56	SK	121	LYS
56	SK	122	SER
56	SK	123	VAL
56	SK	129	MET
56	SK	131	LYS
56	SK	133	ARG
56	SK	137	VAL
56	SK	141	ILE
56	SK	143	ASN
56	SK	149	VAL
56	SK	159	ILE
56	SK	162	THR
56	SK	164	SER
56	SK	165	LEU
56	SK	167	PRO
56	SK	170	LYS
56	SK	174	THR
56	SK	175	LYS
57	SL	4	ILE
57	SL	6	LYS
57	SL	9	TYR
57	SL	10	LYS
57	SL	22	LEU
57	SL	29	ARG
57	SL	30	VAL
57	SL	36	ILE
57	SL	37	THR
57	SL	42	ASN
57	SL	45	LEU
57	SL	49	THR
57	SL	50	TYR

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Mol	Chain	Res	Type
57	SL	57	MET
57	SL	59	SER
57	SL	61	GLU
57	SL	63	ARG
57	SL	65	VAL
57	SL	66	VAL
57	SL	67	LYS
57	SL	69	THR
57	SL	73	ARG
57	SL	78	LEU
57	SL	80	THR
57	SL	81	GLU
57	SL	84	GLU
57	SL	87	ILE
57	SL	91	LEU
57	SL	93	LEU
57	SL	94	THR
57	SL	95	ASP
57	SL	96	ASP
57	SL	97	VAL
57	SL	98	LEU
57	SL	100	THR
58	SM	6	HIS
58	SM	7	GLU
58	SM	12	LYS
58	SM	13	GLN
58	SM	15	GLN
58	SM	18	GLN
58	SM	20	ARG
58	SM	23	ARG
58	SM	26	ASN
58	SM	33	TYR
58	SM	36	ILE
58	SM	41	HIS
58	SM	42	THR
58	SM	45	THR
58	SM	47	ILE
58	SM	54	LYS
58	SM	61	ASN
58	SM	62	VAL
58	SM	63	SER
58	SM	67	ARG

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Mol	Chain	Res	Type
58	SM	68	ILE
58	SM	70	ARG
58	SM	72	VAL
58	SM	77	LYS
58	SM	80	ARG
58	SM	82	ILE
58	SM	84	VAL
58	SM	86	ARG
58	SM	89	LEU
58	SM	102	HIS
58	SM	103	LYS
58	SM	113	PHE
58	SM	114	ARG
58	SM	115	VAL
58	SM	116	LYS
58	SM	123	ILE
58	SM	138	ILE
58	SM	139	LYS
58	SM	140	VAL
58	SM	145	GLU
59	SO	4	THR
59	SO	5	SER
59	SO	17	ARG
59	SO	26	LYS
59	SO	28	ARG
59	SO	29	LYS
59	SO	34	THR
59	SO	37	LYS
59	SO	41	LEU
59	SO	42	GLU
59	SO	45	CYS
59	SO	51	VAL
59	SO	55	ILE
59	SO	58	SER
59	SO	64	SER
59	SO	67	ARG
59	SO	72	VAL
59	SO	76	LYS
59	SO	77	ASN
59	SO	79	LYS
59	SO	80	LYS
59	SO	81	ILE

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Mol	Chain	Res	Type
59	SO	82	THR
59	SO	90	SER
59	SO	91	ILE
59	SO	94	ILE
59	SO	95	ASP
59	SO	99	GLU
59	SO	101	LEU
59	SO	105	PHE
59	SO	107	ARG
59	SO	110	ARG
59	SO	115	ILE
59	SO	118	CYS
59	SO	119	ARG
59	SO	120	PHE
59	SO	121	LYS
59	SO	124	LYS
59	SO	130	LEU
59	SO	133	LEU
59	SO	136	ARG
59	SO	137	LYS
59	SO	138	ARG
60	SP	6	SER
60	SP	7	LYS
60	SP	9	LYS
60	SP	11	ILE
60	SP	14	SER
60	SP	16	ILE
60	SP	25	TRP
60	SP	27	LYS
60	SP	29	THR
60	SP	32	ASP
60	SP	39	LYS
60	SP	42	LYS
60	SP	43	LYS
60	SP	57	GLN
60	SP	60	ILE
60	SP	62	GLN
60	SP	64	LYS
60	SP	70	LYS
60	SP	71	ILE
60	SP	76	LYS
60	SP	78	LYS

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Mol	Chain	Res	Type
60	SP	80	LEU
60	SP	83	GLU
60	SP	86	GLU
60	SP	87	ASP
60	SP	90	CYS
60	SP	91	MET
60	SP	100	LYS
60	SP	103	GLU
60	SP	107	ARG
60	SP	109	LYS
60	SP	111	SER
60	SP	121	ARG
60	SP	125	LEU
60	SP	127	ARG
60	SP	134	ARG
60	SP	138	THR
60	SP	143	SER
60	SP	144	ASP
60	SP	149	LEU
60	SP	150	LEU
61	SQ	28	PHE
61	SQ	33	ILE
61	SQ	37	LYS
61	SQ	42	ILE
61	SQ	48	SER
61	SQ	51	GLU
61	SQ	52	THR
61	SQ	53	ILE
61	SQ	55	ARG
61	SQ	56	VAL
61	SQ	57	SER
61	SQ	60	MET
61	SQ	76	GLN
61	SQ	81	LEU
61	SQ	83	GLU
61	SQ	95	ILE
61	SQ	96	LYS
61	SQ	97	ILE
61	SQ	105	LYS
61	SQ	107	VAL
61	SQ	110	GLN
61	SQ	119	LEU

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Mol	Chain	Res	Type
61	SQ	120	VAL
61	SQ	121	ARG
61	SQ	129	ILE
61	SQ	135	ILE
61	SQ	141	ARG
61	SQ	143	LYS
62	SR	30	ILE
62	SR	32	ASP
62	SR	36	LYS
62	SR	40	ARG
62	SR	43	ARG
62	SR	47	LYS
62	SR	48	HIS
62	SR	58	VAL
62	SR	61	LEU
62	SR	62	ARG
62	SR	63	LEU
62	SR	64	ARG
62	SR	65	ARG
62	SR	68	GLN
62	SR	76	VAL
62	SR	83	MET
62	SR	88	GLU
62	SR	89	MET
62	SR	95	SER
62	SR	96	VAL
62	SR	97	TYR
62	SR	100	ARG
62	SR	103	ILE
62	SR	106	GLU
62	SR	114	ARG
62	SR	117	ARG
62	SR	121	MET
62	SR	124	LYS
62	SR	125	ILE
62	SR	126	VAL
62	SR	128	HIS
62	SR	130	LYS
63	ST	9	LEU
63	ST	10	LEU
63	ST	16	GLU
63	ST	18	ARG

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Mol	Chain	Res	Type
63	ST	19	GLU
63	ST	20	ARG
63	ST	22	LYS
63	ST	27	THR
63	ST	28	LEU
63	ST	30	LYS
63	ST	31	LYS
63	ST	37	VAL
63	ST	41	LYS
63	ST	44	LYS
63	ST	47	ILE
63	ST	48	LEU
63	ST	49	VAL
63	ST	54	LEU
63	ST	56	LEU
63	ST	57	VAL
63	ST	58	ARG
63	ST	60	GLU
63	ST	61	ILE
63	ST	62	LEU
63	ST	63	ARG
63	ST	64	THR
63	ST	65	LYS
63	ST	66	VAL
63	ST	68	GLU
63	ST	70	ILE
63	ST	72	ILE
63	ST	76	SER
63	ST	77	LEU
63	ST	81	LEU
63	ST	83	MET
63	ST	85	ILE
63	ST	87	VAL
63	ST	94	SER
63	ST	96	ILE
63	ST	101	GLN
63	ST	104	SER
63	ST	111	VAL
63	ST	112	LYS
63	ST	113	ASP
63	ST	114	GLU
63	ST	117	ARG

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Mol	Chain	Res	Type
63	ST	119	GLU
63	ST	132	VAL
63	ST	133	VAL
63	ST	134	SER
63	ST	137	ARG
63	ST	144	PHE
63	ST	153	ARG
63	ST	154	GLN
63	ST	155	LYS
63	ST	158	ARG
64	SU	3	LYS
64	SU	5	ARG
64	SU	6	THR
64	SU	7	LYS
64	SU	8	THR
64	SU	9	ILE
64	SU	11	ARG
64	SU	14	ARG
64	SU	23	SER
64	SU	24	LEU
64	SU	27	LYS
64	SU	30	GLN
64	SU	33	LYS
64	SU	41	VAL
64	SU	43	ILE
64	SU	46	SER
64	SU	47	LYS
64	SU	61	MET
64	SU	64	VAL
64	SU	66	LYS
65	SV	8	ASN
65	SV	10	TYR
65	SV	11	ARG
65	SV	12	ASP
65	SV	13	LEU
65	SV	14	LEU
65	SV	19	THR
65	SV	21	ILE
65	SV	25	VAL
65	SV	27	LEU
65	SV	35	LYS
65	SV	37	ILE

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Mol	Chain	Res	Type
65	SV	39	ARG
65	SV	40	ARG
65	SV	41	PHE
65	SV	43	ASN
65	SV	44	VAL
65	SV	46	LEU
65	SV	50	ASN
65	SV	51	ILE
65	SV	53	VAL
65	SV	55	LYS
65	SV	56	ARG
65	SV	68	LEU
65	SV	73	GLU
65	SV	74	ASP
65	SV	76	LEU
65	SV	80	ILE
65	SV	87	ARG
65	SV	92	GLU
65	SV	96	ASP
65	SV	97	MET
65	SV	98	HIS
65	SV	99	ILE
65	SV	100	LEU
65	SV	104	ILE
65	SV	106	SER
65	SV	117	LYS
65	SV	120	CYS
65	SV	125	ARG
65	SV	127	HIS
65	SV	131	LYS
65	SV	132	VAL
65	SV	133	ARG
65	SV	136	HIS
65	SV	137	THR
65	SV	138	LYS
65	SV	139	SER
65	SV	140	THR
65	SV	142	ARG
65	SV	146	VAL
66	SW	4	VAL
66	SW	6	ARG
66	SW	7	VAL

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Mol	Chain	Res	Type
66	SW	10	ASP
66	SW	11	VAL
66	SW	13	ILE
66	SW	19	HIS
66	SW	21	LYS
66	SW	23	ARG
66	SW	27	LYS
66	SW	32	THR
66	SW	33	ASP
66	SW	36	LYS
66	SW	37	THR
66	SW	39	VAL
66	SW	40	SER
66	SW	41	ARG
66	SW	42	GLN
66	SW	53	ILE
66	SW	54	LYS
66	SW	57	SER
66	SW	59	ILE
66	SW	67	SER
66	SW	69	SER
66	SW	70	ILE
66	SW	72	VAL
66	SW	75	LEU
66	SW	78	LYS
66	SW	82	LEU
66	SW	83	GLN
66	SW	87	THR
66	SW	88	THR
66	SW	93	LYS
66	SW	94	ARG
66	SW	96	SER
66	SW	97	CYS
66	SW	98	LYS
66	SW	100	ILE
66	SW	101	ARG
66	SW	102	SER
66	SW	111	LYS
66	SW	112	LEU
66	SW	113	LEU
66	SW	117	GLU
66	SW	123	SER

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Mol	Chain	Res	Type
66	SW	129	MET
67	SX	21	MET
67	SX	22	HIS
67	SX	24	LYS
67	SX	26	THR
67	SX	27	ILE
67	SX	28	ILE
67	SX	30	VAL
67	SX	32	LYS
67	SX	33	ASP
67	SX	39	ARG
67	SX	42	LYS
67	SX	44	ILE
67	SX	46	LYS
67	SX	53	ILE
67	SX	58	ARG
67	SX	63	ARG
67	SX	66	ILE
67	SX	67	THR
67	SX	71	SER
67	SX	75	GLU
67	SX	82	ARG
67	SX	94	VAL
67	SX	101	ILE
67	SX	102	SER
67	SX	107	LYS
67	SX	111	ILE
67	SX	114	ILE
67	SX	117	THR
67	SX	119	GLU
67	SX	120	VAL
67	SX	121	GLU
68	SY	11	SER
68	SY	12	SER
68	SY	16	VAL
68	SY	17	ASP
68	SY	19	TYR
68	SY	22	ARG
68	SY	23	LYS
68	SY	30	LEU
68	SY	31	ILE
68	SY	34	LYS

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Mol	Chain	Res	Type
68	SY	35	ASP
68	SY	41	LEU
68	SY	43	VAL
68	SY	48	ASP
68	SY	49	LYS
68	SY	52	MET
68	SY	53	ILE
68	SY	54	GLU
68	SY	55	ASN
68	SY	58	VAL
68	SY	63	CYS
68	SY	72	VAL
68	SY	73	ASP
68	SY	74	SER
68	SY	77	MET
68	SY	79	LEU
68	SY	81	GLN
68	SY	86	MET
68	SY	87	GLU
69	Sb	3	GLU
69	Sb	4	ILE
69	Sb	5	THR
69	Sb	7	LYS
69	Sb	9	ARG
69	Sb	10	LYS
69	Sb	11	VAL
69	Sb	12	LEU
69	Sb	13	ASN
69	Sb	14	ASN
69	Sb	16	LEU
69	Sb	20	GLN
69	Sb	22	CYS
69	Sb	23	VAL
69	Sb	24	VAL
69	Sb	25	ASP
69	Sb	26	VAL
69	Sb	27	LEU
69	Sb	28	HIS
69	Sb	32	THR
69	Sb	34	GLU
69	Sb	36	LYS
69	Sb	39	ILE

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Mol	Chain	Res	Type
69	Sb	40	LYS
69	Sb	43	VAL
69	Sb	48	LYS
69	Sb	53	LYS
69	Sb	55	ILE
69	Sb	56	VAL
69	Sb	60	PHE
69	Sb	61	LYS
69	Sb	62	THR
69	Sb	70	VAL
69	Sb	72	PHE
69	Sb	73	CYS
69	Sb	78	ASN
69	Sb	82	LEU
69	Sb	91	LYS
69	Sb	92	ILE
69	Sb	93	ARG
69	Sb	96	LEU
69	Sb	97	ILE
69	Sb	101	LYS
69	Sb	103	VAL
69	Sb	104	SER
69	Sb	105	ARG
69	Sb	115	ARG
69	Sb	117	LYS
69	Sb	118	LYS
70	Sc	14	LYS
70	Sc	15	VAL
70	Sc	17	TYR
70	Sc	32	LYS
70	Sc	40	ILE
70	Sc	43	THR
70	Sc	48	ARG
70	Sc	50	ARG
70	Sc	59	VAL
70	Sc	60	MET
70	Sc	62	GLN
70	Sc	63	LEU
70	Sc	68	ASP
70	Sc	71	ILE
70	Sc	73	SER
70	Sc	74	LYS

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Mol	Chain	Res	Type
70	Sc	76	SER
70	Sc	77	ARG
70	Sc	78	MET
70	Sc	79	THR
70	Sc	82	LYS
70	Sc	83	ASN
70	Sc	84	MET
70	Sc	86	LYS
71	Sd	6	ARG
71	Sd	10	ARG
71	Sd	11	SER
71	Sd	15	CYS
71	Sd	18	THR
71	Sd	19	ASN
71	Sd	20	ILE
71	Sd	21	VAL
71	Sd	30	VAL
71	Sd	34	LYS
71	Sd	35	VAL
71	Sd	36	ILE
71	Sd	40	THR
71	Sd	42	ARG
71	Sd	49	ILE
71	Sd	51	ASP
71	Sd	58	VAL
71	Sd	60	GLN
71	Sd	64	ILE
71	Sd	69	ASN
71	Sd	71	VAL
71	Sd	76	SER
71	Sd	83	ILE
71	Sd	90	GLU
71	Sd	91	ASP
71	Sd	93	LYS
71	Sd	96	THR
72	Se	44	MET
72	Se	47	ASP
72	Se	48	LEU
72	Se	52	ASP
72	Se	54	VAL
72	Se	55	GLU
72	Se	56	GLU

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Mol	Chain	Res	Type
72	Se	57	GLN
72	Se	61	LYS
72	Se	62	LEU
72	Se	63	LYS
72	Se	65	LEU
72	Se	71	SER
72	Se	74	LEU
72	Se	75	GLU
72	Se	76	ILE
72	Se	77	LYS
72	Se	81	CYS
72	Se	83	ASP
72	Se	84	ILE
72	Se	85	VAL
72	Se	86	VAL
72	Se	101	THR
72	Se	103	GLN
72	Se	104	ILE
72	Se	105	SER
72	Se	108	THR
72	Se	115	THR
72	Se	116	SER
72	Se	118	VAL
72	Se	119	GLU
72	Se	120	ARG
72	Se	122	ARG
72	Se	123	GLN
73	Sg	5	ILE
73	Sg	9	VAL
73	Sg	10	ILE
73	Sg	11	GLU
73	Sg	15	ARG
73	Sg	16	THR
73	Sg	17	SER
73	Sg	22	ILE
73	Sg	23	THR
73	Sg	25	VAL
73	Sg	26	LYS
73	Sg	27	VAL
73	Sg	30	MET
73	Sg	33	GLU
73	Sg	36	GLN

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Mol	Chain	Res	Type
73	Sg	37	ILE
73	Sg	38	ILE
73	Sg	39	ARG
73	Sg	40	ASN
73	Sg	41	VAL
73	Sg	42	ILE
73	Sg	45	VAL
73	Sg	47	LYS
73	Sg	48	ASP
73	Sg	51	LEU
73	Sg	52	VAL
73	Sg	53	LEU
73	Sg	55	GLU
73	Sg	57	GLU
73	Sg	58	ARG
73	Sg	59	GLU
73	Sg	61	ARG
74	Sh	88	ARG
74	Sh	89	GLU
74	Sh	90	THR
74	Sh	94	THR
74	Sh	96	ILE
74	Sh	101	GLU
74	Sh	102	CYS
74	Sh	103	ARG
74	Sh	104	ILE
74	Sh	105	CYS
74	Sh	110	SER
74	Sh	112	TYR
74	Sh	113	ARG
74	Sh	114	LYS
74	Sh	117	LEU
74	Sh	119	ILE
74	Sh	122	ARG
74	Sh	125	LYS
74	Sh	130	LYS
74	Sh	131	ILE
74	Sh	135	LYS
75	Sj	11	LYS
75	Sj	13	ARG
75	Sj	14	LYS
75	Sj	15	CYS

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Mol	Chain	Res	Type
75	Sj	16	THR
75	Sj	18	LYS
75	Sj	20	GLU
75	Sj	21	LYS
75	Sj	22	LYS
75	Sj	24	LYS
75	Sj	29	ARG
75	Sj	31	ARG
75	Sj	33	TYR
75	Sj	37	LEU
75	Sj	40	LYS
75	Sj	41	ASN
75	Sj	43	VAL
75	Sj	44	ASP
75	Sj	46	THR
75	Sj	47	LEU
75	Sj	49	HIS
75	Sj	50	ASN
75	Sj	52	ARG
75	Sj	53	ARG
75	Sj	54	LEU
75	Sj	60	LEU
75	Sj	61	ILE
75	Sj	63	GLN
75	Sj	64	LYS
75	Sj	65	LEU
75	Sj	67	PHE
77	a	3	HIS
77	a	4	PHE
77	a	5	THR
77	a	6	THR
77	a	9	ILE
77	a	10	ARG
77	a	15	HIS
77	a	18	ARG
77	a	22	MET
77	a	23	SER
77	a	28	VAL
77	a	29	ASP
77	a	32	LYS
77	a	35	LEU
77	a	37	ASP

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Mol	Chain	Res	Type
77	a	55	ARG
77	a	60	ARG
77	a	130	SER
77	a	135	ILE
77	a	138	ILE
77	a	140	SER
77	a	143	HIS
77	a	144	VAL
77	a	145	ASP
77	a	146	PHE
77	a	147	SER
77	a	154	LEU
77	a	155	ARG
77	a	158	ASP
77	a	162	VAL
77	a	164	VAL
77	a	166	CYS
77	a	172	VAL
77	a	178	LEU
77	a	180	GLN
77	a	187	ILE
77	a	189	CYS
77	a	198	VAL
77	a	199	ILE
77	a	200	MET
77	a	207	GLU
77	a	211	LEU
77	a	212	MET
77	a	215	LYS
77	a	216	THR
77	a	226	THR
77	a	230	LYS
77	a	232	LEU
77	a	233	PHE
77	a	236	LYS
77	a	237	LYS
77	a	239	LYS
77	a	246	THR
77	a	247	ASP
77	a	248	LEU
77	a	253	SER
77	a	266	TRP

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Mol	Chain	Res	Type
77	a	269	THR
77	a	271	THR
77	a	280	LYS
77	a	285	LEU
77	a	286	SER
77	a	287	THR
77	a	289	MET
77	a	290	LYS
77	a	296	ARG
77	a	298	LEU
77	a	302	THR
77	a	304	LYS
77	a	306	THR
77	a	308	LYS
77	a	310	GLN
77	a	316	LYS
77	a	317	ASN
77	a	319	ARG
77	a	323	ILE
77	a	326	MET
77	a	328	PRO
77	a	329	ILE
77	a	330	LEU
77	a	332	LEU
77	a	337	MET
77	a	340	GLN
77	a	341	LYS
77	a	342	LYS
77	a	344	TYR
77	a	345	THR
77	a	346	LYS
77	a	347	MET
77	a	351	LEU
77	a	354	THR
77	a	355	LEU
77	a	360	GLU
77	a	366	ARG
77	a	368	LEU
77	a	371	VAL
77	a	383	LEU
77	a	385	MET
77	a	394	LYS

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Mol	Chain	Res	Type
77	a	397	GLN
77	a	401	VAL
77	a	403	THR
77	a	409	LEU
77	a	417	ILE
77	a	426	LEU
77	a	428	LEU
77	a	433	MET
77	a	437	VAL
77	a	439	LYS
77	a	441	ARG
77	a	447	ARG
77	a	452	VAL
77	a	453	VAL
77	a	455	THR
77	a	457	GLN
77	a	459	VAL
77	a	462	MET
77	a	465	GLU
77	a	474	ASP
77	a	475	GLU
77	a	476	LEU
77	a	477	PHE
77	a	478	ILE
77	a	480	ASN
77	a	481	ILE
77	a	482	GLN
77	a	483	ARG
77	a	485	ILE
77	a	487	MET
77	a	492	ILE
77	a	494	GLN
77	a	495	ILE
77	a	498	VAL
77	a	499	PRO
77	a	502	ASN
77	a	506	LEU
77	a	509	ILE
77	a	511	GLN
77	a	513	LEU
77	a	515	LYS
77	a	516	SER

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Mol	Chain	Res	Type
77	a	519	ILE
77	a	521	THR
77	a	529	LYS
77	a	538	VAL
77	a	541	VAL
77	a	543	VAL
77	a	549	LYS
77	a	550	ASP
77	a	553	LYS
77	a	558	MET
77	a	559	LYS
77	a	560	ARG
77	a	561	LEU
77	a	562	ASP
77	a	563	LYS
77	a	567	CYS
77	a	568	VAL
77	a	571	ILE
77	a	572	CYS
77	a	574	LYS
77	a	577	ASN
77	a	579	ASN
77	a	581	ILE
77	a	591	ILE
77	a	593	LEU
77	a	594	LYS
77	a	595	ASP
77	a	598	GLU
77	a	604	MET
77	a	606	ILE
77	a	607	ARG
77	a	608	VAL
77	a	612	VAL
77	a	617	GLU
77	a	620	THR
77	a	623	SER
77	a	626	VAL
77	a	631	SER
77	a	633	ASN
77	a	636	ASN
77	a	641	GLU
77	a	643	GLU

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Mol	Chain	Res	Type
77	a	648	GLU
77	a	649	VAL
77	a	654	LYS
77	a	658	ILE
77	a	663	ASP
77	a	664	SER
77	a	665	LYS
77	a	667	ARG
77	a	673	ASP
77	a	674	LYS
77	a	679	SER
77	a	683	LYS
77	a	691	VAL
77	a	695	SER
77	a	699	THR
77	a	701	LEU
77	a	703	LEU
77	a	706	THR
77	a	712	VAL
77	a	713	LYS
77	a	718	HIS
77	a	719	ILE
77	a	720	VAL
77	a	721	SER
77	a	727	CYS
77	a	728	ARG
77	a	738	VAL
77	a	743	LYS
77	a	745	ARG
77	a	748	THR
77	a	754	ILE
77	a	765	THR
77	a	766	ARG
77	a	769	LEU
77	a	770	TYR
77	a	775	TYR
77	a	779	MET
77	a	780	LEU
77	a	786	LEU
77	a	787	VAL
77	a	793	GLU
77	a	796	MET

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Mol	Chain	Res	Type
77	a	801	SER
77	a	803	MET
77	a	806	ARG
77	a	810	VAL
77	a	811	ILE
77	a	813	GLU
77	a	814	GLU
77	a	819	GLN
77	a	821	LEU
77	a	822	THR
77	a	823	GLU
77	a	825	LYS
77	a	827	HIS
77	a	830	VAL
77	a	832	GLU
77	a	836	PHE
77	a	841	ARG
77	a	852	CYS
77	a	853	VAL
77	a	855	SER
77	a	859	LEU
77	a	860	ILE
77	a	863	SER
77	a	874	ILE
77	a	876	LEU
77	a	880	LYS
77	a	884	MET
77	a	885	LYS
77	a	891	VAL
77	a	897	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (208) such sidechains are listed below:

Mol	Chain	Res	Type
1	LA	86	GLN
1	LA	100	ASN
1	LA	140	ASN
1	LA	144	ASN
1	LA	154	GLN
1	LA	217	GLN
2	LB	3	HIS
2	LB	37	GLN

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Mol	Chain	Res	Type
2	LB	68	HIS
2	LB	69	ASN
2	LB	75	GLN
2	LB	121	ASN
2	LB	164	GLN
2	LB	172	GLN
2	LB	181	GLN
2	LB	246	ASN
2	LB	313	ASN
2	LB	345	HIS
3	LC	14	GLN
3	LC	109	GLN
3	LC	200	ASN
6	LF	7	GLN
6	LF	17	GLN
6	LF	42	ASN
6	LF	183	HIS
7	LG	22	ASN
7	LG	38	ASN
8	LH	38	HIS
8	LH	68	ASN
8	LH	105	GLN
8	LH	107	ASN
8	LH	108	ASN
8	LH	161	ASN
8	LH	228	ASN
9	LI	87	HIS
9	LI	152	HIS
10	LJ	94	HIS
11	LK	14	ASN
11	LK	198	HIS
12	LL	144	GLN
13	LM	37	ASN
13	LM	49	ASN
13	LM	53	ASN
13	LM	81	GLN
13	LM	95	ASN
13	LM	141	ASN
13	LM	199	ASN
14	LN	60	GLN
15	LO	104	GLN
16	LP	26	HIS

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Mol	Chain	Res	Type
16	LP	28	HIS
16	LP	63	HIS
16	LP	69	HIS
17	LQ	53	HIS
17	LQ	103	HIS
18	LR	69	HIS
19	LS	7	GLN
19	LS	149	GLN
20	LT	119	GLN
20	LT	122	ASN
21	LU	26	ASN
21	LU	31	ASN
22	LV	46	ASN
22	LV	68	GLN
22	LV	89	GLN
23	LW	39	ASN
23	LW	101	GLN
23	LW	109	ASN
24	LX	6	HIS
26	LZ	22	ASN
26	LZ	62	HIS
27	La	16	GLN
28	Lb	14	HIS
28	Lb	40	HIS
28	Lb	49	HIS
29	Lc	6	ASN
29	Lc	17	HIS
29	Lc	53	GLN
30	Ld	44	GLN
31	Le	78	HIS
32	Lf	50	GLN
32	Lf	54	GLN
34	Lh	11	HIS
34	Lh	62	HIS
34	Lh	66	GLN
34	Lh	97	GLN
35	Li	46	GLN
36	Lj	72	ASN
38	Ll	33	GLN
38	Ll	53	ASN
39	Ln	22	ASN
39	Ln	62	ASN

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Mol	Chain	Res	Type
39	Ln	83	ASN
39	Ln	171	ASN
39	Ln	199	GLN
39	Ln	214	HIS
41	Lp	87	HIS
42	Lq	25	GLN
42	Lq	33	GLN
43	Ls	92	ASN
43	Ls	117	ASN
46	SA	14	GLN
46	SA	112	ASN
46	SA	130	ASN
46	SA	146	ASN
47	SB	125	ASN
47	SB	146	HIS
47	SB	231	HIS
47	SB	233	GLN
48	SC	28	HIS
48	SC	69	HIS
48	SC	168	HIS
49	SD	60	ASN
49	SD	81	ASN
49	SD	174	ASN
49	SD	190	ASN
49	SD	223	ASN
50	SE	50	ASN
50	SE	53	HIS
50	SE	151	HIS
50	SE	196	GLN
50	SE	201	HIS
50	SE	230	ASN
51	SF	60	ASN
51	SF	178	GLN
52	SG	85	GLN
52	SG	92	HIS
52	SG	204	GLN
53	SH	74	GLN
53	SH	164	ASN
54	SI	18	GLN
54	SI	89	GLN
54	SI	93	ASN
54	SI	103	ASN

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Mol	Chain	Res	Type
54	SI	112	GLN
54	SI	134	GLN
54	SI	139	HIS
55	SJ	42	GLN
55	SJ	92	ASN
55	SJ	101	HIS
56	SK	134	HIS
56	SK	140	GLN
56	SK	143	ASN
57	SL	32	ASN
57	SL	47	ASN
57	SL	74	HIS
58	SM	6	HIS
58	SM	13	GLN
58	SM	15	GLN
58	SM	74	HIS
58	SM	90	HIS
58	SM	104	HIS
59	SO	31	HIS
59	SO	61	GLN
60	SP	62	GLN
61	SQ	110	GLN
62	SR	16	ASN
62	SR	68	GLN
63	ST	33	ASN
63	ST	95	GLN
63	ST	101	GLN
64	SU	20	ASN
64	SU	51	ASN
64	SU	62	ASN
65	SV	8	ASN
65	SV	20	ASN
65	SV	43	ASN
65	SV	50	ASN
65	SV	88	ASN
66	SW	68	HIS
66	SW	83	GLN
67	SX	22	HIS
67	SX	23	GLN
67	SX	115	GLN
68	SY	28	ASN
68	SY	55	ASN

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Mol	Chain	Res	Type
68	SY	56	ASN
69	Sb	45	GLN
70	Sc	28	ASN
70	Sc	44	GLN
70	Sc	83	ASN
71	Sd	8	ASN
71	Sd	17	HIS
71	Sd	24	GLN
71	Sd	55	ASN
71	Sd	69	ASN
71	Sd	81	ASN
71	Sd	82	HIS
72	Se	70	ASN
74	Sh	107	ASN
74	Sh	127	ASN
75	Sj	63	GLN
77	a	27	HIS
77	a	30	HIS
77	a	61	GLN
77	a	180	GLN
77	a	256	ASN
77	a	318	GLN
77	a	398	GLN
77	a	423	ASN
77	a	457	GLN
77	a	547	ASN
77	a	577	ASN
77	a	578	GLN
77	a	636	ASN
77	a	697	HIS
77	a	710	GLN
77	a	718	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	LD	135/142 (95%)	49 (36%)	3 (2%)
44	Lt	2588/2697 (95%)	1025 (39%)	0
45	Lu	74/75 (98%)	42 (56%)	0
5	LE	114/121 (94%)	38 (33%)	5 (4%)
76	St	1453/1454 (99%)	683 (47%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
78	y	10/11 (90%)	10 (100%)	0
All	All	4374/4500 (97%)	1847 (42%)	8 (0%)

All (1847) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	LD	9	C
4	LD	17	G
4	LD	19	U
4	LD	20	G
4	LD	21	C
4	LD	22	C
4	LD	24	C
4	LD	25	G
4	LD	30	G
4	LD	35	G
4	LD	36	C
4	LD	39	C
4	LD	40	G
4	LD	52	G
4	LD	53	G
4	LD	54	A
4	LD	56	C
4	LD	59	G
4	LD	60	A
4	LD	62	A
4	LD	63	C
4	LD	64	G
4	LD	65	C
4	LD	67	G
4	LD	69	G
4	LD	70	C
4	LD	73	A
4	LD	76	C
4	LD	77	G
4	LD	82	C
4	LD	84	C
4	LD	85	C
4	LD	86	G
4	LD	87	A
4	LD	88	G
4	LD	93	A

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Mol	Chain	Res	Type
4	LD	97	A
4	LD	101	U
4	LD	104	A
4	LD	105	A
4	LD	106	C
4	LD	108	C
4	LD	110	G
4	LD	111	C
4	LD	112	G
4	LD	116	C
4	LD	127	C
4	LD	133	G
4	LD	140	G
5	LE	5	U
5	LE	7	G
5	LE	11	A
5	LE	14	C
5	LE	19	G
5	LE	26	C
5	LE	29	C
5	LE	30	U
5	LE	32	A
5	LE	36	C
5	LE	38	U
5	LE	39	U
5	LE	40	C
5	LE	42	G
5	LE	43	A
5	LE	54	G
5	LE	55	A
5	LE	56	A
5	LE	62	G
5	LE	63	U
5	LE	64	C
5	LE	65	A
5	LE	66	G
5	LE	70	C
5	LE	77	U
5	LE	85	U
5	LE	86	C
5	LE	91	A
5	LE	92	C

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Mol	Chain	Res	Type
5	LE	96	G
5	LE	97	U
5	LE	98	G
5	LE	99	G
5	LE	102	A
5	LE	110	U
5	LE	111	G
5	LE	114	G
5	LE	116	A
44	Lt	3	C
44	Lt	4	G
44	Lt	9	U
44	Lt	10	G
44	Lt	15	G
44	Lt	18	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	44	A
44	Lt	48	G
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	71	C
44	Lt	72	C
44	Lt	73	G
44	Lt	74	G
44	Lt	75	G
44	Lt	84	C
44	Lt	85	U
44	Lt	86	A
44	Lt	90	G
44	Lt	92	G
44	Lt	103	G
44	Lt	107	A
44	Lt	108	G

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Mol	Chain	Res	Type
44	Lt	109	C
44	Lt	110	C
44	Lt	111	C
44	Lt	117	G
44	Lt	118	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	130	G
44	Lt	131	G
44	Lt	132	G
44	Lt	150	C
44	Lt	152	G
44	Lt	153	C
44	Lt	156	G
44	Lt	158	G
44	Lt	166	G
44	Lt	167	G
44	Lt	168	G
44	Lt	169	C
44	Lt	170	C
44	Lt	172	C
44	Lt	176	C
44	Lt	178	A
44	Lt	179	G
44	Lt	181	G
44	Lt	185	G
44	Lt	186	C
44	Lt	187	A
44	Lt	188	A
44	Lt	189	G
44	Lt	190	C
44	Lt	191	C
44	Lt	192	C
44	Lt	194	G
44	Lt	198	G
44	Lt	200	C

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Mol	Chain	Res	Type
44	Lt	225	A
44	Lt	230	U
44	Lt	235	G
44	Lt	238	C
44	Lt	239	G
44	Lt	240	U
44	Lt	246	G
44	Lt	250	A
44	Lt	251	G
44	Lt	256	G
44	Lt	257	C
44	Lt	258	G
44	Lt	263	C
44	Lt	267	C
44	Lt	268	C
44	Lt	275	A
44	Lt	281	G
44	Lt	288	G
44	Lt	289	A
44	Lt	292	G
44	Lt	294	U
44	Lt	302	C
44	Lt	303	A
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	329	G
44	Lt	333	C
44	Lt	339	G
44	Lt	343	G
44	Lt	345	U
44	Lt	347	A
44	Lt	349	A
44	Lt	350	A
44	Lt	351	G
44	Lt	352	A
44	Lt	356	G
44	Lt	368	C

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Mol	Chain	Res	Type
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	385	C
44	Lt	388	U
44	Lt	389	C
44	Lt	391	C
44	Lt	397	A
44	Lt	404	G
44	Lt	405	A
44	Lt	408	A
44	Lt	421	G
44	Lt	425	A
44	Lt	429	C
44	Lt	430	G
44	Lt	435	A
44	Lt	436	G
44	Lt	437	C
44	Lt	438	C
44	Lt	439	C
44	Lt	443	C
44	Lt	444	G
44	Lt	446	C
44	Lt	449	A
44	Lt	455	C
44	Lt	459	A
44	Lt	460	G
44	Lt	461	A
44	Lt	463	G
44	Lt	464	C
44	Lt	465	C
44	Lt	466	C
44	Lt	471	C
44	Lt	472	C
44	Lt	477	A
44	Lt	483	C
44	Lt	484	U
44	Lt	485	G

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Mol	Chain	Res	Type
44	Lt	486	C
44	Lt	489	G
44	Lt	491	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	515	U
44	Lt	517	G
44	Lt	518	G
44	Lt	525	A
44	Lt	534	U
44	Lt	535	C
44	Lt	537	A
44	Lt	539	G
44	Lt	542	C
44	Lt	546	G
44	Lt	547	A
44	Lt	549	G
44	Lt	550	G
44	Lt	552	G
44	Lt	554	G
44	Lt	556	C
44	Lt	564	A
44	Lt	566	G
44	Lt	568	C
44	Lt	570	G
44	Lt	578	C
44	Lt	582	C
44	Lt	587	G
44	Lt	590	C
44	Lt	591	U
44	Lt	592	G
44	Lt	596	C
44	Lt	597	G
44	Lt	601	A
44	Lt	605	C
44	Lt	607	C
44	Lt	611	G
44	Lt	612	G

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Mol	Chain	Res	Type
44	Lt	613	A
44	Lt	614	G
44	Lt	616	C
44	Lt	624	G
44	Lt	625	G
44	Lt	630	A
44	Lt	631	A
44	Lt	632	A
44	Lt	633	G
44	Lt	637	C
44	Lt	638	A
44	Lt	639	U
44	Lt	640	C
44	Lt	641	G
44	Lt	642	A
44	Lt	643	A
44	Lt	650	G
44	Lt	651	G
44	Lt	654	G
44	Lt	661	G
44	Lt	662	C
44	Lt	669	A
44	Lt	670	A
44	Lt	676	C
44	Lt	677	C
44	Lt	678	C
44	Lt	679	A
44	Lt	680	G
44	Lt	681	G
44	Lt	688	G
44	Lt	691	G
44	Lt	692	C
44	Lt	694	C
44	Lt	695	C
44	Lt	698	A
44	Lt	699	G
44	Lt	700	U
44	Lt	705	G
44	Lt	708	C
44	Lt	709	G
44	Lt	710	U
44	Lt	715	C

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Mol	Chain	Res	Type
44	Lt	716	G
44	Lt	719	G
44	Lt	720	G
44	Lt	722	C
44	Lt	723	G
44	Lt	725	C
44	Lt	728	G
44	Lt	730	G
44	Lt	732	G
44	Lt	734	G
44	Lt	735	G
44	Lt	736	G
44	Lt	738	C
44	Lt	739	C
44	Lt	740	U
44	Lt	742	C
44	Lt	743	C
44	Lt	744	C
44	Lt	747	C
44	Lt	752	G
44	Lt	753	C
44	Lt	754	C
44	Lt	759	A
44	Lt	760	A
44	Lt	764	C
44	Lt	765	C
44	Lt	767	A
44	Lt	769	G
44	Lt	770	G
44	Lt	776	G
44	Lt	777	C
44	Lt	778	C
44	Lt	779	G
44	Lt	780	C
44	Lt	781	C
44	Lt	782	C
44	Lt	787	G
44	Lt	788	C
44	Lt	790	G
44	Lt	791	G
44	Lt	794	U
44	Lt	796	G

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Mol	Chain	Res	Type
44	Lt	799	G
44	Lt	800	G
44	Lt	804	G
44	Lt	805	G
44	Lt	807	C
44	Lt	808	G
44	Lt	809	A
44	Lt	814	G
44	Lt	818	G
44	Lt	827	G
44	Lt	829	C
44	Lt	830	C
44	Lt	831	C
44	Lt	832	U
44	Lt	834	C
44	Lt	839	A
44	Lt	841	G
44	Lt	843	A
44	Lt	853	A
44	Lt	854	G
44	Lt	855	G
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	878	C
44	Lt	879	A
44	Lt	882	G
44	Lt	887	C
44	Lt	888	C
44	Lt	889	G
44	Lt	890	C
44	Lt	894	G
44	Lt	898	C
44	Lt	899	G
44	Lt	900	C
44	Lt	901	G
44	Lt	906	G

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Mol	Chain	Res	Type
44	Lt	907	G
44	Lt	908	C
44	Lt	913	G
44	Lt	916	G
44	Lt	921	C
44	Lt	922	G
44	Lt	983	C
44	Lt	984	C
44	Lt	986	A
44	Lt	987	A
44	Lt	989	C
44	Lt	990	G
44	Lt	993	C
44	Lt	994	G
44	Lt	995	G
44	Lt	997	C
44	Lt	999	G
44	Lt	1000	G
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	1017	G
44	Lt	1018	A
44	Lt	1019	G
44	Lt	1021	C
44	Lt	1023	C
44	Lt	1025	G
44	Lt	1026	A
44	Lt	1028	C
44	Lt	1030	G
44	Lt	1031	C
44	Lt	1032	G
44	Lt	1036	G
44	Lt	1037	G
44	Lt	1038	C
44	Lt	1043	G
44	Lt	1045	G
44	Lt	1046	C

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Mol	Chain	Res	Type
44	Lt	1047	G
44	Lt	1053	G
44	Lt	1062	C
44	Lt	1067	G
44	Lt	1070	G
44	Lt	1073	C
44	Lt	1074	C
44	Lt	1075	G
44	Lt	1076	G
44	Lt	1079	G
44	Lt	1080	C
44	Lt	1081	G
44	Lt	1085	G
44	Lt	1089	C
44	Lt	1095	G
44	Lt	1096	G
44	Lt	1109	G
44	Lt	1110	G
44	Lt	1117	G
44	Lt	1119	G
44	Lt	1120	C
44	Lt	1122	G
44	Lt	1125	C
44	Lt	1126	U
44	Lt	1132	G
44	Lt	1134	A
44	Lt	1135	G
44	Lt	1136	U
44	Lt	1138	G
44	Lt	1140	C
44	Lt	1141	G
44	Lt	1143	U
44	Lt	1150	C
44	Lt	1151	G
44	Lt	1152	C
44	Lt	1153	C
44	Lt	1154	C
44	Lt	1156	G
44	Lt	1159	G
44	Lt	1160	G
44	Lt	1161	A
44	Lt	1165	A

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Mol	Chain	Res	Type
44	Lt	1166	G
44	Lt	1167	G
44	Lt	1168	G
44	Lt	1170	G
44	Lt	1171	A
44	Lt	1172	G
44	Lt	1178	U
44	Lt	1179	U
44	Lt	1182	G
44	Lt	1189	C
44	Lt	1191	G
44	Lt	1192	C
44	Lt	1193	A
44	Lt	1195	C
44	Lt	1196	U
44	Lt	1198	G
44	Lt	1199	C
44	Lt	1203	G
44	Lt	1204	G
44	Lt	1206	U
44	Lt	1207	G
44	Lt	1217	U
44	Lt	1220	G
44	Lt	1225	G
44	Lt	1226	G
44	Lt	1231	A
44	Lt	1233	A
44	Lt	1236	G
44	Lt	1237	G
44	Lt	1239	A
44	Lt	1241	G
44	Lt	1242	G
44	Lt	1243	G
44	Lt	1245	C
44	Lt	1248	G
44	Lt	1249	C
44	Lt	1250	C
44	Lt	1252	G
44	Lt	1253	C
44	Lt	1256	G
44	Lt	1257	U
44	Lt	1258	C

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Mol	Chain	Res	Type
44	Lt	1260	A
44	Lt	1261	A
44	Lt	1262	C
44	Lt	1269	C
44	Lt	1272	G
44	Lt	1273	C
44	Lt	1275	G
44	Lt	1278	A
44	Lt	1279	C
44	Lt	1280	U
44	Lt	1281	C
44	Lt	1282	C
44	Lt	1286	A
44	Lt	1290	G
44	Lt	1298	C
44	Lt	1299	G
44	Lt	1300	C
44	Lt	1308	C
44	Lt	1309	C
44	Lt	1310	C
44	Lt	1311	G
44	Lt	1313	C
44	Lt	1316	C
44	Lt	1318	G
44	Lt	1323	C
44	Lt	1324	G
44	Lt	1328	A
44	Lt	1332	G
44	Lt	1338	C
44	Lt	1344	G
44	Lt	1345	C
44	Lt	1346	G
44	Lt	1349	G
44	Lt	1350	C
44	Lt	1355	G
44	Lt	1361	G
44	Lt	1365	G
44	Lt	1366	C
44	Lt	1369	C
44	Lt	1377	C
44	Lt	1381	A
44	Lt	1382	C

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Mol	Chain	Res	Type
44	Lt	1383	G
44	Lt	1384	C
44	Lt	1387	U
44	Lt	1389	C
44	Lt	1392	G
44	Lt	1395	G
44	Lt	1399	G
44	Lt	1400	G
44	Lt	1401	G
44	Lt	1406	G
44	Lt	1407	G
44	Lt	1412	G
44	Lt	1423	G
44	Lt	1434	C
44	Lt	1438	U
44	Lt	1439	G
44	Lt	1440	A
44	Lt	1443	A
44	Lt	1447	G
44	Lt	1448	G
44	Lt	1449	G
44	Lt	1451	G
44	Lt	1453	C
44	Lt	1454	G
44	Lt	1455	C
44	Lt	1456	C
44	Lt	1461	G
44	Lt	1464	C
44	Lt	1466	C
44	Lt	1470	A
44	Lt	1472	C
44	Lt	1473	G
44	Lt	1474	A
44	Lt	1476	C
44	Lt	1479	A
44	Lt	1480	G
44	Lt	1481	C
44	Lt	1482	A
44	Lt	1483	G
44	Lt	1485	A
44	Lt	1486	C
44	Lt	1489	C

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Mol	Chain	Res	Type
44	Lt	1490	G
44	Lt	1491	G
44	Lt	1498	C
44	Lt	1499	A
44	Lt	1503	U
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	1518	A
44	Lt	1524	G
44	Lt	1525	C
44	Lt	1526	U
44	Lt	1528	A
44	Lt	1531	G
44	Lt	1538	G
44	Lt	1543	C
44	Lt	1550	C
44	Lt	1564	A
44	Lt	1567	G
44	Lt	1570	U
44	Lt	1571	G
44	Lt	1574	U
44	Lt	1575	C
44	Lt	1576	U
44	Lt	1577	G
44	Lt	1578	A
44	Lt	1579	C
44	Lt	1580	G
44	Lt	1582	C
44	Lt	1585	G
44	Lt	1586	C
44	Lt	1587	C
44	Lt	1588	G
44	Lt	1589	G
44	Lt	1590	G
44	Lt	1593	A
44	Lt	1596	A
44	Lt	1597	C
44	Lt	1599	G

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Mol	Chain	Res	Type
44	Lt	1600	G
44	Lt	1601	A
44	Lt	1604	G
44	Lt	1605	G
44	Lt	1606	A
44	Lt	1611	G
44	Lt	1618	C
44	Lt	1620	A
44	Lt	1622	U
44	Lt	1624	U
44	Lt	1626	U
44	Lt	1628	C
44	Lt	1629	U
44	Lt	1631	G
44	Lt	1633	A
44	Lt	1634	A
44	Lt	1635	C
44	Lt	1646	G
44	Lt	1647	A
44	Lt	1648	G
44	Lt	1649	G
44	Lt	1650	G
44	Lt	1656	C
44	Lt	1658	C
44	Lt	1659	G
44	Lt	1663	C
44	Lt	1665	G
44	Lt	1672	C
44	Lt	1676	A
44	Lt	1679	U
44	Lt	1683	C
44	Lt	1686	A
44	Lt	1692	A
44	Lt	1693	C
44	Lt	1695	A
44	Lt	1696	C
44	Lt	1697	C
44	Lt	1699	U
44	Lt	1702	C
44	Lt	1703	C
44	Lt	1706	G
44	Lt	1707	A

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Mol	Chain	Res	Type
44	Lt	1708	A
44	Lt	1713	U
44	Lt	1715	C
44	Lt	1716	G
44	Lt	1719	G
44	Lt	1720	A
44	Lt	1721	A
44	Lt	1727	G
44	Lt	1731	A
44	Lt	1732	A
44	Lt	1733	C
44	Lt	1734	G
44	Lt	1735	G
44	Lt	1736	C
44	Lt	1737	G
44	Lt	1738	G
44	Lt	1739	G
44	Lt	1741	G
44	Lt	1744	A
44	Lt	1748	U
44	Lt	1749	G
44	Lt	1750	A
44	Lt	1755	C
44	Lt	1760	G
44	Lt	1761	G
44	Lt	1764	G
44	Lt	1765	C
44	Lt	1767	A
44	Lt	1769	A
44	Lt	1771	G
44	Lt	1772	C
44	Lt	1786	U
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

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Mol	Chain	Res	Type
44	Lt	1811	G
44	Lt	1817	C
44	Lt	1822	U
44	Lt	1823	G
44	Lt	1824	U
44	Lt	1833	G
44	Lt	1842	C
44	Lt	1843	G
44	Lt	1845	G
44	Lt	1846	C
44	Lt	1853	C
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	1870	G
44	Lt	1873	C
44	Lt	1876	C
44	Lt	1881	G
44	Lt	1882	G
44	Lt	1885	C
44	Lt	1886	A
44	Lt	1889	A
44	Lt	1890	A
44	Lt	1891	G
44	Lt	1892	A
44	Lt	1895	C
44	Lt	1897	U
44	Lt	1899	U
44	Lt	1902	G
44	Lt	1906	G
44	Lt	1907	A
44	Lt	1912	A
44	Lt	1914	C
44	Lt	1915	C
44	Lt	1925	G
44	Lt	1929	C

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Mol	Chain	Res	Type
44	Lt	1936	G
44	Lt	1940	G
44	Lt	1941	C
44	Lt	1942	G
44	Lt	1943	C
44	Lt	1944	A
44	Lt	1946	C
44	Lt	1947	G
44	Lt	1948	C
44	Lt	1949	A
44	Lt	1950	C
44	Lt	1954	G
44	Lt	1955	G
44	Lt	1956	A
44	Lt	1957	G
44	Lt	1958	G
44	Lt	1960	C
44	Lt	1962	C
44	Lt	1963	G
44	Lt	1964	C
44	Lt	1965	C
44	Lt	1966	C
44	Lt	1967	C
44	Lt	1968	U
44	Lt	1969	G
44	Lt	1970	A
44	Lt	1971	G
44	Lt	1972	A
44	Lt	1973	C
44	Lt	1974	A
44	Lt	1976	C
44	Lt	1977	C
44	Lt	1980	A
44	Lt	1981	C
44	Lt	1983	G
44	Lt	1984	C
44	Lt	1985	C
44	Lt	1989	G
44	Lt	1990	C
44	Lt	1997	G
44	Lt	2000	C
44	Lt	2004	C

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Mol	Chain	Res	Type
44	Lt	2006	G
44	Lt	2007	U
44	Lt	2008	C
44	Lt	2009	G
44	Lt	2010	C
44	Lt	2012	C
44	Lt	2014	G
44	Lt	2017	A
44	Lt	2018	C
44	Lt	2022	C
44	Lt	2023	C
44	Lt	2024	C
44	Lt	2027	G
44	Lt	2030	G
44	Lt	2031	G
44	Lt	2033	A
44	Lt	2038	G
44	Lt	2041	U
44	Lt	2042	G
44	Lt	2047	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	2057	C
44	Lt	2059	A
44	Lt	2061	A
44	Lt	2062	C
44	Lt	2063	C
44	Lt	2064	G
44	Lt	2065	G
44	Lt	2066	A
44	Lt	2067	C
44	Lt	2068	C
44	Lt	2069	G
44	Lt	2072	G
44	Lt	2073	G
44	Lt	2075	G
44	Lt	2076	U
44	Lt	2079	C

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Mol	Chain	Res	Type
44	Lt	2080	A
44	Lt	2081	C
44	Lt	2084	C
44	Lt	2089	U
44	Lt	2090	C
44	Lt	2092	G
44	Lt	2093	C
44	Lt	2098	A
44	Lt	2100	G
44	Lt	2101	G
44	Lt	2104	A
44	Lt	2105	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
44	Lt	2118	A
44	Lt	2120	A
44	Lt	2128	A
44	Lt	2129	A
44	Lt	2130	G
44	Lt	2134	G
44	Lt	2137	C
44	Lt	2138	G
44	Lt	2139	A
44	Lt	2140	C
44	Lt	2143	G
44	Lt	2144	C
44	Lt	2152	G
44	Lt	2153	U
44	Lt	2163	G
44	Lt	2164	G
44	Lt	2166	C
44	Lt	2171	A
44	Lt	2177	G
44	Lt	2184	C
44	Lt	2185	G
44	Lt	2186	A
44	Lt	2193	G

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Mol	Chain	Res	Type
44	Lt	2196	G
44	Lt	2200	C
44	Lt	2201	G
44	Lt	2202	G
44	Lt	2203	C
44	Lt	2205	G
44	Lt	2206	C
44	Lt	2207	G
44	Lt	2211	G
44	Lt	2217	G
44	Lt	2218	U
44	Lt	2219	G
44	Lt	2220	G
44	Lt	2222	A
44	Lt	2223	G
44	Lt	2224	A
44	Lt	2225	A
44	Lt	2226	A
44	Lt	2227	A
44	Lt	2230	U
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	2241	U
44	Lt	2242	A
44	Lt	2243	A
44	Lt	2244	C
44	Lt	2245	U
44	Lt	2246	G
44	Lt	2254	G
44	Lt	2255	C
44	Lt	2258	C
44	Lt	2260	G
44	Lt	2265	C
44	Lt	2266	C
44	Lt	2268	G
44	Lt	2270	A

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Mol	Chain	Res	Type
44	Lt	2272	C
44	Lt	2273	G
44	Lt	2274	A
44	Lt	2276	G
44	Lt	2279	G
44	Lt	2283	U
44	Lt	2286	G
44	Lt	2289	C
44	Lt	2290	C
44	Lt	2291	U
44	Lt	2292	U
44	Lt	2294	G
44	Lt	2296	U
44	Lt	2298	U
44	Lt	2299	C
44	Lt	2310	A
44	Lt	2311	C
44	Lt	2315	C
44	Lt	2317	G
44	Lt	2321	G
44	Lt	2322	C
44	Lt	2324	C
44	Lt	2326	G
44	Lt	2328	C
44	Lt	2334	A
44	Lt	2339	C
44	Lt	2354	U
44	Lt	2355	U
44	Lt	2356	C
44	Lt	2357	A
44	Lt	2358	A
44	Lt	2360	G
44	Lt	2363	U
44	Lt	2364	C
44	Lt	2365	G
44	Lt	2367	G
44	Lt	2368	A
44	Lt	2369	G
44	Lt	2372	G
44	Lt	2373	G
44	Lt	2376	U
44	Lt	2377	U

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Mol	Chain	Res	Type
44	Lt	2382	C
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	2412	G
44	Lt	2414	C
44	Lt	2416	C
44	Lt	2417	C
44	Lt	2418	G
44	Lt	2420	G
44	Lt	2421	G
44	Lt	2424	A
44	Lt	2429	A
44	Lt	2430	C
44	Lt	2431	G
44	Lt	2434	G
44	Lt	2436	G
44	Lt	2439	A
44	Lt	2445	A
44	Lt	2446	G
44	Lt	2447	A
44	Lt	2448	G
44	Lt	2451	A
44	Lt	2452	C
44	Lt	2457	G
44	Lt	2464	G
44	Lt	2466	C
44	Lt	2467	G
44	Lt	2471	G
44	Lt	2472	C
44	Lt	2473	C
44	Lt	2474	C
44	Lt	2475	C
44	Lt	2486	G
44	Lt	2488	C
44	Lt	2495	G
44	Lt	2496	C
44	Lt	2497	G
44	Lt	2503	C

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Mol	Chain	Res	Type
44	Lt	2508	G
44	Lt	2509	C
44	Lt	2510	G
44	Lt	2511	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	2536	C
44	Lt	2539	A
44	Lt	2545	C
44	Lt	2546	A
44	Lt	2547	C
44	Lt	2552	C
44	Lt	2553	C
44	Lt	2563	G
44	Lt	2566	C
44	Lt	2573	G
44	Lt	2574	C
44	Lt	2575	G
44	Lt	2577	C
44	Lt	2578	C
44	Lt	2580	A
44	Lt	2581	G
44	Lt	2583	C
44	Lt	2584	C
44	Lt	2585	C
44	Lt	2586	G
44	Lt	2587	U
44	Lt	2591	C
44	Lt	2592	C
44	Lt	2593	G
44	Lt	2594	U
44	Lt	2598	C
44	Lt	2601	G
44	Lt	2605	C
44	Lt	2608	C
44	Lt	2609	C
44	Lt	2610	G
44	Lt	2611	C

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Mol	Chain	Res	Type
44	Lt	2612	C
44	Lt	2617	G
44	Lt	2618	A
44	Lt	2627	G
44	Lt	2628	G
44	Lt	2629	C
44	Lt	2630	G
44	Lt	2631	C
44	Lt	2635	G
44	Lt	2638	C
44	Lt	2642	U
44	Lt	2648	G
44	Lt	2649	C
44	Lt	2651	G
44	Lt	2653	G
44	Lt	2655	C
44	Lt	2657	U
44	Lt	2658	G
44	Lt	2668	G
44	Lt	2675	G
44	Lt	2680	U
44	Lt	2682	C
44	Lt	2683	A
44	Lt	2684	G
44	Lt	2687	C
44	Lt	2688	G
45	Lu	4	A
45	Lu	7	G
45	Lu	8	U
45	Lu	9	G
45	Lu	10	G
45	Lu	12	G
45	Lu	13	C
45	Lu	15	G
45	Lu	16	C
45	Lu	17	G
45	Lu	18	G
45	Lu	19	A
45	Lu	20	A
45	Lu	22	C
45	Lu	23	G
45	Lu	24	U

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Mol	Chain	Res	Type
45	Lu	30	G
45	Lu	31	C
45	Lu	32	C
45	Lu	35	U
45	Lu	36	A
45	Lu	37	A
45	Lu	38	C
45	Lu	42	G
45	Lu	44	G
45	Lu	45	G
45	Lu	46	U
45	Lu	47	C
45	Lu	48	G
45	Lu	50	U
45	Lu	51	G
45	Lu	52	G
45	Lu	53	A
45	Lu	56	G
45	Lu	57	A
45	Lu	58	A
45	Lu	59	A
45	Lu	60	C
45	Lu	67	C
45	Lu	73	C
45	Lu	74	C
45	Lu	75	A
76	St	2	A
76	St	3	U
76	St	8	U
76	St	10	G
76	St	11	A
76	St	17	C
76	St	20	G
76	St	23	C
76	St	25	C
76	St	26	G
76	St	31	U
76	St	32	C
76	St	33	U
76	St	35	C
76	St	41	G
76	St	43	C

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Mol	Chain	Res	Type
76	St	44	G
76	St	45	A
76	St	46	A
76	St	54	A
76	St	56	G
76	St	57	C
76	St	59	C
76	St	60	G
76	St	61	C
76	St	62	U
76	St	63	C
76	St	64	A
76	St	65	C
76	St	66	C
76	St	67	C
76	St	68	G
76	St	69	G
76	St	70	G
76	St	71	A
76	St	77	C
76	St	81	C
76	St	82	G
76	St	83	G
76	St	84	C
76	St	87	A
76	St	91	C
76	St	94	C
76	St	96	G
76	St	98	U
76	St	101	A
76	St	102	C
76	St	104	C
76	St	106	C
76	St	108	G
76	St	114	G
76	St	115	U
76	St	116	C
76	St	117	C
76	St	118	C
76	St	119	U
76	St	121	C
76	St	122	U

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Mol	Chain	Res	Type
76	St	123	A
76	St	124	G
76	St	125	C
76	St	127	G
76	St	128	G
76	St	129	A
76	St	130	C
76	St	133	C
76	St	136	U
76	St	137	G
76	St	138	G
76	St	144	C
76	St	146	G
76	St	147	C
76	St	148	G
76	St	151	A
76	St	152	A
76	St	153	G
76	St	154	A
76	St	158	G
76	St	159	C
76	St	161	C
76	St	162	G
76	St	163	C
76	St	166	G
76	St	170	G
76	St	171	C
76	St	172	G
76	St	173	C
76	St	174	G
76	St	175	C
76	St	176	C
76	St	179	G
76	St	180	C
76	St	182	G
76	St	183	G
76	St	184	C
76	St	185	G
76	St	187	G
76	St	188	C
76	St	189	A
76	St	194	G

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Mol	Chain	Res	Type
76	St	195	A
76	St	196	C
76	St	198	C
76	St	199	A
76	St	200	G
76	St	201	C
76	St	202	G
76	St	204	C
76	St	205	G
76	St	206	G
76	St	207	C
76	St	211	C
76	St	219	U
76	St	221	C
76	St	222	G
76	St	224	G
76	St	229	C
76	St	231	C
76	St	232	C
76	St	234	G
76	St	235	G
76	St	237	C
76	St	240	C
76	St	242	C
76	St	245	U
76	St	246	C
76	St	247	G
76	St	249	G
76	St	250	G
76	St	251	C
76	St	254	G
76	St	257	G
76	St	260	G
76	St	265	G
76	St	272	G
76	St	274	C
76	St	277	A
76	St	283	A
76	St	286	G
76	St	290	G
76	St	291	A
76	St	293	U

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Mol	Chain	Res	Type
76	St	294	C
76	St	299	G
76	St	300	A
76	St	302	C
76	St	304	G
76	St	305	G
76	St	306	C
76	St	309	G
76	St	310	C
76	St	311	G
76	St	313	G
76	St	314	A
76	St	315	C
76	St	317	G
76	St	326	U
76	St	327	C
76	St	328	C
76	St	329	A
76	St	330	A
76	St	331	G
76	St	333	A
76	St	335	G
76	St	336	G
76	St	337	C
76	St	338	A
76	St	339	G
76	St	340	C
76	St	348	G
76	St	350	A
76	St	352	U
76	St	353	U
76	St	354	G
76	St	355	C
76	St	357	C
76	St	358	A
76	St	360	U
76	St	361	G
76	St	365	G
76	St	366	G
76	St	368	G
76	St	369	C
76	St	370	G

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Mol	Chain	Res	Type
76	St	372	G
76	St	374	G
76	St	377	A
76	St	378	G
76	St	382	C
76	St	383	G
76	St	386	G
76	St	387	A
76	St	388	G
76	St	390	G
76	St	394	G
76	St	395	A
76	St	396	G
76	St	397	C
76	St	398	G
76	St	399	A
76	St	401	G
76	St	405	G
76	St	406	C
76	St	412	G
76	St	413	C
76	St	417	C
76	St	418	G
76	St	419	C
76	St	420	C
76	St	421	G
76	St	422	C
76	St	423	G
76	St	424	C
76	St	425	A
76	St	426	G
76	St	427	C
76	St	429	G
76	St	431	G
76	St	435	A
76	St	436	A
76	St	437	G
76	St	438	G
76	St	439	U
76	St	441	U
76	St	442	G
76	St	443	U

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Mol	Chain	Res	Type
76	St	445	C
76	St	446	C
76	St	448	G
76	St	449	C
76	St	451	G
76	St	452	C
76	St	454	G
76	St	455	C
76	St	456	G
76	St	458	U
76	St	459	A
76	St	462	U
76	St	463	C
76	St	468	U
76	St	471	G
76	St	474	A
76	St	475	G
76	St	487	G
76	St	489	U
76	St	490	G
76	St	491	C
76	St	492	U
76	St	493	G
76	St	494	C
76	St	498	U
76	St	499	G
76	St	500	A
76	St	502	A
76	St	503	C
76	St	504	G
76	St	509	U
76	St	510	A
76	St	514	G
76	St	518	C
76	St	519	C
76	St	520	C
76	St	521	C
76	St	522	G
76	St	524	C
76	St	525	G
76	St	527	C
76	St	530	G

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Mol	Chain	Res	Type
76	St	531	A
76	St	532	G
76	St	534	A
76	St	535	A
76	St	537	C
76	St	540	G
76	St	541	A
76	St	544	G
76	St	545	C
76	St	546	U
76	St	550	G
76	St	552	C
76	St	553	A
76	St	554	G
76	St	555	G
76	St	557	C
76	St	558	C
76	St	559	G
76	St	560	U
76	St	561	U
76	St	567	C
76	St	568	G
76	St	569	C
76	St	570	C
76	St	571	G
76	St	573	G
76	St	581	G
76	St	582	C
76	St	583	G
76	St	584	C
76	St	585	A
76	St	586	G
76	St	587	C
76	St	588	G
76	St	589	G
76	St	592	G
76	St	593	C
76	St	594	G
76	St	595	G
76	St	596	C
76	St	597	G
76	St	598	C

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Mol	Chain	Res	Type
76	St	599	G
76	St	600	C
76	St	602	G
76	St	603	C
76	St	604	C
76	St	605	G
76	St	606	C
76	St	607	C
76	St	609	C
76	St	610	A
76	St	611	G
76	St	612	C
76	St	614	C
76	St	616	G
76	St	617	A
76	St	626	G
76	St	627	G
76	St	630	G
76	St	634	C
76	St	638	G
76	St	639	G
76	St	640	U
76	St	647	C
76	St	650	G
76	St	652	A
76	St	658	G
76	St	659	A
76	St	660	A
76	St	667	U
76	St	668	G
76	St	675	C
76	St	676	C
76	St	680	A
76	St	685	C
76	St	686	G
76	St	687	G
76	St	688	C
76	St	689	C
76	St	693	C
76	St	694	A
76	St	696	G
76	St	698	G

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Mol	Chain	Res	Type
76	St	699	C
76	St	700	C
76	St	701	U
76	St	706	A
76	St	712	C
76	St	713	C
76	St	714	U
76	St	718	U
76	St	720	A
76	St	739	G
76	St	742	C
76	St	744	A
76	St	746	A
76	St	747	A
76	St	751	G
76	St	753	U
76	St	754	C
76	St	756	G
76	St	758	C
76	St	759	A
76	St	765	G
76	St	770	C
76	St	774	G
76	St	775	C
76	St	777	G
76	St	780	A
76	St	782	C
76	St	784	G
76	St	785	U
76	St	786	G
76	St	787	C
76	St	793	C
76	St	794	G
76	St	796	G
76	St	797	G
76	St	800	G
76	St	802	C
76	St	805	G
76	St	806	C
76	St	807	G
76	St	808	C
76	St	809	G

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Mol	Chain	Res	Type
76	St	810	U
76	St	811	C
76	St	814	G
76	St	820	C
76	St	823	C
76	St	824	C
76	St	830	A
76	St	834	G
76	St	835	G
76	St	836	G
76	St	837	A
76	St	838	G
76	St	840	C
76	St	841	U
76	St	842	C
76	St	843	C
76	St	844	G
76	St	845	G
76	St	852	G
76	St	853	G
76	St	855	G
76	St	861	U
76	St	872	C
76	St	881	G
76	St	882	A
76	St	888	U
76	St	889	U
76	St	891	A
76	St	894	G
76	St	898	G
76	St	902	C
76	St	904	A
76	St	907	A
76	St	910	C
76	St	911	G
76	St	917	U
76	St	923	G
76	St	925	U
76	St	927	A
76	St	929	U
76	St	930	C
76	St	932	G

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Mol	Chain	Res	Type
76	St	938	A
76	St	940	G
76	St	943	C
76	St	944	G
76	St	945	C
76	St	949	U
76	St	950	C
76	St	952	C
76	St	955	G
76	St	959	C
76	St	960	G
76	St	961	G
76	St	962	A
76	St	963	C
76	St	964	G
76	St	965	C
76	St	967	C
76	St	968	G
76	St	969	G
76	St	970	A
76	St	971	G
76	St	972	G
76	St	973	A
76	St	974	C
76	St	977	A
76	St	982	C
76	St	984	G
76	St	985	G
76	St	986	C
76	St	987	G
76	St	988	C
76	St	989	G
76	St	990	C
76	St	993	U
76	St	994	C
76	St	995	G
76	St	997	G
76	St	998	A
76	St	999	U
76	St	1000	C
76	St	1001	G
76	St	1005	G

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Mol	Chain	Res	Type
76	St	1006	G
76	St	1007	G
76	St	1009	G
76	St	1014	U
76	St	1015	G
76	St	1016	C
76	St	1021	C
76	St	1026	C
76	St	1027	C
76	St	1028	C
76	St	1029	A
76	St	1030	G
76	St	1032	C
76	St	1035	U
76	St	1036	G
76	St	1039	G
76	St	1042	A
76	St	1043	G
76	St	1044	C
76	St	1048	C
76	St	1049	U
76	St	1050	G
76	St	1053	C
76	St	1054	C
76	St	1056	U
76	St	1057	U
76	St	1058	G
76	St	1062	C
76	St	1063	A
76	St	1064	A
76	St	1066	G
76	St	1067	A
76	St	1074	C
76	St	1080	C
76	St	1087	C
76	St	1088	G
76	St	1089	C
76	St	1090	C
76	St	1091	G
76	St	1096	A
76	St	1098	G
76	St	1100	C

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Mol	Chain	Res	Type
76	St	1103	G
76	St	1104	C
76	St	1105	G
76	St	1107	C
76	St	1110	C
76	St	1111	G
76	St	1112	G
76	St	1114	A
76	St	1115	G
76	St	1117	A
76	St	1120	G
76	St	1122	G
76	St	1128	A
76	St	1130	A
76	St	1131	G
76	St	1132	C
76	St	1133	A
76	St	1134	G
76	St	1135	G
76	St	1137	C
76	St	1138	U
76	St	1139	G
76	St	1141	G
76	St	1147	C
76	St	1148	U
76	St	1149	C
76	St	1150	A
76	St	1151	G
76	St	1152	A
76	St	1153	C
76	St	1154	G
76	St	1157	C
76	St	1161	G
76	St	1162	C
76	St	1163	C
76	St	1164	G
76	St	1165	C
76	St	1166	A
76	St	1172	G
76	St	1175	A
76	St	1177	A
76	St	1178	C

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Mol	Chain	Res	Type
76	St	1179	U
76	St	1180	G
76	St	1184	G
76	St	1187	C
76	St	1188	C
76	St	1189	A
76	St	1190	G
76	St	1192	C
76	St	1193	G
76	St	1194	G
76	St	1195	C
76	St	1196	G
76	St	1204	G
76	St	1208	G
76	St	1209	C
76	St	1211	C
76	St	1212	G
76	St	1213	G
76	St	1214	A
76	St	1215	G
76	St	1219	C
76	St	1224	G
76	St	1225	U
76	St	1226	G
76	St	1227	G
76	St	1230	G
76	St	1233	A
76	St	1234	C
76	St	1237	C
76	St	1238	G
76	St	1242	U
76	St	1243	G
76	St	1244	G
76	St	1245	A
76	St	1246	A
76	St	1247	C
76	St	1252	C
76	St	1256	G
76	St	1257	C
76	St	1261	A
76	St	1262	G
76	St	1263	G

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Mol	Chain	Res	Type
76	St	1264	A
76	St	1265	A
76	St	1266	U
76	St	1267	G
76	St	1270	U
76	St	1271	U
76	St	1272	G
76	St	1273	U
76	St	1276	G
76	St	1278	G
76	St	1285	C
76	St	1289	C
76	St	1290	C
76	St	1292	C
76	St	1294	C
76	St	1295	G
76	St	1303	C
76	St	1305	U
76	St	1306	C
76	St	1307	C
76	St	1310	G
76	St	1319	A
76	St	1321	A
76	St	1322	C
76	St	1323	A
76	St	1324	C
76	St	1325	C
76	St	1326	G
76	St	1333	G
76	St	1341	C
76	St	1345	U
76	St	1346	G
76	St	1349	C
76	St	1350	G
76	St	1351	C
76	St	1353	G
76	St	1354	C
76	St	1355	G
76	St	1368	G
76	St	1370	C
76	St	1371	G
76	St	1372	C

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Mol	Chain	Res	Type
76	St	1373	G
76	St	1374	C
76	St	1378	G
76	St	1386	A
76	St	1397	C
76	St	1399	G
76	St	1400	G
76	St	1401	A
76	St	1403	G
76	St	1405	A
76	St	1406	G
76	St	1408	A
76	St	1409	G
76	St	1410	A
76	St	1411	A
76	St	1412	G
76	St	1413	U
76	St	1415	G
76	St	1416	U
76	St	1417	A
76	St	1421	A
76	St	1422	G
76	St	1423	G
76	St	1424	U
76	St	1426	U
76	St	1428	C
76	St	1435	G
76	St	1437	A
76	St	1445	A
76	St	1446	U
76	St	1447	G
76	St	1448	G
76	St	1449	A
76	St	1450	U
76	St	1451	C
76	St	1453	U
76	St	1454	U
78	y	32	A
78	y	33	A
78	y	34	A
78	y	35	U
78	y	36	G

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Mol	Chain	Res	Type
78	y	37	G
78	y	38	A
78	y	39	U
78	y	40	A
78	y	41	A

All (8) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	LD	23	U
4	LD	87	A
4	LD	111	C
5	LE	38	U
5	LE	63	U
5	LE	85	U
5	LE	96	G
5	LE	110	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
79	PO4	a	901	-	4,4,4	0.77	0	6,6,6	0.49	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
80	GDP	a	902	-	29,30,30	1.23	4 (13%)	45,47,47	1.74	7 (15%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
80	GDP	a	902	-	-	5/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
80	a	902	GDP	C6-N1	-3.02	1.33	1.38
80	a	902	GDP	C5-C4	2.77	1.46	1.38
80	a	902	GDP	C4-N9	-2.40	1.31	1.38
80	a	902	GDP	C5-N7	-2.37	1.34	1.39

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
80	a	902	GDP	C5-C4-N3	-5.58	119.51	128.39
80	a	902	GDP	C2-N3-C4	4.76	120.50	112.30
80	a	902	GDP	N9-C4-N3	4.16	134.27	125.95
80	a	902	GDP	C6-C5-N7	3.44	136.55	130.29
80	a	902	GDP	O6-C6-C5	-2.35	120.32	126.53
80	a	902	GDP	C5-C6-N1	2.17	118.77	113.25
80	a	902	GDP	C4-C5-N7	-2.16	107.25	110.67

There are no chirality outliers.

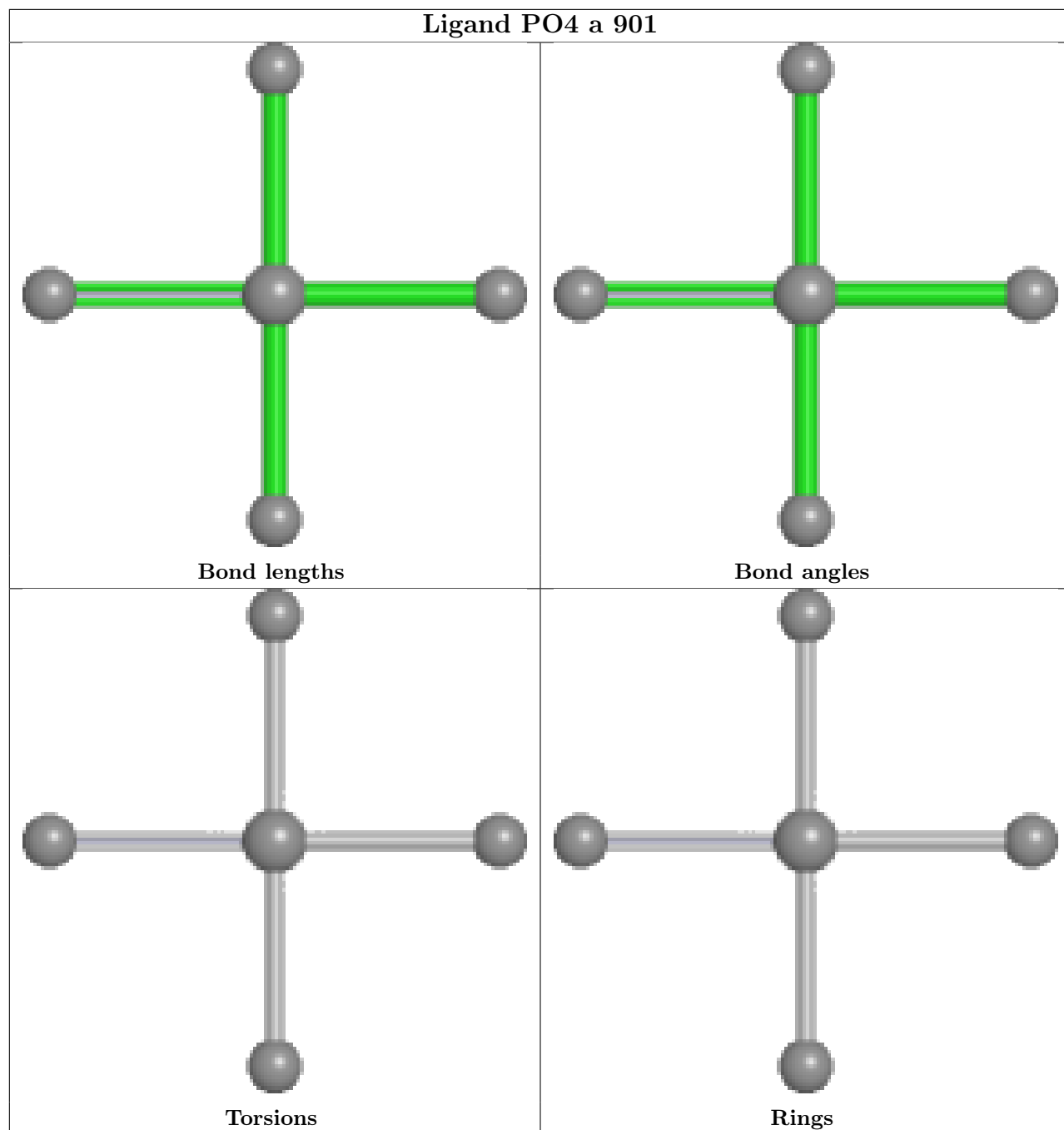
All (5) torsion outliers are listed below:

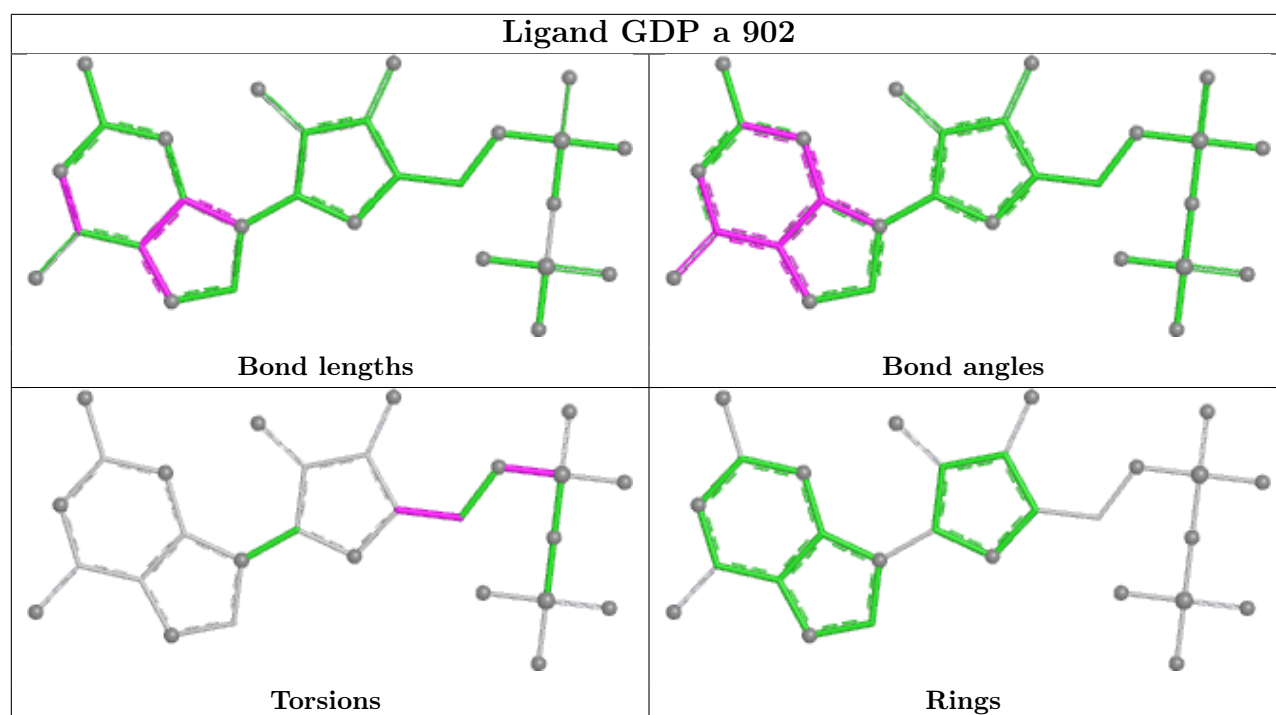
Mol	Chain	Res	Type	Atoms
80	a	902	GDP	C5'-O5'-PA-O1A
80	a	902	GDP	O4'-C4'-C5'-O5'
80	a	902	GDP	C3'-C4'-C5'-O5'
80	a	902	GDP	C5'-O5'-PA-O3A
80	a	902	GDP	C5'-O5'-PA-O2A

There are no ring outliers.

No monomer is involved in short contacts.

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

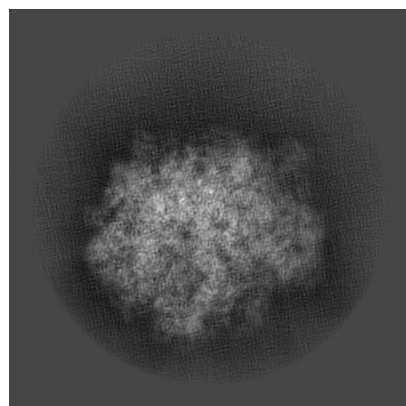
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16225. These allow visual inspection of the internal detail of the map and identification of artifacts.

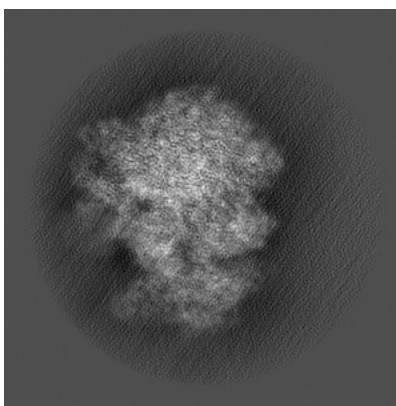
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

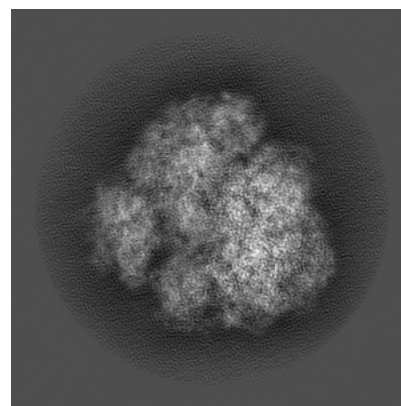
6.1.1 Primary map



X

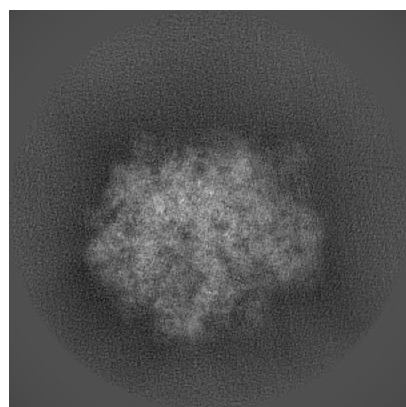


Y

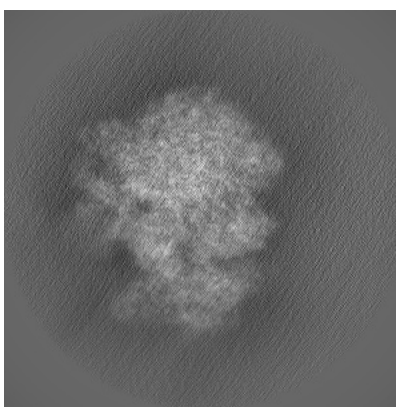


Z

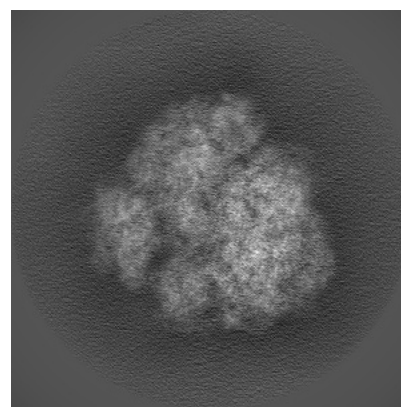
6.1.2 Raw map



X



Y

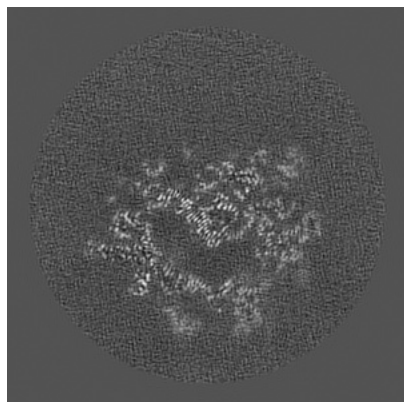


Z

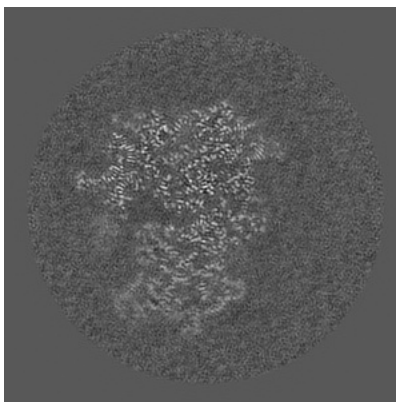
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

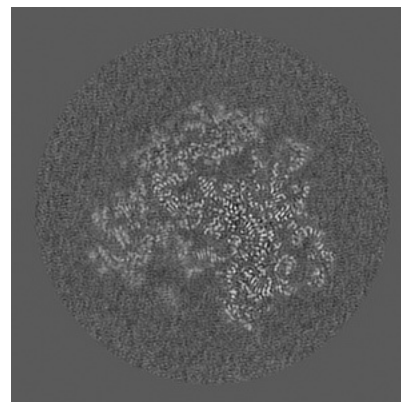
6.2.1 Primary map



X Index: 250

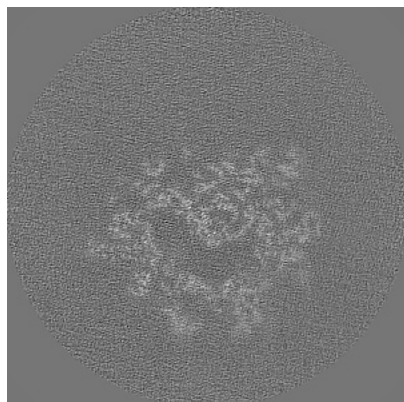


Y Index: 250

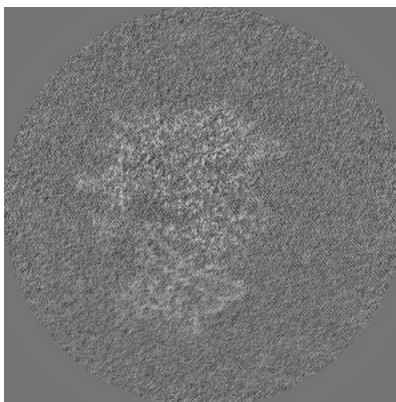


Z Index: 250

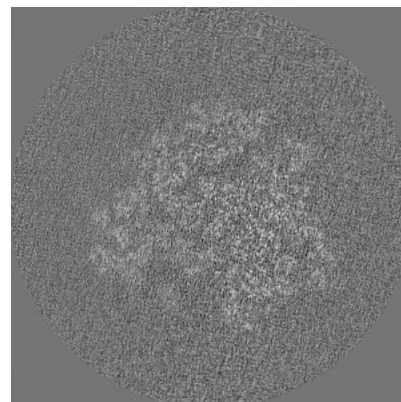
6.2.2 Raw map



X Index: 250



Y Index: 250

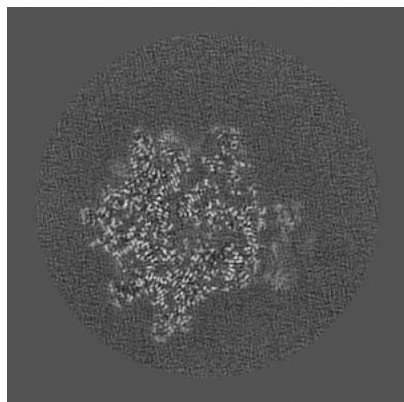


Z Index: 250

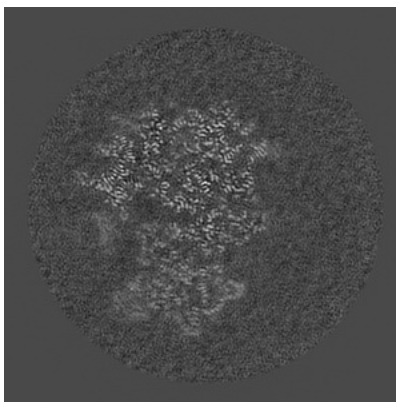
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

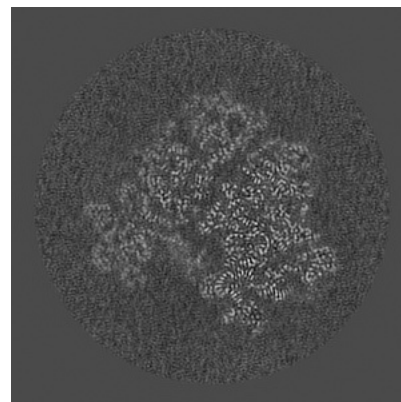
6.3.1 Primary map



X Index: 306

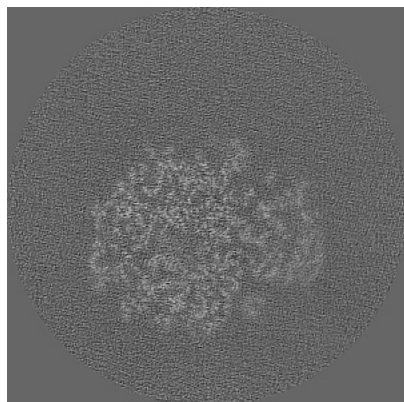


Y Index: 248

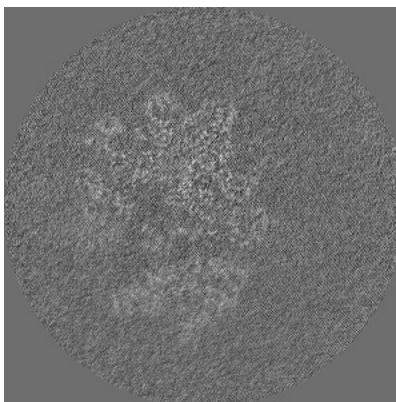


Z Index: 240

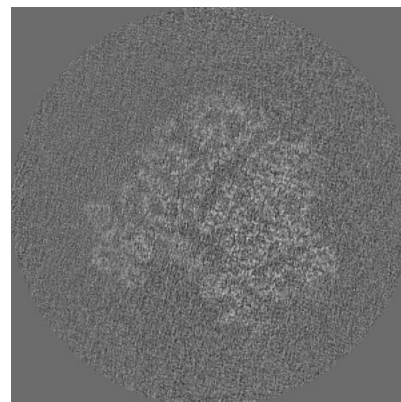
6.3.2 Raw map



X Index: 276



Y Index: 236

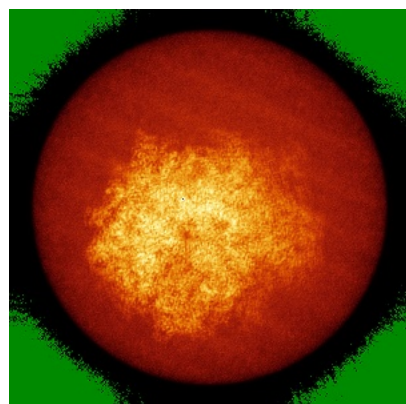


Z Index: 240

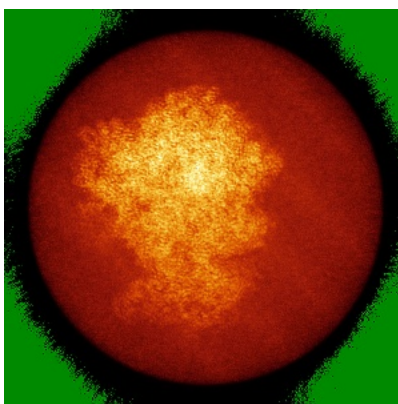
The images above show the largest variance slices of the map in three orthogonal directions.

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

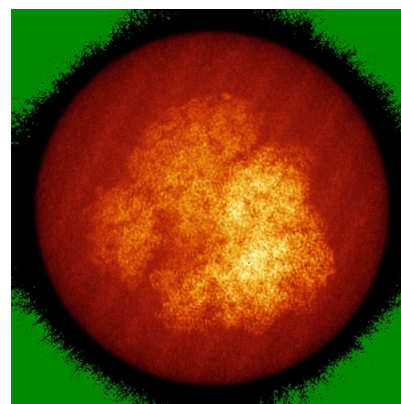
6.4.1 Primary map



X

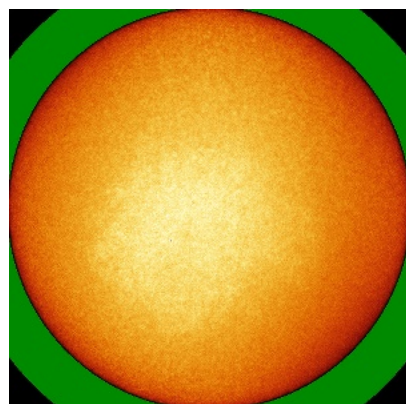


Y

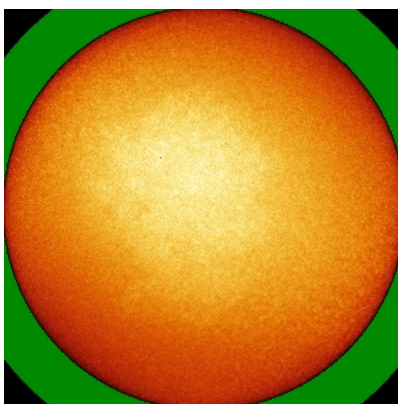


Z

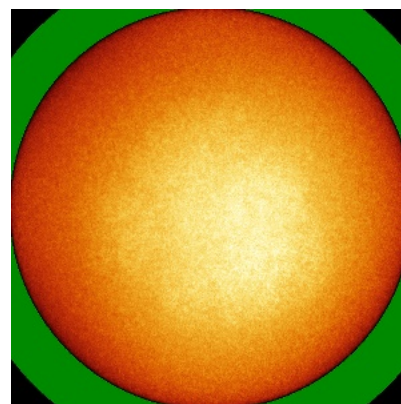
6.4.2 Raw map



X



Y

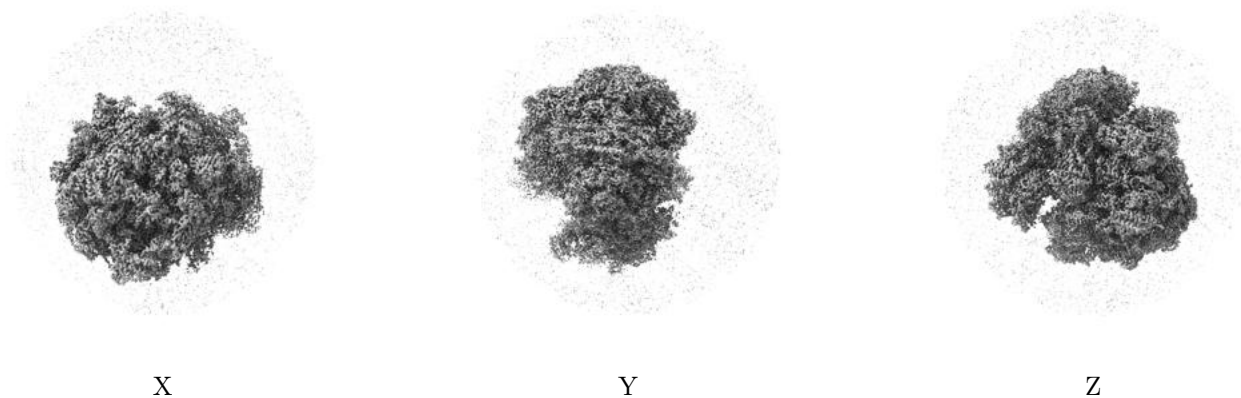


Z

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

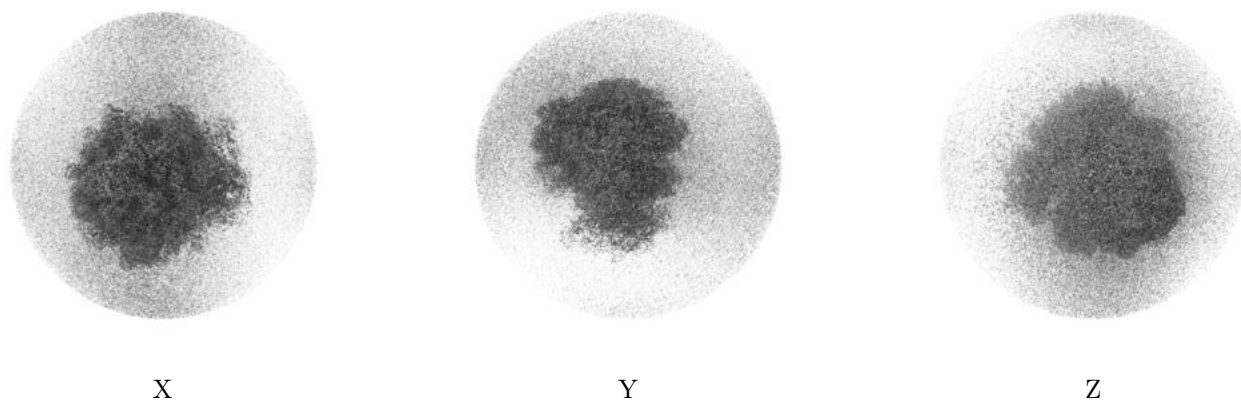
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.74. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

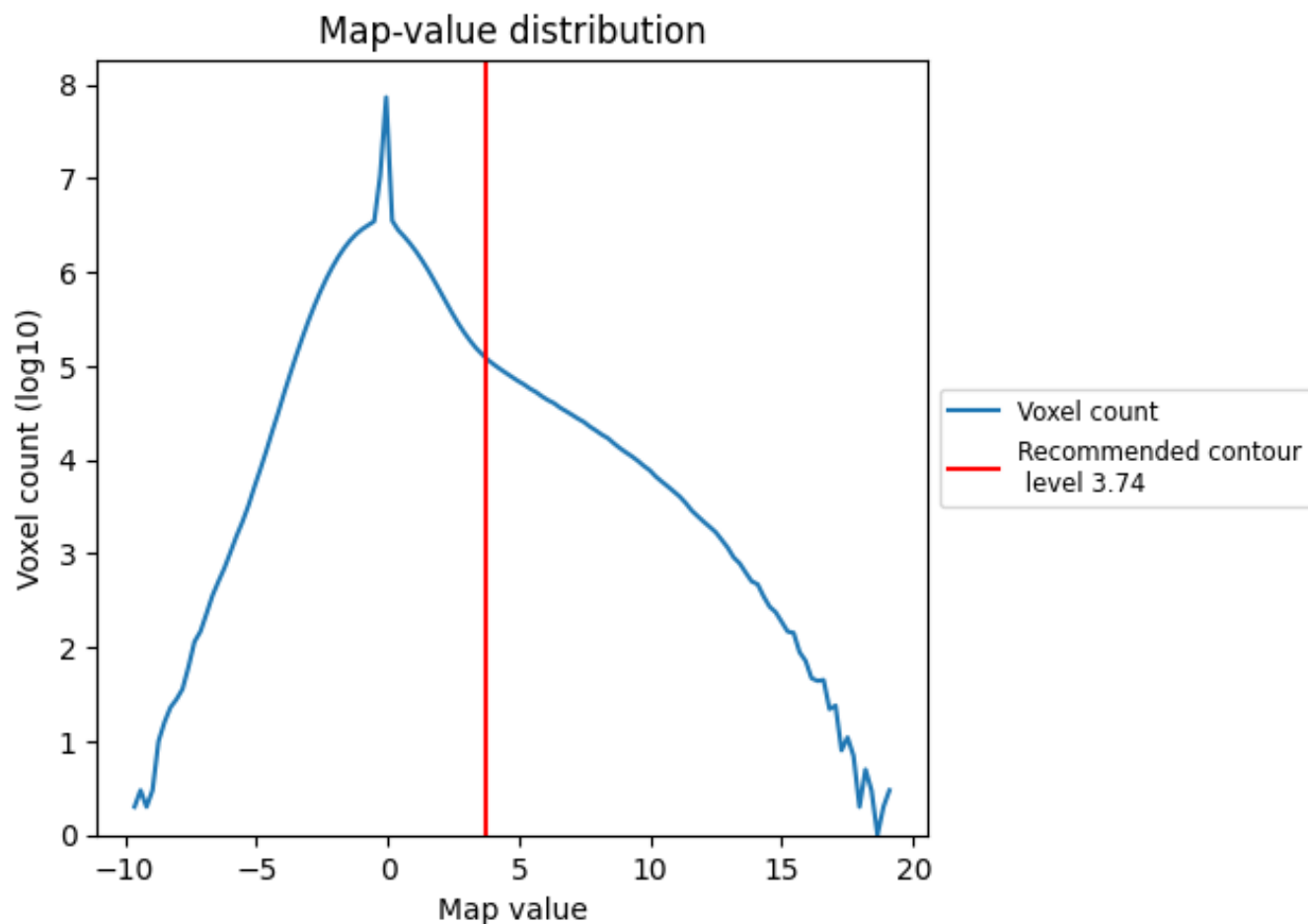
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

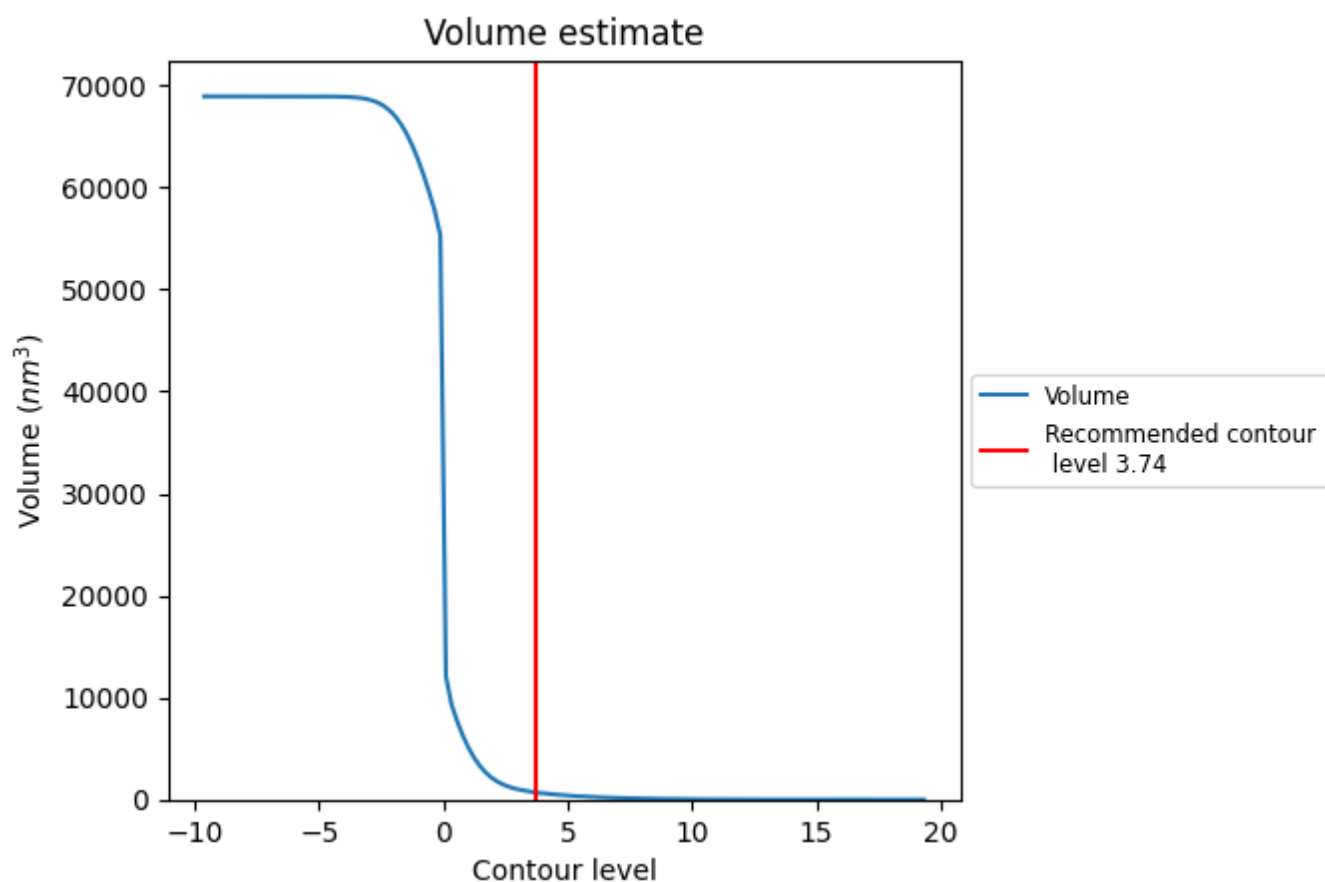
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

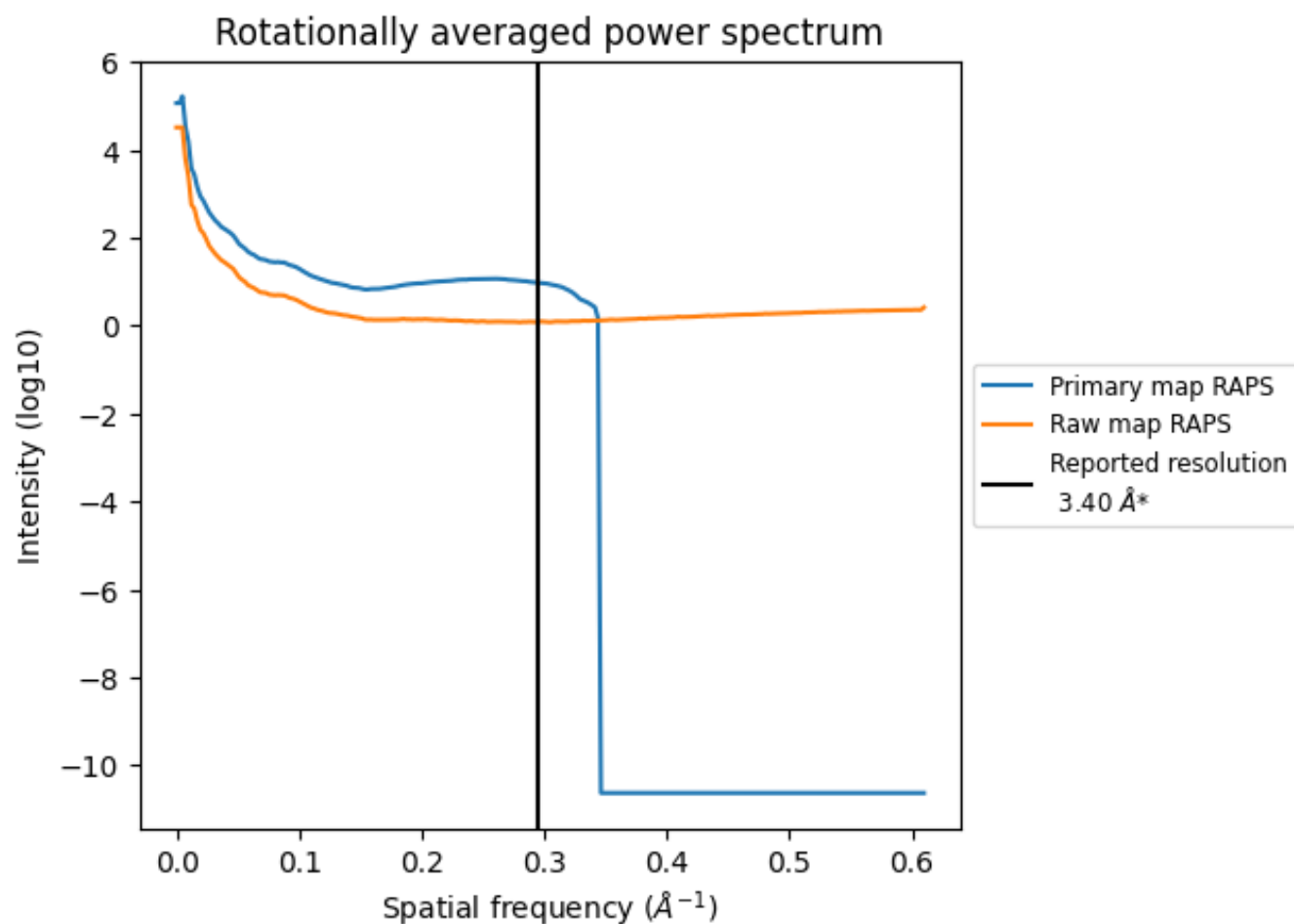
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 690 nm³; this corresponds to an approximate mass of 623 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 ⓘ

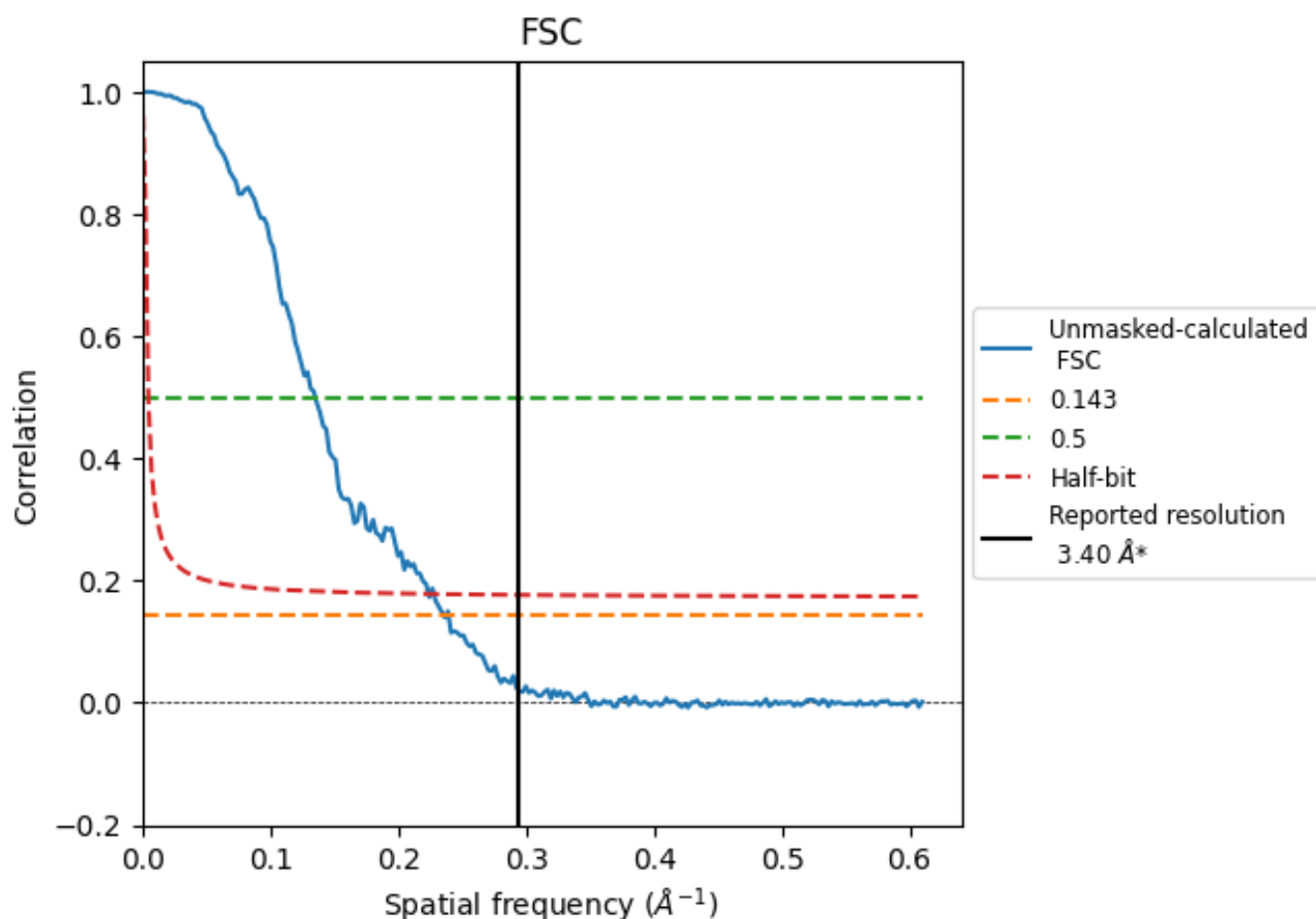


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

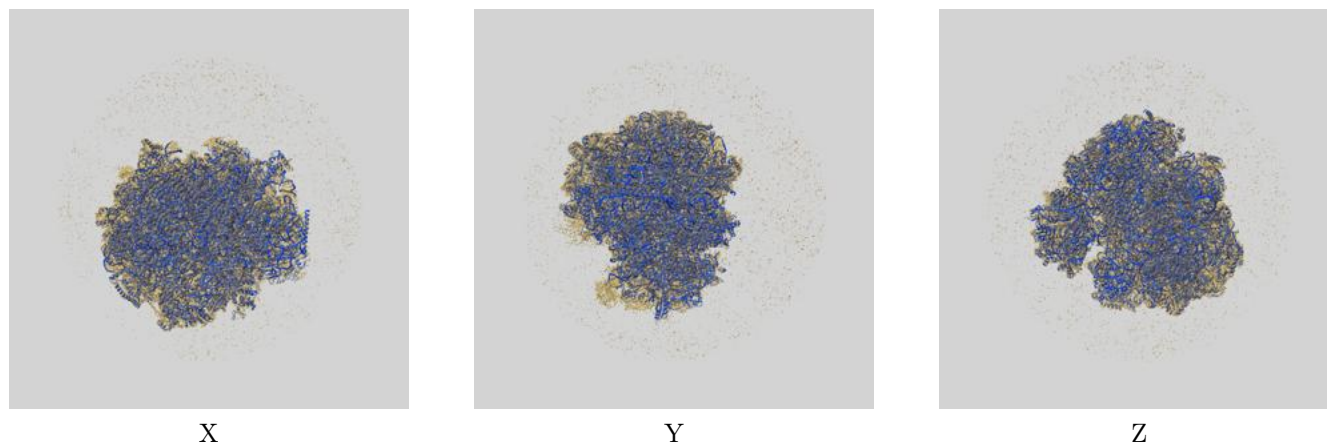
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.24	7.39	4.47

*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 4.24 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

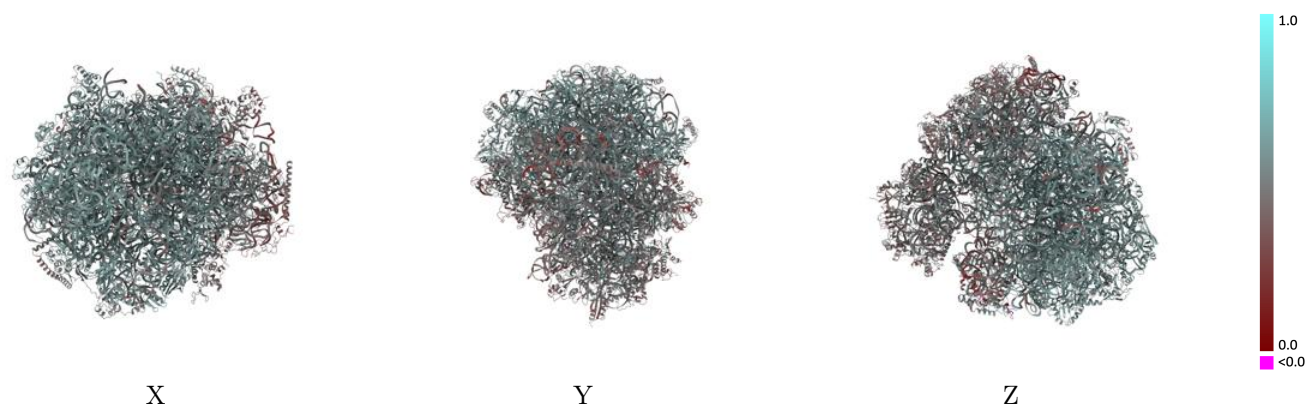
This section contains information regarding the fit between EMDB map EMD-16225 and PDB model 8BSI. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



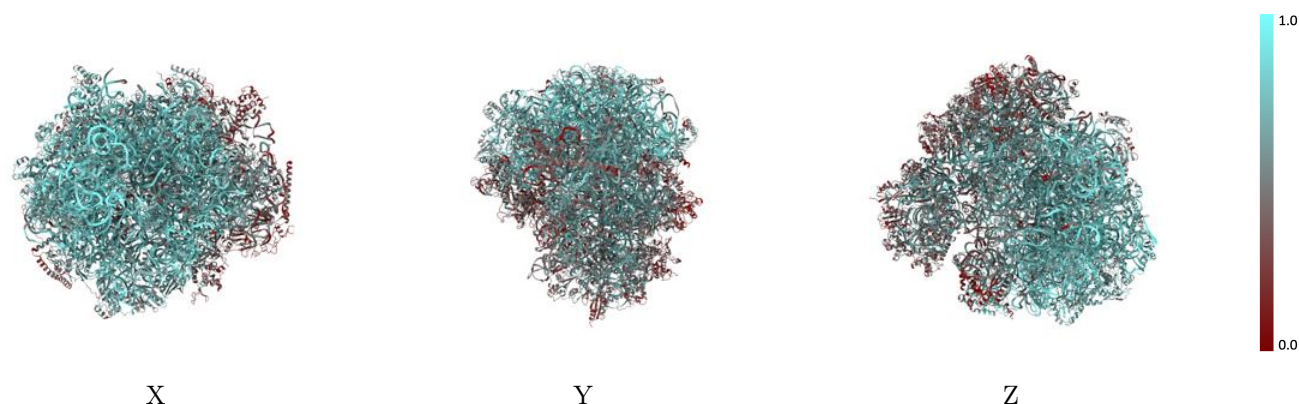
The images above show the 3D surface view of the map at the recommended contour level 3.74 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



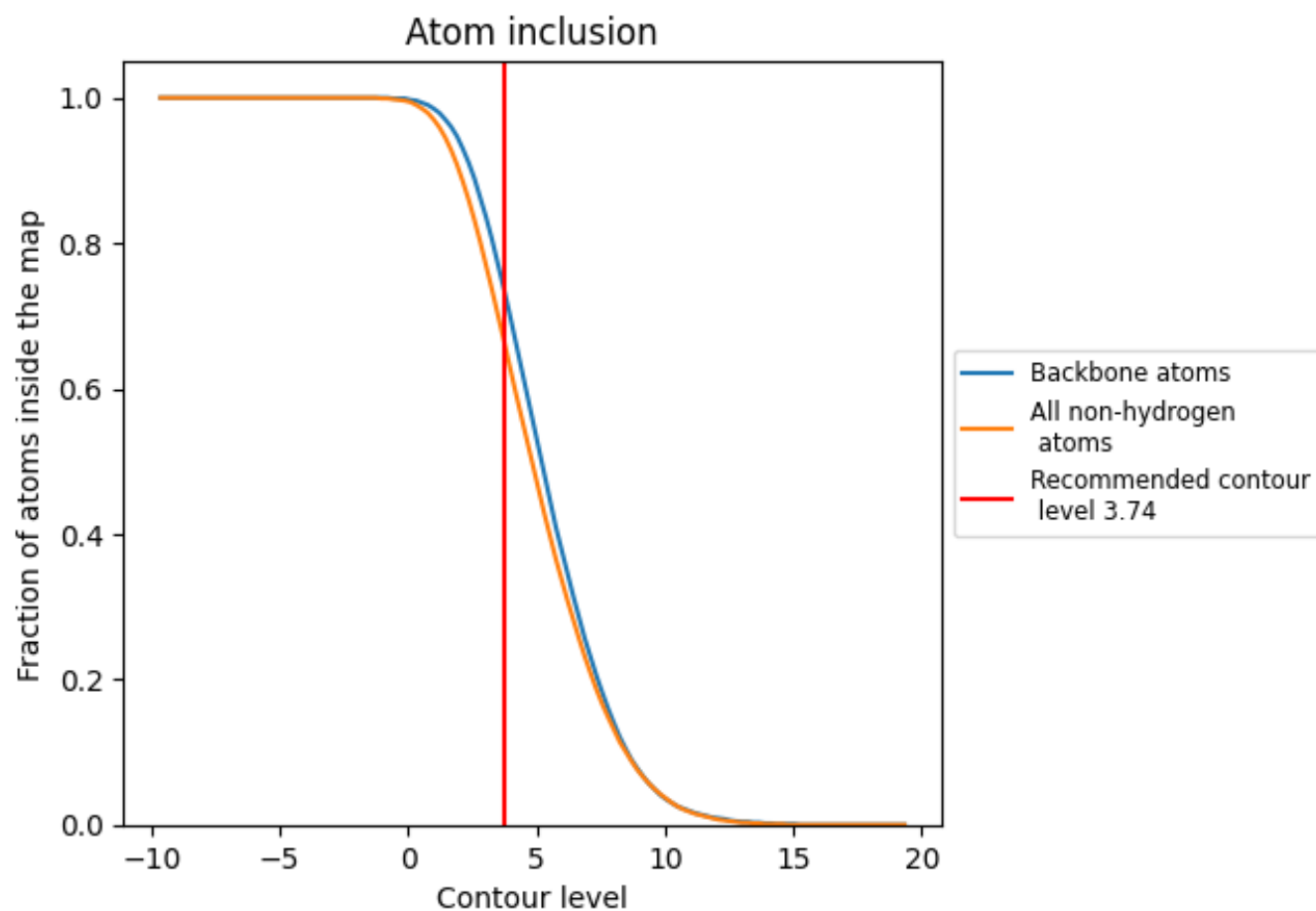
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3.74).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 66% 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 (3.74) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6650	 0.5210
LA	 0.7600	 0.5890
LB	 0.7430	 0.5740
LC	 0.7010	 0.5640
LD	 0.8600	 0.5680
LE	 0.8460	 0.5520
LF	 0.6370	 0.5300
LG	 0.7250	 0.5820
LH	 0.6250	 0.5430
LI	 0.6690	 0.5520
LJ	 0.6530	 0.5520
LK	 0.3790	 0.5020
LL	 0.5530	 0.5150
LM	 0.7030	 0.5640
LN	 0.6460	 0.5380
LO	 0.8000	 0.5940
LP	 0.7130	 0.5610
LQ	 0.7070	 0.5610
LR	 0.6890	 0.5650
LS	 0.6080	 0.5410
LT	 0.7110	 0.5620
LU	 0.6880	 0.5630
LV	 0.5030	 0.4820
LW	 0.6620	 0.5680
LX	 0.6360	 0.5380
LY	 0.7290	 0.5730
LZ	 0.7160	 0.5600
La	 0.5760	 0.5180
Lb	 0.7710	 0.5880
Lc	 0.6760	 0.5450
Ld	 0.5690	 0.5240
Le	 0.6740	 0.5590
Lf	 0.7130	 0.5680
Lg	 0.7210	 0.5790
Lh	 0.6420	 0.5510



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Chain	Atom inclusion	Q-score
Li	 0.6960	 0.5590
Lj	 0.6420	 0.5490
Lk	 0.7510	 0.5830
Ll	 0.5180	 0.4730
Ln	 0.1210	 0.3160
Lo	 0.6560	 0.5610
Lp	 0.7320	 0.5870
Lq	 0.7200	 0.5850
Ls	 0.6910	 0.5240
Lt	 0.8160	 0.5560
Lu	 0.5770	 0.4630
SA	 0.3410	 0.4300
SB	 0.5190	 0.4960
SC	 0.4640	 0.4820
SD	 0.5500	 0.5000
SE	 0.4380	 0.4750
SF	 0.4560	 0.4630
SG	 0.2830	 0.4200
SH	 0.2630	 0.4270
SI	 0.4980	 0.5070
SJ	 0.5110	 0.5040
SK	 0.4460	 0.4730
SL	 0.4550	 0.4240
SM	 0.5240	 0.5270
SO	 0.5480	 0.5440
SP	 0.4870	 0.4910
SQ	 0.5830	 0.5360
SR	 0.4050	 0.4620
ST	 0.4190	 0.4580
SU	 0.4290	 0.4470
SV	 0.3880	 0.4150
SW	 0.3970	 0.4430
SX	 0.3620	 0.4410
SY	 0.3860	 0.4500
Sb	 0.2970	 0.4140
Sc	 0.3600	 0.4280
Sd	 0.5720	 0.5280
Se	 0.2880	 0.4380
Sg	 0.3690	 0.4650
Sh	 0.5300	 0.5060
Sj	 0.3760	 0.4660
St	 0.6830	 0.4870

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Chain	Atom inclusion	Q-score
a	 0.3680	 0.4460
y	 0.2630	 0.3370