



Full wwPDB EM Validation Report ⓘ

Mar 23, 2026 – 05:33 PM UTC

PDB ID : 6C0F / pdb_00006c0f
EMDB ID : EMD-7324
Title : Yeast nucleolar pre-60S ribosomal subunit (state 2)
Authors : Sanghai, Z.A.; Miller, L.; Barandun, J.; Hunziker, M.; Chaker-Margot, M.;
Klinge, S.
Deposited on : 2017-12-29
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

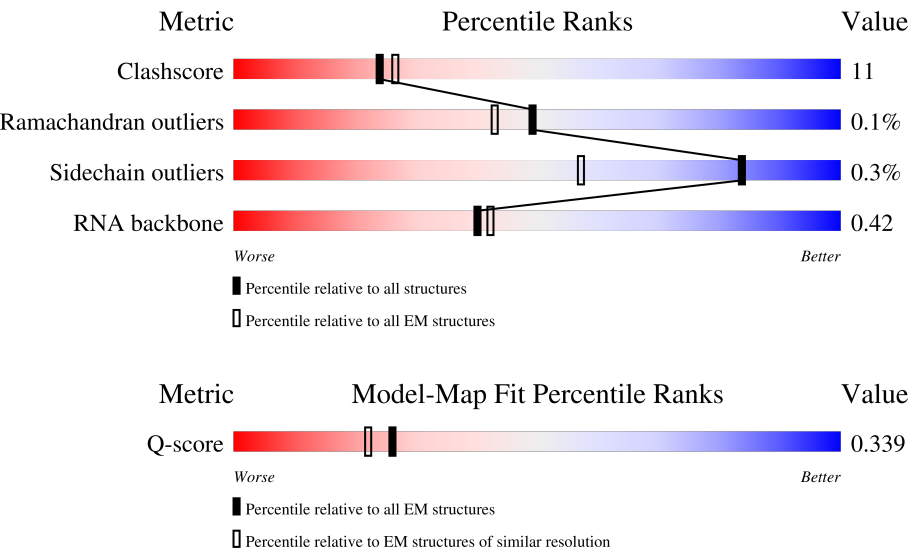
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.70 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.



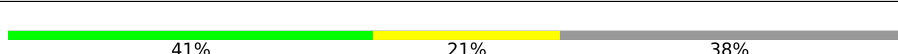
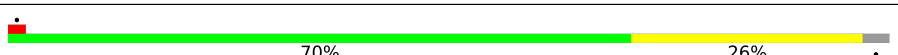
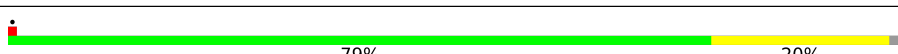
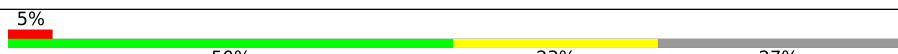
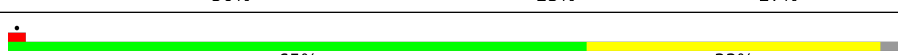
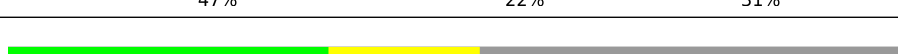
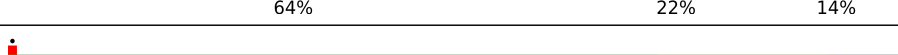
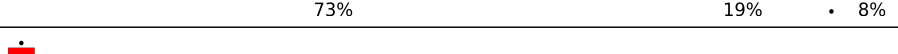
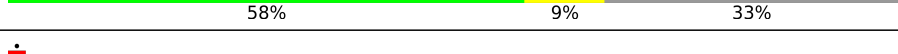
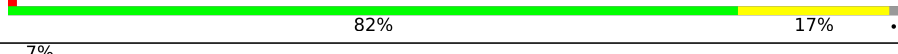
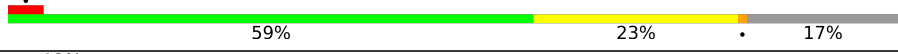
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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

Mol	Chain	Length	Quality of chain
1	1	3395	17%19%60%
2	2	158	49%44%8%
3	6	232	11%15%12%62%

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Mol	Chain	Length	Quality of chain
4	A	463	
5	B	387	
6	C	362	
7	D	306	
8	E	176	
9	F	244	
10	G	256	
11	I	295	
12	K	376	
13	L	199	
14	M	138	
15	N	204	
16	O	199	
17	P	184	
18	Q	186	
19	S	172	
20	V	137	
21	W	647	
22	Y	127	
23	7	231	
24	8	434	
25	b	291	
26	e	130	
27	f	107	
28	h	120	

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Mol	Chain	Length	Quality of chain
29	i	100	
30	j	88	
31	x	28	
32	m	74	
33	n	605	
34	o	220	
35	p	505	
36	q	285	
37	s	807	
38	t	322	
39	u	199	
40	v	453	
41	w	250	
42	y	245	
43	z	278	

2 Entry composition

There are 44 unique types of molecules in this entry. The entry contains 91742 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called *Saccharomyces cerevisiae* S288c 35S pre-ribosomal RNA miscRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	1357	Total	C	N	O	P	0	0
			29055	12970	5242	9486	1357		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	U	deletion	GB 259147931

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 3 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	6	87	Total	C	N	O	P	0	0
			1838	823	309	619	87		

- Molecule 4 is a protein called Ribosome biogenesis protein NSA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	394	Total	C	N	O	S	0	0
			3126	1997	525	593	11		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	324	Total	C	N	O	S	0	0
			2577	1635	478	458	6		

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	314	Total	C	N	O	S	0	0
			2418	1531	454	430	3		

- Molecule 7 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	190	Total	C	N	O	S	0	0
			1578	996	297	275	10		

- Molecule 8 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	170	Total	C	N	O	S	0	0
			1366	882	244	239	1		

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	242	Total	C	N	O	S	0	0
			1941	1249	352	339	1		

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	187	Total	C	N	O	S	0	0
			1453	934	253	264	2		

- Molecule 11 is a protein called Ribosome production factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	288	Total	C	N	O	S	0	0
			2429	1544	439	442	4		

- Molecule 12 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	260	Total	C	N	O	S	0	0
			2099	1352	346	398	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
13	L	106	Total	C	N	O	0	0
			845	531	174	140		

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	128	Total	C	N	O	S	0	0
			997	641	190	164	2		

- Molecule 15 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	176	Total	C	N	O	S	0	0
			1509	946	319	243	1		

- Molecule 16 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	184	Total	C	N	O	S	0	0
			1451	936	268	246	1		

- Molecule 17 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	P	124	Total	C	N	O	0	0
			975	612	184	179		

- Molecule 18 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	132	Total	C	N	O	S	0	0
			1015	648	191	175	1		

- Molecule 19 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 20 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	122	Total	C	N	O	S	0	0
			903	567	169	160	7		

- Molecule 21 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	98	Total	C	N	O	S	0	0
			806	509	132	164	1		

- Molecule 22 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Y	126	Total	C	N	O	S	0	0
			993	625	192	176			

- Molecule 23 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	7	156	Total	C	N	O	S	0	0
			1295	813	250	228	4		

- Molecule 24 is a protein called Ribosomal RNA-processing protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	8	98	Total	C	N	O	S	0	0
			836	515	165	154	2		

- Molecule 25 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	242	Total	C	N	O	S	0	0
			1919	1221	344	350	4		

- Molecule 26 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	e	114	Total	C	N	O	S	0	0
			914	580	181	152	1		

- Molecule 27 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 28 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 29 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	i	84	Total	C	N	O	S	0	0
			665	413	136	114	2		

- Molecule 30 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	j	72	Total	C	N	O	S	0	0
			575	350	125	95	5		

- Molecule 31 is a protein called Brx1-associated peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	x	28	Total	C	N	O	0	0
			140	84	28	28		

- Molecule 32 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	m	74	Total	C	N	O	0	0
			370	222	74	74		

- Molecule 33 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	n	341	Total	C	N	O	S	0	0
			2794	1823	470	492	9		

- Molecule 34 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	o	133	Total	C	N	O	S	0	0
			1107	716	198	189	4		

- Molecule 35 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	p	437	Total	C	N	O	S	0	0
			3486	2247	600	627	12		

- Molecule 36 is a protein called Protein MAK11.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	q	285	Total	C	N	O	S	0	0
			1409	839	285	285			

- Molecule 37 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	s	157	Total	C	N	O	S	0	0
			1069	672	203	191	3		

- Molecule 38 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	t	248	Total	C	N	O	S	0	0
			1965	1254	350	358	3		

- Molecule 39 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	u	129	Total	C	N	O	S	0	0
			1088	682	220	178	8		

- Molecule 40 is a protein called Ribosome biogenesis protein SSF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	v	225	Total	C	N	O	S	0	0
			1795	1142	320	324	9		

- Molecule 41 is a protein called Ribosomal RNA-processing protein 15.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	w	70	Total	C	N	O	0	0
			562	357	96	109		

- Molecule 42 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	y	226	Total	C	N	O	S	0	0
			1709	1060	296	346	7		

- Molecule 43 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	z	243	Total	C	N	O	S	0	0
			2058	1334	353	366	5		

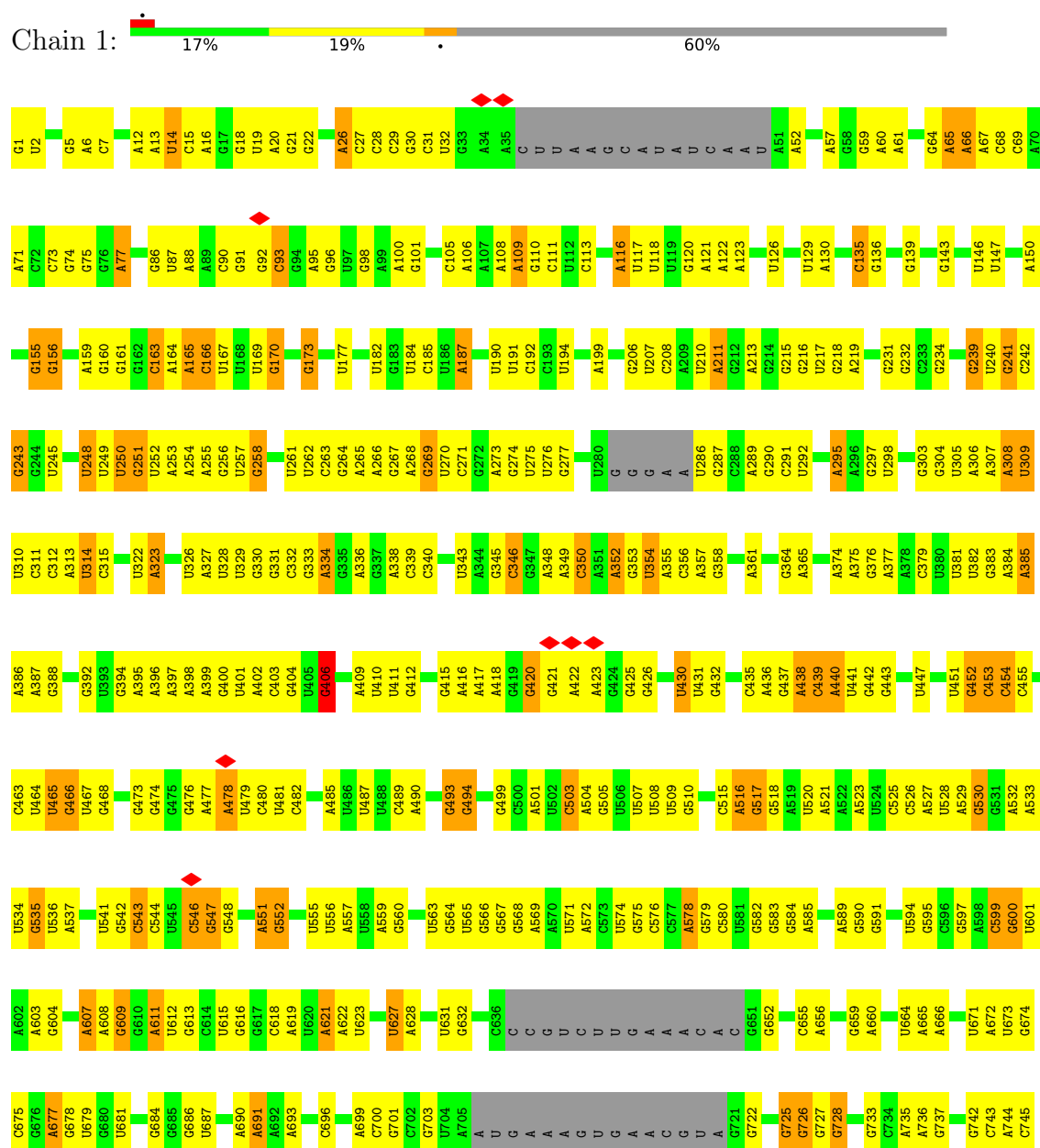
- Molecule 44 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
44	D	1	Total	Zn	0
			1	1	
44	j	1	Total	Zn	0
			1	1	
44	u	1	Total	Zn	0
			1	1	

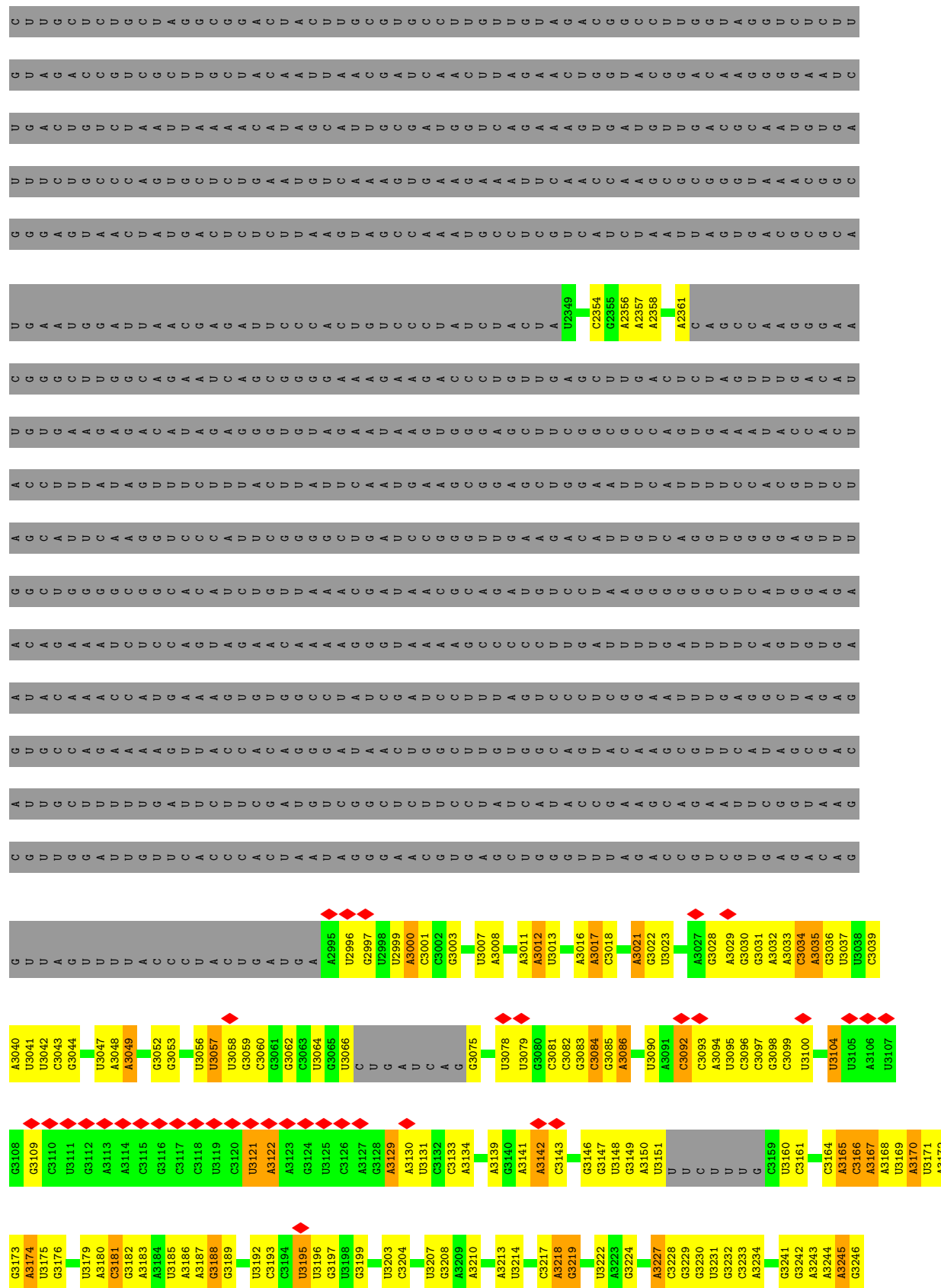
3 Residue-property plots

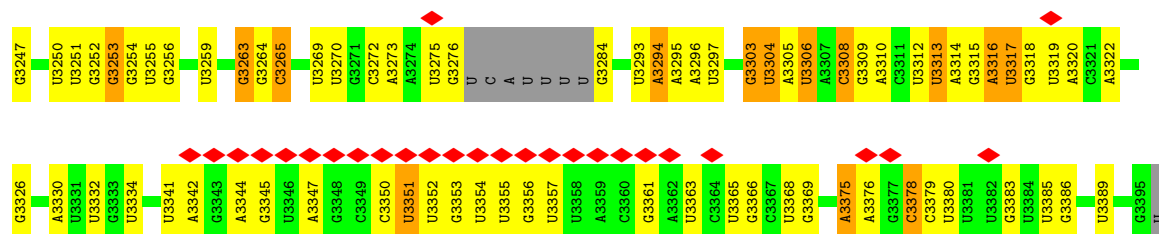
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: *Saccharomyces cerevisiae* S288c 35S pre-ribosomal RNA miscRNA

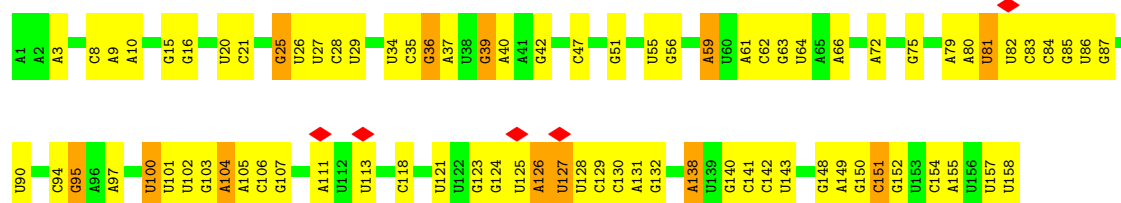




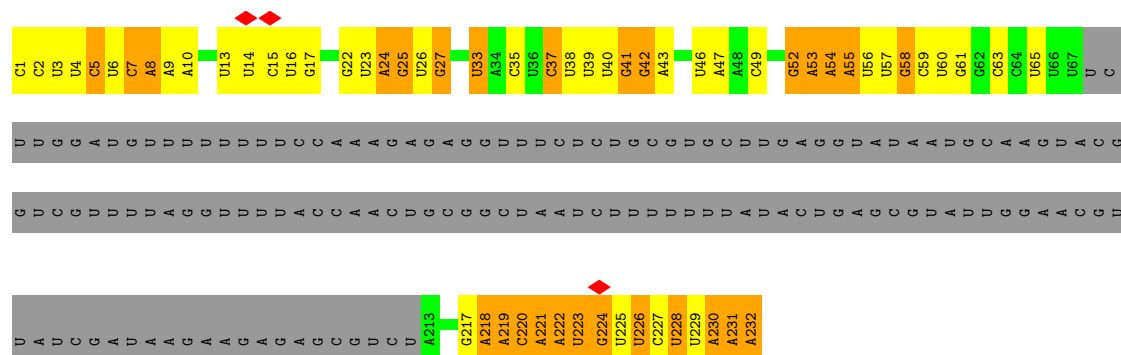




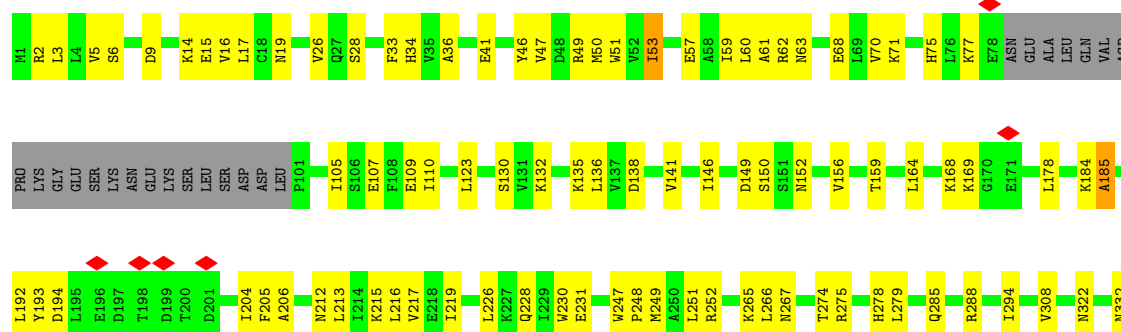
• Molecule 2: 5.8S rRNA



• Molecule 3: ITS2

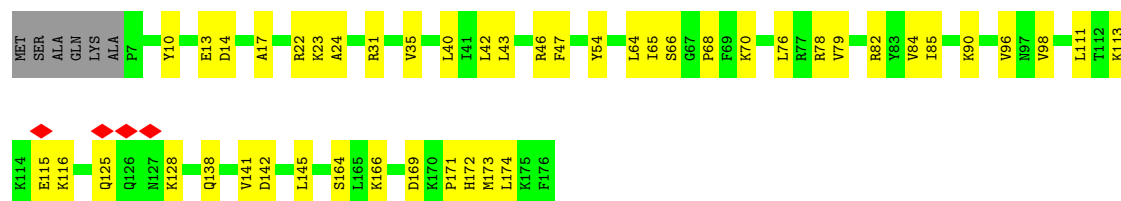


• Molecule 4: Ribosome biogenesis protein NSA1

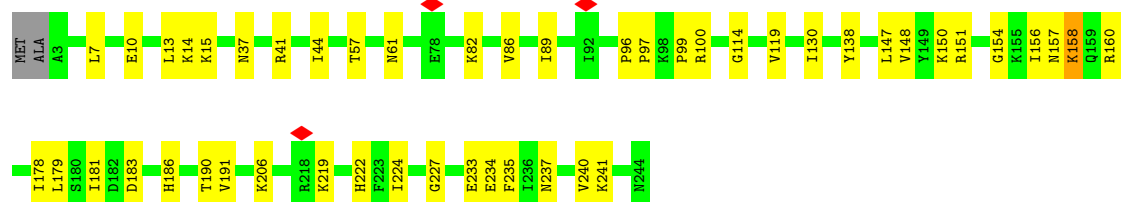
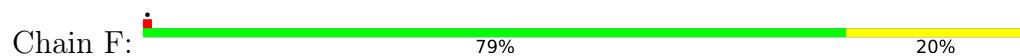




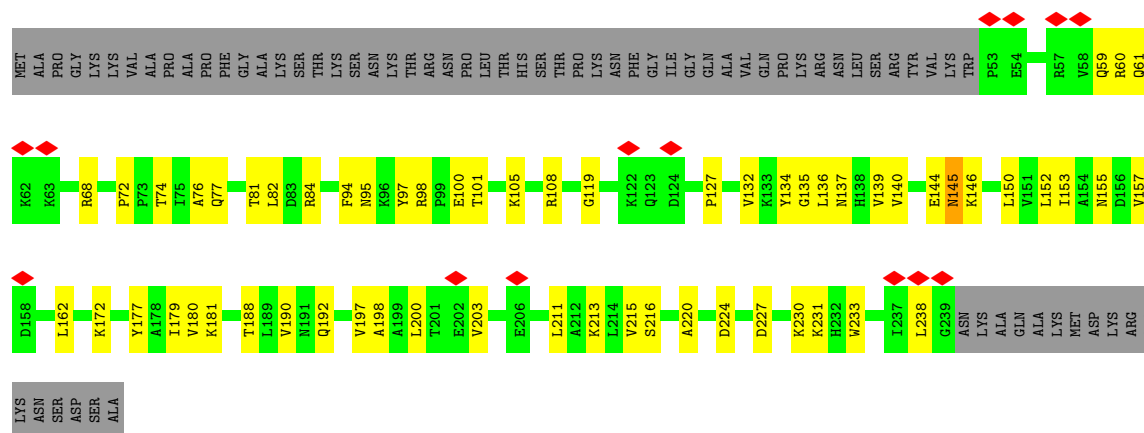
• Molecule 8: 60S ribosomal protein L6-A



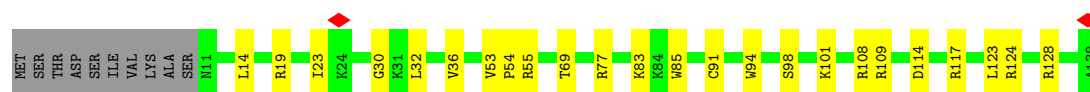
• Molecule 9: 60S ribosomal protein L7-A



• Molecule 10: 60S ribosomal protein L8-A



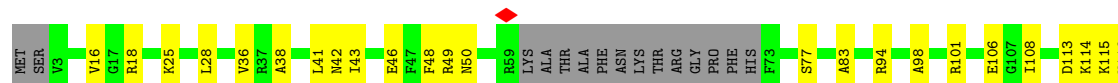
• Molecule 11: Ribosome production factor 1



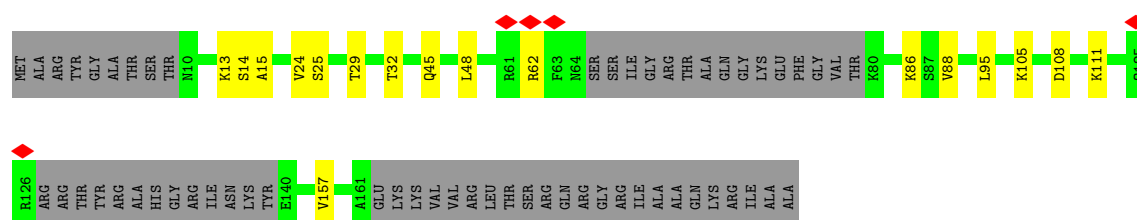
- Molecule 15: 60S ribosomal protein L15-A



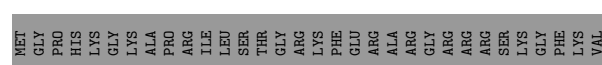
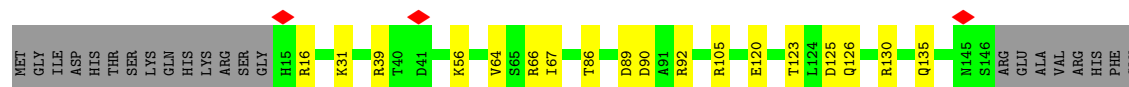
- Molecule 16: 60S ribosomal protein L16-A



- Molecule 17: 60S ribosomal protein L17-A



- Molecule 18: 60S ribosomal protein L18-A



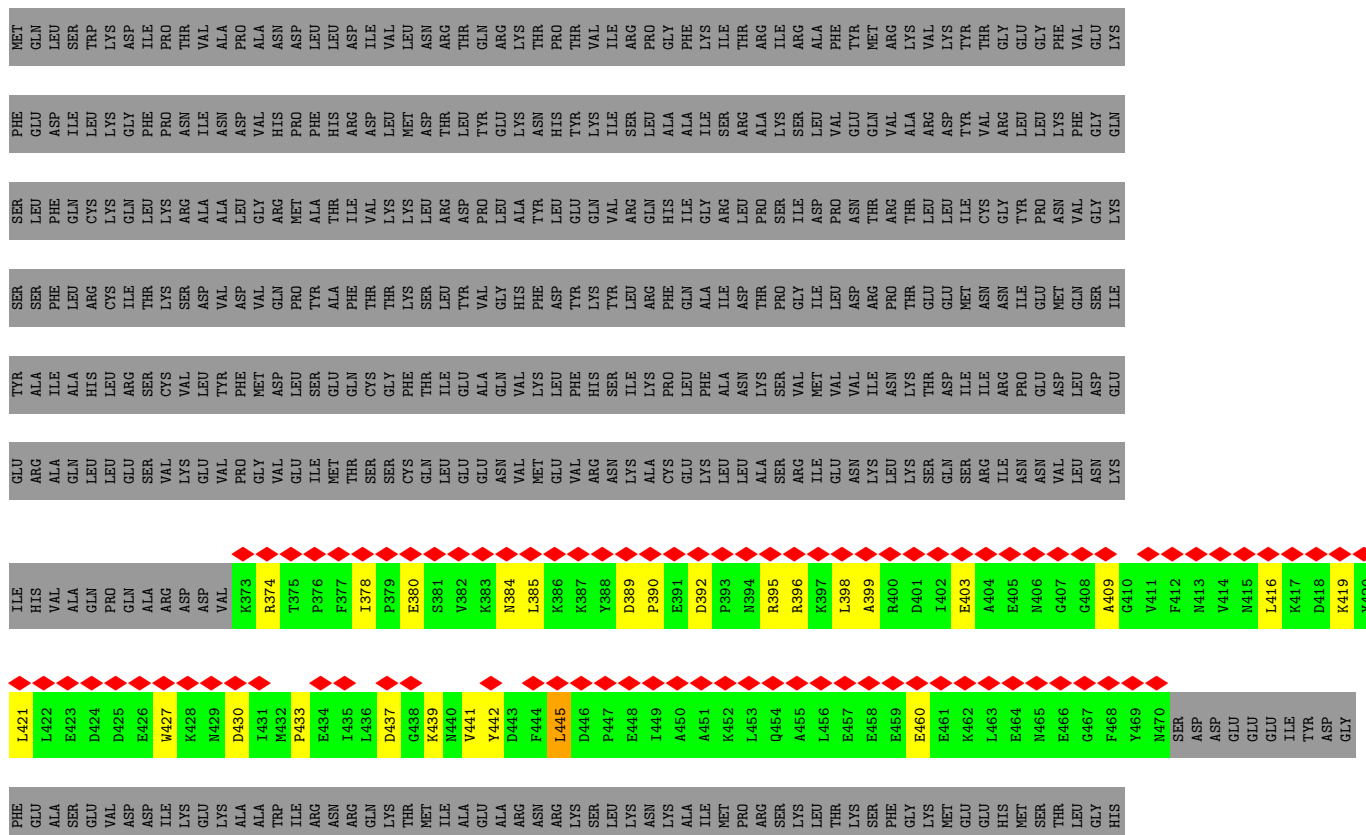
- Molecule 19: 60S ribosomal protein L20-A



- Molecule 20: 60S ribosomal protein L23-A

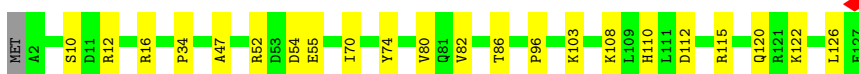


- Molecule 21: Nucleolar GTP-binding protein 1

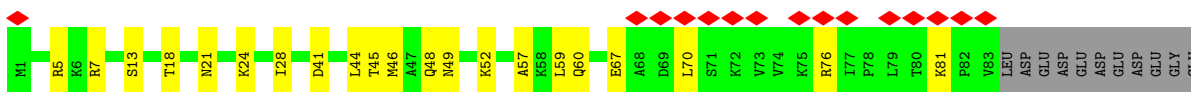


LYS
ALA
ASP
ARG
MET
MET
ALA
LYS
MET
GLU
ARG
GLU
ARG
GLU
ASN
ARG
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LYS
GLN
GLY
GLU
SER
SER
ASP
ARG
HIS
ASN
ALA
VAL
SER
SER
LEU
SER
LYS
LYS
HIS
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GLY
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THR
ASP
PHE
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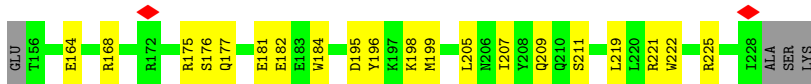
Chain Y: 82% 17%



Chain 7:



ASP	GLN	GLN	ASP	ASN	TYR	ASN	ALA	ALA	THR	VAL	GLU	LEU	ASP	GLU	ASN	GLU	ILE	PRO	GLU	GLY	GLY	ALA	ARG	ALA	ILE	GLN	ARG	ASP	LYS	ASN	GLY	ASP	VAL	VAL	VAL	VAL	TYR	GLY	LYS	LYS	LYS	LYS	ASN	PHE	ASP	ASP	ASP	GLU	ASP	VAL	VAL	ASN	ASN	GLU	ILE	LYS	ALA	ARG	ASP	THR	THR	ILE
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Chain 8: 11% 19% 77%

MET	SER	ASN	SER	LEU	GLU	GLU	ARG	LEU	ARG	ALA	ALA	ASN	SER	ALA	PHE	ASP	GLY	LEU	LEU	ALA	ALA	ILE	PRO	ALA	LYS	TYR	TYR	ASP	GLU	LYS	SER	GLN	GLU	GLN	TRP	LYS	LYS	LYS	LYS	THR	LYS	ASN	ASP	LYS	LEU	LEU	GLU	PRO	GLN	ARG
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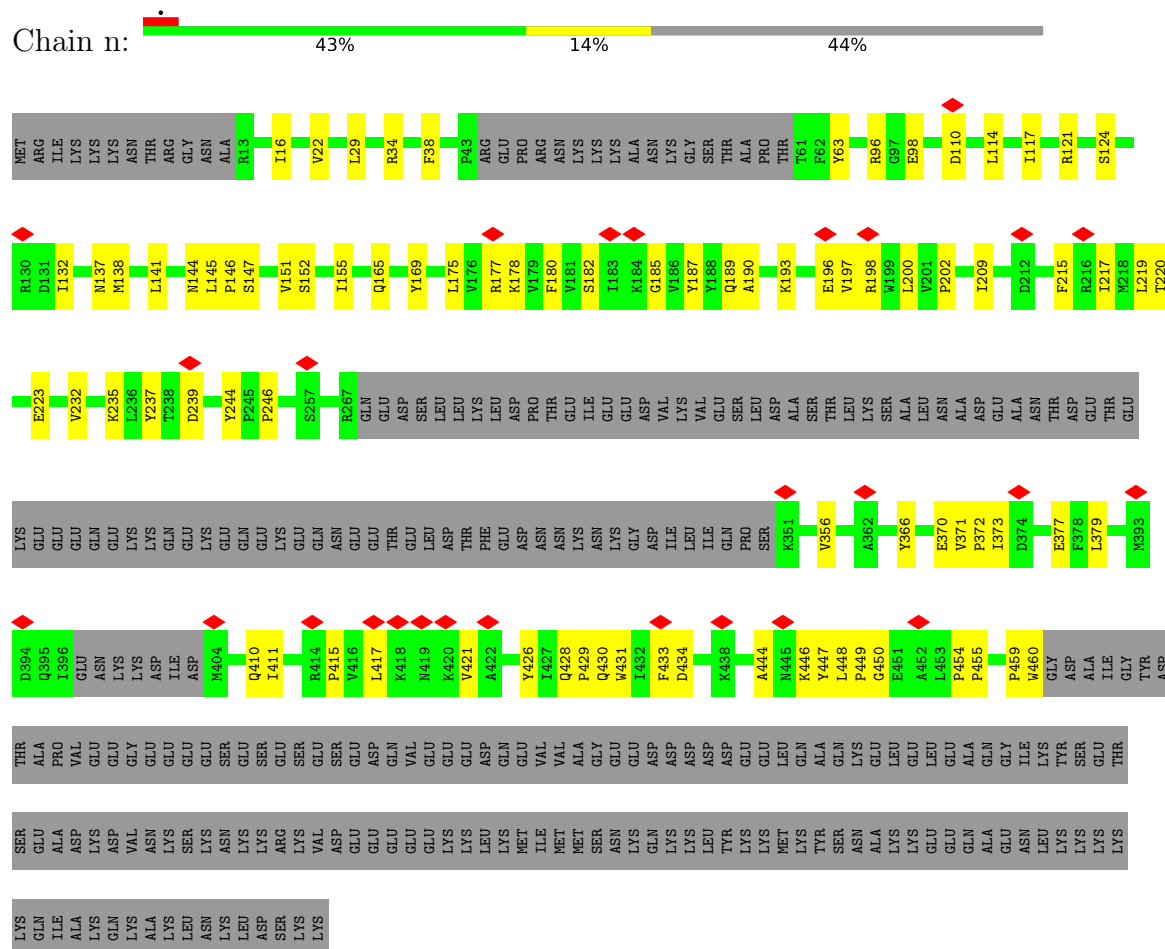
ASP	ASP	GLU	THR	SER	SER	THR	LEU	GLU	VAL	MET	LYS	LYS	LYS	GLU	ASP	ALA	LYS	PRO	VAL	VAL	LEU	PRO	GLY	GLY	LYS	LYS	PHE	LYS	LYS	HIS	MET	LYS	MET	GLN	LYS	GLN	LYS	LYS	GLU	GLU	ALA	ALA	THR	SER	SER	LYS	VAL	LEU	ASN	ASP	VAL	GLU	VAL	VAL	ASN	ASP	PRO	PRO	MET	ILE	ILE	ILE	ALA
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[illegible][illegible]

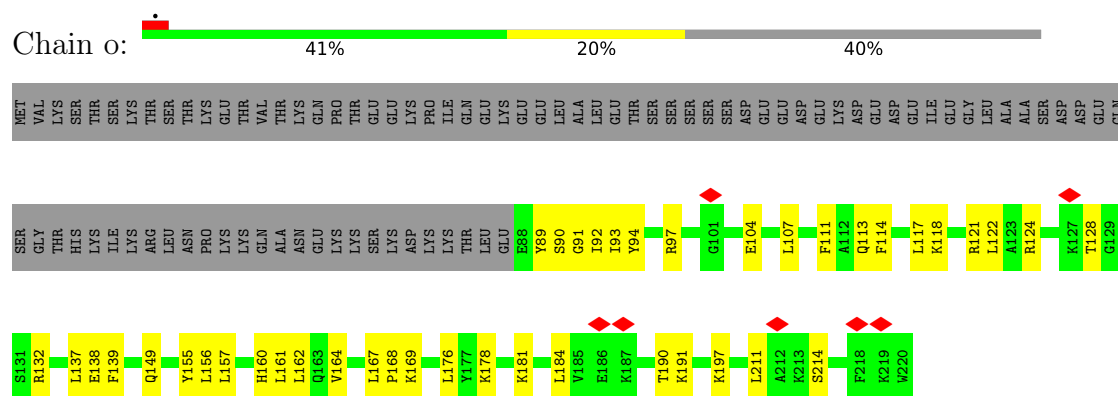
LEU	GLU	ASN	ASN	ASN	ASN	SER	SER	LYS	LYS	ARG	PHE	LYS	LYS	GLY	LYS	LYS	ASP	GLU	SER	ILE	ASN	ASN	ALA	ASP	GLY	VAL	MET	PHE	GLN	ASN	ILE	ILE	PHE	ASP	ASP	GLY	ALA	ALA	ARG	ALA	THR	SER	SER	ASP	LEU	GLN	ARG	LEU	LEU	ARG	LYS	LYS	GLY	PRO	ALA	LYS	ASN	D296	L303	L304	L305
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A306	A307	A308	A309	A310	A311	A312	A313	A314	A315	A316	A317	A318	A319	A320	A321	A322	A323	A324	A325	A326	A327	A328	A329	A330	A331	A332	A333	A334	A335	A336	A337	A338	A339	A340	A341	A342	A343	A344	A345	A346	A347	A348	A349	A350	A351	A352	A353	A354	A355	A356	A357	A358	A359	A360	A361	A362	A363	A364	A365	A366	A367	A368	A369	A370	A371	A372	A373	A374	A375	A376	A377	A378	A379	A380	A381	A382	A383	A384	A385	A386	A387	A388	A389	A390	A391	A392	A393	A394	A395	A396	A397	A398	A399	A400	A401	A402	A403	A404	A405	A406	A407	A408	A409	A410	A411	A412	A413	A414	A415	A416	A417	A418	A419	A420	A421	A422	A423	A424	A425	A426	A427	A428	A429	A430	A431	A432	A433	A434	A435	A436	A437	A438	A439	A440	A441	A442	A443	A444	A445	A446	A447	A448	A449	A450	A451	A452	A453	A454	A455	A456	A457	A458	A459	A460	A461	A462	A463	A464	A465	A466	A467	A468	A469	A470	A471	A472	A473	A474	A475	A476	A477	A478	A479	A480	A481	A482	A483	A484	A485	A486	A487	A488	A489	A490	A491	A492	A493	A494	A495	A496	A497	A498	A499	A500	A501	A502	A503	A504	A505	A506	A507	A508	A509	A510	A511	A512	A513	A514	A515	A516	A517	A518	A519	A520	A521	A522	A523	A524	A525	A526	A527	A528	A529	A530	A531	A532	A533	A534	A535	A536	A537	A538	A539	A540	A541	A542	A543	A544	A545	A546	A547	A548	A549	A550	A551	A552	A553	A554	A555	A556	A557	A558	A559	A560	A561	A562	A563	A564	A565	A566	A567	A568	A569	A570	A571	A572	A573	A574	A575	A576	A577	A578	A579	A580	A581	A582	A583	A584	A585	A586	A587	A588	A589	A590	A591	A592	A593	A594	A595	A596	A597	A598	A599	A600	A601	A602	A603	A604	A605	A606	A607	A608	A609	A610	A611	A612	A613	A614	A615	A616	A617	A618	A619	A620	A621	A622	A623	A624	A625	A626	A627	A628	A629	A630	A631	A632	A633	A634	A635	A636	A637	A638	A639	A640	A641	A642	A643	A644	A645	A646	A647	A648	A649	A650	A651	A652	A653	A654	A655	A656	A657	A658	A659	A660	A661	A662	A663	A664	A665	A666	A667	A668	A669	A670	A671	A672	A673	A674	A675	A676	A677	A678	A679	A680	A681	A682	A683	A684	A685	A686	A687	A688	A689	A690	A691	A692	A693	A694	A695	A696	A697	A698	A699	A700	A701	A702	A703	A704	A705	A706	A707	A708	A709	A710	A711	A712	A713	A714	A715	A716	A717	A718	A719	A720	A721	A722	A723	A724	A725	A726	A727	A728	A729	A730	A731	A732	A733	A734	A735	A736	A737	A738	A739	A740	A741	A742	A743	A744	A745	A746	A747	A748	A749	A750	A751	A752	A753	A754	A755	A756	A757	A758	A759	A760	A761	A762	A763	A764	A765	A766	A767	A768	A769	A770	A771	A772	A773	A774	A775	A776	A777	A778	A779	A780	A781	A782	A783	A784	A785	A786	A787	A788	A789	A790	A791	A792	A793	A794	A795	A796	A797	A798	A799	A800	A801	A802	A803	A804	A805	A806	A807	A808	A809	A810	A811	A812	A813	A814	A815	A816	A817	A818	A819	A820	A821	A822	A823	A824	A825	A826	A827	A828	A829	A830	A831	A832	A833	A834	A835	A836	A837	A838	A839	A840	A841	A842	A843	A844	A845	A846	A847	A848	A849	A850	A851	A852	A853	A854	A855	A856	A857	A858	A859	A860	A861	A862	A863	A864	A865	A866	A867	A868	A869	A870	A871	A872	A873	A874	A875	A876	A877	A878	A879	A880	A881	A882	A883	A884	A885	A886	A887	A888	A889	A890	A891	A892	A893	A894	A895	A896	A897	A898	A899	A900	A901	A902	A903	A904	A905	A906	A907	A908	A909	A910	A911	A912	A913	A914	A915	A916	A917	A918	A919	A920	A921	A922	A923	A924	A925	A926	A927	A928	A929	A930	A931	A932	A933	A934	A935	A936	A937	A938	A939	A940	A941	A942	A943	A944	A945	A946	A947	A948	A949	A950	A951	A952	A953	A954	A955	A956	A957	A958	A959	A960	A961	A962	A963	A964	A965	A966	A967	A968	A969	A970	A971	A972	A973	A974	A975	A976	A977	A978	A979	A980	A981	A982	A983	A984	A985	A986	A987	A988	A989	A990	A991	A992	A993	A994	A995	A996	A997	A998	A999	A1000
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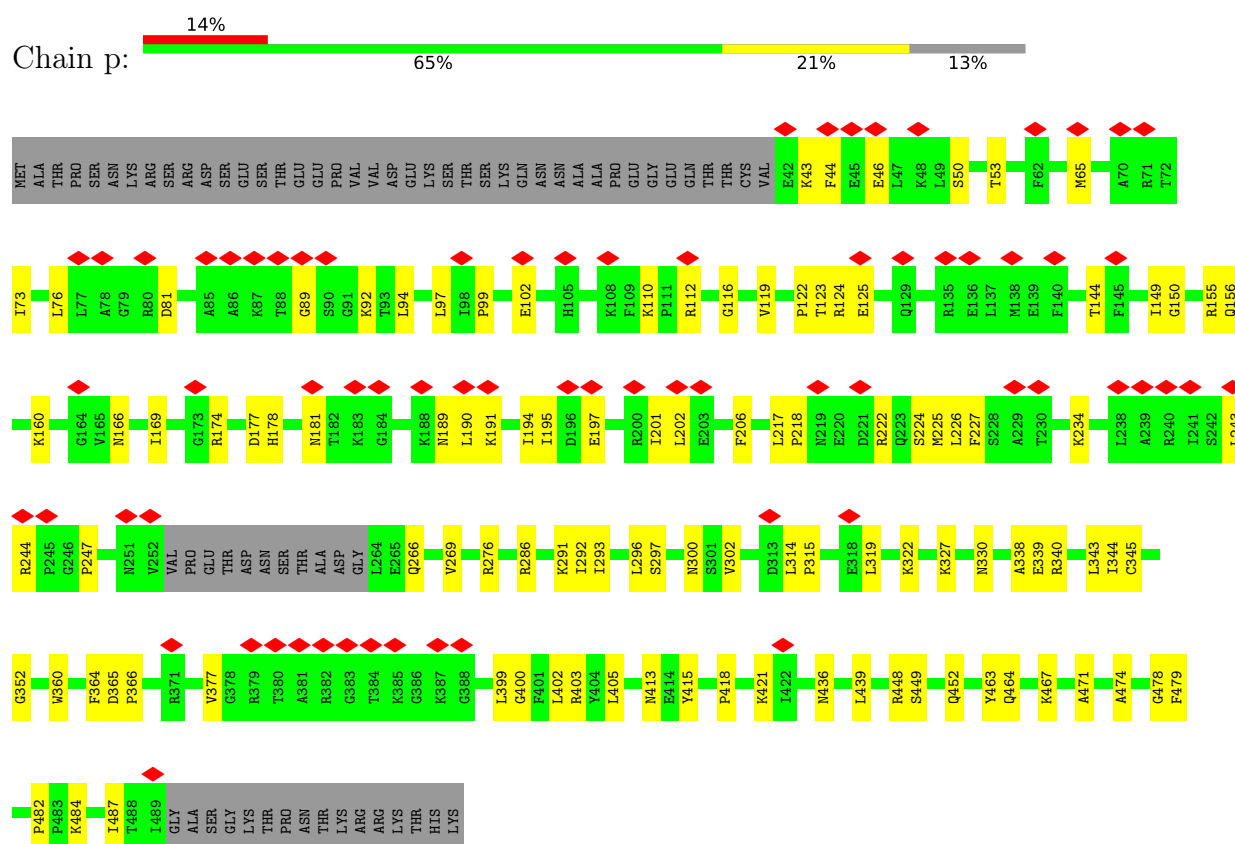
E378	R379	Q380	K381	R382	E384	E385	N386	L387	R388	I389	R390	K391	D392	N393	LYS	GLY	LYS	LYS	LYS	ARG	ASN	GLN	GLN	GLU	LYS	MET	LYS	ARG	TYR	VAL	GLY	SER	ALA	ALA	PRO	LYS	LYS	ARG	ALA	PHE	GLU	GLY	ARG	LEU	LYS	THR	GLY	LYS	LYS	LYS	GLY	PRO	ASP
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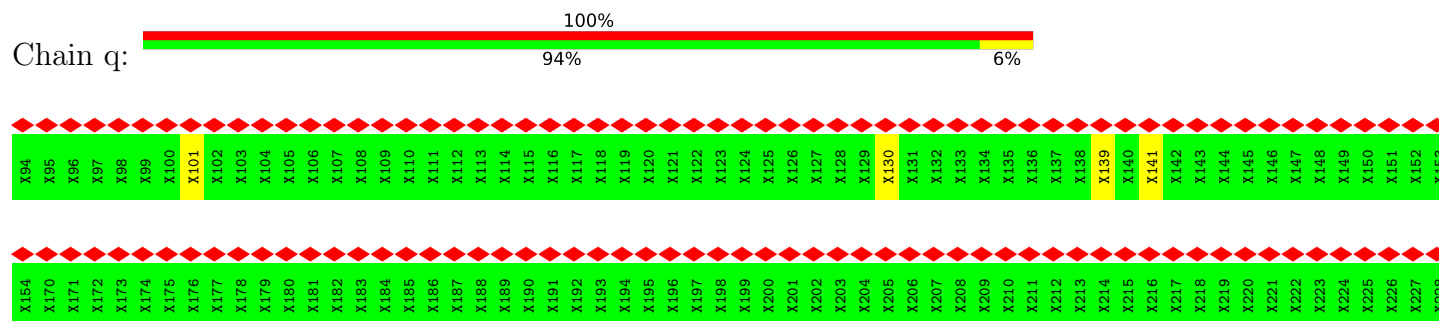
• Molecule 34: Ribosome biogenesis protein 15



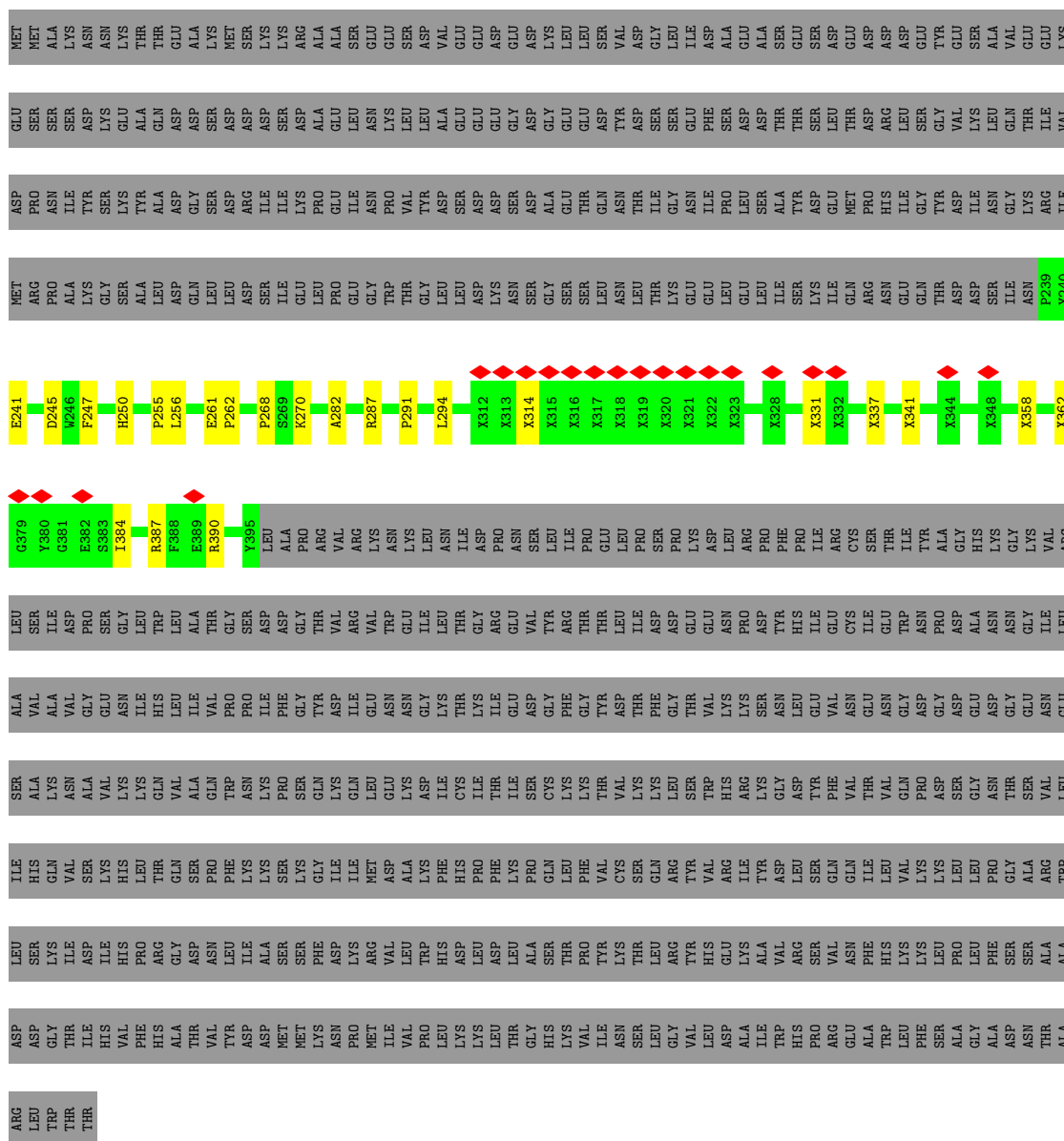
• Molecule 35: ATP-dependent RNA helicase HAS1



• Molecule 36: Protein MAK11

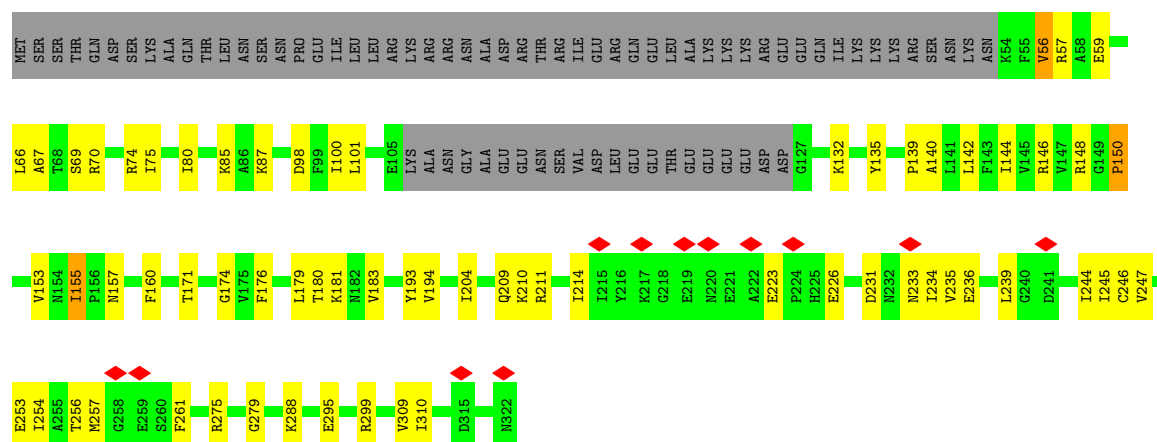


- Molecule 37: Ribosome biogenesis protein ERB1



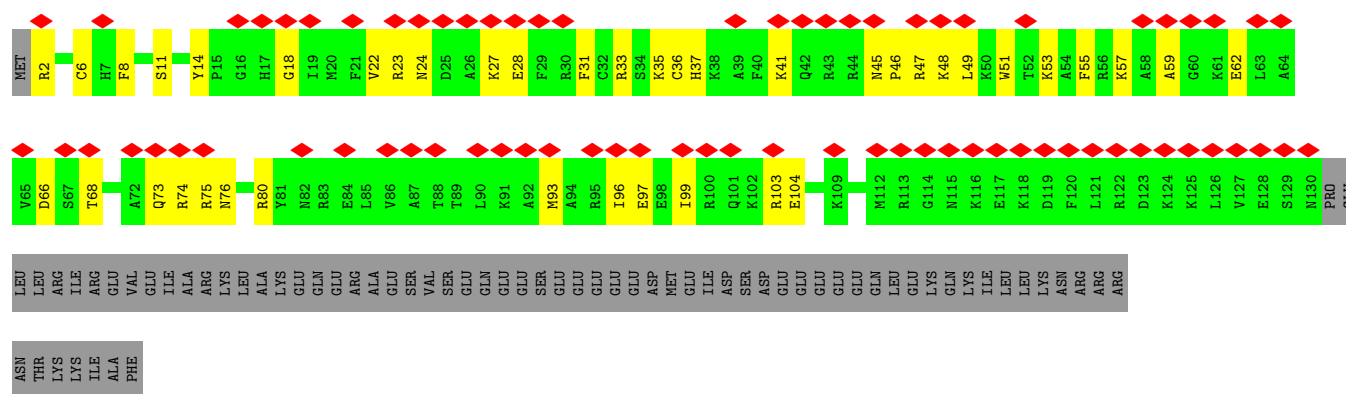
- Molecule 38: Ribosome biogenesis protein RLP7

Chain t: 



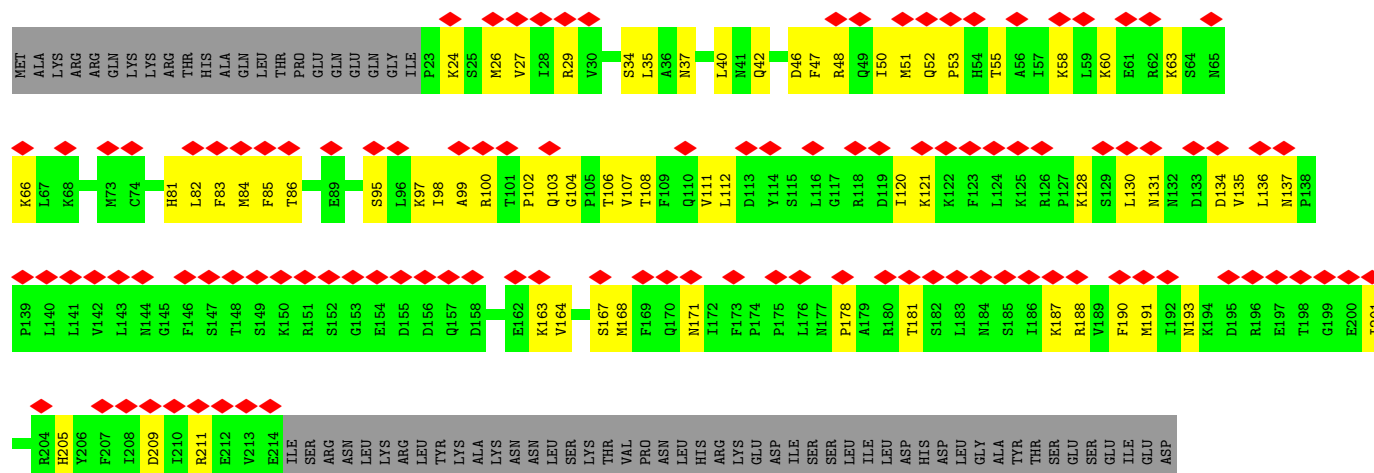
• Molecule 39: Ribosome biogenesis protein RLP24

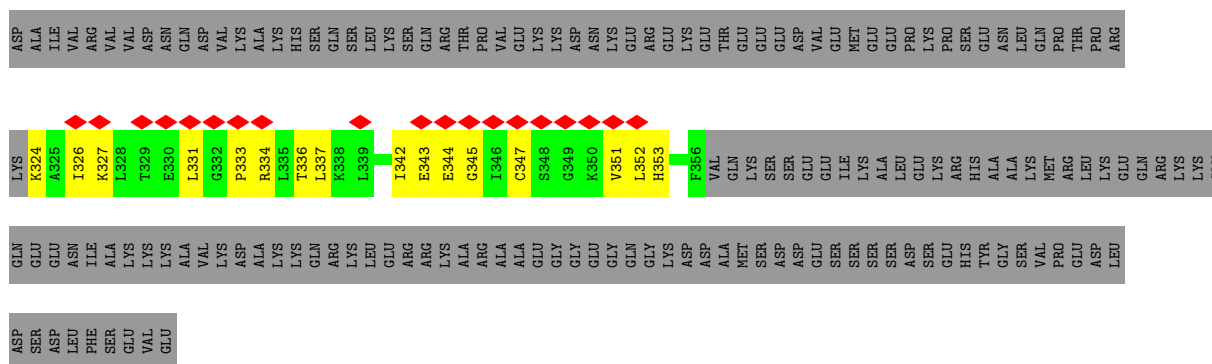
Chain u: 



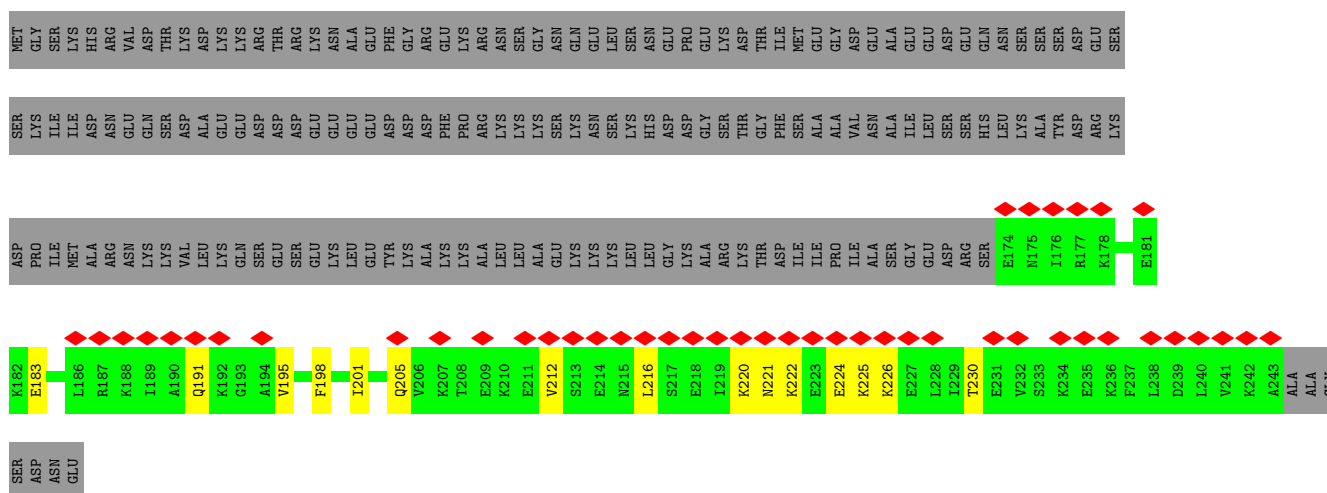
• Molecule 40: Ribosome biogenesis protein SSF1

Chain v: 

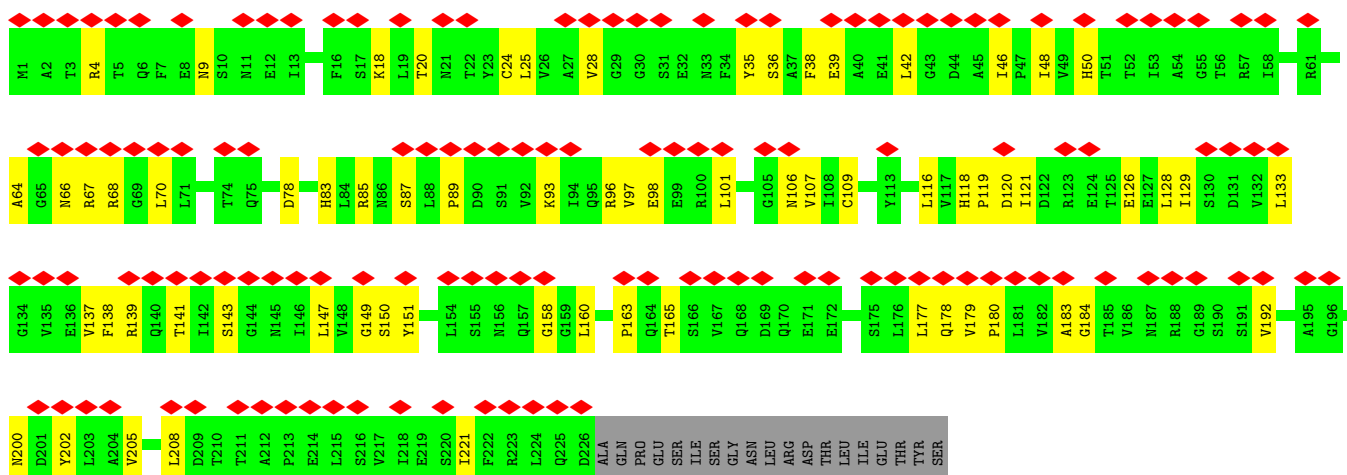




- Molecule 41: Ribosomal RNA-processing protein 15

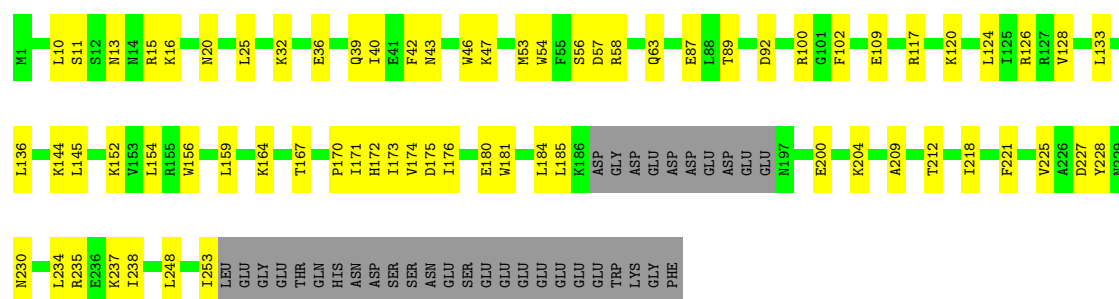


- Molecule 42: Eukaryotic translation initiation factor 6



- Molecule 43: Ribosomal RNA-processing protein 1

App Type	Percentage
Shopping app	63%
Social media app	25%
Productivity app	13%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	201114	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.56	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.173	Depositor
Minimum map value	-0.043	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	624.0, 624.0, 624.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3, 1.3, 1.3	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.35	0/32512	0.44	3/50669 (0.0%)
2	2	0.35	0/3746	0.44	0/5832
3	6	0.33	0/2050	0.57	0/3186
4	A	0.35	0/3182	0.63	4/4288 (0.1%)
5	B	0.29	0/2628	0.65	2/3529 (0.1%)
6	C	0.38	0/2462	0.71	0/3333
7	D	0.40	0/1609	0.63	0/2157
8	E	0.32	0/1390	0.65	2/1866 (0.1%)
9	F	0.33	0/1979	0.68	2/2661 (0.1%)
10	G	0.37	0/1477	0.79	4/1994 (0.2%)
11	I	0.36	0/2476	0.66	0/3323
12	K	0.30	0/2133	0.69	2/2879 (0.1%)
13	L	0.38	0/858	0.75	0/1154
14	M	0.31	0/1012	0.59	0/1362
15	N	0.36	0/1540	0.63	0/2060
16	O	0.32	0/1476	0.64	0/1980
17	P	0.30	0/991	0.58	0/1334
18	Q	0.35	0/1030	0.63	0/1393
19	S	0.30	0/1473	0.67	2/1980 (0.1%)
20	V	0.20	0/917	0.50	0/1235
21	W	0.23	0/821	0.52	0/1106
22	Y	0.37	0/1004	0.66	0/1341
23	7	0.37	0/1312	0.72	2/1744 (0.1%)
24	8	0.21	0/840	0.46	0/1105
25	b	0.32	0/1868	0.69	0/2522
26	e	0.33	0/931	0.62	0/1243
27	f	0.37	0/868	0.63	0/1168
28	h	0.31	0/978	0.70	0/1301
29	i	0.30	0/672	0.66	0/894
30	j	0.29	0/587	0.63	0/778
33	n	0.30	0/2862	0.62	0/3870
34	o	0.31	0/1129	0.64	2/1502 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	p	0.31	0/3552	0.68	2/4789 (0.0%)
37	s	0.34	0/720	0.68	0/964
38	t	0.34	0/1991	0.74	0/2679
39	u	0.26	0/1109	0.59	0/1474
40	v	0.26	0/1825	0.69	0/2453
41	w	0.21	0/563	0.59	0/748
42	y	0.25	0/1730	0.60	0/2354
43	z	0.33	0/2104	0.63	0/2832
All	All	0.33	0/94407	0.57	27/135082 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	A	0	2
7	D	0	1
9	F	0	1
10	G	0	1
19	S	0	4
28	h	0	1
33	n	0	1
36	q	0	1
37	s	0	1
38	t	0	3
All	All	0	16

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	S	13	ARG	CA-C-N	6.71	138.17	121.80
19	S	13	ARG	C-N-CA	6.71	138.17	121.80
10	G	119	GLY	CA-C-N	6.41	133.24	121.70
10	G	119	GLY	C-N-CA	6.41	133.24	121.70
10	G	145	ASN	CA-C-N	6.03	132.56	121.70
10	G	145	ASN	C-N-CA	6.03	132.56	121.70
9	F	157	ASN	CA-C-N	5.84	132.70	121.54
9	F	157	ASN	C-N-CA	5.84	132.70	121.54
4	A	265	LYS	CA-C-N	5.68	132.38	121.54
4	A	265	LYS	C-N-CA	5.68	132.38	121.54

Continued on next page...

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	7	44	LEU	CA-C-N	5.63	132.30	121.54
23	7	44	LEU	C-N-CA	5.63	132.30	121.54
4	A	414	GLU	CA-C-N	5.60	128.10	120.77
4	A	414	GLU	C-N-CA	5.60	128.10	120.77
12	K	186	ILE	CA-C-N	5.55	127.76	120.60
12	K	186	ILE	C-N-CA	5.55	127.76	120.60
34	o	214	SER	CA-C-N	5.53	131.65	121.70
34	o	214	SER	C-N-CA	5.53	131.65	121.70
35	p	338	ALA	CA-C-N	5.45	131.95	121.54
35	p	338	ALA	C-N-CA	5.45	131.95	121.54
1	1	3351	U	C2'-C3'-O3'	5.12	117.18	109.50
1	1	406	G	O4'-C1'-N9	5.10	116.15	108.50
8	E	98	VAL	CA-C-N	5.08	128.81	120.63
8	E	98	VAL	C-N-CA	5.08	128.81	120.63
5	B	347	SER	CA-C-N	5.07	131.22	121.54
5	B	347	SER	C-N-CA	5.07	131.22	121.54
1	1	3351	U	C4'-C3'-O3'	5.05	116.98	109.40

There are no chirality outliers.

All (16) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	185	ALA	Peptide
4	A	53	ILE	Peptide
7	D	56	ASP	Peptide
9	F	158	LYS	Peptide
10	G	76	ALA	Peptide
19	S	12	ARG	Peptide
19	S	13	ARG	Peptide
19	S	22	PRO	Peptide
19	S	83	SER	Peptide
28	h	83	LYS	Peptide
33	n	175	LEU	Peptide
36	q	344	UNK	Peptide
37	s	337	UNK	Peptide
38	t	150	PRO	Peptide
38	t	223	GLU	Peptide
38	t	245	ILE	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	29055	0	14598	537	0
2	2	3353	0	1695	63	0
3	6	1838	0	927	52	0
4	A	3126	0	3178	92	0
5	B	2577	0	2655	76	0
6	C	2418	0	2541	58	0
7	D	1578	0	1619	57	0
8	E	1366	0	1466	36	0
9	F	1941	0	2037	41	0
10	G	1453	0	1536	50	0
11	I	2429	0	2472	90	0
12	K	2099	0	2180	62	0
13	L	845	0	898	30	0
14	M	997	0	1090	24	0
15	N	1509	0	1561	40	0
16	O	1451	0	1554	35	0
17	P	975	0	988	14	0
18	Q	1015	0	1096	16	0
19	S	1437	0	1475	32	0
20	V	903	0	946	29	0
21	W	806	0	777	24	0
22	Y	993	0	1081	18	0
23	7	1295	0	1383	34	0
24	8	836	0	897	13	0
25	b	1919	0	1858	51	0
26	e	914	0	977	18	0
27	f	850	0	880	20	0
28	h	969	0	1078	28	0
29	i	665	0	721	18	0
30	j	575	0	579	17	0
31	x	140	0	34	1	0
32	m	370	0	76	3	0
33	n	2794	0	2845	64	0
34	o	1107	0	1159	36	0
35	p	3486	0	3618	77	0
36	q	1409	0	308	9	0
37	s	1069	0	820	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	t	1965	0	2077	53	0
39	u	1088	0	1118	35	0
40	v	1795	0	1877	63	0
41	w	562	0	614	16	0
42	y	1709	0	1701	52	0
43	z	2058	0	2096	51	0
44	D	1	0	0	0	0
44	j	1	0	0	0	0
44	u	1	0	0	0	0
All	All	91742	0	75086	1716	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 11.

All (1716) 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)
38:t:139:PRO:HA	38:t:179:LEU:O	1.61	0.99
1:1:182:U:H3	1:1:234:G:H1	1.07	0.97
1:1:160:G:H1	1:1:261:U:H3	1.09	0.97
1:1:509:U:H3	1:1:582:G:H1	1.10	0.95
4:A:57:GLU:OE2	4:A:169:LYS:NZ	1.99	0.95
1:1:528:U:H3	1:1:564:G:H1	1.09	0.95
40:v:334:ARG:NH1	41:w:183:GLU:OE2	1.99	0.94
25:b:273:LYS:O	25:b:277:ASN:HB2	1.67	0.94
1:1:438:A:OP2	11:I:104:LYS:NZ	2.02	0.92
25:b:32:ARG:NH1	31:x:168:UNK:O	2.03	0.92
39:u:2:ARG:NH1	42:y:78:ASP:OD2	2.03	0.91
1:1:3222:U:H3	1:1:3263:G:H1	1.17	0.91
1:1:129:U:H3	1:1:139:G:H1	0.93	0.90
1:1:3213:A:H62	14:M:124:ARG:HH12	1.20	0.90
8:E:31:ARG:NH1	27:f:107:ILE:O	2.05	0.89
1:1:3214:U:OP2	14:M:128:ARG:NH1	2.05	0.89
43:z:100:ARG:NH1	43:z:152:LYS:O	2.08	0.87
1:1:364:G:N7	30:j:52:LYS:NZ	2.22	0.87
1:1:3210:A:OP1	14:M:109:ARG:NH1	2.07	0.87
1:1:599:C:OP1	6:C:332:LYS:NZ	2.08	0.86
33:n:189:GLN:HA	33:n:197:VAL:O	1.74	0.86
3:6:39:U:O4	34:o:191:LYS:NZ	2.08	0.86
1:1:674:G:O6	18:Q:56:LYS:NZ	2.09	0.86
3:6:8:A:OP1	38:t:132:LYS:NZ	2.09	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:600:G:N2	1:1:603:A:OP2	2.08	0.85
1:1:3181:C:OP2	16:O:171:LYS:NZ	2.09	0.85
1:1:3021:A:N6	1:1:3033:A:OP2	2.08	0.85
1:1:251:G:O6	23:7:175:ARG:NH1	2.09	0.85
3:6:229:U:O5'	38:t:275:ARG:NH1	2.08	0.85
1:1:431:U:OP1	27:f:65:ARG:NH1	2.08	0.85
1:1:440:A:OP1	26:e:113:LYS:NZ	2.09	0.85
1:1:687:U:OP2	13:L:36:ARG:NH2	2.08	0.85
1:1:3039:C:OP1	5:B:62:ARG:NH1	2.08	0.85
1:1:173:G:H1	1:1:245:U:H3	1.23	0.84
33:n:190:ALA:O	33:n:196:GLU:HA	1.78	0.84
1:1:678:G:OP1	25:b:273:LYS:NZ	2.09	0.84
21:W:419:LYS:NZ	42:y:35:TYR:OH	2.10	0.84
1:1:216:G:OP1	22:Y:16:ARG:NH1	2.10	0.84
1:1:353:G:OP2	23:7:7:ARG:NH2	2.11	0.84
43:z:47:LYS:NZ	43:z:109:GLU:OE2	2.11	0.84
1:1:1884:A:OP1	24:8:339:LYS:NZ	2.11	0.83
35:p:150:GLY:HA2	35:p:174:ARG:HH11	1.44	0.83
42:y:85:ARG:NH1	42:y:89:PRO:O	2.11	0.83
5:B:31:ALA:O	5:B:339:ARG:NH1	2.12	0.83
30:j:48:ASN:OD1	30:j:54:LYS:NZ	2.12	0.83
1:1:297:G:OP2	1:1:297:G:N2	2.11	0.83
40:v:29:ARG:NH1	40:v:37:ASN:O	2.12	0.83
15:N:37:HIS:HE1	15:N:63:ARG:HH11	1.27	0.82
21:W:439:LYS:NZ	39:u:97:GLU:OE1	2.13	0.82
1:1:297:G:O6	15:N:12:ARG:NH1	2.13	0.82
1:1:71:A:OP1	25:b:253:LYS:NZ	2.13	0.81
25:b:90:GLU:OE2	25:b:92:ARG:NE	2.11	0.81
1:1:465:U:OP2	43:z:15:ARG:NH2	2.12	0.81
41:w:220:LYS:HG2	41:w:225:LYS:HZ2	1.44	0.81
1:1:761:A:OP2	1:1:769:G:N2	2.13	0.81
1:1:1447:G:N2	1:1:2356:A:OP2	2.12	0.81
1:1:696:C:OP2	6:C:119:ARG:NH2	2.12	0.81
35:p:81:ASP:OD2	35:p:244:ARG:N	2.12	0.81
1:1:177:U:O2	1:1:241:G:N1	2.12	0.80
1:1:726:G:N1	1:1:743:C:OP2	2.14	0.80
4:A:132:LYS:HZ1	4:A:136:LEU:HA	1.46	0.80
4:A:388:ASP:OD2	4:A:391:THR:N	2.14	0.80
1:1:518:G:OP2	1:1:518:G:N2	2.12	0.79
2:2:56:G:OP1	30:j:68:LYS:NZ	2.15	0.79
38:t:85:LYS:NZ	38:t:98:ASP:OD1	2.16	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:100:A:OP1	15:N:193:ARG:NH1	2.14	0.79
6:C:203:ARG:HB3	6:C:246:ARG:HH11	1.46	0.79
19:S:109:ASP:OD1	19:S:113:ARG:NH1	2.15	0.79
1:1:609:G:N7	6:C:308:LYS:NZ	2.31	0.79
10:G:144:GLU:OE2	15:N:6:TYR:OH	2.01	0.79
1:1:678:G:OP2	25:b:270:ARG:NE	2.16	0.79
1:1:91:G:OP2	1:1:93:C:N4	2.15	0.79
1:1:91:G:N2	1:1:95:A:OP2	2.16	0.79
1:1:727:G:OP2	1:1:742:G:N2	2.11	0.78
14:M:108:ARG:NH1	16:O:196:ALA:O	2.17	0.78
1:1:560:G:OP1	14:M:83:LYS:NZ	2.16	0.78
1:1:951:A:OP2	1:1:1367:G:N1	2.14	0.78
7:D:160:LYS:NZ	17:P:105:LYS:O	2.16	0.78
40:v:134:ASP:O	40:v:187:LYS:NZ	2.16	0.78
1:1:21:G:OP2	2:2:36:G:N1	2.16	0.78
1:1:3241:G:OP2	5:B:153:LYS:NZ	2.16	0.78
3:6:53:A:H3'	10:G:213:LYS:HZ3	1.46	0.78
11:I:104:LYS:N	11:I:152:GLU:OE2	2.13	0.77
14:M:114:ASP:OD1	14:M:117:ARG:NH1	2.16	0.77
1:1:722:G:H1	1:1:748:U:H3	1.29	0.77
1:1:358:G:N2	1:1:361:A:OP2	2.14	0.77
33:n:147:SER:OG	38:t:211:ARG:NH1	2.17	0.77
2:2:21:C:OP1	6:C:193:LYS:NZ	2.16	0.76
1:1:3097:C:OP1	5:B:349:LYS:NZ	2.18	0.76
17:P:108:ASP:OD2	17:P:111:LYS:N	2.13	0.76
1:1:346:C:N4	1:1:349:A:OP2	2.19	0.76
3:6:7:C:OP2	12:K:128:LYS:NZ	2.18	0.76
2:2:75:G:OP2	22:Y:74:TYR:OH	2.03	0.76
1:1:3139:A:O3'	5:B:20:LYS:NZ	2.19	0.76
3:6:5:C:N4	3:6:24:A:OP2	2.19	0.76
8:E:166:LYS:N	8:E:169:ASP:OD2	2.18	0.75
1:1:1:G:OP2	1:1:1:G:N2	2.18	0.75
1:1:194:U:OP2	4:A:357:ARG:NH1	2.19	0.75
1:1:533:A:O2'	1:1:535:G:OP2	2.03	0.75
9:F:138:TYR:H	9:F:233:GLU:HA	1.52	0.75
1:1:622:A:OP1	27:f:60:ARG:NH1	2.20	0.75
40:v:42:GLN:NE2	40:v:46:ASP:OD2	2.20	0.75
1:1:608:A:O2'	6:C:326:ARG:NH1	2.19	0.74
39:u:66:ASP:OD1	39:u:103:ARG:NH1	2.18	0.74
17:P:14:SER:O	17:P:105:LYS:NZ	2.21	0.74
1:1:1363:A:OP1	9:F:160:ARG:NH1	2.21	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:221:THR:O	12:K:225:ASN:HB2	1.87	0.74
4:A:41:GLU:OE1	4:A:62:ARG:NH1	2.21	0.74
40:v:51:MET:O	40:v:188:ARG:NH1	2.20	0.74
1:1:217:U:O2	22:Y:103:LYS:NZ	2.20	0.74
5:B:147:GLU:OE1	5:B:150:ARG:NH1	2.20	0.74
1:1:66:A:N3	15:N:176:LYS:NZ	2.33	0.74
35:p:300:ASN:OD1	35:p:322:LYS:NZ	2.20	0.73
1:1:3242:G:N2	1:1:3245:A:OP2	2.21	0.73
1:1:576:C:OP1	9:F:241:LYS:NZ	2.19	0.73
1:1:508:U:H3	1:1:583:G:H1	1.35	0.73
1:1:3189:G:H1	1:1:3203:U:H3	1.37	0.73
1:1:420:G:H1	2:2:3:A:H61	1.34	0.73
4:A:403:ARG:NH1	11:I:272:ARG:HH11	1.87	0.73
18:Q:120:GLU:OE2	18:Q:130:ARG:NH2	2.21	0.73
7:D:4:GLU:OE2	18:Q:31:LYS:NZ	2.20	0.72
33:n:178:LYS:HG3	33:n:189:GLN:HE21	1.54	0.72
7:D:44:PRO:O	7:D:65:LYS:NZ	2.22	0.72
1:1:262:U:H4'	35:p:448:ARG:NH1	2.04	0.72
1:1:185:C:OP1	22:Y:122:LYS:NZ	2.22	0.72
4:A:213:LEU:O	4:A:215:LYS:NZ	2.23	0.72
1:1:3092:C:O2'	1:1:3094:A:OP2	2.07	0.72
1:1:699:A:OP1	13:L:68:LYS:NZ	2.23	0.71
35:p:81:ASP:OD1	35:p:224:SER:N	2.18	0.71
1:1:3306:U:O2'	1:1:3308:C:OP2	2.05	0.71
16:O:77:SER:N	16:O:106:GLU:OE2	2.22	0.70
1:1:3037:U:O2'	5:B:348:ARG:NH1	2.25	0.70
33:n:147:SER:O	38:t:211:ARG:NH1	2.24	0.70
1:1:261:U:OP2	35:p:160:LYS:NZ	2.21	0.70
1:1:297:G:N3	29:i:41:ARG:NH1	2.39	0.70
1:1:1348:U:OP1	18:Q:39:ARG:NH1	2.23	0.70
2:2:103:G:OP2	2:2:105:A:O2'	2.10	0.70
40:v:134:ASP:OD1	40:v:187:LYS:NZ	2.25	0.70
2:2:121:U:H3	2:2:132:G:H1	1.38	0.70
2:2:36:G:OP2	28:h:86:ARG:N	2.21	0.70
4:A:50:MET:HA	4:A:59:ILE:O	1.92	0.70
35:p:76:LEU:HB3	35:p:99:PRO:HG2	1.73	0.69
40:v:81:HIS:HA	40:v:99:ALA:O	1.91	0.69
3:6:22:G:N7	12:K:96:LYS:NZ	2.41	0.69
11:I:77:ASP:O	11:I:81:LEU:HB2	1.92	0.69
34:o:197:LYS:HZ3	34:o:197:LYS:HB3	1.56	0.69
39:u:76:ASN:ND2	42:y:98:GLU:OE2	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:94:C:H3'	30:j:72:ARG:HH12	1.58	0.69
1:1:297:G:H2'	29:i:41:ARG:HH12	1.57	0.69
1:1:3326:G:H1	1:1:3380:U:H3	1.38	0.69
14:M:14:LEU:H	14:M:19:ARG:HH11	1.38	0.69
38:t:146:ARG:HE	38:t:171:THR:HG22	1.57	0.69
39:u:33:ARG:HE	39:u:35:LYS:HE2	1.58	0.69
6:C:160:GLN:HG2	6:C:214:GLY:HA3	1.75	0.69
25:b:110:ILE:HG22	25:b:226:ILE:HG12	1.75	0.69
35:p:144:THR:H	35:p:166:ASN:HB2	1.58	0.69
1:1:733:G:N2	1:1:736:A:OP2	2.24	0.68
4:A:47:VAL:HG22	4:A:62:ARG:HH22	1.57	0.68
1:1:432:G:H1	1:1:627:U:H3	1.40	0.68
14:M:36:VAL:HG11	14:M:55:ARG:HH12	1.59	0.68
1:1:525:C:OP2	14:M:77:ARG:NH2	2.24	0.68
1:1:3195:U:O2'	1:1:3197:G:N2	2.26	0.68
33:n:200:LEU:HD21	37:s:387:ARG:HH12	1.58	0.68
2:2:36:G:OP2	28:h:85:THR:OG1	2.11	0.68
43:z:133:LEU:HB3	43:z:184:LEU:HD11	1.76	0.68
1:1:544:C:H2'	1:1:547:G:H1	1.60	0.67
34:o:121:ARG:HD3	34:o:176:LEU:HB2	1.75	0.67
1:1:528:U:O2	1:1:564:G:N2	2.26	0.67
1:1:441:U:OP2	7:D:128:ARG:NH1	2.26	0.67
7:D:131:GLU:OE2	11:I:126:ARG:NH1	2.28	0.67
10:G:95:ASN:HD22	10:G:98:ARG:HH11	1.43	0.67
14:M:14:LEU:H	14:M:19:ARG:NH1	1.92	0.67
40:v:84:MET:HB2	40:v:97:LYS:HB2	1.77	0.67
5:B:369:ARG:HH11	39:u:11:SER:HB3	1.59	0.67
9:F:10:GLU:HG2	43:z:172:HIS:HE1	1.60	0.67
1:1:3013:U:H3	1:1:3041:U:H3	1.41	0.67
4:A:403:ARG:HH11	11:I:272:ARG:HD2	1.60	0.67
36:q:313:UNK:HA	36:q:356:UNK:HA	1.77	0.67
1:1:126:U:OP1	15:N:144:ARG:NH2	2.28	0.66
1:1:1404:G:N2	1:1:1407:A:OP2	2.25	0.66
23:7:209:GLN:NE2	35:p:436:ASN:OD1	2.29	0.66
38:t:146:ARG:NH1	38:t:193:TYR:HB3	2.10	0.66
13:L:46:ILE:HG22	13:L:49:ARG:HB2	1.78	0.66
1:1:754:G:N2	1:1:778:U:O2	2.28	0.66
5:B:375:GLU:OE2	39:u:14:TYR:OH	2.13	0.65
1:1:466:G:O4'	43:z:58:ARG:NH1	2.28	0.65
1:1:3000:A:O3'	5:B:120:LYS:NZ	2.29	0.65
1:1:3322:A:N3	40:v:131:ASN:ND2	2.45	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1399:A:N7	2:2:8:C:O2'	2.28	0.65
8:E:65:ILE:O	8:E:76:LEU:HA	1.97	0.65
43:z:171:ILE:HD12	43:z:237:LYS:HD3	1.77	0.65
13:L:44:ALA:HB2	23:7:28:ILE:HD12	1.79	0.65
1:1:338:A:H4'	6:C:197:ARG:HH12	1.60	0.65
1:1:292:U:OP1	15:N:68:ARG:NH1	2.28	0.64
42:y:107:VAL:HG13	42:y:118:HIS:HB2	1.79	0.64
3:6:224:G:N7	38:t:157:ASN:ND2	2.44	0.64
4:A:375:LEU:HB3	4:A:387:PHE:HB2	1.79	0.64
42:y:18:LYS:HB3	42:y:25:LEU:HB2	1.78	0.64
16:O:98:ALA:HA	16:O:101:ARG:HH11	1.62	0.64
15:N:189:LYS:O	15:N:192:LYS:HB3	1.97	0.64
7:D:19:ILE:HD11	7:D:29:ARG:HE	1.63	0.64
19:S:7:TYR:HA	19:S:62:ASN:O	1.97	0.64
4:A:248:PRO:HA	4:A:274:THR:HA	1.79	0.64
22:Y:112:ASP:H	22:Y:115:ARG:HB2	1.61	0.64
11:I:200:ASN:HB2	11:I:233:HIS:HA	1.80	0.63
42:y:42:LEU:HB2	42:y:48:ILE:HD11	1.81	0.63
21:W:385:LEU:HD21	21:W:396:ARG:HH12	1.62	0.63
7:D:39:THR:H	7:D:42:SER:HB2	1.60	0.63
8:E:113:LYS:HD3	8:E:116:LYS:HG2	1.79	0.63
1:1:353:G:N2	1:1:365:A:OP2	2.22	0.63
1:1:155:G:H4'	1:1:156:G:H2'	1.80	0.63
7:D:159:GLU:OE1	17:P:13:LYS:NZ	2.32	0.63
11:I:74:VAL:HG11	11:I:212:ARG:HH12	1.62	0.63
1:1:597:G:OP2	9:F:37:ASN:ND2	2.31	0.63
2:2:39:G:O2'	2:2:105:A:N1	2.32	0.63
1:1:3265:C:OP2	8:E:70:LYS:NZ	2.25	0.63
18:Q:123:THR:OG1	18:Q:125:ASP:OD1	2.10	0.63
3:6:53:A:H3'	10:G:213:LYS:NZ	2.14	0.62
16:O:28:LEU:HD22	16:O:94:ARG:NH1	2.14	0.62
1:1:1159:A:N3	1:1:1160:C:N4	2.47	0.62
5:B:53:MET:HG2	5:B:77:THR:HG22	1.80	0.62
1:1:609:G:P	6:C:326:ARG:HH12	2.23	0.62
40:v:209:ASP:HB3	40:v:327:LYS:HB2	1.81	0.62
1:1:590:G:O2'	6:C:309:ARG:NH1	2.33	0.62
1:1:3309:G:H3'	1:1:3310:A:H8	1.64	0.62
8:E:138:GLN:O	8:E:142:ASP:HB2	2.00	0.62
1:1:3166:C:H42	1:1:3284:G:H1	1.46	0.62
35:p:194:ILE:HG22	35:p:225:MET:HB2	1.80	0.62
1:1:3049:A:O2'	5:B:364:LYS:NZ	2.26	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3222:U:O2	1:1:3263:G:N2	2.30	0.62
33:n:137:ASN:HB3	37:s:387:ARG:HH12	1.65	0.62
1:1:563:U:H2'	1:1:564:G:H8	1.65	0.62
1:1:264:G:H2'	35:p:155:ARG:NH1	2.14	0.61
3:6:25:G:N7	12:K:93:LYS:NZ	2.47	0.61
5:B:112:ASP:O	5:B:116:ARG:HB2	1.99	0.61
7:D:104:PHE:O	7:D:108:CYS:HB2	1.99	0.61
1:1:3210:A:H5''	14:M:109:ARG:NH1	2.15	0.61
1:1:571:U:H2'	1:1:572:A:H8	1.65	0.61
13:L:29:ALA:HB2	15:N:201:ARG:NH1	2.15	0.61
35:p:276:ARG:NH2	35:p:364:PHE:O	2.33	0.61
1:1:394:G:OP2	11:I:290:LYS:NZ	2.25	0.61
1:1:1416:C:OP2	7:D:143:ARG:NH2	2.33	0.61
1:1:3082:C:H2'	1:1:3083:G:H8	1.65	0.61
43:z:54:TRP:O	43:z:117:ARG:NH2	2.34	0.61
1:1:312:C:H2'	1:1:313:A:H8	1.66	0.61
4:A:216:LEU:HB2	4:A:230:TRP:HB3	1.82	0.61
2:2:141:C:O2	15:N:112:ASN:ND2	2.34	0.61
35:p:124:ARG:HG3	35:p:149:ILE:HD13	1.82	0.61
1:1:105:C:HO2'	1:1:684:G:HO2'	1.47	0.61
1:1:464:U:OP1	7:D:75:LYS:NZ	2.34	0.61
38:t:150:PRO:HG2	38:t:153:VAL:HG21	1.83	0.61
4:A:278:HIS:HA	4:A:294:ILE:O	2.00	0.61
18:Q:86:THR:HG22	18:Q:105:ARG:HB2	1.83	0.61
39:u:18:GLY:HA3	39:u:31:PHE:O	2.00	0.61
41:w:222:LYS:HE2	41:w:225:LYS:HB2	1.83	0.61
1:1:499:G:H5''	27:f:48:ARG:HH12	1.66	0.60
10:G:137:ASN:HD22	15:N:3:ALA:H	1.49	0.60
37:s:282:ALA:HA	37:s:287:ARG:HH11	1.66	0.60
42:y:109:CYS:HB3	42:y:149:GLY:HA2	1.82	0.60
7:D:156:ALA:HB2	11:I:235:GLN:HE21	1.67	0.60
1:1:591:G:N2	1:1:612:U:OP1	2.34	0.60
2:2:36:G:OP2	28:h:86:ARG:HG3	2.01	0.60
13:L:115:ARG:NH2	23:7:60:GLN:OE1	2.35	0.60
33:n:444:ALA:HA	33:n:447:TYR:HD2	1.66	0.60
34:o:104:GLU:OE2	34:o:122:LEU:HB3	2.02	0.60
38:t:101:LEU:HB3	38:t:310:ILE:HA	1.84	0.60
35:p:339:GLU:OE2	35:p:340:ARG:NH2	2.35	0.60
11:I:60:ILE:HG12	11:I:291:LYS:NZ	2.17	0.60
5:B:220:VAL:O	5:B:334:ARG:NH1	2.35	0.60
33:n:137:ASN:HB3	37:s:387:ARG:NH1	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:p:266:GLN:HE21	35:p:377:VAL:HG21	1.67	0.60
35:p:76:LEU:HA	35:p:225:MET:HE1	1.83	0.60
35:p:194:ILE:HA	35:p:225:MET:O	2.02	0.60
11:I:64:ARG:HH12	11:I:295:LEU:HD11	1.66	0.59
1:1:507:U:OP1	9:F:150:LYS:NZ	2.34	0.59
1:1:664:U:H3	1:1:798:G:H1	1.50	0.59
1:1:3303:G:H8	1:1:3303:G:OP2	1.85	0.59
35:p:89:GLY:HA3	35:p:352:GLY:HA2	1.84	0.59
33:n:138:MET:SD	37:s:390:ARG:NH2	2.75	0.59
35:p:144:THR:HB	35:p:166:ASN:H	1.67	0.59
43:z:225:VAL:HA	43:z:235:ARG:HG3	1.84	0.59
1:1:700:C:H2'	1:1:701:G:H8	1.67	0.59
1:1:1189:C:N3	1:1:1315:U:O2'	2.34	0.59
12:K:82:VAL:HB	12:K:280:PHE:O	2.01	0.59
33:n:152:SER:H	33:n:155:ILE:HD12	1.67	0.59
10:G:152:LEU:HB2	10:G:198:ALA:HB3	1.84	0.59
1:1:254:A:OP2	37:s:270:LYS:NZ	2.33	0.59
10:G:97:TYR:HD2	10:G:200:LEU:HD11	1.68	0.59
5:B:41:VAL:HA	5:B:185:GLY:HA3	1.84	0.59
23:7:207:ILE:HD12	37:s:268:PRO:HG2	1.84	0.59
43:z:87:GLU:HA	43:z:144:LYS:HG3	1.85	0.59
1:1:501:A:OP1	8:E:82:ARG:NH2	2.36	0.59
4:A:267:ASN:OD1	4:A:285:GLN:NE2	2.35	0.59
5:B:173:GLN:HE21	5:B:175:LYS:HB3	1.68	0.59
1:1:508:U:O2	1:1:583:G:N2	2.33	0.59
11:I:149:ILE:HB	11:I:161:THR:HB	1.84	0.59
1:1:728:G:N7	1:1:742:G:N2	2.50	0.59
1:1:1334:U:H5''	9:F:206:LYS:HB3	1.84	0.59
9:F:7:LEU:H	43:z:63:GLN:HE22	1.50	0.59
23:7:222:TRP:CD1	23:7:225:ARG:HH11	2.21	0.59
11:I:69:THR:HB	11:I:205:ARG:H	1.67	0.58
25:b:97:LEU:HG	25:b:114:ILE:HD13	1.85	0.58
40:v:103:GLN:NE2	40:v:344:GLU:OE2	2.36	0.58
42:y:143:SER:HB2	42:y:165:THR:HA	1.83	0.58
1:1:383:G:O2'	1:1:386:A:N6	2.37	0.58
2:2:95:G:OP2	30:j:72:ARG:NH1	2.35	0.58
2:2:97:A:O2'	28:h:59:ASN:ND2	2.37	0.58
4:A:185:ALA:O	4:A:212:ASN:ND2	2.36	0.58
10:G:95:ASN:ND2	10:G:98:ARG:HH11	2.01	0.58
22:Y:70:ILE:HG13	22:Y:82:VAL:HG22	1.85	0.58
23:7:45:THR:OG1	23:7:48:GLN:NE2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:348:A:N3	1:1:352:A:O2'	2.35	0.58
1:1:447:U:H3	1:1:487:U:H3	1.51	0.58
4:A:251:LEU:O	4:A:252:ARG:NH1	2.33	0.58
4:A:340:LYS:NZ	4:A:361:THR:HA	2.19	0.58
5:B:213:GLU:HB3	5:B:282:ILE:HD12	1.86	0.58
11:I:268:LYS:NZ	26:e:129:GLU:OE1	2.37	0.58
15:N:37:HIS:HE1	15:N:63:ARG:NH1	1.97	0.58
1:1:595:G:O6	8:E:22:ARG:NH2	2.37	0.58
1:1:691:A:N1	2:2:28:C:O2'	2.37	0.58
1:1:3056:U:O4	1:1:3086:A:N6	2.37	0.58
4:A:219:ILE:HA	4:A:226:LEU:HA	1.85	0.58
4:A:266:LEU:O	4:A:285:GLN:NE2	2.36	0.58
11:I:191:THR:H	11:I:228:GLN:HE22	1.51	0.58
25:b:42:ASN:ND2	25:b:94:HIS:O	2.34	0.58
16:O:194:LEU:O	16:O:199:TYR:N	2.37	0.58
21:W:392:ASP:HB3	21:W:395:ARG:HD3	1.86	0.58
35:p:43:LYS:HB2	35:p:46:GLU:HG3	1.86	0.58
35:p:474:ALA:HB1	35:p:479:PHE:HB2	1.86	0.58
1:1:722:G:N2	1:1:748:U:O2	2.36	0.58
3:6:38:U:OP1	34:o:190:THR:N	2.36	0.58
1:1:3092:C:OP2	1:1:3094:A:N6	2.37	0.58
16:O:115:LYS:O	16:O:117:ARG:NH1	2.36	0.58
25:b:188:VAL:HB	25:b:219:PHE:HB2	1.86	0.58
42:y:180:PRO:HB2	42:y:221:ILE:HD11	1.85	0.58
1:1:269:G:H5''	15:N:14:LYS:HE2	1.85	0.58
1:1:509:U:O2	1:1:582:G:N2	2.31	0.57
5:B:121:ASN:HB3	5:B:124:LYS:HZ3	1.69	0.57
11:I:243:ARG:HG3	11:I:260:GLY:H	1.68	0.57
42:y:18:LYS:NZ	42:y:64:ALA:HA	2.19	0.57
35:p:124:ARG:NH2	35:p:452:GLN:OE1	2.38	0.57
43:z:230:ASN:HB3	43:z:235:ARG:HH11	1.68	0.57
21:W:421:LEU:O	39:u:80:ARG:NH2	2.37	0.57
34:o:92:ILE:HG23	34:o:167:LEU:HB2	1.87	0.57
35:p:110:LYS:NZ	35:p:112:ARG:NH1	2.52	0.57
1:1:1329:U:OP1	27:f:17:GLN:NE2	2.37	0.57
4:A:363:SER:HB3	4:A:380:LEU:HD12	1.86	0.57
10:G:192:GLN:O	33:n:96:ARG:NH2	2.37	0.57
27:f:47:LYS:HA	27:f:104:PRO:HD2	1.86	0.57
36:q:242:UNK:HA	36:q:247:UNK:H	1.68	0.57
37:s:358:UNK:O	37:s:362:UNK:N	2.38	0.57
1:1:271:C:O2	29:i:82:ARG:NH2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:o:118:LYS:N	34:o:138:GLU:O	2.38	0.57
12:K:282:LYS:HZ2	12:K:284:ASN:HA	1.69	0.57
25:b:34:LEU:HB3	25:b:86:VAL:HG23	1.87	0.57
33:n:117:ILE:O	33:n:121:ARG:HB2	2.05	0.57
39:u:23:ARG:NH1	39:u:27:LYS:HD2	2.20	0.57
20:V:27:ASP:HB2	20:V:111:GLY:HA3	1.85	0.57
25:b:112:PHE:HD2	25:b:221:MET:HE2	1.70	0.57
1:1:32:U:H3	1:1:52:A:H61	1.53	0.57
5:B:314:TYR:HA	5:B:333:LYS:HE2	1.85	0.57
25:b:111:LYS:HG2	25:b:224:ILE:HD12	1.87	0.57
42:y:163:PRO:HA	42:y:183:ALA:HB1	1.86	0.57
1:1:19:U:H3	2:2:140:G:H1	1.53	0.57
1:1:3148:U:H2'	1:1:3149:G:H8	1.70	0.57
18:Q:120:GLU:HB2	43:z:164:LYS:HZ3	1.69	0.57
2:2:128:U:OP1	2:2:129:C:N4	2.33	0.56
3:6:33:U:O2'	12:K:286:SER:O	2.22	0.56
5:B:221:THR:HG22	5:B:273:HIS:H	1.69	0.56
1:1:297:G:H2'	29:i:41:ARG:NH1	2.19	0.56
11:I:96:PHE:HB3	11:I:147:ILE:HG22	1.87	0.56
42:y:106:ASN:HB3	42:y:147:LEU:HD22	1.88	0.56
3:6:55:A:P	34:o:97:ARG:HH11	2.28	0.56
4:A:376:LEU:HD21	4:A:409:MET:HB2	1.86	0.56
5:B:109:HIS:N	5:B:200:GLU:OE2	2.37	0.56
6:C:260:GLN:HB3	23:7:70:LEU:HD22	1.87	0.56
11:I:233:HIS:O	11:I:239:ILE:HA	2.06	0.56
24:8:332:MET:HB2	40:v:164:VAL:HG22	1.87	0.56
33:n:455:PRO:HB3	37:s:341:UNK:HA	1.86	0.56
36:q:372:UNK:O	36:q:382:UNK:HA	2.05	0.56
38:t:279:GLY:HA2	38:t:288:LYS:HD2	1.87	0.56
42:y:129:ILE:HG23	42:y:133:LEU:HD12	1.86	0.56
1:1:3242:G:OP2	5:B:154:TYR:OH	2.19	0.56
4:A:192:LEU:HD23	4:A:205:PHE:HB3	1.87	0.56
16:O:116:LYS:NZ	19:S:165:TYR:HB3	2.20	0.56
20:V:135:VAL:HG22	42:y:101:LEU:HB3	1.85	0.56
25:b:109:THR:OG1	25:b:227:LEU:O	2.23	0.56
1:1:684:G:OP2	13:L:28:GLN:NE2	2.37	0.56
1:1:1393:A:OP1	26:e:125:ARG:NH2	2.39	0.56
23:7:184:TRP:NE1	23:7:205:LEU:O	2.35	0.56
40:v:97:LYS:HA	40:v:107:VAL:O	2.06	0.56
1:1:618:C:O2'	1:1:621:A:N3	2.37	0.56
12:K:66:LEU:HD22	35:p:418:PRO:HD3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:28:ARG:HH22	19:S:64:ILE:HD13	1.71	0.56
20:V:16:GLY:N	20:V:52:ALA:O	2.38	0.56
1:1:64:G:H22	1:1:322:U:H2'	1.70	0.56
4:A:57:GLU:HA	4:A:70:VAL:O	2.05	0.56
4:A:403:ARG:NH1	11:I:272:ARG:NH1	2.52	0.56
6:C:299:ILE:HG23	18:Q:39:ARG:HB3	1.88	0.56
19:S:42:TRP:HE1	19:S:58:ILE:HD11	1.70	0.56
20:V:135:VAL:HG13	42:y:101:LEU:HA	1.88	0.56
34:o:149:GLN:NE2	34:o:164:VAL:O	2.32	0.56
39:u:68:THR:HB	39:u:96:ILE:HG23	1.88	0.56
2:2:36:G:O2'	2:2:104:A:N1	2.37	0.56
27:f:75:HIS:HB2	27:f:82:ARG:HG3	1.88	0.56
1:1:173:G:O6	1:1:245:U:O4	2.24	0.56
1:1:679:U:H3	1:1:701:G:H1	1.52	0.56
5:B:36:ASP:HB3	5:B:39:LYS:HE3	1.88	0.56
7:D:141:VAL:HG22	7:D:144:ARG:HH21	1.70	0.56
9:F:186:HIS:O	9:F:190:THR:OG1	2.24	0.56
11:I:272:ARG:NE	11:I:279:GLU:OE2	2.39	0.56
1:1:264:G:H2'	35:p:155:ARG:HH12	1.71	0.56
11:I:97:LEU:HB2	11:I:123:PHE:HA	1.87	0.56
38:t:146:ARG:HA	38:t:194:VAL:HG12	1.88	0.56
7:D:53:VAL:HG21	7:D:112:PHE:HB2	1.88	0.55
20:V:87:ARG:NH1	20:V:120:LYS:HE2	2.21	0.55
1:1:336:A:O2'	6:C:48:GLN:NE2	2.38	0.55
11:I:140:ILE:HG13	11:I:165:LEU:HD12	1.89	0.55
12:K:282:LYS:NZ	12:K:284:ASN:HA	2.21	0.55
30:j:27:PHE:HA	30:j:34:CYS:HA	1.87	0.55
35:p:190:LEU:HD23	35:p:222:ARG:HG3	1.89	0.55
35:p:297:SER:N	35:p:365:ASP:OD2	2.39	0.55
1:1:1175:C:H5''	16:O:25:LYS:HD3	1.88	0.55
10:G:188:THR:HG22	33:n:96:ARG:HG2	1.88	0.55
11:I:164:HIS:HB3	11:I:168:GLY:HA3	1.88	0.55
16:O:108:ILE:HB	16:O:160:ARG:NH1	2.21	0.55
25:b:284:LEU:HD21	43:z:43:ASN:HB3	1.87	0.55
28:h:77:PRO:HD2	28:h:80:LEU:HD12	1.89	0.55
43:z:230:ASN:O	43:z:235:ARG:NH1	2.39	0.55
1:1:28:C:O2'	1:1:61:A:N3	2.39	0.55
4:A:14:LYS:HA	4:A:36:ALA:O	2.06	0.55
11:I:100:ASN:HA	11:I:126:ARG:HD3	1.89	0.55
27:f:15:SER:OG	27:f:16:TYR:N	2.39	0.55
35:p:116:GLY:HA2	35:p:191:LYS:H	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6:38:U:O2	3:6:41:G:O6	2.25	0.55
28:h:87:ALA:HA	28:h:90:ARG:HB2	1.88	0.55
4:A:168:LYS:NZ	4:A:178:LEU:HD21	2.21	0.55
34:o:128:THR:HG23	34:o:181:LYS:HG2	1.87	0.55
39:u:74:ARG:HE	42:y:96:ARG:NH1	2.05	0.55
1:1:309:U:O4'	25:b:72:GLN:NE2	2.39	0.55
8:E:171:PRO:HA	8:E:174:LEU:HB2	1.88	0.55
16:O:108:ILE:HB	16:O:160:ARG:HH12	1.71	0.55
34:o:90:SER:HB2	34:o:169:LYS:HA	1.88	0.55
1:1:505:G:OP1	6:C:320:ASN:ND2	2.40	0.55
11:I:94:LYS:NZ	11:I:142:ARG:O	2.33	0.55
13:L:105:ASN:OD1	29:i:17:VAL:N	2.40	0.55
16:O:108:ILE:HD12	16:O:160:ARG:HH12	1.72	0.55
40:v:29:ARG:HH11	40:v:40:LEU:HB3	1.72	0.55
1:1:675:C:O2'	1:1:679:U:OP1	2.24	0.55
1:1:1168:U:H2'	1:1:1169:A:H8	1.72	0.55
5:B:57:VAL:HG22	5:B:73:VAL:HG12	1.88	0.55
11:I:42:ARG:HA	41:w:220:LYS:NZ	2.22	0.55
14:M:23:ILE:O	14:M:30:GLY:N	2.37	0.55
2:2:150:G:O2'	10:G:59:GLN:NE2	2.40	0.54
3:6:55:A:OP1	34:o:97:ARG:NH1	2.36	0.54
7:D:159:GLU:CD	17:P:13:LYS:HZ2	2.15	0.54
23:7:81:LYS:HE3	25:b:280:ALA:H	1.72	0.54
1:1:381:U:OP2	11:I:34:ARG:NH2	2.34	0.54
4:A:3:LEU:HB2	4:A:16:VAL:HB	1.89	0.54
6:C:5:GLN:NE2	43:z:11:SER:O	2.40	0.54
6:C:203:ARG:HB3	6:C:246:ARG:NH1	2.18	0.54
20:V:81:GLN:O	20:V:98:ASN:ND2	2.40	0.54
1:1:170:G:H1	1:1:248:U:H3	1.53	0.54
3:6:231:A:H1'	3:6:232:A:H5'	1.89	0.54
11:I:98:THR:HG22	11:I:126:ARG:HD2	1.89	0.54
11:I:227:ARG:HB3	11:I:246:TYR:HB2	1.89	0.54
1:1:90:C:OP1	25:b:44:ARG:NH2	2.40	0.54
15:N:23:GLN:NE2	15:N:122:ASN:OD1	2.38	0.54
16:O:42:ASN:HA	16:O:136:THR:O	2.08	0.54
20:V:87:ARG:HH21	20:V:93:LEU:HD11	1.72	0.54
41:w:221:ASN:HA	41:w:226:LYS:HD2	1.90	0.54
1:1:608:A:N1	8:E:22:ARG:NH1	2.55	0.54
11:I:189:ARG:H	11:I:245:ARG:HH12	1.56	0.54
33:n:200:LEU:HD21	37:s:387:ARG:NH1	2.23	0.54
12:K:81:ILE:HB	12:K:246:VAL:HB	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:p:150:GLY:HA2	35:p:174:ARG:NH1	2.20	0.54
39:u:57:LYS:NZ	39:u:62:GLU:OE1	2.38	0.54
40:v:104:GLY:O	40:v:345:GLY:N	2.39	0.54
1:1:1346:G:O2'	6:C:307:GLN:NE2	2.41	0.54
1:1:3375:A:O2'	1:1:3378:C:OP2	2.24	0.54
4:A:49:ARG:H	4:A:61:ALA:HB3	1.73	0.54
4:A:146:ILE:HG22	4:A:152:ASN:HD21	1.71	0.54
12:K:181:LEU:HD23	12:K:207:ILE:HB	1.90	0.54
12:K:212:HIS:HA	12:K:217:PHE:HA	1.89	0.54
15:N:37:HIS:CE1	15:N:63:ARG:HH11	2.17	0.54
16:O:121:PRO:HA	16:O:124:LEU:HD23	1.90	0.54
1:1:655:C:H2'	1:1:656:A:H8	1.73	0.54
3:6:228:U:OP1	38:t:171:THR:N	2.33	0.54
4:A:15:GLU:HB3	4:A:36:ALA:HB3	1.88	0.54
1:1:1362:G:H2'	1:1:1363:A:H8	1.72	0.54
1:1:3039:C:H2'	1:1:3040:A:H8	1.73	0.54
21:W:433:PRO:HG2	21:W:441:VAL:HG11	1.89	0.54
43:z:218:ILE:HA	43:z:221:PHE:HD2	1.73	0.54
1:1:754:G:C2	1:1:778:U:O2	2.61	0.54
7:D:25:GLN:OE1	26:e:92:TYR:OH	2.26	0.54
20:V:45:ARG:NH1	20:V:46:LEU:HB3	2.23	0.54
33:n:117:ILE:O	33:n:121:ARG:CB	2.56	0.54
35:p:399:LEU:O	35:p:402:LEU:HB2	2.07	0.54
42:y:28:VAL:HG12	42:y:50:HIS:HB3	1.89	0.54
1:1:5:G:H2'	1:1:6:A:H8	1.72	0.53
1:1:3231:U:H2'	1:1:3232:G:H8	1.73	0.53
1:1:3297:U:OP2	5:B:121:ASN:ND2	2.41	0.53
4:A:184:LYS:HD2	4:A:215:LYS:HE3	1.89	0.53
10:G:61:GLN:HB3	15:N:28:TRP:HH2	1.74	0.53
15:N:18:VAL:HG13	15:N:19:LEU:HD12	1.90	0.53
40:v:137:ASN:HD22	40:v:187:LYS:HD2	1.73	0.53
11:I:65:VAL:HG11	11:I:292:LYS:NZ	2.24	0.53
19:S:43:TYR:O	19:S:47:LYS:NZ	2.39	0.53
35:p:292:ILE:HG12	35:p:360:TRP:HB2	1.91	0.53
42:y:4:ARG:HB3	42:y:208:LEU:HD23	1.90	0.53
1:1:1887:A:OP1	24:8:353:ARG:NH2	2.41	0.53
5:B:194:TRP:O	5:B:198:HIS:ND1	2.33	0.53
19:S:136:LYS:HE3	19:S:137:ARG:HH22	1.74	0.53
30:j:45:ARG:HH11	30:j:47:TYR:HE2	1.55	0.53
1:1:451:U:H2'	1:1:452:G:C8	2.44	0.53
1:1:1190:A:H2'	16:O:49:ARG:HH12	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:139:GLN:HG3	5:B:141:GLY:H	1.74	0.53
12:K:290:PRO:HD2	34:o:211:LEU:HD11	1.90	0.53
35:p:123:THR:HG22	35:p:125:GLU:H	1.73	0.53
38:t:67:ALA:HB1	38:t:153:VAL:HG22	1.90	0.53
1:1:3316:A:O2'	1:1:3317:U:OP2	2.22	0.53
5:B:44:THR:HA	5:B:340:LYS:HE3	1.91	0.53
23:7:45:THR:O	23:7:49:ASN:HB2	2.08	0.53
39:u:18:GLY:CA	39:u:31:PHE:O	2.57	0.53
41:w:220:LYS:HG2	41:w:225:LYS:NZ	2.22	0.53
1:1:109:A:N1	1:1:322:U:O2'	2.35	0.53
1:1:627:U:H4'	1:1:1399:A:H1'	1.91	0.53
1:1:677:A:N1	1:1:703:G:O2'	2.41	0.53
1:1:3227:A:H8	1:1:3227:A:OP2	1.92	0.53
12:K:85:ASN:HA	12:K:277:ARG:H	1.73	0.53
13:L:34:SER:HA	13:L:37:ASN:HD22	1.73	0.53
38:t:74:ARG:HD3	38:t:75:ILE:HG13	1.90	0.53
42:y:158:GLY:HA2	42:y:179:VAL:HB	1.90	0.53
3:6:27:G:OP1	34:o:130:ASN:ND2	2.39	0.53
19:S:25:PHE:O	19:S:41:TYR:OH	2.25	0.53
20:V:131:SER:O	42:y:106:ASN:ND2	2.42	0.53
35:p:474:ALA:O	35:p:478:GLY:N	2.41	0.53
1:1:75:G:O3'	13:L:70:ARG:NH2	2.42	0.53
4:A:70:VAL:HG22	4:A:110:ILE:HG12	1.90	0.53
1:1:182:U:O4	1:1:234:G:O6	2.27	0.53
35:p:202:LEU:HD11	35:p:234:LYS:HB2	1.90	0.53
41:w:212:VAL:HA	41:w:216:LEU:HB2	1.91	0.53
1:1:532:A:H2'	1:1:533:A:C8	2.44	0.53
1:1:744:A:OP1	18:Q:66:ARG:NH2	2.42	0.53
4:A:2:ARG:HG2	4:A:17:LEU:HG	1.90	0.53
4:A:411:ASP:OD1	4:A:412:ASP:N	2.42	0.53
5:B:205:VAL:O	5:B:209:PHE:N	2.37	0.53
7:D:113:THR:HG21	8:E:10:TYR:HB3	1.90	0.53
1:1:184:U:H3	1:1:232:G:H1	1.58	0.52
1:1:3255:U:H2'	1:1:3256:G:H8	1.74	0.52
33:n:421:VAL:N	33:n:426:TYR:OH	2.42	0.52
1:1:2357:A:H2'	1:1:2358:A:H8	1.74	0.52
15:N:38:ARG:HE	15:N:60:VAL:HG13	1.73	0.52
1:1:406:G:OP1	1:1:1415:U:O2'	2.26	0.52
2:2:36:G:C8	28:h:86:ARG:HG2	2.44	0.52
35:p:452:GLN:HG2	35:p:487:ILE:HD11	1.92	0.52
1:1:1452:A:N6	24:8:361:SER:OG	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:33:PRO:HG2	5:B:340:LYS:HG3	1.92	0.52
15:N:184:LYS:O	15:N:187:ARG:HB3	2.09	0.52
1:1:686:G:OP2	13:L:39:ARG:NH2	2.39	0.52
3:6:53:A:O2'	3:6:55:A:N6	2.42	0.52
13:L:83:ALA:HA	13:L:117:LYS:HE3	1.91	0.52
16:O:36:VAL:HB	16:O:108:ILE:HG12	1.92	0.52
34:o:117:LEU:HA	34:o:139:PHE:HA	1.92	0.52
1:1:208:C:OP2	6:C:163:LYS:NZ	2.43	0.52
2:2:26:U:O2'	6:C:51:ALA:O	2.26	0.52
2:2:29:U:H5''	13:L:27:ASP:HB3	1.91	0.52
11:I:272:ARG:N	11:I:277:GLU:O	2.38	0.52
33:n:144:ASN:HD22	33:n:202:PRO:HG2	1.74	0.52
33:n:415:PRO:HD3	37:s:375:ARG:NH1	2.25	0.52
1:1:67:A:O2'	1:1:315:C:O2	2.26	0.52
1:1:345:G:O2'	2:2:25:G:N3	2.42	0.52
1:1:1381:A:H2'	1:1:1382:G:H8	1.75	0.52
1:1:1385:C:O3'	7:D:29:ARG:NH2	2.43	0.52
19:S:13:ARG:NH1	19:S:51:VAL:HG12	2.25	0.52
23:7:182:GLU:OE1	23:7:225:ARG:NH1	2.41	0.52
35:p:73:ILE:HA	35:p:76:LEU:HB2	1.92	0.52
35:p:201:ILE:HG23	35:p:206:PHE:HB2	1.92	0.52
1:1:15:C:H2'	1:1:16:A:H8	1.74	0.52
1:1:655:C:H2'	1:1:656:A:C8	2.45	0.52
1:1:1168:U:O2	1:1:1330:A:N7	2.43	0.52
16:O:43:ILE:HB	16:O:136:THR:HB	1.92	0.52
39:u:23:ARG:HH12	39:u:27:LYS:HD2	1.75	0.52
43:z:89:THR:HG23	43:z:92:ASP:H	1.75	0.52
1:1:411:U:H2'	1:1:412:G:H8	1.75	0.52
1:1:1362:G:H2'	1:1:1363:A:C8	2.45	0.52
1:1:3062:G:H1	1:1:3081:C:H42	1.56	0.52
7:D:28:CYS:HB2	7:D:33:ASN:HD22	1.74	0.52
11:I:201:ASN:HB2	11:I:234:ASN:HB3	1.91	0.52
19:S:74:ASN:O	19:S:129:ILE:N	2.41	0.52
19:S:96:ASP:OD2	19:S:102:ALA:N	2.43	0.52
20:V:87:ARG:NH1	20:V:121:GLU:OE2	2.43	0.52
1:1:425:G:H2'	1:1:426:G:H8	1.75	0.51
1:1:591:G:O2'	8:E:17:ALA:O	2.25	0.51
1:1:1447:G:N7	17:P:25:SER:OG	2.42	0.51
2:2:79:A:OP2	2:2:79:A:H8	1.92	0.51
6:C:315:LYS:HD3	6:C:320:ASN:HD21	1.75	0.51
7:D:132:ARG:HD3	26:e:128:LEU:HB3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:50:GLN:O	11:I:54:GLU:HB2	2.10	0.51
21:W:403:GLU:OE2	21:W:409:ALA:HA	2.10	0.51
25:b:151:LEU:HD11	32:m:201:UNK:HA	1.92	0.51
28:h:44:ILE:HA	28:h:47:VAL:HG12	1.91	0.51
38:t:101:LEU:N	38:t:309:VAL:O	2.41	0.51
1:1:275:U:H3	1:1:290:G:H1	1.57	0.51
3:6:46:U:O2'	12:K:245:ASN:ND2	2.43	0.51
3:6:65:U:O2'	3:6:222:A:N6	2.40	0.51
5:B:328:ILE:HD11	5:B:336:VAL:HG11	1.92	0.51
7:D:132:ARG:NH2	11:I:152:GLU:O	2.42	0.51
10:G:172:LYS:NZ	37:s:250:HIS:O	2.31	0.51
27:f:16:TYR:OH	27:f:89:LEU:O	2.27	0.51
33:n:16:ILE:H	33:n:63:TYR:H	1.57	0.51
35:p:189:ASN:HB3	35:p:191:LYS:HE3	1.91	0.51
38:t:295:GLU:HB3	38:t:299:ARG:NH1	2.26	0.51
40:v:29:ARG:HA	40:v:85:PHE:HB2	1.91	0.51
42:y:106:ASN:ND2	42:y:150:SER:OG	2.43	0.51
7:D:73:PRO:HA	7:D:76:LEU:HB2	1.92	0.51
8:E:40:LEU:HD13	8:E:84:VAL:HG11	1.92	0.51
11:I:59:THR:HG23	11:I:62:ASN:H	1.73	0.51
16:O:116:LYS:HZ1	19:S:165:TYR:HB3	1.74	0.51
23:7:41:ASP:OD2	23:7:52:LYS:HE2	2.11	0.51
40:v:130:LEU:HB2	40:v:331:LEU:HD11	1.91	0.51
1:1:482:C:O3'	7:D:85:ASN:ND2	2.44	0.51
1:1:1419:A:OP1	2:2:20:U:O2'	2.26	0.51
21:W:460:GLU:OE2	39:u:99:ILE:HG21	2.10	0.51
41:w:222:LYS:HE3	41:w:224:GLU:HB3	1.92	0.51
43:z:56:SER:O	43:z:120:LYS:NZ	2.38	0.51
1:1:22:G:O6	28:h:86:ARG:NH2	2.43	0.51
1:1:664:U:H2'	1:1:665:A:H8	1.76	0.51
1:1:1389:G:H5''	26:e:101:SER:HB3	1.93	0.51
1:1:3233:C:H2'	1:1:3234:A:C8	2.46	0.51
1:1:3296:A:OP2	5:B:121:ASN:HB2	2.11	0.51
1:1:3304:U:N3	5:B:333:LYS:O	2.43	0.51
4:A:60:LEU:HB3	4:A:62:ARG:HH21	1.74	0.51
10:G:213:LYS:NZ	34:o:160:HIS:HB3	2.25	0.51
12:K:256:PRO:HA	12:K:259:PHE:HD2	1.76	0.51
25:b:31:GLN:HA	25:b:84:ASN:HD22	1.76	0.51
33:n:34:ARG:O	33:n:38:PHE:HB2	2.11	0.51
38:t:233:ASN:HA	38:t:236:GLU:HG2	1.91	0.51
12:K:40:ALA:HB1	12:K:289:LEU:HD13	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:135:GLN:NE2	43:z:230:ASN:O	2.42	0.51
1:1:3037:U:H4'	5:B:348:ARG:HH11	1.76	0.51
2:2:40:A:OP2	2:2:103:G:N1	2.44	0.51
9:F:89:ILE:HG23	9:F:219:LYS:HE2	1.91	0.51
11:I:147:ILE:HD11	11:I:163:ILE:HD12	1.92	0.51
17:P:48:LEU:HD22	17:P:88:VAL:HG13	1.92	0.51
24:8:334:GLN:HG3	24:8:340:ILE:HD12	1.93	0.51
40:v:201:ILE:HG13	40:v:337:LEU:HB2	1.92	0.51
1:1:1434:G:OP1	1:1:1437:C:N4	2.43	0.51
34:o:93:ILE:HB	34:o:137:LEU:HB2	1.93	0.51
43:z:174:VAL:HG11	43:z:238:ILE:HG12	1.93	0.51
1:1:14:U:H3	2:2:118:C:H1'	1.76	0.51
1:1:291:C:OP2	15:N:128:LYS:NZ	2.44	0.51
3:6:58:G:N1	34:o:124:ARG:O	2.38	0.51
5:B:119:TYR:HE2	5:B:127:LYS:HA	1.76	0.51
21:W:442:TYR:HA	21:W:445:LEU:HD22	1.93	0.51
33:n:114:LEU:HD11	33:n:223:GLU:HG2	1.92	0.51
6:C:198:ARG:NH1	22:Y:12:ARG:NH1	2.59	0.51
33:n:151:VAL:HG22	33:n:219:LEU:HD21	1.93	0.51
40:v:98:ILE:O	40:v:106:THR:HA	2.11	0.51
4:A:193:TYR:HB3	4:A:204:ILE:HB	1.94	0.50
28:h:85:THR:OG1	28:h:86:ARG:N	2.44	0.50
33:n:189:GLN:HB3	33:n:198:ARG:HG2	1.92	0.50
35:p:243:LEU:HD13	35:p:247:PRO:HG3	1.92	0.50
38:t:144:ILE:O	38:t:174:GLY:CA	2.59	0.50
43:z:154:LEU:HB3	43:z:159:LEU:HD12	1.93	0.50
1:1:185:C:H5''	22:Y:122:LYS:HG2	1.92	0.50
4:A:5:VAL:HG22	4:A:407:ILE:HG12	1.93	0.50
8:E:166:LYS:O	27:f:6:ARG:NH2	2.45	0.50
10:G:72:PRO:HG3	15:N:18:VAL:HA	1.94	0.50
35:p:177:ASP:O	35:p:181:ASN:HB2	2.11	0.50
1:1:687:U:H4'	23:7:67:GLU:OE2	2.12	0.50
4:A:71:LYS:N	4:A:109:GLU:O	2.37	0.50
5:B:47:LEU:HB3	5:B:335:ILE:HD11	1.93	0.50
10:G:100:GLU:CD	10:G:108:ARG:HH12	2.20	0.50
14:M:19:ARG:HA	14:M:69:THR:HG22	1.93	0.50
14:M:123:LEU:HD22	16:O:190:VAL:HG23	1.93	0.50
33:n:235:LYS:O	33:n:239:ASP:HB2	2.11	0.50
36:q:414:UNK:O	36:q:421:UNK:HA	2.11	0.50
1:1:439:C:H5	7:D:132:ARG:HB2	1.77	0.50
1:1:3185:U:O2'	19:S:170:THR:OG1	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:9:A:H2'	2:2:10:A:H8	1.76	0.50
3:6:3:U:O2	38:t:70:ARG:NH2	2.44	0.50
4:A:17:LEU:O	4:A:33:PHE:N	2.44	0.50
20:V:67:PRO:HA	20:V:70:ARG:HB2	1.94	0.50
23:7:184:TRP:HD1	23:7:205:LEU:HD12	1.76	0.50
35:p:174:ARG:HG3	35:p:178:HIS:HD2	1.76	0.50
42:y:177:LEU:HB3	42:y:179:VAL:HG22	1.93	0.50
1:1:160:G:N2	1:1:261:U:O2	2.33	0.50
2:2:107:G:H4'	2:2:138:A:H5'	1.92	0.50
8:E:66:SER:HB3	8:E:76:LEU:HD23	1.92	0.50
10:G:162:LEU:HD23	15:N:7:LEU:HD21	1.93	0.50
12:K:104:HIS:HB2	12:K:258:GLU:OE2	2.12	0.50
15:N:186:GLY:O	15:N:189:LYS:HB3	2.10	0.50
34:o:89:TYR:HA	34:o:168:PRO:HA	1.94	0.50
1:1:147:U:OP2	10:G:136:LEU:HB2	2.12	0.50
1:1:3066:U:H2'	1:1:3075:G:H22	1.77	0.50
6:C:102:PRO:HB2	6:C:104:LYS:HE2	1.94	0.50
19:S:12:ARG:HB3	19:S:24:LEU:HD23	1.92	0.50
21:W:460:GLU:OE2	39:u:99:ILE:HD13	2.12	0.50
33:n:193:LYS:NZ	33:n:239:ASP:OD2	2.33	0.50
35:p:190:LEU:HD21	35:p:217:LEU:HD22	1.92	0.50
43:z:227:ASP:O	43:z:235:ARG:NH1	2.45	0.50
1:1:1178:G:N3	1:1:1328:C:O2'	2.44	0.50
7:D:59:LYS:HD2	7:D:81:LYS:HE3	1.94	0.50
12:K:125:LEU:HB2	12:K:154:ILE:HG22	1.93	0.50
1:1:1334:U:O3'	9:F:151:ARG:NH1	2.41	0.50
2:2:95:G:OP1	30:j:76:ASN:ND2	2.39	0.50
22:Y:70:ILE:HA	22:Y:82:VAL:HA	1.92	0.50
40:v:181:THR:O	41:w:205:GLN:NE2	2.43	0.50
2:2:104:A:OP1	30:j:21:ARG:NH2	2.44	0.50
3:6:38:U:O2	3:6:41:G:C6	2.65	0.50
4:A:46:TYR:N	4:A:63:ASN:OD1	2.45	0.50
4:A:247:TRP:CD1	4:A:275:ARG:HB2	2.46	0.50
4:A:308:VAL:HG12	4:A:333:VAL:HG12	1.92	0.50
6:C:120:TYR:HD1	6:C:277:PRO:HG2	1.76	0.50
9:F:97:PRO:HB3	9:F:100:ARG:HH11	1.77	0.50
10:G:135:GLY:O	10:G:139:VAL:N	2.44	0.50
10:G:203:VAL:HG21	10:G:211:LEU:HD22	1.93	0.50
21:W:398:LEU:HB3	42:y:36:SER:HB2	1.94	0.50
25:b:113:TYR:HB3	25:b:222:THR:HB	1.93	0.50
35:p:119:VAL:HB	35:p:169:ILE:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:19:U:H2'	1:1:20:A:C8	2.46	0.49
5:B:58:ARG:HA	5:B:357:LYS:HG3	1.94	0.49
11:I:94:LYS:HB2	11:I:144:PHE:HA	1.94	0.49
12:K:36:ARG:NH1	12:K:291:LEU:O	2.40	0.49
15:N:183:THR:O	15:N:187:ARG:N	2.42	0.49
22:Y:55:GLU:HB3	22:Y:108:LYS:HB3	1.92	0.49
24:8:311:MET:O	24:8:319:GLN:NE2	2.45	0.49
1:1:693:A:OP1	6:C:45:ASN:ND2	2.45	0.49
2:2:94:C:H3'	30:j:72:ARG:NH1	2.25	0.49
4:A:194:ASP:OD1	4:A:322:ASN:ND2	2.44	0.49
4:A:340:LYS:HZ3	4:A:361:THR:HA	1.75	0.49
13:L:36:ARG:O	13:L:40:ALA:N	2.40	0.49
4:A:334:ILE:HA	4:A:343:PHE:O	2.13	0.49
6:C:261:VAL:O	6:C:271:LYS:NZ	2.44	0.49
9:F:86:VAL:O	9:F:114:GLY:HA2	2.13	0.49
12:K:97:LEU:HA	12:K:236:VAL:O	2.11	0.49
21:W:399:ALA:N	42:y:39:GLU:OE1	2.45	0.49
42:y:38:PHE:HE1	42:y:205:VAL:HG11	1.77	0.49
1:1:1425:U:O2'	6:C:36:HIS:NE2	2.40	0.49
2:2:130:C:H2'	2:2:131:A:H8	1.77	0.49
11:I:42:ARG:HA	41:w:220:LYS:HZ1	1.77	0.49
22:Y:86:THR:HA	22:Y:96:PRO:HA	1.94	0.49
33:n:124:SER:HB3	37:s:314:UNK:HA	1.95	0.49
38:t:235:VAL:HG21	38:t:247:VAL:HG22	1.94	0.49
1:1:129:U:H2'	1:1:130:A:C8	2.48	0.49
1:1:381:U:O4	11:I:30:ARG:NH2	2.45	0.49
3:6:37:C:P	12:K:277:ARG:HH12	2.34	0.49
8:E:13:GLU:OE2	26:e:89:THR:N	2.45	0.49
13:L:54:LEU:HA	23:7:59:LEU:HD22	1.93	0.49
1:1:338:A:H4'	6:C:197:ARG:NH1	2.27	0.49
1:1:761:A:OP2	1:1:770:G:N2	2.45	0.49
2:2:154:C:H2'	2:2:155:A:C8	2.48	0.49
5:B:296:THR:HB	5:B:299:ASP:H	1.76	0.49
10:G:100:GLU:OE2	10:G:108:ARG:NH1	2.45	0.49
11:I:64:ARG:HD2	11:I:293:PHE:HB2	1.94	0.49
12:K:280:PHE:HB3	12:K:288:VAL:HB	1.95	0.49
36:q:141:UNK:O	39:u:47:ARG:NE	2.45	0.49
40:v:106:THR:HG23	40:v:345:GLY:HA2	1.95	0.49
43:z:133:LEU:HD23	43:z:136:LEU:HD12	1.93	0.49
1:1:135:C:HO2'	28:h:95:PHE:H	1.61	0.49
1:1:1178:G:OP2	16:O:25:LYS:NZ	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:50:LYS:HA	5:B:79:VAL:HA	1.94	0.49
38:t:135:TYR:HE2	38:t:181:LYS:HG2	1.78	0.49
1:1:86:G:N2	1:1:87:U:O4	2.44	0.49
1:1:377:A:N6	1:1:400:G:O2'	2.46	0.49
1:1:594:U:O4	6:C:304:GLN:NE2	2.42	0.49
4:A:19:ASN:HB2	4:A:33:PHE:HE2	1.78	0.49
28:h:101:THR:HG23	28:h:104:GLN:H	1.77	0.49
29:i:70:ARG:NH1	29:i:84:LYS:HG2	2.26	0.49
33:n:430:GLN:HA	33:n:433:PHE:HD2	1.77	0.49
38:t:142:LEU:HD11	38:t:179:LEU:HD22	1.94	0.49
42:y:121:ILE:HG22	42:y:139:ARG:NH1	2.28	0.49
43:z:167:THR:HG23	43:z:234:LEU:HD12	1.93	0.49
1:1:27:C:O2'	1:1:327:A:N3	2.39	0.49
1:1:100:A:H3'	1:1:101:G:H21	1.78	0.49
1:1:722:G:N1	1:1:748:U:N3	2.49	0.49
1:1:3146:G:H2'	1:1:3147:G:C8	2.47	0.49
2:2:8:C:H2'	2:2:9:A:H8	1.78	0.49
4:A:135:LYS:HE3	11:I:140:ILE:HD13	1.95	0.49
16:O:108:ILE:HD12	16:O:160:ARG:NH1	2.28	0.49
1:1:608:A:C6	8:E:22:ARG:NH1	2.81	0.49
1:1:760:G:N2	1:1:770:G:O2'	2.46	0.49
1:1:1389:G:OP1	26:e:104:ASN:ND2	2.44	0.49
1:1:3028:G:H8	1:1:3028:G:OP2	1.96	0.49
4:A:206:ALA:HB2	4:A:216:LEU:HD23	1.95	0.49
4:A:332:ASN:HD22	4:A:346:ASP:HA	1.78	0.49
4:A:346:ASP:OD1	4:A:350:ARG:N	2.46	0.49
15:N:36:ILE:HG12	15:N:64:VAL:HG23	1.95	0.49
16:O:46:GLU:O	16:O:50:ASN:ND2	2.46	0.49
24:8:333:LEU:HD22	24:8:338:ILE:HD12	1.95	0.49
25:b:32:ARG:HB2	25:b:83:CYS:HA	1.93	0.49
25:b:93:LYS:HD3	25:b:249:ARG:HH12	1.77	0.49
33:n:446:LYS:HD3	33:n:454:PRO:HD3	1.94	0.49
38:t:209:GLN:HG3	38:t:210:LYS:HG3	1.95	0.49
1:1:268:A:H61	1:1:295:A:H3'	1.77	0.48
1:1:477:A:H1'	1:1:480:C:H41	1.78	0.48
1:1:671:U:H2'	1:1:672:A:H8	1.78	0.48
1:1:3344:A:N6	1:1:3361:G:O2'	2.45	0.48
2:2:143:U:OP1	15:N:38:ARG:NH2	2.45	0.48
12:K:37:VAL:HG12	12:K:260:VAL:HG22	1.95	0.48
12:K:93:LYS:HG3	12:K:240:ARG:NH1	2.28	0.48
42:y:66:ASN:ND2	42:y:133:LEU:O	2.41	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:343:U:H1'	6:C:95:ARG:HG3	1.95	0.48
1:1:600:G:H5'	1:1:601:U:OP2	2.13	0.48
1:1:3149:G:O2'	5:B:129:ALA:O	2.28	0.48
1:1:3213:A:N6	14:M:124:ARG:HH12	2.01	0.48
2:2:81:U:O4	22:Y:52:ARG:NH2	2.46	0.48
7:D:65:LYS:HG3	7:D:76:LEU:HD11	1.95	0.48
12:K:67:LEU:HD11	35:p:269:VAL:HG21	1.96	0.48
12:K:100:LEU:O	12:K:233:GLN:HA	2.13	0.48
25:b:192:GLU:HB2	25:b:215:ILE:HD13	1.94	0.48
33:n:430:GLN:HG3	33:n:434:ASP:OD2	2.13	0.48
35:p:366:PRO:HB3	35:p:463:TYR:CZ	2.48	0.48
43:z:92:ASP:OD1	43:z:145:LEU:HD13	2.13	0.48
4:A:53:ILE:HB	4:A:57:GLU:HG3	1.95	0.48
4:A:123:LEU:HD23	4:A:136:LEU:HG	1.96	0.48
6:C:193:LYS:HG3	6:C:198:ARG:HG3	1.94	0.48
10:G:155:ASN:HD21	10:G:181:LYS:HG3	1.78	0.48
19:S:10:ILE:HB	19:S:59:VAL:HB	1.94	0.48
33:n:177:ARG:HG3	33:n:356:VAL:HG21	1.95	0.48
35:p:484:LYS:HB2	37:s:255:PRO:HG2	1.94	0.48
1:1:477:A:H5''	1:1:478:A:H5'	1.94	0.48
4:A:377:GLN:HB3	4:A:385:ARG:HB2	1.96	0.48
25:b:269:GLU:HA	25:b:272:ILE:HD12	1.95	0.48
38:t:180:THR:H	38:t:183:VAL:HB	1.78	0.48
38:t:239:LEU:HB3	38:t:244:ILE:HB	1.95	0.48
1:1:677:A:N6	1:1:786:A:O4'	2.46	0.48
2:2:8:C:H2'	2:2:9:A:C8	2.48	0.48
3:6:230:A:H2'	38:t:148:ARG:HH12	1.79	0.48
39:u:45:ASN:HB3	39:u:48:LYS:HG2	1.96	0.48
1:1:215:G:OP1	22:Y:12:ARG:NH1	2.46	0.48
1:1:353:G:O2'	1:1:364:G:O6	2.24	0.48
1:1:1448:U:H2'	1:1:1449:A:H8	1.78	0.48
1:1:2354:C:OP1	17:P:86:LYS:NZ	2.43	0.48
6:C:35:VAL:HG11	6:C:244:LEU:HD21	1.96	0.48
7:D:56:ASP:OD1	7:D:57:ASN:N	2.46	0.48
34:o:157:LEU:HB3	34:o:162:LEU:HD13	1.96	0.48
39:u:55:PHE:O	39:u:59:ALA:HB2	2.12	0.48
10:G:153:ILE:O	10:G:180:VAL:N	2.46	0.48
11:I:234:ASN:HD21	11:I:295:LEU:HD22	1.79	0.48
1:1:440:A:OP2	1:1:441:U:H5	1.97	0.48
1:1:1336:U:H2'	1:1:1337:A:H8	1.79	0.48
3:6:22:G:N2	12:K:184:ASP:O	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:81:ILE:N	12:K:246:VAL:O	2.41	0.48
21:W:378:ILE:HG12	42:y:202:TYR:HB3	1.94	0.48
1:1:326:U:H2'	1:1:327:A:H8	1.79	0.48
6:C:45:ASN:HA	6:C:110:ASN:HD22	1.79	0.48
42:y:18:LYS:HZ3	42:y:64:ALA:HA	1.76	0.48
1:1:1183:C:H2'	1:1:1184:A:H8	1.78	0.48
1:1:3052:G:H2'	1:1:3053:G:C8	2.49	0.48
1:1:3093:C:OP2	20:V:48:ARG:NH1	2.47	0.48
2:2:27:U:H4'	6:C:51:ALA:HB3	1.96	0.48
2:2:154:C:H5''	10:G:181:LYS:HD3	1.96	0.48
3:6:42:G:H2'	3:6:43:A:C8	2.49	0.48
4:A:337:ASP:OD2	4:A:339:LYS:HB2	2.14	0.48
9:F:235:PHE:HE2	19:S:33:ASN:HD22	1.60	0.48
18:Q:125:ASP:OD1	18:Q:126:GLN:N	2.47	0.48
25:b:289:LEU:HD11	43:z:47:LYS:HD3	1.95	0.48
33:n:237:TYR:HD2	33:n:244:TYR:HA	1.79	0.48
40:v:52:GLN:HE21	40:v:55:THR:HG23	1.78	0.48
2:2:42:G:H1	2:2:102:U:H3	1.62	0.47
2:2:55:U:HO2'	23:7:13:SER:HG	1.58	0.47
7:D:97:LEU:O	7:D:105:ARG:NH2	2.47	0.47
26:e:67:SER:HG	26:e:69:SER:HG	1.60	0.47
1:1:298:U:OP2	29:i:33:ALA:N	2.47	0.47
8:E:111:LEU:HG	8:E:115:GLU:HG2	1.95	0.47
10:G:172:LYS:NZ	37:s:247:PHE:O	2.26	0.47
19:S:12:ARG:NH2	19:S:57:GLU:OE2	2.46	0.47
21:W:441:VAL:HG22	39:u:93:MET:HE1	1.96	0.47
34:o:104:GLU:HA	34:o:107:LEU:HD12	1.96	0.47
1:1:1327:C:H2'	1:1:1328:C:H6	1.79	0.47
1:1:1349:G:H2'	9:F:15:LYS:HB2	1.96	0.47
1:1:3210:A:H5''	14:M:109:ARG:HH12	1.80	0.47
3:6:35:C:O2'	12:K:84:ASN:OD1	2.28	0.47
6:C:7:THR:HG23	43:z:13:ASN:HD22	1.79	0.47
9:F:178:ILE:HG23	9:F:183:ASP:HB2	1.97	0.47
11:I:191:THR:N	11:I:228:GLN:HE22	2.11	0.47
15:N:114:ARG:HD3	15:N:137:PRO:HG3	1.96	0.47
19:S:11:GLY:O	19:S:25:PHE:N	2.44	0.47
25:b:41:VAL:HG13	25:b:46:ARG:HB2	1.96	0.47
25:b:113:TYR:HB2	25:b:224:ILE:HD11	1.96	0.47
40:v:167:SER:O	40:v:171:ASN:ND2	2.47	0.47
1:1:105:C:H2'	1:1:106:A:H8	1.79	0.47
1:1:306:A:H2'	1:1:308:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:612:U:H2'	1:1:613:G:H8	1.80	0.47
5:B:140:ASP:OD1	5:B:141:GLY:N	2.48	0.47
15:N:114:ARG:NH1	15:N:151:ILE:O	2.47	0.47
24:8:343:ASP:OD2	24:8:346:LEU:HD12	2.15	0.47
43:z:40:ILE:HA	43:z:43:ASN:HD22	1.80	0.47
1:1:1312:C:O2'	16:O:83:ALA:O	2.33	0.47
1:1:3150:A:HO2'	1:1:3294:A:HO2'	1.61	0.47
1:1:3315:G:H3'	5:B:123:TYR:HB2	1.97	0.47
2:2:154:C:H2'	2:2:155:A:H8	1.79	0.47
11:I:170:THR:HB	11:I:271:GLN:HB2	1.97	0.47
12:K:295:GLN:HG2	34:o:197:LYS:HG2	1.96	0.47
35:p:119:VAL:HG13	35:p:194:ILE:HD11	1.96	0.47
40:v:100:ARG:HG2	40:v:102:PRO:HD2	1.95	0.47
1:1:615:U:H2'	1:1:616:G:H8	1.78	0.47
1:1:3182:G:O3'	16:O:161:LYS:NZ	2.45	0.47
1:1:3314:A:H2'	1:1:3315:G:C8	2.50	0.47
7:D:71:HIS:HD2	7:D:72:THR:HG23	1.80	0.47
7:D:175:TYR:HB3	7:D:179:PRO:HB3	1.95	0.47
11:I:204:THR:OG1	11:I:295:LEU:O	2.32	0.47
16:O:130:LYS:NZ	16:O:133:ARG:HH21	2.13	0.47
23:7:76:ARG:HH11	25:b:278:VAL:HG13	1.80	0.47
40:v:29:ARG:HE	40:v:35:LEU:HD23	1.79	0.47
1:1:21:G:P	2:2:36:G:H1	2.33	0.47
1:1:263:C:H5	35:p:156:GLN:HE21	1.62	0.47
1:1:303:G:H2'	1:1:304:G:C8	2.49	0.47
1:1:454:C:OP2	1:1:455:C:OP2	2.33	0.47
1:1:546:C:H5''	1:1:547:G:C5	2.48	0.47
1:1:565:U:H2'	1:1:566:G:H8	1.78	0.47
1:1:584:G:H2'	1:1:585:A:H8	1.80	0.47
1:1:1195:A:H1'	1:1:1319:G:H4'	1.96	0.47
1:1:2999:U:H2'	1:1:3000:A:C8	2.49	0.47
2:2:9:A:H2'	2:2:10:A:C8	2.50	0.47
3:6:1:C:N3	38:t:59:GLU:HG2	2.30	0.47
3:6:9:A:H2'	3:6:10:A:H8	1.80	0.47
5:B:147:GLU:CD	5:B:150:ARG:HH11	2.23	0.47
8:E:96:VAL:HG11	8:E:141:VAL:HG13	1.96	0.47
23:7:196:TYR:HA	23:7:199:MET:HG2	1.95	0.47
35:p:174:ARG:HG3	35:p:178:HIS:CD2	2.50	0.47
42:y:70:LEU:N	42:y:93:LYS:O	2.44	0.47
1:1:1448:U:H2'	1:1:1449:A:C8	2.50	0.47
4:A:149:ASP:OD1	4:A:150:SER:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:180:LEU:HB2	11:I:224:ILE:HG22	1.96	0.47
10:G:145:ASN:H	10:G:146:LYS:HA	1.80	0.47
11:I:204:THR:O	11:I:208:GLN:N	2.41	0.47
25:b:50:GLN:HA	25:b:61:LYS:HZ1	1.80	0.47
25:b:78:ALA:O	25:b:82:ASN:N	2.48	0.47
1:1:5:G:H2'	1:1:6:A:C8	2.50	0.47
1:1:1389:G:O6	6:C:186:LYS:NZ	2.41	0.47
1:1:3007:U:H2'	1:1:3008:A:H8	1.80	0.47
1:1:3052:G:H2'	1:1:3053:G:H8	1.78	0.47
3:6:24:A:H5'	3:6:217:G:H22	1.80	0.47
5:B:183:LEU:O	5:B:191:LYS:NZ	2.34	0.47
7:D:51:ALA:HA	7:D:63:TYR:O	2.14	0.47
12:K:230:TYR:HD2	12:K:231:MET:HB3	1.79	0.47
18:Q:64:VAL:HA	18:Q:67:ILE:HD12	1.97	0.47
25:b:39:ARG:HA	25:b:64:LYS:HD2	1.97	0.47
28:h:38:ARG:HG2	28:h:41:LEU:HB2	1.97	0.47
29:i:74:LYS:HD2	29:i:80:PHE:HD1	1.79	0.47
4:A:70:VAL:HA	4:A:110:ILE:HA	1.97	0.47
21:W:427:TRP:HA	21:W:430:ASP:OD2	2.15	0.47
33:n:429:PRO:HG3	37:s:374:LEU:HD22	1.96	0.47
35:p:149:ILE:O	35:p:174:ARG:NH1	2.48	0.47
38:t:135:TYR:HE1	38:t:179:LEU:HD21	1.80	0.47
38:t:253:GLU:HA	38:t:256:THR:HB	1.96	0.47
1:1:611:A:O4'	8:E:23:LYS:NZ	2.48	0.46
1:1:3170:A:OP2	1:1:3174:A:N6	2.48	0.46
3:6:219:A:H8	3:6:219:A:OP2	1.98	0.46
5:B:108:GLU:HB2	5:B:137:TYR:CD2	2.50	0.46
5:B:188:ILE:HA	5:B:191:LYS:HD2	1.97	0.46
20:V:112:SER:O	20:V:132:ASN:ND2	2.45	0.46
42:y:119:PRO:HG2	42:y:141:THR:HG23	1.96	0.46
1:1:392:G:H5'	11:I:59:THR:HA	1.96	0.46
1:1:530:G:H8	1:1:530:G:OP2	1.98	0.46
1:1:3016:A:HO2'	1:1:3017:A:H8	1.63	0.46
24:8:332:MET:HE1	40:v:163:LYS:HE2	1.98	0.46
40:v:111:VAL:HA	40:v:337:LEU:HD23	1.97	0.46
1:1:156:G:H5'	29:i:25:LYS:HD3	1.96	0.46
1:1:182:U:O2	1:1:234:G:N2	2.38	0.46
4:A:231:GLU:HB3	4:A:288:ARG:NH1	2.30	0.46
5:B:58:ARG:NE	5:B:74:GLU:OE1	2.48	0.46
7:D:106:HIS:HD2	7:D:107:LYS:NZ	2.14	0.46
9:F:224:ILE:HG23	19:S:36:ILE:HG23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:146:ASP:HA	11:I:163:ILE:O	2.15	0.46
13:L:89:TYR:O	13:L:92:THR:OG1	2.29	0.46
38:t:157:ASN:HA	38:t:160:PHE:HB3	1.96	0.46
1:1:26:A:N3	1:1:328:U:O2'	2.44	0.46
1:1:608:A:C5	8:E:22:ARG:HD3	2.51	0.46
3:6:219:A:H5'	38:t:87:LYS:NZ	2.30	0.46
7:D:34:VAL:O	7:D:111:ARG:NH1	2.49	0.46
24:8:327:LYS:NZ	40:v:352:LEU:O	2.33	0.46
30:j:28:HIS:N	30:j:33:THR:O	2.47	0.46
1:1:129:U:O4	1:1:139:G:O6	2.34	0.46
1:1:541:U:H2'	1:1:542:G:C8	2.50	0.46
1:1:623:U:OP2	27:f:60:ARG:NH1	2.49	0.46
3:6:47:A:O2'	12:K:284:ASN:ND2	2.47	0.46
4:A:75:HIS:HB2	4:A:107:GLU:OE2	2.15	0.46
14:M:36:VAL:HG21	14:M:55:ARG:NH1	2.31	0.46
17:P:15:ALA:HA	17:P:105:LYS:NZ	2.30	0.46
40:v:24:LYS:HA	40:v:55:THR:HG22	1.96	0.46
1:1:330:G:H2'	1:1:331:G:H8	1.80	0.46
1:1:411:U:H2'	1:1:412:G:C8	2.50	0.46
1:1:746:A:H2'	1:1:747:A:C8	2.51	0.46
1:1:1191:U:OP2	16:O:49:ARG:HD2	2.16	0.46
1:1:1354:G:N7	7:D:26:ASN:ND2	2.46	0.46
1:1:3313:U:H5'	1:1:3314:A:OP2	2.16	0.46
16:O:38:ALA:H	16:O:106:GLU:HA	1.80	0.46
26:e:79:VAL:HG13	26:e:111:ARG:HG2	1.97	0.46
40:v:29:ARG:HB2	40:v:34:SER:HB2	1.96	0.46
1:1:74:G:O5'	13:L:104:ARG:NH2	2.49	0.46
1:1:334:A:OP1	23:7:18:THR:OG1	2.29	0.46
1:1:417:A:H2'	1:1:418:A:C8	2.50	0.46
1:1:535:G:N2	1:1:536:U:O4	2.46	0.46
1:1:1318:A:OP1	16:O:18:ARG:NH2	2.43	0.46
1:1:3133:C:H2'	1:1:3134:A:H8	1.80	0.46
4:A:168:LYS:HZ3	4:A:178:LEU:HD21	1.79	0.46
13:L:23:LYS:N	15:N:197:LEU:O	2.45	0.46
16:O:148:LYS:H	16:O:148:LYS:HD2	1.80	0.46
25:b:56:LEU:O	25:b:59:SER:OG	2.29	0.46
43:z:228:TYR:C	43:z:235:ARG:HH12	2.24	0.46
1:1:340:C:OP2	6:C:195:ARG:NH2	2.45	0.46
1:1:664:U:H2'	1:1:665:A:C8	2.51	0.46
2:2:97:A:OP1	28:h:67:ARG:NH2	2.49	0.46
5:B:77:THR:HG21	5:B:328:ILE:HG22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:54:TYR:HA	8:E:65:ILE:HG22	1.97	0.46
10:G:81:THR:OG1	10:G:179:ILE:O	2.30	0.46
10:G:136:LEU:HA	10:G:197:VAL:HG21	1.98	0.46
11:I:127:LYS:HB2	11:I:130:TYR:HE2	1.81	0.46
35:p:99:PRO:HA	35:p:102:GLU:HB2	1.97	0.46
35:p:400:GLY:O	35:p:403:ARG:HG2	2.16	0.46
1:1:123:A:OP1	10:G:105:LYS:NZ	2.47	0.46
1:1:163:C:H2'	1:1:164:A:C8	2.51	0.46
1:1:589:A:O2'	1:1:1338:C:OP1	2.34	0.46
5:B:71:GLU:OE2	5:B:357:LYS:NZ	2.49	0.46
5:B:137:TYR:HE1	5:B:144:ILE:HG21	1.81	0.46
6:C:138:ARG:HE	6:C:243:HIS:HB2	1.80	0.46
19:S:11:GLY:N	19:S:41:TYR:OH	2.49	0.46
28:h:93:THR:H	28:h:96:GLU:HB2	1.81	0.46
40:v:164:VAL:HG12	40:v:168:MET:HE3	1.97	0.46
1:1:515:C:O2'	6:C:342:LYS:O	2.31	0.46
1:1:745:C:H2'	1:1:746:A:H8	1.79	0.46
1:1:1410:U:H4'	26:e:75:LEU:HD11	1.97	0.46
7:D:17:HIS:HB3	7:D:29:ARG:H	1.81	0.46
10:G:213:LYS:HZ3	34:o:160:HIS:HB3	1.81	0.46
36:q:130:UNK:O	36:q:139:UNK:N	2.48	0.46
39:u:37:HIS:CD2	39:u:41:LYS:HE3	2.50	0.46
39:u:73:GLN:HE21	39:u:75:ARG:HH11	1.64	0.46
1:1:441:U:H5''	1:1:442:G:H5'	1.97	0.45
1:1:504:A:H2'	1:1:505:G:H8	1.81	0.45
1:1:671:U:O3'	18:Q:16:ARG:NH2	2.49	0.45
1:1:3313:U:H3'	1:1:3314:A:H8	1.82	0.45
22:Y:54:ASP:HB3	22:Y:110:HIS:H	1.82	0.45
42:y:42:LEU:HD13	42:y:46:ILE:HD11	1.98	0.45
1:1:69:C:OP1	15:N:178:HIS:N	2.48	0.45
1:1:165:A:H5'	1:1:166:C:OP2	2.15	0.45
1:1:437:G:N7	11:I:155:LYS:NZ	2.54	0.45
9:F:99:PRO:HB3	9:F:130:ILE:HG22	1.98	0.45
11:I:289:GLU:OE2	11:I:292:LYS:HE2	2.16	0.45
13:L:34:SER:O	13:L:37:ASN:HB2	2.17	0.45
21:W:442:TYR:CB	39:u:2:ARG:HH12	2.29	0.45
33:n:132:ILE:HD12	33:n:232:VAL:HG11	1.97	0.45
35:p:300:ASN:HD22	35:p:449:SER:HB3	1.81	0.45
39:u:6:CYS:N	39:u:11:SER:O	2.46	0.45
42:y:126:GLU:OE1	42:y:139:ARG:NH2	2.48	0.45
42:y:150:SER:HB3	42:y:192:VAL:HG13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1:G:O5'	3:6:232:A:O2'	2.26	0.45
1:1:551:A:OP2	1:1:551:A:H2'	2.16	0.45
1:1:1404:G:OP1	26:e:65:PHE:N	2.49	0.45
1:1:1412:G:OP1	26:e:105:ARG:NH2	2.46	0.45
1:1:1436:U:O2	24:8:383:ARG:NH1	2.49	0.45
1:1:3322:A:O2'	40:v:131:ASN:OD1	2.24	0.45
3:6:227:C:H41	38:t:153:VAL:HB	1.82	0.45
4:A:230:TRP:HZ2	4:A:288:ARG:HA	1.82	0.45
11:I:101:VAL:HG23	11:I:126:ARG:HE	1.80	0.45
12:K:99:LEU:HB3	12:K:233:GLN:HB3	1.98	0.45
14:M:98:SER:HA	14:M:101:LYS:HD2	1.97	0.45
23:7:5:ARG:HH12	30:j:67:LEU:CD1	2.29	0.45
39:u:49:LEU:HD23	39:u:51:TRP:HE1	1.80	0.45
1:1:87:U:H2'	1:1:88:A:H8	1.82	0.45
1:1:239:G:H5''	28:h:94:LYS:NZ	2.32	0.45
1:1:305:U:H5	25:b:92:ARG:HH12	1.64	0.45
1:1:794:U:H2'	1:1:795:G:H8	1.81	0.45
1:1:1361:U:H2'	1:1:1362:G:C8	2.52	0.45
1:1:3183:A:N1	1:1:3188:G:O2'	2.48	0.45
8:E:68:PRO:HG3	8:E:145:LEU:HD23	1.98	0.45
10:G:220:ALA:HA	10:G:224:ASP:OD2	2.17	0.45
14:M:85:TRP:NE1	14:M:91:CYS:SG	2.87	0.45
33:n:431:TRP:HB2	33:n:447:TYR:CG	2.51	0.45
1:1:250:U:O4	23:7:176:SER:N	2.50	0.45
1:1:255:A:H2'	1:1:256:G:H8	1.81	0.45
1:1:3150:A:O2'	1:1:3294:A:O2'	2.30	0.45
11:I:74:VAL:HG11	11:I:212:ARG:NH1	2.31	0.45
12:K:64:LYS:HA	35:p:413:ASN:HD21	1.80	0.45
13:L:25:HIS:HE2	15:N:198:SER:HG	1.64	0.45
15:N:13:LYS:HE3	29:i:45:ARG:HH11	1.81	0.45
33:n:169:TYR:HB2	33:n:237:TYR:HE1	1.81	0.45
33:n:217:ILE:O	33:n:220:THR:OG1	2.31	0.45
38:t:231:ASP:OD2	38:t:234:ILE:HG13	2.16	0.45
1:1:417:A:H2'	1:1:418:A:H8	1.82	0.45
1:1:608:A:H5'	6:C:322:GLN:HB2	1.98	0.45
11:I:244:HIS:HB3	11:I:256:LEU:HD22	1.99	0.45
13:L:46:ILE:HD12	13:L:49:ARG:NH1	2.31	0.45
20:V:87:ARG:HH11	20:V:120:LYS:HE2	1.80	0.45
23:7:222:TRP:HD1	23:7:225:ARG:HH11	1.65	0.45
40:v:48:ARG:HH12	40:v:60:LYS:HB3	1.82	0.45
1:1:86:G:O2'	1:1:98:G:O6	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:269:G:N2	1:1:270:U:O4	2.38	0.45
1:1:384:A:C5'	11:I:35:ARG:HH12	2.30	0.45
1:1:485:A:H5''	7:D:127:LEU:HD11	1.98	0.45
1:1:671:U:H2'	1:1:672:A:C8	2.51	0.45
1:1:3379:C:H4'	5:B:315:GLY:HA2	1.99	0.45
4:A:49:ARG:NH2	4:A:141:VAL:O	2.50	0.45
8:E:14:ASP:OD1	8:E:14:ASP:N	2.50	0.45
9:F:10:GLU:HG2	43:z:172:HIS:CE1	2.48	0.45
11:I:60:ILE:HG12	11:I:291:LYS:HZ3	1.80	0.45
20:V:36:ILE:HA	20:V:60:ALA:HA	1.99	0.45
35:p:110:LYS:HZ2	35:p:112:ARG:NH1	2.15	0.45
41:w:212:VAL:HG21	41:w:230:THR:HG22	1.99	0.45
1:1:304:G:N7	25:b:69:LYS:NZ	2.61	0.45
1:1:438:A:H8	11:I:102:ASN:HD21	1.65	0.45
1:1:3049:A:H5''	5:B:53:MET:HB2	1.99	0.45
3:6:52:G:H22	10:G:216:SER:HB2	1.81	0.45
4:A:206:ALA:HA	4:A:215:LYS:O	2.17	0.45
4:A:336:THR:HG22	4:A:342:VAL:HG22	1.98	0.45
7:D:53:VAL:HG11	7:D:112:PHE:HA	1.97	0.45
12:K:83:VAL:HB	12:K:244:LEU:HB3	1.98	0.45
12:K:143:GLN:O	12:K:146:SER:OG	2.32	0.45
12:K:158:LYS:HA	12:K:161:LYS:HG2	1.99	0.45
19:S:14:LEU:HG	19:S:56:GLY:HA2	1.98	0.45
19:S:23:LYS:HZ3	19:S:25:PHE:HZ	1.64	0.45
35:p:296:LEU:N	35:p:345:CYS:O	2.48	0.45
1:1:187:A:N1	1:1:211:A:O2'	2.39	0.45
1:1:489:C:H2'	1:1:490:A:C8	2.52	0.45
1:1:1316:C:OP2	16:O:130:LYS:HE2	2.17	0.45
1:1:1880:U:H2'	1:1:1881:A:H8	1.82	0.45
2:2:47:C:H1'	2:2:61:A:H2'	1.99	0.45
2:2:59:A:H3'	2:2:59:A:OP2	2.16	0.45
4:A:156:VAL:HB	4:A:164:LEU:HD11	1.99	0.45
5:B:116:ARG:HG2	5:B:175:LYS:HE2	1.99	0.45
7:D:110:GLN:HE22	8:E:14:ASP:HB3	1.81	0.45
20:V:54:LEU:HD21	20:V:119:GLY:HA3	1.99	0.45
20:V:80:ARG:HB2	20:V:99:ALA:HB3	1.98	0.45
33:n:141:LEU:HD11	37:s:384:ILE:HD13	1.98	0.45
33:n:193:LYS:HZ3	33:n:239:ASP:CG	2.19	0.45
1:1:354:U:H2'	1:1:355:A:H8	1.82	0.45
1:1:547:G:H2'	1:1:547:G:OP2	2.17	0.45
1:1:565:U:H2'	1:1:566:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:612:U:H2'	1:1:613:G:C8	2.52	0.45
1:1:3018:C:OP1	42:y:9:ASN:ND2	2.36	0.45
1:1:3039:C:P	5:B:62:ARG:HH11	2.36	0.45
1:1:3294:A:H5'	5:B:126:LYS:HD2	1.98	0.45
3:6:222:A:H4'	3:6:223:U:OP1	2.15	0.45
9:F:234:GLU:O	9:F:237:ASN:HB2	2.16	0.45
12:K:240:ARG:HD3	34:o:184:LEU:HD11	1.98	0.45
25:b:141:GLN:HG2	25:b:181:ILE:HD12	1.99	0.45
25:b:225:LEU:HD22	25:b:235:LYS:NZ	2.31	0.45
32:m:197:UNK:O	32:m:201:UNK:CB	2.64	0.45
1:1:15:C:H2'	1:1:16:A:C8	2.51	0.44
1:1:412:G:OP1	17:P:62:ARG:NH1	2.49	0.44
1:1:551:A:OP2	1:1:551:A:H8	2.00	0.44
1:1:3007:U:H2'	1:1:3008:A:C8	2.53	0.44
4:A:60:LEU:HB2	4:A:68:GLU:HB2	1.99	0.44
20:V:104:ASN:HD21	20:V:108:GLU:HB2	1.81	0.44
21:W:380:GLU:O	21:W:384:ASN:HB2	2.17	0.44
25:b:118:HIS:CD2	25:b:218:ARG:HD2	2.52	0.44
42:y:67:ARG:HG3	42:y:68:ARG:HG3	1.99	0.44
43:z:100:ARG:HH12	43:z:156:TRP:CG	2.34	0.44
1:1:65:A:H61	1:1:323:A:H62	1.65	0.44
1:1:655:C:OP2	26:e:27:ARG:NH1	2.43	0.44
1:1:3192:U:H2'	1:1:3193:C:C6	2.52	0.44
1:1:3308:C:H3'	1:1:3309:G:H21	1.82	0.44
4:A:217:VAL:HG22	4:A:228:GLN:HA	1.99	0.44
4:A:334:ILE:HG12	4:A:344:LYS:HG2	1.99	0.44
5:B:301:THR:HG22	21:W:437:ASP:H	1.82	0.44
11:I:41:GLU:OE2	11:I:51:ARG:HD3	2.18	0.44
19:S:8:GLN:HB3	19:S:62:ASN:HB2	1.98	0.44
29:i:70:ARG:HH12	29:i:84:LYS:HG2	1.82	0.44
34:o:111:PHE:HA	34:o:114:PHE:HD2	1.82	0.44
35:p:197:GLU:N	35:p:227:PHE:O	2.42	0.44
43:z:200:GLU:HB3	43:z:204:LYS:NZ	2.32	0.44
1:1:353:G:C6	30:j:52:LYS:HE2	2.52	0.44
1:1:3083:G:N2	1:1:3332:U:O3'	2.50	0.44
3:6:41:G:N2	3:6:42:G:N3	2.66	0.44
4:A:279:LEU:HD23	4:A:294:ILE:HD12	1.99	0.44
5:B:86:VAL:HG22	5:B:162:VAL:HG12	1.99	0.44
9:F:44:ILE:HD11	9:F:179:LEU:HG	1.99	0.44
9:F:156:ILE:C	9:F:158:LYS:H	2.25	0.44
12:K:81:ILE:HD11	12:K:263:VAL:HG22	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:b:236:ILE:HG13	32:m:197:UNK:HA	1.98	0.44
1:1:578:A:H2'	6:C:334:PHE:HD2	1.82	0.44
1:1:3090:U:OP1	5:B:270:ARG:NH2	2.50	0.44
5:B:21:ARG:HB3	5:B:272:TYR:HD2	1.82	0.44
6:C:235:LEU:HA	6:C:238:LEU:HB2	1.98	0.44
12:K:78:LEU:HA	12:K:250:ASN:HA	1.98	0.44
12:K:98:LYS:HB3	12:K:236:VAL:HB	1.99	0.44
33:n:178:LYS:HZ2	33:n:459:PRO:HB2	1.81	0.44
33:n:428:GLN:HE21	33:n:449:PRO:HB3	1.83	0.44
34:o:155:TYR:HE2	34:o:157:LEU:HD13	1.81	0.44
1:1:254:A:O3'	28:h:106:LYS:NZ	2.48	0.44
1:1:722:G:O6	1:1:748:U:O4	2.35	0.44
5:B:303:LYS:HZ2	5:B:371:GLN:HB3	1.82	0.44
7:D:90:LEU:HD23	7:D:93:ILE:HD12	1.99	0.44
9:F:82:LYS:HE2	9:F:191:VAL:HB	1.99	0.44
12:K:221:THR:O	12:K:225:ASN:CB	2.63	0.44
21:W:396:ARG:NH2	42:y:39:GLU:O	2.50	0.44
1:1:387:A:H8	1:1:387:A:OP2	2.01	0.44
12:K:298:LEU:HA	12:K:301:LEU:HD23	2.00	0.44
13:L:24:VAL:HG22	15:N:199:LEU:HB2	2.00	0.44
20:V:87:ARG:HH12	20:V:120:LYS:HB3	1.83	0.44
28:h:38:ARG:HD3	28:h:39:PRO:HD2	1.99	0.44
29:i:70:ARG:NH1	29:i:84:LYS:HA	2.32	0.44
29:i:94:ILE:HG23	29:i:98:ARG:HD3	1.99	0.44
1:1:551:A:O2'	1:1:552:G:O5'	2.32	0.44
1:1:745:C:H2'	1:1:746:A:C8	2.52	0.44
10:G:140:VAL:HG21	15:N:3:ALA:HB2	1.99	0.44
10:G:213:LYS:HD3	34:o:160:HIS:HA	2.00	0.44
10:G:231:LYS:HE2	37:s:245:ASP:OD2	2.18	0.44
11:I:193:HIS:CG	11:I:226:GLY:HA3	2.53	0.44
12:K:70:ASP:OD2	12:K:72:GLU:HB3	2.18	0.44
22:Y:34:PRO:HA	22:Y:47:ALA:HA	2.00	0.44
25:b:187:TRP:HB3	25:b:189:ARG:NH1	2.33	0.44
34:o:124:ARG:HD3	34:o:178:LYS:HA	1.99	0.44
35:p:293:ILE:HG12	35:p:343:LEU:HB3	1.99	0.44
1:1:64:G:O2'	1:1:77:A:N3	2.42	0.44
1:1:350:C:O3'	11:I:11:ASN:ND2	2.51	0.44
1:1:516:A:H2'	1:1:517:G:C8	2.53	0.44
1:1:536:U:H2'	1:1:537:A:H8	1.83	0.44
1:1:3309:G:OP2	1:1:3309:G:N2	2.49	0.44
4:A:9:ASP:OD2	4:A:382:ARG:NH1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:132:VAL:HG12	10:G:200:LEU:HD12	2.00	0.44
28:h:35:LYS:HA	28:h:38:ARG:HB3	2.00	0.44
28:h:43:LYS:O	28:h:46:THR:OG1	2.31	0.44
39:u:45:ASN:HD22	39:u:46:PRO:HD2	1.83	0.44
1:1:415:G:H2'	1:1:416:A:C8	2.53	0.44
1:1:673:U:H2'	1:1:674:G:C8	2.53	0.44
1:1:1391:C:C4	26:e:103:LYS:HD3	2.52	0.44
9:F:10:GLU:HG3	9:F:14:LYS:HE3	2.00	0.44
11:I:268:LYS:HG2	11:I:269:ARG:HG3	2.00	0.44
17:P:45:GLN:HE21	17:P:95:LEU:HB3	1.82	0.44
21:W:389:ASP:OD2	21:W:392:ASP:HB2	2.17	0.44
25:b:45:HIS:CE1	25:b:97:LEU:HD13	2.53	0.44
36:q:308:UNK:O	36:q:319:UNK:HA	2.17	0.44
40:v:26:MET:HB2	40:v:82:LEU:HA	1.99	0.44
1:1:1390:A:N6	1:1:1418:A:O2'	2.51	0.43
1:1:1886:A:N6	40:v:103:GLN:OE1	2.51	0.43
1:1:3121:U:H1'	1:1:3122:A:H5''	2.00	0.43
7:D:56:ASP:HB3	7:D:61:TYR:HE2	1.82	0.43
10:G:101:THR:HG21	33:n:98:GLU:OE2	2.18	0.43
18:Q:89:ASP:OD1	18:Q:90:ASP:N	2.51	0.43
25:b:36:ILE:HD13	25:b:74:LEU:HD22	1.99	0.43
35:p:92:LYS:NZ	35:p:197:GLU:OE2	2.51	0.43
35:p:302:VAL:HG13	35:p:344:ILE:HG22	1.99	0.43
38:t:155:ILE:H	38:t:155:ILE:HG13	1.55	0.43
39:u:66:ASP:CG	39:u:103:ARG:HH11	2.23	0.43
43:z:176:ILE:HG22	43:z:180:GLU:HG2	1.99	0.43
1:1:622:A:H5''	27:f:60:ARG:HH12	1.81	0.43
1:1:3148:U:H2'	1:1:3149:G:C8	2.51	0.43
3:6:49:C:H5'	12:K:71:GLU:OE2	2.18	0.43
9:F:10:GLU:HA	9:F:13:LEU:HD12	2.00	0.43
10:G:227:ASP:OD1	10:G:227:ASP:N	2.51	0.43
11:I:189:ARG:H	11:I:245:ARG:NH1	2.16	0.43
13:L:75:PHE:O	13:L:101:ARG:NH1	2.51	0.43
15:N:124:ASP:N	15:N:127:TYR:O	2.41	0.43
25:b:74:LEU:HD23	25:b:77:ILE:HD12	2.00	0.43
33:n:182:SER:OG	33:n:185:GLY:O	2.35	0.43
38:t:140:ALA:HB3	38:t:179:LEU:HD23	1.99	0.43
40:v:97:LYS:HG2	40:v:108:THR:HG22	1.99	0.43
1:1:350:C:O2'	1:1:352:A:OP1	2.35	0.43
1:1:476:G:H2'	1:1:477:A:C8	2.53	0.43
1:1:1354:G:H4'	7:D:40:ARG:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1448:U:O2	1:1:2356:A:N7	2.51	0.43
1:1:3035:A:H5'	1:1:3036:G:OP2	2.18	0.43
7:D:53:VAL:HG12	7:D:115:LEU:HD12	2.00	0.43
12:K:73:GLU:HG3	12:K:76:LYS:HE2	2.01	0.43
15:N:107:GLY:HA3	15:N:160:GLU:OE2	2.19	0.43
39:u:53:LYS:CE	39:u:57:LYS:HZ3	2.30	0.43
40:v:50:ILE:HD11	40:v:333:PRO:HD2	2.00	0.43
40:v:211:ARG:HH21	40:v:327:LYS:HE2	1.83	0.43
1:1:147:U:C4	10:G:157:VAL:HG13	2.54	0.43
1:1:354:U:H2'	1:1:355:A:C8	2.54	0.43
1:1:753:C:H2'	1:1:754:G:C8	2.54	0.43
1:1:791:A:H2'	1:1:792:G:C8	2.54	0.43
1:1:3017:A:H2'	1:1:3018:C:C6	2.54	0.43
1:1:3043:C:H2'	1:1:3044:G:H8	1.82	0.43
1:1:3234:A:H2	1:1:3253:G:H22	1.64	0.43
3:6:229:U:H2'	38:t:275:ARG:HH11	1.83	0.43
8:E:43:LEU:HD11	8:E:85:ILE:HG13	2.00	0.43
10:G:134:TYR:HB3	10:G:190:VAL:HG21	2.00	0.43
13:L:43:ALA:HB2	13:L:51:LEU:HD11	1.99	0.43
16:O:46:GLU:OE2	16:O:48:PHE:HB3	2.19	0.43
35:p:436:ASN:HB3	35:p:439:LEU:HB2	2.00	0.43
38:t:214:ILE:O	38:t:226:GLU:HA	2.18	0.43
40:v:84:MET:HE1	40:v:347:CYS:HB2	2.00	0.43
1:1:772:U:H2'	1:1:773:G:C8	2.54	0.43
1:1:1348:U:H1'	1:1:1350:A:H1'	2.01	0.43
1:1:1349:G:H3'	9:F:15:LYS:HD2	1.99	0.43
1:1:3060:C:H1'	1:1:3332:U:H1'	1.99	0.43
1:1:3151:U:OP2	5:B:132:LYS:NZ	2.45	0.43
5:B:89:VAL:HG23	5:B:105:VAL:HB	2.00	0.43
5:B:281:LYS:NZ	5:B:350:ALA:O	2.47	0.43
7:D:10:ILE:HG23	7:D:15:CYS:HB2	2.01	0.43
12:K:283:THR:HG22	12:K:285:ARG:H	1.84	0.43
16:O:16:VAL:HA	16:O:41:LEU:HD21	2.00	0.43
20:V:132:ASN:ND2	42:y:151:TYR:OH	2.49	0.43
33:n:209:ILE:HD11	33:n:215:PHE:HZ	1.82	0.43
38:t:66:LEU:O	38:t:69:SER:OG	2.27	0.43
42:y:118:HIS:CE1	42:y:120:ASP:HB2	2.53	0.43
1:1:517:G:H8	1:1:517:G:OP2	2.01	0.43
1:1:1381:A:H2'	1:1:1382:G:C8	2.53	0.43
1:1:1404:G:H5'	1:1:1405:U:OP2	2.18	0.43
1:1:3164:C:OP1	11:I:189:ARG:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:97:A:OP1	28:h:63:ARG:NH2	2.43	0.43
4:A:17:LEU:HD13	4:A:34:HIS:HB3	2.01	0.43
4:A:247:TRP:NE1	4:A:249:MET:SD	2.90	0.43
6:C:181:VAL:HG11	6:C:224:GLY:HA3	2.00	0.43
7:D:132:ARG:HH21	11:I:100:ASN:HD21	1.67	0.43
12:K:125:LEU:HG	12:K:181:LEU:HB2	1.99	0.43
19:S:75:PHE:O	19:S:93:GLU:HA	2.19	0.43
26:e:19:ARG:NH1	26:e:28:VAL:HG13	2.33	0.43
33:n:366:TYR:HD2	33:n:410:GLN:HG2	1.84	0.43
38:t:235:VAL:HG13	38:t:239:LEU:HD12	2.00	0.43
43:z:32:LYS:HE2	43:z:36:GLU:OE2	2.19	0.43
43:z:248:LEU:HB3	43:z:253:ILE:HB	2.01	0.43
1:1:1176:C:H2'	1:1:1177:G:C2	2.54	0.43
4:A:168:LYS:HZ3	4:A:168:LYS:HB3	1.82	0.43
20:V:45:ARG:HH12	20:V:46:LEU:HB3	1.81	0.43
21:W:390:PRO:O	21:W:395:ARG:NH1	2.50	0.43
23:7:177:GLN:HB3	23:7:181:GLU:OE2	2.19	0.43
1:1:584:G:H2'	1:1:585:A:C8	2.53	0.43
1:1:1166:G:H5''	27:f:73:ARG:NH1	2.33	0.43
1:1:3250:U:H2'	1:1:3251:U:H6	1.84	0.43
2:2:151:C:O2'	10:G:60:ARG:NE	2.52	0.43
4:A:340:LYS:NZ	4:A:360:ILE:O	2.32	0.43
8:E:125:GLN:HB3	8:E:128:LYS:HE3	2.01	0.43
25:b:45:HIS:HE1	25:b:97:LEU:HD13	1.83	0.43
33:n:460:TRP:CD1	37:s:331:UNK:HA	2.54	0.43
35:p:94:LEU:HA	35:p:97:LEU:HB2	2.01	0.43
35:p:195:ILE:O	35:p:226:LEU:HA	2.19	0.43
39:u:53:LYS:NZ	39:u:57:LYS:NZ	2.66	0.43
1:1:257:U:H2'	1:1:258:G:H8	1.84	0.43
1:1:273:A:H2'	1:1:274:G:C8	2.54	0.43
1:1:631:U:H2'	1:1:632:G:C8	2.54	0.43
1:1:3305:A:OP1	5:B:223:GLY:N	2.51	0.43
3:6:55:A:O2'	34:o:94:TYR:OH	2.32	0.43
5:B:288:GLY:N	5:B:320:ASP:OD1	2.46	0.43
6:C:20:LEU:HD11	6:C:252:GLU:HG3	2.01	0.43
10:G:74:THR:O	10:G:77:GLN:NE2	2.52	0.43
10:G:233:TRP:NE1	37:s:241:GLU:O	2.39	0.43
25:b:118:HIS:HB2	25:b:218:ARG:HB3	2.01	0.43
33:n:22:VAL:HG21	33:n:29:LEU:HA	2.01	0.43
33:n:415:PRO:HG3	37:s:375:ARG:HH12	1.83	0.43
33:n:449:PRO:HA	33:n:450:GLY:HA2	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:p:291:LYS:HD3	35:p:339:GLU:HA	2.01	0.43
40:v:46:ASP:HB3	40:v:333:PRO:HD3	2.01	0.43
40:v:326:ILE:HD12	41:w:195:VAL:HG22	2.00	0.43
1:1:493:G:O2'	1:1:494:G:O5'	2.34	0.43
1:1:627:U:H2'	1:1:628:A:C8	2.54	0.43
5:B:152:LYS:HG2	5:B:189:SER:HA	2.01	0.43
6:C:193:LYS:HA	6:C:198:ARG:HA	2.01	0.43
6:C:205:PRO:HG2	6:C:225:VAL:HG22	1.99	0.43
7:D:144:ARG:HH22	11:I:284:PRO:HB3	1.83	0.43
34:o:156:LEU:HA	34:o:161:LEU:HA	2.01	0.43
35:p:327:LYS:HA	35:p:330:ASN:HD22	1.84	0.43
40:v:343:GLU:HG2	40:v:351:VAL:HG22	2.01	0.43
1:1:660:A:N1	1:1:941:G:O2'	2.45	0.42
1:1:753:C:N4	1:1:754:G:O6	2.52	0.42
1:1:3208:G:O2'	19:S:161:LYS:NZ	2.52	0.42
7:D:104:PHE:O	7:D:108:CYS:CB	2.67	0.42
9:F:82:LYS:HA	9:F:119:VAL:HB	2.00	0.42
25:b:95:GLN:OE1	25:b:249:ARG:NH2	2.51	0.42
30:j:17:THR:N	30:j:27:PHE:O	2.52	0.42
35:p:474:ALA:O	35:p:479:PHE:N	2.40	0.42
40:v:48:ARG:HD3	40:v:58:LYS:HA	2.01	0.42
1:1:177:U:O2	1:1:241:G:C6	2.70	0.42
1:1:409:A:H61	2:2:15:G:H1'	1.84	0.42
1:1:452:G:H2'	1:1:453:C:H5"	2.01	0.42
1:1:526:C:H2'	1:1:527:A:H8	1.83	0.42
1:1:659:G:N1	1:1:1434:G:OP2	2.45	0.42
1:1:737:G:OP2	1:1:737:G:H8	2.02	0.42
1:1:3272:C:OP1	8:E:78:ARG:NH2	2.52	0.42
4:A:247:TRP:O	4:A:275:ARG:N	2.50	0.42
12:K:144:LEU:HB3	12:K:149:ILE:HG13	2.00	0.42
12:K:205:THR:HA	12:K:206:PRO:HD3	1.88	0.42
13:L:27:ASP:OD1	13:L:27:ASP:N	2.47	0.42
14:M:36:VAL:HG11	14:M:55:ARG:NH1	2.29	0.42
15:N:122:ASN:OD1	15:N:123:GLN:N	2.52	0.42
25:b:141:GLN:HE21	25:b:181:ILE:HB	1.84	0.42
33:n:187:TYR:CZ	33:n:200:LEU:HD13	2.54	0.42
35:p:110:LYS:HZ3	35:p:112:ARG:NH1	2.16	0.42
40:v:53:PRO:HG3	40:v:136:LEU:HD22	2.01	0.42
1:1:364:G:OP2	30:j:52:LYS:HE3	2.19	0.42
1:1:3047:U:H4'	5:B:53:MET:HE1	2.01	0.42
1:1:3245:A:H5'	1:1:3246:G:H5"	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6:9:A:H2'	3:6:10:A:C8	2.53	0.42
6:C:268:ALA:HA	23:7:76:ARG:HE	1.83	0.42
6:C:329:PRO:HB3	9:F:41:ARG:NH1	2.34	0.42
12:K:190:LEU:HD13	12:K:206:PRO:HG2	2.01	0.42
12:K:211:THR:HG22	12:K:222:LEU:HD13	2.00	0.42
19:S:141:LYS:HA	19:S:144:LEU:HD12	2.00	0.42
23:7:199:MET:HE1	23:7:219:LEU:HD11	2.01	0.42
1:1:385:A:O5'	11:I:31:HIS:ND1	2.52	0.42
1:1:580:C:OP1	6:C:321:LYS:NZ	2.52	0.42
1:1:1185:C:H2'	1:1:1186:G:C8	2.55	0.42
1:1:3034:C:H5''	1:1:3035:A:OP2	2.18	0.42
4:A:2:ARG:HA	4:A:16:VAL:O	2.19	0.42
5:B:308:MET:N	5:B:361:THR:O	2.49	0.42
6:C:329:PRO:HB3	9:F:41:ARG:HH11	1.83	0.42
9:F:190:THR:OG1	9:F:190:THR:O	2.36	0.42
11:I:81:LEU:HD13	11:I:212:ARG:HD3	2.01	0.42
11:I:139:CYS:HB3	11:I:144:PHE:HB2	2.02	0.42
12:K:301:LEU:HD12	12:K:302:GLU:HB2	2.01	0.42
40:v:52:GLN:HG3	40:v:55:THR:H	1.83	0.42
40:v:112:LEU:HB3	40:v:336:THR:HB	2.02	0.42
1:1:116:A:N1	1:1:264:G:H4'	2.34	0.42
1:1:326:U:H2'	1:1:327:A:C8	2.55	0.42
1:1:379:C:O3'	11:I:55:ASN:ND2	2.52	0.42
1:1:383:G:H2'	11:I:31:HIS:CE1	2.53	0.42
1:1:3017:A:H2'	1:1:3018:C:H6	1.84	0.42
4:A:367:ILE:HA	4:A:376:LEU:O	2.19	0.42
4:A:380:LEU:HD13	11:I:279:GLU:HG2	2.01	0.42
9:F:147:LEU:HD11	9:F:240:VAL:HG11	2.01	0.42
19:S:42:TRP:CE2	19:S:53:LYS:HG3	2.55	0.42
38:t:176:PHE:CE1	38:t:204:ILE:HG12	2.54	0.42
40:v:190:PHE:HD1	40:v:205:HIS:HB3	1.85	0.42
1:1:303:G:C6	25:b:69:LYS:NZ	2.88	0.42
1:1:435:C:H2'	1:1:436:A:C8	2.55	0.42
1:1:622:A:H5''	27:f:60:ARG:NH1	2.35	0.42
1:1:3213:A:H5''	14:M:128:ARG:NH1	2.33	0.42
2:2:157:U:OP1	10:G:84:ARG:NH2	2.52	0.42
5:B:382:THR:HG22	39:u:104:GLU:OE2	2.19	0.42
11:I:232:LEU:HA	11:I:240:PHE:O	2.19	0.42
23:7:195:ASP:OD2	23:7:198:LYS:HD2	2.19	0.42
29:i:36:ARG:HA	37:s:256:LEU:HD13	2.01	0.42
29:i:46:GLU:CD	37:s:247:PHE:HB3	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:v:135:VAL:HG13	40:v:187:LYS:HB3	2.00	0.42
42:y:160:LEU:HD11	42:y:184:GLY:HA3	2.01	0.42
1:1:276:U:H2'	1:1:277:G:C8	2.54	0.42
1:1:594:U:P	1:1:609:G:H1	2.42	0.42
1:1:789:A:O2'	6:C:114:ASN:ND2	2.49	0.42
1:1:1183:C:H2'	1:1:1184:A:C8	2.53	0.42
4:A:275:ARG:NH1	4:A:338:TYR:HE2	2.17	0.42
4:A:361:THR:OG1	4:A:381:ASP:OD1	2.36	0.42
4:A:385:ARG:HA	4:A:396:VAL:O	2.19	0.42
5:B:290:ASP:O	5:B:293:ASN:ND2	2.53	0.42
7:D:69:ARG:NH1	7:D:78:GLU:OE2	2.52	0.42
8:E:42:LEU:HD22	8:E:79:VAL:HG11	2.01	0.42
9:F:10:GLU:OE1	43:z:126:ARG:NH2	2.52	0.42
10:G:81:THR:OG1	10:G:82:LEU:N	2.52	0.42
14:M:36:VAL:HG21	14:M:55:ARG:HH12	1.84	0.42
16:O:194:LEU:O	16:O:198:GLY:N	2.53	0.42
17:P:29:THR:HA	17:P:32:THR:HG22	2.02	0.42
24:8:314:LYS:NZ	24:8:322:GLN:HE22	2.17	0.42
34:o:90:SER:OG	34:o:91:GLY:N	2.53	0.42
35:p:50:SER:O	35:p:53:THR:OG1	2.29	0.42
42:y:20:THR:O	42:y:200:ASN:ND2	2.47	0.42
1:1:381:U:H2'	1:1:382:U:H6	1.84	0.42
1:1:950:G:N2	1:1:1368:U:OP2	2.51	0.42
1:1:1193:A:N6	1:1:1317:A:H62	2.17	0.42
4:A:51:TRP:HB3	4:A:59:ILE:HD12	2.00	0.42
9:F:44:ILE:HD13	9:F:44:ILE:HA	1.83	0.42
10:G:68:ARG:HG3	10:G:238:LEU:HA	2.01	0.42
15:N:6:TYR:CE1	29:i:40:VAL:HG22	2.55	0.42
23:7:177:GLN:HE21	23:7:221:ARG:HD2	1.84	0.42
25:b:225:LEU:HD13	25:b:235:LYS:NZ	2.34	0.42
28:h:76:GLN:HG2	28:h:80:LEU:HB2	2.02	0.42
35:p:122:PRO:HG3	35:p:201:ILE:HG13	2.01	0.42
38:t:254:ILE:HG23	38:t:261:PHE:HE1	1.84	0.42
1:1:672:A:P	18:Q:16:ARG:HH22	2.43	0.42
2:2:126:A:H4'	2:2:127:U:OP2	2.17	0.42
7:D:68:GLU:HG3	43:z:57:ASP:HA	2.01	0.42
12:K:125:LEU:O	12:K:154:ILE:HA	2.20	0.42
13:L:46:ILE:HD12	13:L:46:ILE:HG23	1.86	0.42
40:v:178:PRO:HB2	41:w:201:ILE:HG12	2.02	0.42
43:z:10:LEU:HD11	43:z:25:LEU:HD11	2.01	0.42
43:z:102:PHE:CE2	43:z:128:VAL:HG11	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:392:G:H5''	11:I:60:ILE:HG13	2.00	0.42
1:1:946:U:H2'	1:1:947:G:C8	2.55	0.42
1:1:3021:A:H2	1:1:3033:A:H62	1.67	0.42
1:1:3146:G:H2'	1:1:3147:G:H8	1.84	0.42
2:2:72:A:OP2	22:Y:52:ARG:HD3	2.20	0.42
7:D:10:ILE:O	7:D:18:ARG:NH2	2.53	0.42
7:D:106:HIS:ND1	8:E:10:TYR:OH	2.40	0.42
14:M:53:VAL:HA	14:M:54:PRO:HD3	1.92	0.42
20:V:80:ARG:NH1	20:V:116:GLY:HA3	2.35	0.42
20:V:96:GLU:OE1	39:u:24:ASN:N	2.53	0.42
25:b:88:PHE:O	25:b:99:LEU:HA	2.20	0.42
27:f:69:GLY:HA3	27:f:85:PHE:HA	2.02	0.42
33:n:165:GLN:HG2	33:n:246:PRO:HG3	2.02	0.42
33:n:448:LEU:HD12	33:n:449:PRO:HD2	2.01	0.42
40:v:342:ILE:HB	40:v:353:HIS:HB3	2.01	0.42
42:y:126:GLU:HG3	42:y:137:VAL:HG11	2.02	0.42
1:1:725:G:H3'	1:1:726:G:C8	2.55	0.41
1:1:1438:U:H1'	6:C:94:CYS:HA	2.01	0.41
1:1:2357:A:H2'	1:1:2358:A:C8	2.54	0.41
1:1:3000:A:H2'	1:1:3001:C:C6	2.55	0.41
1:1:3183:A:H2	1:1:3188:G:H4'	1.85	0.41
2:2:66:A:H5'	28:h:10:ARG:HH22	1.85	0.41
7:D:86:TYR:HE1	7:D:113:THR:HG22	1.85	0.41
11:I:164:HIS:CD2	11:I:166:PRO:HD2	2.55	0.41
11:I:245:ARG:NH2	17:P:157:VAL:O	2.53	0.41
34:o:149:GLN:HG2	34:o:164:VAL:HG13	2.01	0.41
35:p:44:PHE:CD1	35:p:65:MET:HG2	2.55	0.41
35:p:471:ALA:HA	35:p:482:PRO:HG3	2.02	0.41
36:q:270:UNK:HA	36:q:285:UNK:O	2.19	0.41
40:v:324:LYS:HD2	41:w:198:PHE:HE2	1.84	0.41
1:1:163:C:OP1	23:7:211:SER:OG	2.30	0.41
1:1:425:G:H2'	1:1:426:G:C8	2.54	0.41
1:1:1385:C:O2'	7:D:29:ARG:NH2	2.45	0.41
1:1:3104:U:O2	1:1:3129:A:N7	2.53	0.41
1:1:3304:U:H1'	5:B:334:ARG:HH21	1.84	0.41
4:A:382:ARG:NH1	4:A:402:SER:HA	2.35	0.41
10:G:94:PHE:CE1	10:G:200:LEU:HD13	2.55	0.41
11:I:77:ASP:O	11:I:81:LEU:CB	2.65	0.41
20:V:17:LEU:O	20:V:52:ALA:N	2.41	0.41
20:V:24:ASN:ND2	20:V:97:ASP:OD2	2.53	0.41
20:V:104:ASN:OD1	20:V:108:GLU:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:n:370:GLU:HG2	38:t:246:CYS:SG	2.60	0.41
40:v:35:LEU:HD21	40:v:63:LYS:HE2	2.01	0.41
1:1:3313:U:H4'	5:B:173:GLN:HG3	2.02	0.41
3:6:54:A:H3'	3:6:55:A:C8	2.55	0.41
4:A:336:THR:HG23	4:A:367:ILE:HD13	2.03	0.41
6:C:244:LEU:HA	6:C:244:LEU:HD23	1.86	0.41
9:F:156:ILE:HD12	9:F:161:VAL:HG11	2.01	0.41
19:S:7:TYR:O	19:S:28:ARG:HA	2.20	0.41
33:n:379:LEU:HD23	33:n:379:LEU:HA	1.93	0.41
39:u:22:VAL:HG22	39:u:28:GLU:HG2	2.01	0.41
40:v:120:ILE:HG12	40:v:334:ARG:HH21	1.86	0.41
40:v:191:MET:HE3	40:v:193:ASN:HD21	1.84	0.41
42:y:116:LEU:HD23	42:y:138:PHE:HB2	2.03	0.41
1:1:791:A:H2'	1:1:792:G:H8	1.84	0.41
1:1:1168:U:H2'	1:1:1169:A:C8	2.54	0.41
1:1:3097:C:H2'	1:1:3098:G:C8	2.56	0.41
1:1:3218:A:H5''	1:1:3219:G:C5	2.55	0.41
1:1:3252:G:H2'	1:1:3253:G:C8	2.55	0.41
5:B:56:ILE:HD12	5:B:359:ILE:HG12	2.02	0.41
11:I:240:PHE:HB3	11:I:242:ARG:NH1	2.35	0.41
16:O:113:ASP:OD2	16:O:114:LYS:NZ	2.54	0.41
19:S:40:ARG:HH22	19:S:119:ARG:HA	1.84	0.41
20:V:80:ARG:HH12	20:V:116:GLY:HA3	1.85	0.41
22:Y:120:GLN:HE21	22:Y:126:LEU:HB3	1.85	0.41
27:f:6:ARG:NH1	27:f:8:TYR:O	2.53	0.41
33:n:145:LEU:HA	33:n:146:PRO:HD3	1.92	0.41
33:n:146:PRO:HA	38:t:210:LYS:HE2	2.03	0.41
38:t:257:MET:HG2	38:t:261:PHE:HB2	2.02	0.41
43:z:176:ILE:HG21	43:z:176:ILE:HD13	1.87	0.41
1:1:473:G:H2'	1:1:474:G:C8	2.56	0.41
1:1:3057:U:OP1	40:v:66:LYS:N	2.41	0.41
1:1:3095:U:H2'	1:1:3096:C:C6	2.56	0.41
1:1:3303:G:O2'	1:1:3305:A:N7	2.50	0.41
4:A:77:LYS:HB2	4:A:105:ILE:HG23	2.02	0.41
4:A:375:LEU:HD23	4:A:387:PHE:HD2	1.85	0.41
6:C:317:PRO:C	6:C:319:LYS:H	2.29	0.41
9:F:14:LYS:HE2	43:z:175:ASP:OD2	2.20	0.41
10:G:95:ASN:ND2	10:G:98:ARG:NH1	2.68	0.41
17:P:15:ALA:HA	17:P:105:LYS:HZ2	1.86	0.41
35:p:190:LEU:HD13	35:p:218:PRO:HD2	2.02	0.41
40:v:121:LYS:HE2	40:v:128:LYS:HZ2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:z:170:PRO:HA	43:z:173:ILE:HD12	2.03	0.41
1:1:297:G:C2	29:i:41:ARG:NH1	2.88	0.41
1:1:377:A:H1'	1:1:392:G:N2	2.35	0.41
1:1:442:G:H2'	1:1:443:G:H8	1.85	0.41
1:1:607:A:OP1	8:E:24:ALA:N	2.48	0.41
1:1:655:C:OP2	26:e:27:ARG:HD3	2.20	0.41
1:1:665:A:H2'	1:1:666:A:C8	2.55	0.41
1:1:1340:G:OP2	26:e:61:LYS:HD2	2.21	0.41
3:6:55:A:OP2	34:o:97:ARG:NE	2.36	0.41
6:C:276:LEU:HA	6:C:277:PRO:HD3	1.77	0.41
8:E:64:LEU:HD11	8:E:76:LEU:HD22	2.02	0.41
8:E:164:SER:OG	27:f:4:SER:OG	2.32	0.41
9:F:96:PRO:HA	9:F:97:PRO:HD3	1.94	0.41
12:K:118:VAL:HG23	35:p:286:ARG:HH11	1.85	0.41
14:M:32:LEU:HD11	14:M:94:TRP:CD1	2.56	0.41
28:h:31:LEU:O	28:h:35:LYS:HB2	2.20	0.41
33:n:180:PHE:CZ	33:n:182:SER:HB3	2.56	0.41
34:o:113:GLN:HE22	38:t:56:VAL:HG23	1.85	0.41
37:s:261:GLU:HA	37:s:262:PRO:HD3	1.89	0.41
40:v:326:ILE:O	41:w:191:GLN:NE2	2.54	0.41
42:y:101:LEU:HD11	42:y:107:VAL:HG11	2.02	0.41
43:z:46:TRP:CE2	43:z:102:PHE:HB2	2.55	0.41
43:z:53:MET:HE3	43:z:124:LEU:HD12	2.03	0.41
1:1:20:A:OP2	28:h:90:ARG:NH2	2.53	0.41
1:1:242:C:O2'	1:1:243:G:H8	2.04	0.41
1:1:504:A:H2'	1:1:505:G:C8	2.56	0.41
1:1:946:U:H2'	1:1:947:G:H8	1.84	0.41
2:2:121:U:O2	2:2:132:G:N2	2.36	0.41
9:F:222:HIS:O	9:F:227:GLY:N	2.50	0.41
11:I:191:THR:OG1	11:I:228:GLN:NE2	2.53	0.41
12:K:295:GLN:NE2	34:o:197:LYS:O	2.53	0.41
25:b:35:LEU:HG	25:b:59:SER:HB2	2.02	0.41
35:p:464:GLN:HB2	35:p:467:LYS:HG3	2.02	0.41
38:t:100:ILE:HD11	38:t:135:TYR:HD1	1.86	0.41
38:t:144:ILE:HD12	38:t:144:ILE:HA	1.89	0.41
42:y:24:CYS:HB3	42:y:48:ILE:HG23	2.02	0.41
1:1:215:G:H2'	1:1:216:G:H8	1.86	0.41
1:1:356:C:H2'	1:1:357:A:H8	1.86	0.41
1:1:503:C:H2'	1:1:504:A:C8	2.55	0.41
1:1:3039:C:H2'	1:1:3040:A:C8	2.54	0.41
1:1:3189:G:N2	1:1:3203:U:O2	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:7:46:MET:HE2	23:7:57:ALA:HB1	2.02	0.41
27:f:49:ILE:HD11	27:f:71:VAL:HG23	2.03	0.41
35:p:269:VAL:HG22	35:p:415:TYR:HB2	2.03	0.41
38:t:144:ILE:O	38:t:174:GLY:HA2	2.19	0.41
40:v:27:VAL:HA	40:v:83:PHE:HB2	2.03	0.41
40:v:47:PHE:HD1	40:v:50:ILE:HD12	1.84	0.41
1:1:213:A:N3	22:Y:10:SER:OG	2.48	0.41
1:1:528:U:H2'	1:1:529:A:C8	2.55	0.41
1:1:541:U:H2'	1:1:542:G:H8	1.86	0.41
1:1:574:U:H2'	1:1:575:G:C8	2.56	0.41
1:1:608:A:O3'	6:C:326:ARG:NH1	2.53	0.41
1:1:665:A:H2'	1:1:666:A:H8	1.85	0.41
1:1:725:G:H3'	1:1:726:G:H8	1.85	0.41
1:1:787:G:H2'	1:1:788:C:C6	2.55	0.41
1:1:1191:U:OP2	16:O:49:ARG:NH1	2.42	0.41
1:1:1439:U:H2'	1:1:1440:G:C8	2.56	0.41
1:1:1451:C:H5'	24:8:365:TRP:HZ2	1.85	0.41
1:1:3043:C:H2'	1:1:3044:G:C8	2.55	0.41
1:1:3084:C:O2'	1:1:3332:U:OP1	2.31	0.41
1:1:3141:A:H5''	1:1:3142:A:H4'	2.03	0.41
1:1:3385:U:H2'	1:1:3386:G:C8	2.56	0.41
2:2:27:U:H2'	2:2:28:C:C6	2.56	0.41
3:6:226:U:H6	3:6:226:U:H2'	1.75	0.41
5:B:69:LYS:HZ2	21:W:416:LEU:HG	1.85	0.41
5:B:103:THR:OG1	5:B:147:GLU:OE2	2.18	0.41
5:B:221:THR:OG1	5:B:222:LYS:N	2.53	0.41
8:E:172:HIS:CD2	8:E:173:MET:HG3	2.56	0.41
9:F:57:THR:O	9:F:61:ASN:ND2	2.53	0.41
9:F:148:VAL:HG12	9:F:181:ILE:HD11	2.03	0.41
11:I:242:ARG:HG2	11:I:258:GLU:OE2	2.21	0.41
12:K:38:ILE:HA	12:K:41:VAL:HG12	2.02	0.41
19:S:13:ARG:NH1	19:S:50:LYS:O	2.54	0.41
20:V:40:LYS:HD3	20:V:59:MET:HE2	2.03	0.41
20:V:101:VAL:HB	20:V:109:MET:HE1	2.02	0.41
23:7:21:ASN:HA	23:7:24:LYS:HE2	2.03	0.41
27:f:52:VAL:HG22	27:f:66:VAL:HG22	2.02	0.41
30:j:82:SER:OG	30:j:83:ALA:N	2.53	0.41
38:t:146:ARG:HG2	38:t:171:THR:HA	2.02	0.41
39:u:8:PHE:HB3	39:u:36:CYS:HB3	2.03	0.41
40:v:191:MET:HE2	40:v:191:MET:HB3	1.96	0.41
1:1:108:A:OP1	13:L:42:ARG:NH2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:215:G:H2'	1:1:216:G:C8	2.55	0.41
1:1:563:U:H2'	1:1:564:G:C8	2.51	0.41
1:1:3167:A:H1'	1:1:3284:G:N2	2.36	0.41
2:2:64:U:H5''	28:h:49:LYS:HG3	2.03	0.41
12:K:123:VAL:H	12:K:152:ASP:HB2	1.86	0.41
13:L:35:ARG:O	13:L:38:ALA:HB3	2.21	0.41
15:N:46:ASP:N	15:N:46:ASP:OD1	2.53	0.41
21:W:374:ARG:NH1	42:y:178:GLN:HB2	2.36	0.41
33:n:373:ILE:O	33:n:377:GLU:HB2	2.21	0.41
43:z:170:PRO:HB2	43:z:234:LEU:HD11	2.02	0.41
1:1:29:C:H2'	1:1:30:G:H8	1.85	0.40
1:1:489:C:H2'	1:1:490:A:H8	1.86	0.40
1:1:542:G:H2'	1:1:543:C:C6	2.57	0.40
1:1:1384:U:H2'	1:1:1385:C:C6	2.56	0.40
3:6:58:G:C2	34:o:132:ARG:NH1	2.88	0.40
3:6:220:C:H5'	3:6:221:A:OP1	2.21	0.40
4:A:138:ASP:OD2	4:A:159:THR:HB	2.21	0.40
6:C:210:ALA:O	6:C:257:LYS:NZ	2.55	0.40
7:D:167:MET:HE2	11:I:252:GLU:OE2	2.21	0.40
12:K:88:PHE:HE2	12:K:239:PRO:HD2	1.85	0.40
33:n:141:LEU:HD13	37:s:387:ARG:HG3	2.02	0.40
33:n:372:PRO:HD2	37:s:374:LEU:HD21	2.04	0.40
33:n:428:GLN:N	33:n:447:TYR:O	2.37	0.40
35:p:421:LYS:HD3	35:p:421:LYS:HA	1.82	0.40
39:u:2:ARG:HH11	42:y:78:ASP:HB2	1.86	0.40
42:y:97:VAL:HG22	42:y:128:LEU:HD23	2.02	0.40
1:1:68:C:N4	1:1:314:U:O2'	2.46	0.40
1:1:289:A:H2'	1:1:290:G:H8	1.87	0.40
3:6:218:A:H1'	38:t:80:ILE:HG23	2.03	0.40
7:D:106:HIS:HD2	7:D:107:LYS:HZ3	1.67	0.40
8:E:35:VAL:HB	8:E:90:LYS:NZ	2.36	0.40
10:G:150:LEU:HD21	10:G:215:VAL:HG22	2.04	0.40
11:I:119:PRO:HD3	11:I:219:PRO:HD3	2.03	0.40
11:I:161:THR:HA	11:I:171:PHE:O	2.21	0.40
11:I:165:LEU:O	11:I:167:GLU:N	2.52	0.40
15:N:59:PHE:HD1	15:N:133:ILE:HD11	1.86	0.40
21:W:399:ALA:HB3	42:y:36:SER:HB3	2.04	0.40
35:p:314:LEU:HA	35:p:315:PRO:HD3	1.86	0.40
1:1:383:G:OP2	41:w:222:LYS:HD2	2.22	0.40
1:1:430:U:H1'	27:f:90:PRO:HB3	2.03	0.40
1:1:3012:A:H2	1:1:3042:U:H3	1.70	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:100:U:OP2	2:2:101:U:OP2	2.37	0.40
2:2:149:A:H2'	2:2:150:G:C8	2.56	0.40
6:C:188:ARG:HG2	6:C:190:GLY:H	1.86	0.40
8:E:46:ARG:NH1	8:E:47:PHE:CE1	2.89	0.40
10:G:177:TYR:OH	10:G:230:LYS:NZ	2.55	0.40
11:I:238:TYR:HE1	11:I:266:LYS:HD2	1.86	0.40
12:K:282:LYS:HD3	12:K:288:VAL:HG12	2.03	0.40
19:S:8:GLN:NE2	19:S:26:ARG:HE	2.20	0.40
23:7:45:THR:O	23:7:49:ASN:CB	2.69	0.40
30:j:67:LEU:HD22	30:j:70:VAL:HG21	2.03	0.40
33:n:110:ASP:OD1	33:n:110:ASP:N	2.54	0.40
33:n:371:VAL:HG11	33:n:411:ILE:HG22	2.02	0.40
37:s:291:PRO:HA	37:s:294:LEU:HD12	2.04	0.40
43:z:181:TRP:O	43:z:185:LEU:HG	2.21	0.40
1:1:156:G:H1'	13:L:77:LEU:HD11	2.02	0.40
1:1:567:G:H2'	1:1:568:G:C8	2.57	0.40
1:1:3165:A:OP2	11:I:189:ARG:HD3	2.21	0.40
1:1:3365:U:H2'	1:1:3366:G:C8	2.56	0.40
3:6:231:A:O2'	3:6:232:A:N3	2.44	0.40
4:A:6:SER:OG	4:A:47:VAL:O	2.33	0.40
4:A:26:VAL:HG12	4:A:28:SER:H	1.85	0.40
4:A:130:SER:HB2	11:I:133:LYS:HE3	2.03	0.40
4:A:194:ASP:OD1	4:A:194:ASP:N	2.50	0.40
4:A:213:LEU:HD12	4:A:231:GLU:OE2	2.22	0.40
7:D:67:PRO:O	43:z:117:ARG:NH1	2.55	0.40
9:F:224:ILE:HG23	19:S:36:ILE:HG12	2.04	0.40
11:I:202:PHE:CE1	11:I:234:ASN:HB2	2.57	0.40
12:K:250:ASN:HB3	12:K:253:TRP:CD2	2.55	0.40
23:7:164:GLU:O	23:7:168:ARG:N	2.55	0.40
28:h:38:ARG:NH1	28:h:41:LEU:HD13	2.37	0.40
29:i:41:ARG:O	29:i:45:ARG:HG2	2.20	0.40
36:q:101:UNK:HA	36:q:421:UNK:O	2.21	0.40
40:v:211:ARG:HE	40:v:327:LYS:HE3	1.87	0.40
43:z:209:ALA:O	43:z:212:THR:OG1	2.28	0.40
1:1:159:A:H2'	1:1:160:G:H8	1.87	0.40
1:1:273:A:H2'	1:1:274:G:H8	1.86	0.40
1:1:286:U:H2'	1:1:287:G:C8	2.56	0.40
1:1:1427:U:H2'	1:1:1428:A:C8	2.56	0.40
2:2:142:C:H2'	2:2:143:U:C6	2.57	0.40
3:6:8:A:H2'	3:6:9:A:C8	2.57	0.40
6:C:11:LEU:HD23	6:C:11:LEU:HA	1.93	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:31:GLU:HB3	7:D:54:LYS:HZ1	1.86	0.40
9:F:154:GLY:O	9:F:161:VAL:N	2.35	0.40
13:L:54:LEU:HB3	13:L:95:ILE:HA	2.03	0.40
18:Q:90:ASP:CG	18:Q:92:ARG:HE	2.29	0.40
28:h:35:LYS:HD2	28:h:44:ILE:HG21	2.04	0.40
38:t:100:ILE:O	38:t:132:LYS:HA	2.22	0.40
40:v:86:THR:O	40:v:95:SER:N	2.50	0.40
42:y:83:HIS:O	42:y:87:SER:OG	2.31	0.40
42:y:109:CYS:SG	42:y:116:LEU:HB2	2.62	0.40
43:z:16:LYS:O	43:z:20:ASN:ND2	2.54	0.40
43:z:39:GLN:HA	43:z:42:PHE:HD2	1.86	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	
4	A	390/463 (84%)	368 (94%)	22 (6%)	0	100	100
5	B	320/387 (83%)	302 (94%)	18 (6%)	0	100	100
6	C	310/362 (86%)	285 (92%)	23 (7%)	2 (1%)	21	52
7	D	188/306 (61%)	177 (94%)	11 (6%)	0	100	100
8	E	168/176 (96%)	158 (94%)	10 (6%)	0	100	100
9	F	240/244 (98%)	225 (94%)	15 (6%)	0	100	100
10	G	185/256 (72%)	170 (92%)	14 (8%)	1 (0%)	24	56
11	I	286/295 (97%)	272 (95%)	14 (5%)	0	100	100
12	K	256/376 (68%)	243 (95%)	13 (5%)	0	100	100
13	L	104/199 (52%)	96 (92%)	7 (7%)	1 (1%)	12	43
14	M	126/138 (91%)	123 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	N	172/204 (84%)	162 (94%)	10 (6%)	0	100	100
16	O	180/199 (90%)	173 (96%)	7 (4%)	0	100	100
17	P	118/184 (64%)	113 (96%)	5 (4%)	0	100	100
18	Q	130/186 (70%)	128 (98%)	2 (2%)	0	100	100
19	S	169/172 (98%)	154 (91%)	15 (9%)	0	100	100
20	V	120/137 (88%)	115 (96%)	5 (4%)	0	100	100
21	W	96/647 (15%)	94 (98%)	2 (2%)	0	100	100
22	Y	124/127 (98%)	118 (95%)	6 (5%)	0	100	100
23	7	152/231 (66%)	137 (90%)	15 (10%)	0	100	100
24	8	96/434 (22%)	96 (100%)	0	0	100	100
25	b	220/291 (76%)	207 (94%)	13 (6%)	0	100	100
26	e	110/130 (85%)	106 (96%)	4 (4%)	0	100	100
27	f	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
28	h	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
29	i	82/100 (82%)	78 (95%)	4 (5%)	0	100	100
30	j	70/88 (80%)	66 (94%)	4 (6%)	0	100	100
33	n	333/605 (55%)	322 (97%)	11 (3%)	0	100	100
34	o	131/220 (60%)	123 (94%)	8 (6%)	0	100	100
35	p	433/505 (86%)	422 (98%)	11 (2%)	0	100	100
37	s	82/807 (10%)	77 (94%)	5 (6%)	0	100	100
38	t	244/322 (76%)	220 (90%)	23 (9%)	1 (0%)	30	60
39	u	127/199 (64%)	127 (100%)	0	0	100	100
40	v	221/453 (49%)	207 (94%)	14 (6%)	0	100	100
41	w	68/250 (27%)	64 (94%)	4 (6%)	0	100	100
42	y	224/245 (91%)	214 (96%)	10 (4%)	0	100	100
43	z	239/278 (86%)	228 (95%)	11 (5%)	0	100	100
All	All	6735/10443 (64%)	6380 (95%)	350 (5%)	5 (0%)	49	78

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	C	268	ALA
6	C	292	SER

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Mol	Chain	Res	Type
13	L	63	VAL
10	G	127	PRO
38	t	56	VAL

5.3.2 Protein sidechains [i](#)

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	
4	A	352/410 (86%)	352 (100%)	0	100	100
5	B	272/323 (84%)	272 (100%)	0	100	100
6	C	257/289 (89%)	256 (100%)	1 (0%)	84	81
7	D	171/274 (62%)	171 (100%)	0	100	100
8	E	149/153 (97%)	149 (100%)	0	100	100
9	F	204/205 (100%)	204 (100%)	0	100	100
10	G	152/208 (73%)	152 (100%)	0	100	100
11	I	271/276 (98%)	271 (100%)	0	100	100
12	K	241/346 (70%)	240 (100%)	1 (0%)	84	81
13	L	85/159 (54%)	85 (100%)	0	100	100
14	M	100/109 (92%)	100 (100%)	0	100	100
15	N	153/176 (87%)	153 (100%)	0	100	100
16	O	150/162 (93%)	149 (99%)	1 (1%)	76	77
17	P	100/146 (68%)	99 (99%)	1 (1%)	68	74
18	Q	108/151 (72%)	108 (100%)	0	100	100
19	S	155/156 (99%)	155 (100%)	0	100	100
20	V	94/105 (90%)	94 (100%)	0	100	100
21	W	87/573 (15%)	86 (99%)	1 (1%)	65	73
22	Y	109/110 (99%)	108 (99%)	1 (1%)	70	75
23	7	141/205 (69%)	141 (100%)	0	100	100
24	8	90/388 (23%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	b	203/247 (82%)	201 (99%)	2 (1%)	68	74
26	e	97/111 (87%)	97 (100%)	0	100	100
27	f	90/91 (99%)	90 (100%)	0	100	100
28	h	104/105 (99%)	104 (100%)	0	100	100
29	i	70/82 (85%)	67 (96%)	3 (4%)	26	50
30	j	60/71 (84%)	59 (98%)	1 (2%)	53	67
33	n	309/548 (56%)	308 (100%)	1 (0%)	86	83
34	o	118/199 (59%)	118 (100%)	0	100	100
35	p	381/440 (87%)	379 (100%)	2 (0%)	81	80
37	s	77/653 (12%)	77 (100%)	0	100	100
38	t	219/287 (76%)	217 (99%)	2 (1%)	70	75
39	u	114/180 (63%)	114 (100%)	0	100	100
40	v	208/413 (50%)	208 (100%)	0	100	100
41	w	63/219 (29%)	63 (100%)	0	100	100
42	y	194/211 (92%)	194 (100%)	0	100	100
43	z	225/257 (88%)	225 (100%)	0	100	100
All	All	5973/9038 (66%)	5956 (100%)	17 (0%)	84	83

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	C	3	ARG
12	K	248	LEU
16	O	148	LYS
17	P	24	VAL
21	W	445	LEU
22	Y	80	VAL
25	b	99	LEU
25	b	109	THR
29	i	43	LEU
29	i	58	ILE
29	i	60	LEU
30	j	67	LEU
33	n	417	LEU
35	p	319	LEU
35	p	405	LEU

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Mol	Chain	Res	Type
38	t	57	ARG
38	t	155	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (125) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	34	HIS
4	A	75	HIS
4	A	152	ASN
4	A	332	ASN
5	B	109	HIS
5	B	173	GLN
5	B	184	ASN
6	C	45	ASN
6	C	48	GLN
6	C	110	ASN
6	C	114	ASN
6	C	260	GLN
6	C	307	GLN
6	C	320	ASN
7	D	11	ASN
7	D	23	ASN
7	D	33	ASN
7	D	110	GLN
8	E	57	HIS
8	E	61	ASN
8	E	167	ASN
9	F	37	ASN
9	F	61	ASN
9	F	244	ASN
10	G	59	GLN
10	G	95	ASN
10	G	137	ASN
11	I	11	ASN
11	I	88	ASN
11	I	100	ASN
11	I	102	ASN
11	I	193	HIS
11	I	203	GLN
11	I	220	GLN
11	I	228	GLN
12	K	101	ASN

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Mol	Chain	Res	Type
12	K	200	ASN
12	K	214	ASN
12	K	245	ASN
12	K	275	GLN
13	L	37	ASN
13	L	106	GLN
14	M	105	GLN
15	N	37	HIS
15	N	195	ASN
16	O	29	ASN
16	O	31	GLN
16	O	50	ASN
16	O	55	HIS
17	P	10	ASN
17	P	45	GLN
17	P	54	HIS
17	P	97	ASN
18	Q	145	ASN
19	S	8	GLN
19	S	89	ASN
19	S	108	GLN
20	V	132	ASN
21	W	384	ASN
21	W	413	ASN
21	W	415	ASN
22	Y	120	GLN
23	7	48	GLN
23	7	49	ASN
23	7	177	GLN
23	7	209	GLN
24	8	322	GLN
25	b	45	HIS
25	b	75	ASN
25	b	82	ASN
25	b	118	HIS
25	b	158	HIS
25	b	175	HIS
26	e	20	HIS
26	e	52	GLN
27	f	42	GLN
28	h	59	ASN
29	i	91	ASN

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Mol	Chain	Res	Type
29	i	92	ASN
29	i	100	HIS
30	j	69	HIS
33	n	160	GLN
33	n	164	ASN
33	n	189	GLN
33	n	386	ASN
33	n	428	GLN
33	n	445	ASN
35	p	69	GLN
35	p	141	HIS
35	p	153	ASN
35	p	156	GLN
35	p	189	ASN
35	p	266	GLN
35	p	287	ASN
35	p	310	ASN
35	p	323	GLN
35	p	330	ASN
35	p	337	ASN
35	p	397	ASN
35	p	413	ASN
35	p	441	GLN
38	t	92	HIS
38	t	172	ASN
38	t	225	HIS
38	t	284	ASN
39	u	37	HIS
39	u	45	ASN
39	u	73	GLN
39	u	76	ASN
40	v	38	HIS
40	v	42	GLN
40	v	137	ASN
40	v	171	ASN
41	w	191	GLN
41	w	199	ASN
41	w	221	ASN
42	y	106	ASN
42	y	162	HIS
42	y	168	GLN
42	y	225	GLN

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Mol	Chain	Res	Type
43	z	13	ASN
43	z	20	ASN
43	z	43	ASN
43	z	63	GLN
43	z	91	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1343/3395 (39%)	352 (26%)	28 (2%)
2	2	157/158 (99%)	35 (22%)	3 (1%)
3	6	85/232 (36%)	44 (51%)	5 (5%)
All	All	1585/3785 (41%)	431 (27%)	36 (2%)

All (431) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	7	C
1	1	12	A
1	1	13	A
1	1	14	U
1	1	18	G
1	1	26	A
1	1	31	C
1	1	57	A
1	1	59	G
1	1	60	A
1	1	65	A
1	1	66	A
1	1	73	C
1	1	77	A
1	1	92	G
1	1	93	C
1	1	96	G
1	1	109	A
1	1	110	G
1	1	111	C
1	1	113	C
1	1	116	A
1	1	117	U

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Mol	Chain	Res	Type
1	1	118	U
1	1	120	G
1	1	121	A
1	1	122	A
1	1	135	C
1	1	136	G
1	1	143	G
1	1	146	U
1	1	150	A
1	1	155	G
1	1	156	G
1	1	161	G
1	1	163	C
1	1	165	A
1	1	166	C
1	1	167	U
1	1	169	U
1	1	170	G
1	1	173	G
1	1	187	A
1	1	190	U
1	1	191	U
1	1	192	C
1	1	199	A
1	1	206	G
1	1	207	U
1	1	210	U
1	1	211	A
1	1	218	G
1	1	219	A
1	1	231	G
1	1	240	U
1	1	241	G
1	1	243	G
1	1	248	U
1	1	249	U
1	1	250	U
1	1	251	G
1	1	252	U
1	1	253	A
1	1	258	G
1	1	265	A

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Mol	Chain	Res	Type
1	1	266	A
1	1	267	G
1	1	269	G
1	1	295	A
1	1	307	A
1	1	308	A
1	1	309	U
1	1	310	U
1	1	311	C
1	1	314	U
1	1	323	A
1	1	329	U
1	1	332	C
1	1	333	G
1	1	334	A
1	1	339	C
1	1	346	C
1	1	350	C
1	1	352	A
1	1	354	U
1	1	374	A
1	1	375	A
1	1	376	G
1	1	385	A
1	1	388	G
1	1	395	A
1	1	396	A
1	1	397	A
1	1	398	A
1	1	399	A
1	1	401	U
1	1	402	A
1	1	403	C
1	1	404	G
1	1	410	U
1	1	421	G
1	1	422	A
1	1	423	A
1	1	430	U
1	1	438	A
1	1	439	C
1	1	440	A

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Mol	Chain	Res	Type
1	1	453	C
1	1	454	C
1	1	463	C
1	1	465	U
1	1	466	G
1	1	467	U
1	1	468	G
1	1	478	A
1	1	479	U
1	1	481	U
1	1	494	G
1	1	503	C
1	1	510	G
1	1	516	A
1	1	517	G
1	1	520	U
1	1	521	A
1	1	523	A
1	1	530	G
1	1	534	U
1	1	535	G
1	1	543	C
1	1	546	C
1	1	547	G
1	1	548	G
1	1	551	A
1	1	552	G
1	1	555	U
1	1	556	U
1	1	557	A
1	1	559	A
1	1	569	A
1	1	578	A
1	1	579	G
1	1	599	C
1	1	600	G
1	1	604	G
1	1	607	A
1	1	609	G
1	1	611	A
1	1	619	A
1	1	621	A

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Mol	Chain	Res	Type
1	1	627	U
1	1	652	G
1	1	677	A
1	1	681	U
1	1	690	A
1	1	691	A
1	1	725	G
1	1	726	G
1	1	728	G
1	1	735	A
1	1	749	C
1	1	750	G
1	1	756	U
1	1	757	C
1	1	762	U
1	1	763	G
1	1	764	U
1	1	765	C
1	1	766	U
1	1	767	U
1	1	770	G
1	1	771	A
1	1	775	A
1	1	776	U
1	1	777	U
1	1	779	G
1	1	780	A
1	1	781	G
1	1	785	G
1	1	801	A
1	1	944	C
1	1	951	A
1	1	1158	A
1	1	1159	A
1	1	1172	G
1	1	1178	G
1	1	1179	A
1	1	1180	A
1	1	1181	U
1	1	1185	C
1	1	1192	C
1	1	1193	A

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Mol	Chain	Res	Type
1	1	1313	G
1	1	1316	C
1	1	1330	A
1	1	1331	U
1	1	1345	G
1	1	1348	U
1	1	1349	G
1	1	1350	A
1	1	1351	U
1	1	1352	A
1	1	1353	U
1	1	1354	G
1	1	1355	A
1	1	1386	A
1	1	1391	C
1	1	1392	G
1	1	1399	A
1	1	1400	G
1	1	1404	G
1	1	1408	G
1	1	1417	G
1	1	1418	A
1	1	1419	A
1	1	1421	G
1	1	1434	G
1	1	1435	A
1	1	1436	U
1	1	1437	C
1	1	1446	A
1	1	1448	U
1	1	1452	A
1	1	1453	A
1	1	1454	A
1	1	1879	A
1	1	1880	U
1	1	1885	U
1	1	1887	A
1	1	2361	A
1	1	2996	U
1	1	2997	G
1	1	3000	A
1	1	3003	G

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Mol	Chain	Res	Type
1	1	3011	A
1	1	3012	A
1	1	3017	A
1	1	3021	A
1	1	3022	G
1	1	3023	U
1	1	3029	A
1	1	3030	G
1	1	3031	G
1	1	3032	A
1	1	3034	C
1	1	3035	A
1	1	3048	A
1	1	3049	A
1	1	3057	U
1	1	3058	U
1	1	3059	G
1	1	3064	U
1	1	3078	U
1	1	3079	U
1	1	3084	C
1	1	3085	G
1	1	3086	A
1	1	3092	C
1	1	3099	C
1	1	3100	U
1	1	3104	U
1	1	3109	G
1	1	3122	A
1	1	3129	A
1	1	3130	A
1	1	3131	U
1	1	3142	A
1	1	3143	C
1	1	3160	U
1	1	3161	C
1	1	3165	A
1	1	3166	C
1	1	3167	A
1	1	3168	A
1	1	3169	U
1	1	3170	A

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Mol	Chain	Res	Type
1	1	3171	U
1	1	3172	A
1	1	3173	G
1	1	3174	A
1	1	3175	U
1	1	3176	G
1	1	3179	U
1	1	3180	A
1	1	3181	C
1	1	3186	A
1	1	3187	A
1	1	3188	G
1	1	3195	U
1	1	3196	U
1	1	3199	G
1	1	3204	C
1	1	3207	U
1	1	3217	C
1	1	3218	A
1	1	3219	G
1	1	3224	G
1	1	3227	A
1	1	3228	C
1	1	3229	G
1	1	3230	G
1	1	3243	A
1	1	3244	A
1	1	3245	A
1	1	3247	G
1	1	3253	G
1	1	3254	G
1	1	3259	U
1	1	3263	G
1	1	3264	G
1	1	3265	C
1	1	3269	U
1	1	3270	U
1	1	3273	A
1	1	3275	U
1	1	3276	G
1	1	3293	U
1	1	3294	A

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Mol	Chain	Res	Type
1	1	3295	A
1	1	3303	G
1	1	3304	U
1	1	3306	U
1	1	3308	C
1	1	3312	U
1	1	3313	U
1	1	3316	A
1	1	3317	U
1	1	3318	G
1	1	3319	U
1	1	3320	A
1	1	3330	A
1	1	3334	U
1	1	3341	U
1	1	3342	A
1	1	3345	G
1	1	3347	A
1	1	3350	C
1	1	3351	U
1	1	3352	U
1	1	3353	G
1	1	3354	U
1	1	3355	U
1	1	3356	G
1	1	3357	U
1	1	3363	U
1	1	3368	U
1	1	3369	G
1	1	3375	A
1	1	3376	A
1	1	3378	C
1	1	3383	G
1	1	3389	U
2	2	16	G
2	2	25	G
2	2	34	U
2	2	35	C
2	2	36	G
2	2	37	A
2	2	39	G
2	2	51	G

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Mol	Chain	Res	Type
2	2	59	A
2	2	62	C
2	2	63	G
2	2	80	A
2	2	81	U
2	2	82	U
2	2	83	C
2	2	84	C
2	2	85	G
2	2	86	U
2	2	87	G
2	2	90	U
2	2	95	G
2	2	100	U
2	2	104	A
2	2	106	C
2	2	111	A
2	2	113	U
2	2	124	G
2	2	125	U
2	2	126	A
2	2	127	U
2	2	138	A
2	2	148	G
2	2	151	C
2	2	152	G
2	2	158	U
3	6	2	C
3	6	4	U
3	6	5	C
3	6	6	U
3	6	7	C
3	6	8	A
3	6	13	U
3	6	14	U
3	6	15	C
3	6	16	U
3	6	17	G
3	6	23	U
3	6	24	A
3	6	25	G
3	6	26	U

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Mol	Chain	Res	Type
3	6	27	G
3	6	33	U
3	6	37	C
3	6	40	U
3	6	41	G
3	6	42	G
3	6	52	G
3	6	53	A
3	6	54	A
3	6	55	A
3	6	56	U
3	6	57	U
3	6	58	G
3	6	59	C
3	6	60	U
3	6	61	G
3	6	63	C
3	6	218	A
3	6	219	A
3	6	220	C
3	6	221	A
3	6	223	U
3	6	224	G
3	6	225	U
3	6	226	U
3	6	228	U
3	6	230	A
3	6	231	A
3	6	232	A

All (36) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	13	A
1	1	239	G
1	1	250	U
1	1	307	A
1	1	309	U
1	1	406	G
1	1	420	G
1	1	452	G
1	1	465	U

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Mol	Chain	Res	Type
1	1	493	G
1	1	761	A
1	1	765	C
1	1	1329	U
1	1	1886	A
1	1	3030	G
1	1	3078	U
1	1	3121	U
1	1	3166	C
1	1	3168	A
1	1	3169	U
1	1	3218	A
1	1	3228	C
1	1	3269	U
1	1	3293	U
1	1	3316	A
1	1	3341	U
1	1	3350	C
1	1	3351	U
2	2	36	G
2	2	123	G
2	2	126	A
3	6	16	U
3	6	25	G
3	6	60	U
3	6	222	A
3	6	225	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
36	q	5

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	q	398:UNK	C	400:UNK	N	14.84
1	q	136:UNK	C	137:UNK	N	9.43
1	q	114:UNK	C	115:UNK	N	7.34
1	q	257:UNK	C	259:UNK	N	6.77
1	q	242:UNK	C	247:UNK	N	4.06

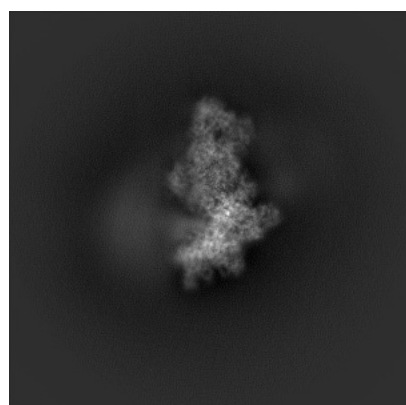
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7324. These allow visual inspection of the internal detail of the map and identification of artifacts.

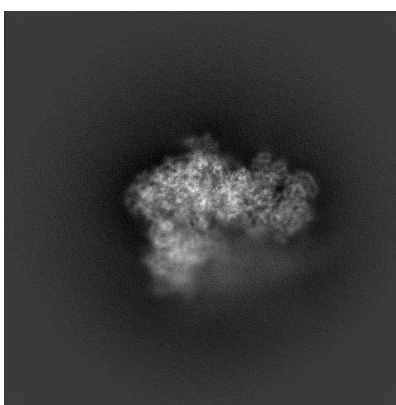
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

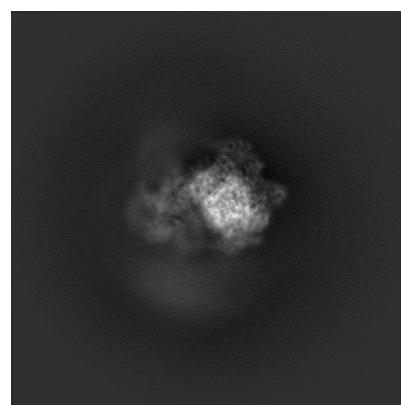
6.1.1 Primary map



X



Y

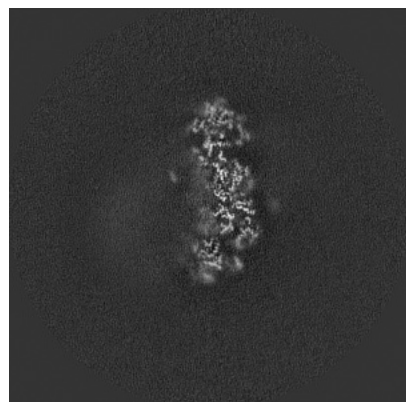


Z

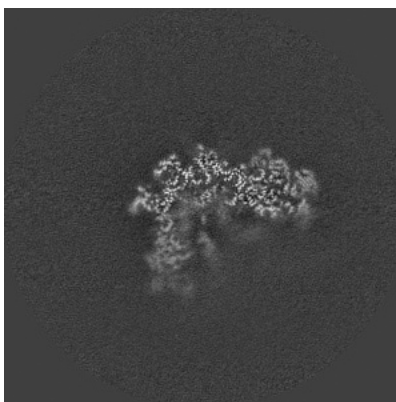
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

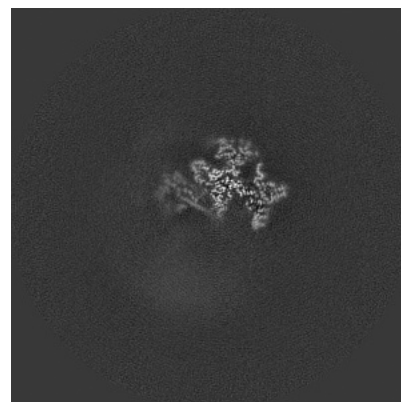
6.2.1 Primary map



X Index: 240



Y Index: 240

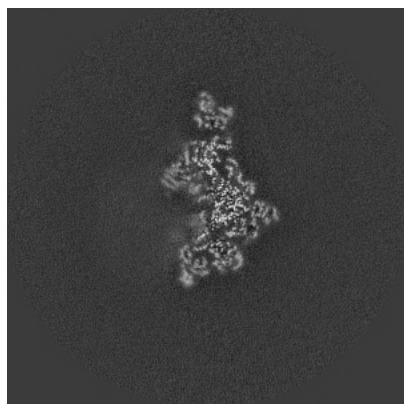


Z Index: 240

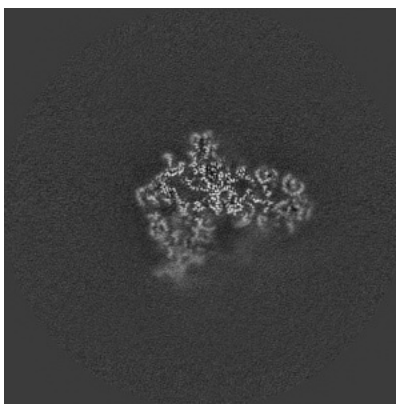
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

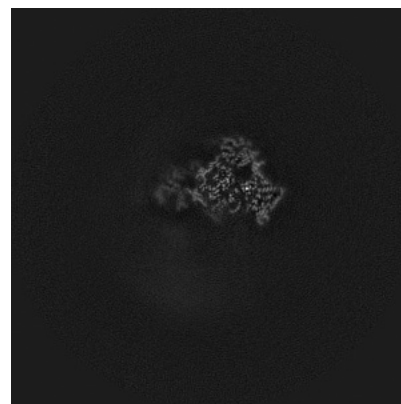
6.3.1 Primary map



X Index: 264



Y Index: 257

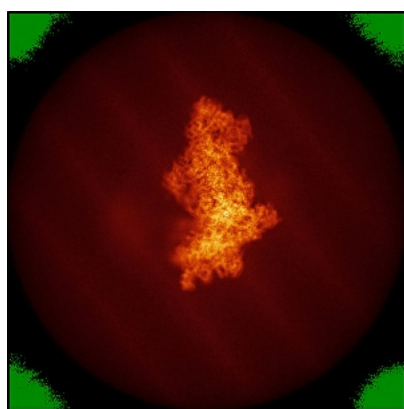


Z Index: 235

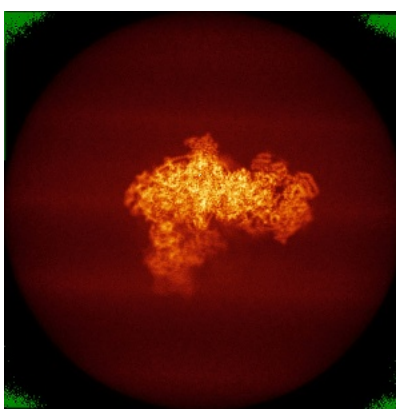
The images above show the largest variance slices of the map in three orthogonal directions.

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

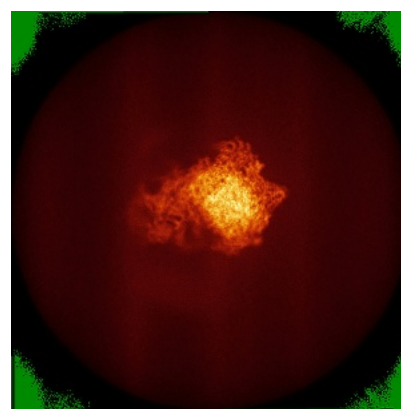
6.4.1 Primary map



X



Y

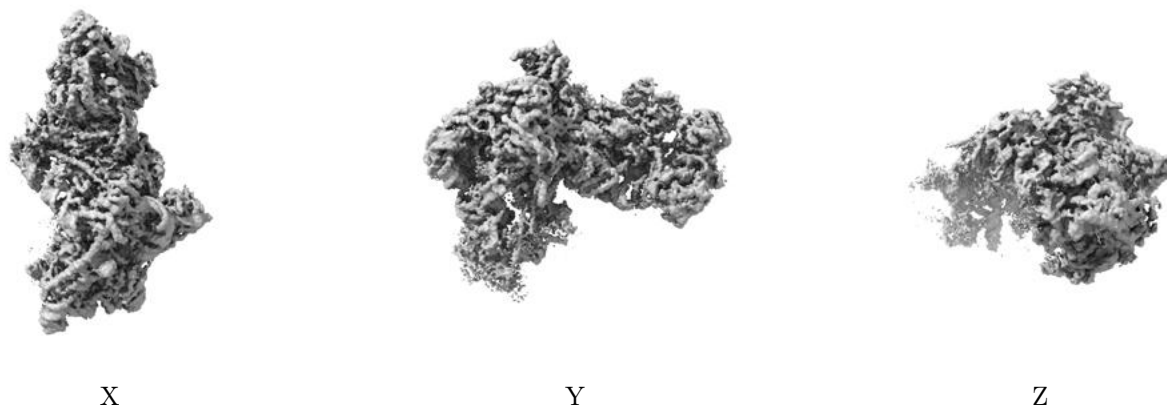


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

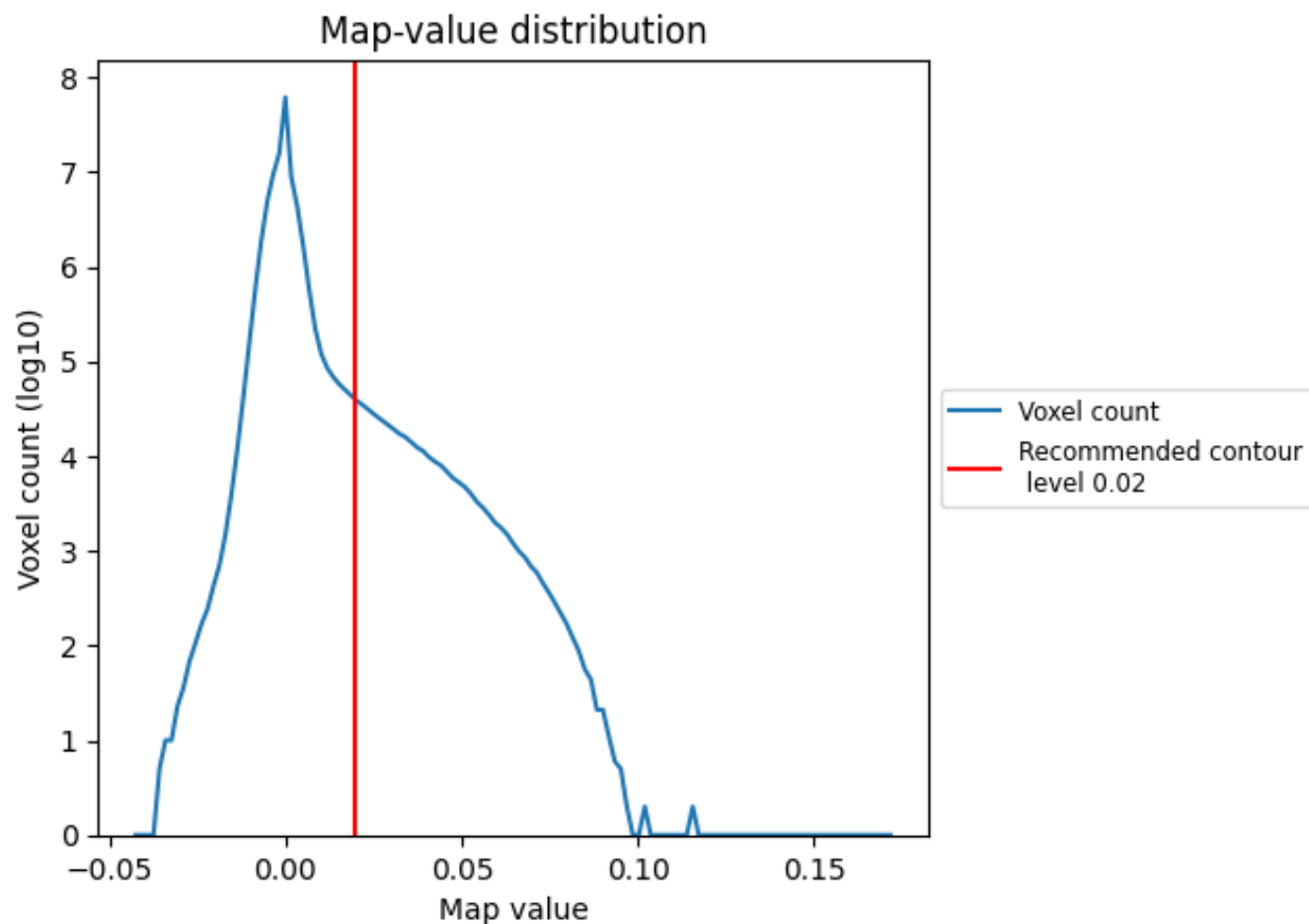
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

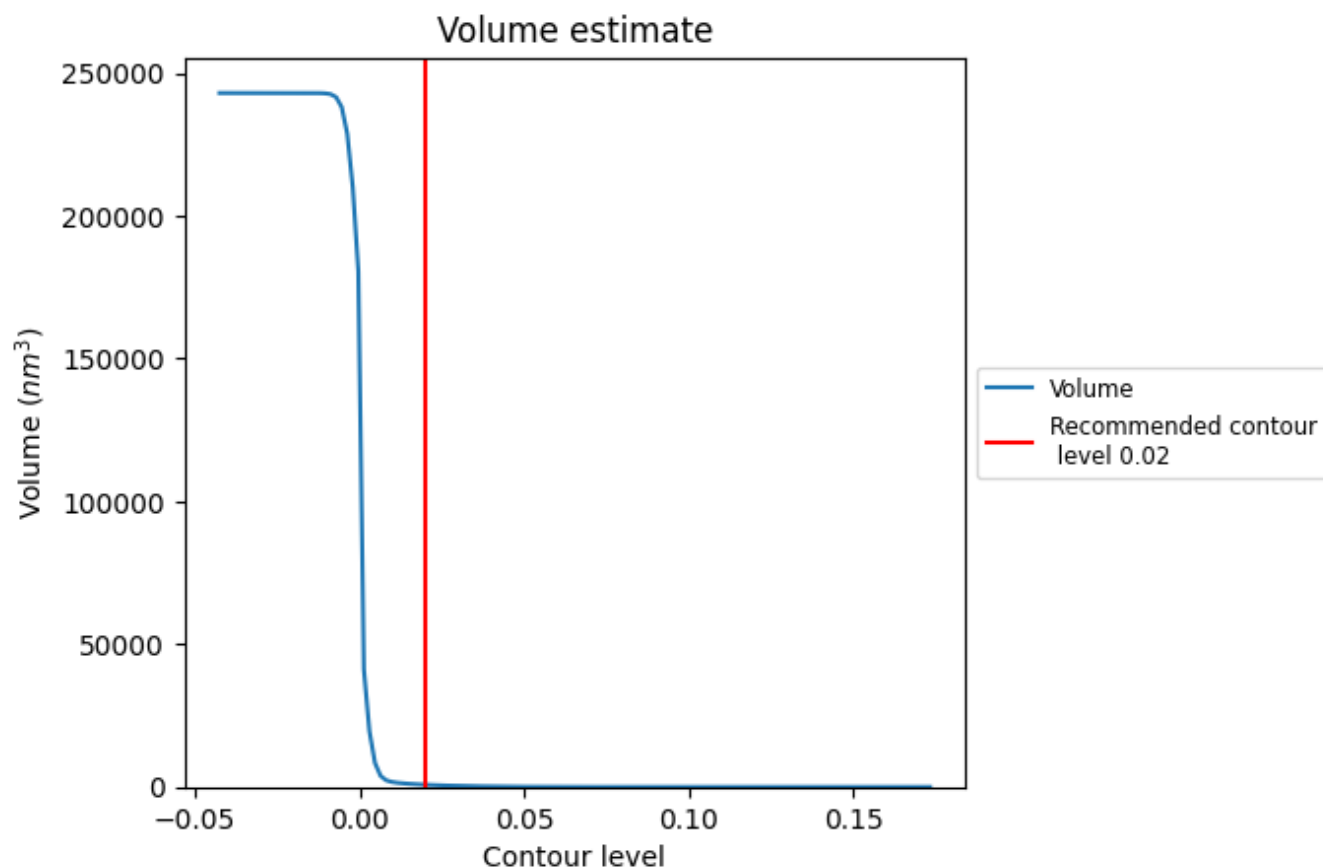
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

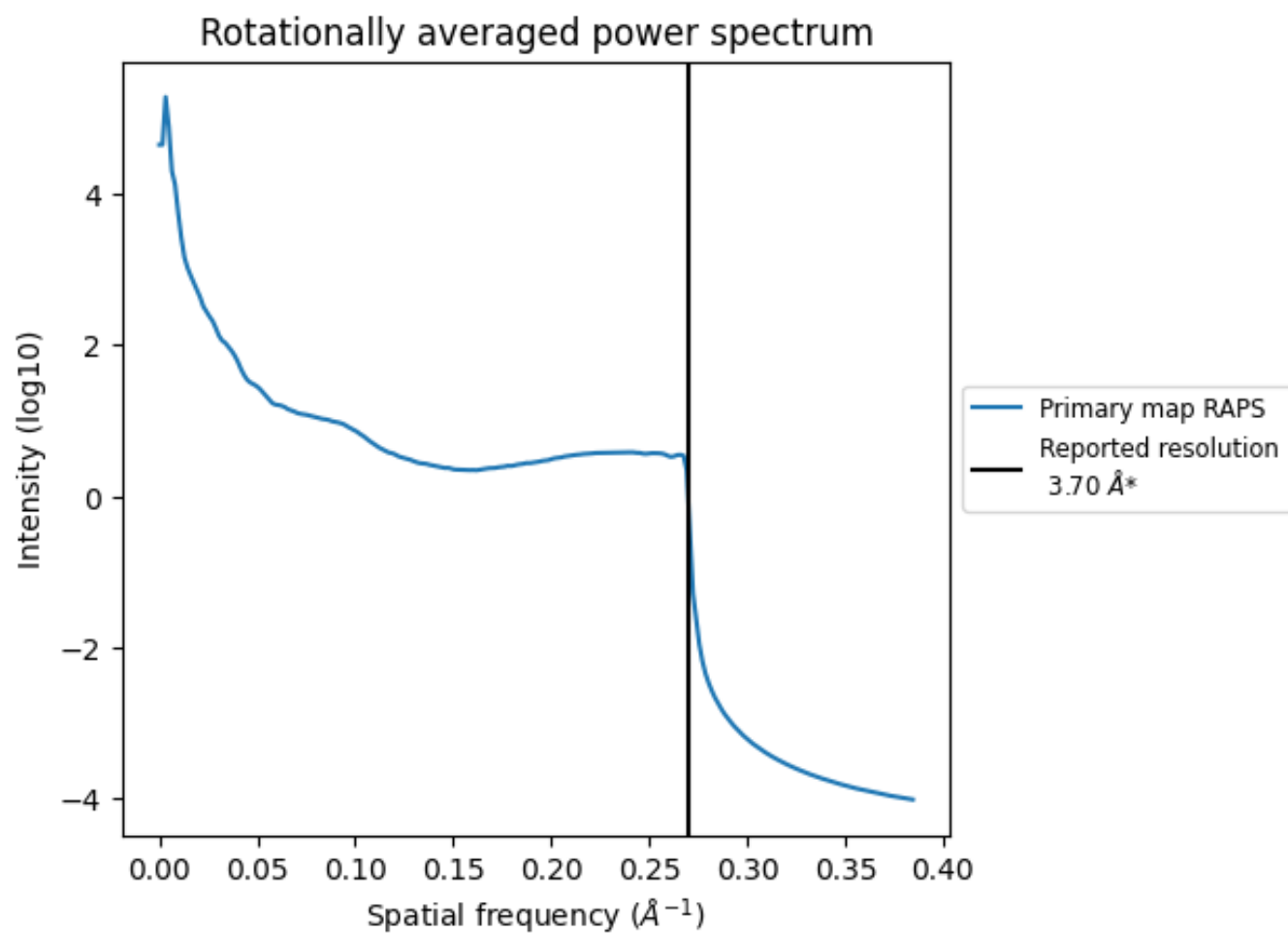
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 766 nm³; this corresponds to an approximate mass of 692 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 0.270 Å⁻¹

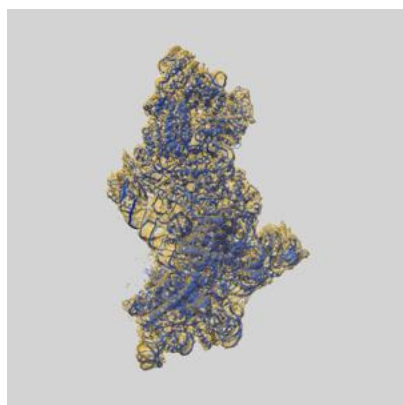
8 Fourier-Shell correlation ⓘ

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

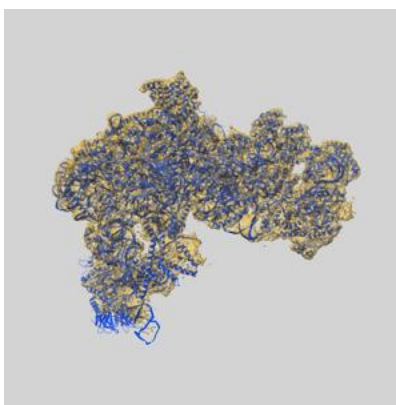
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7324 and PDB model 6C0F. Per-residue inclusion information can be found in section [3](#) on page [12](#).

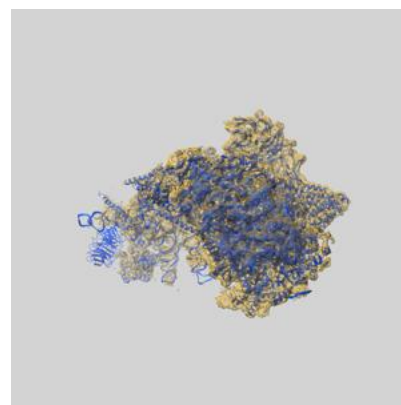
9.1 Map-model overlay [i](#)



X



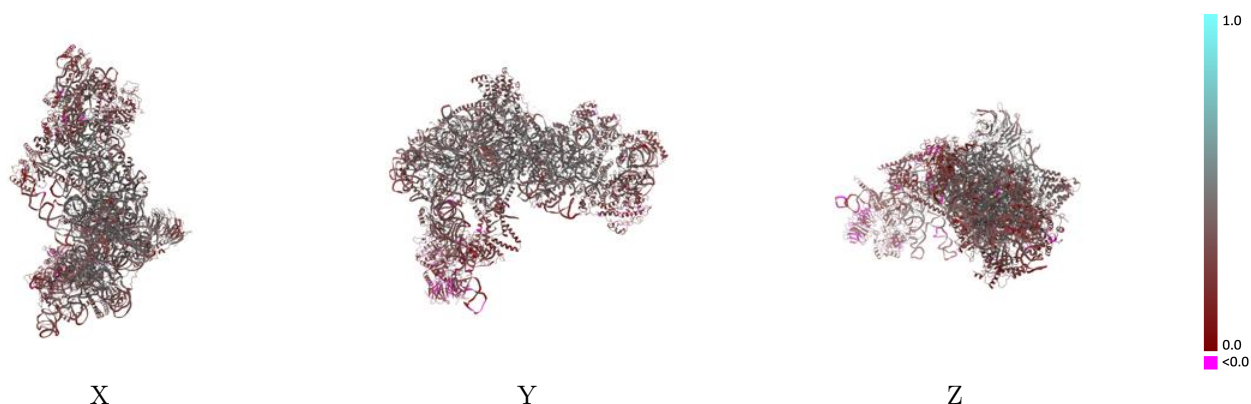
Y



Z

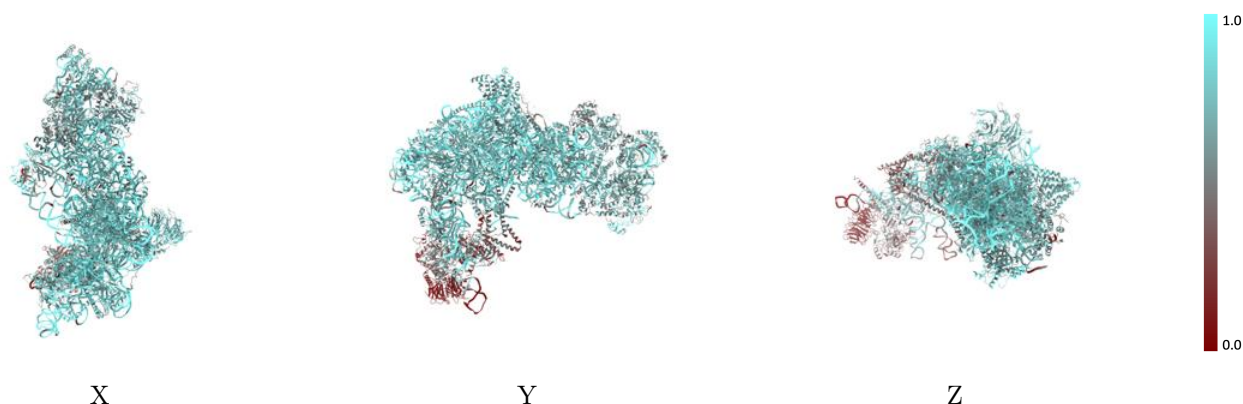
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



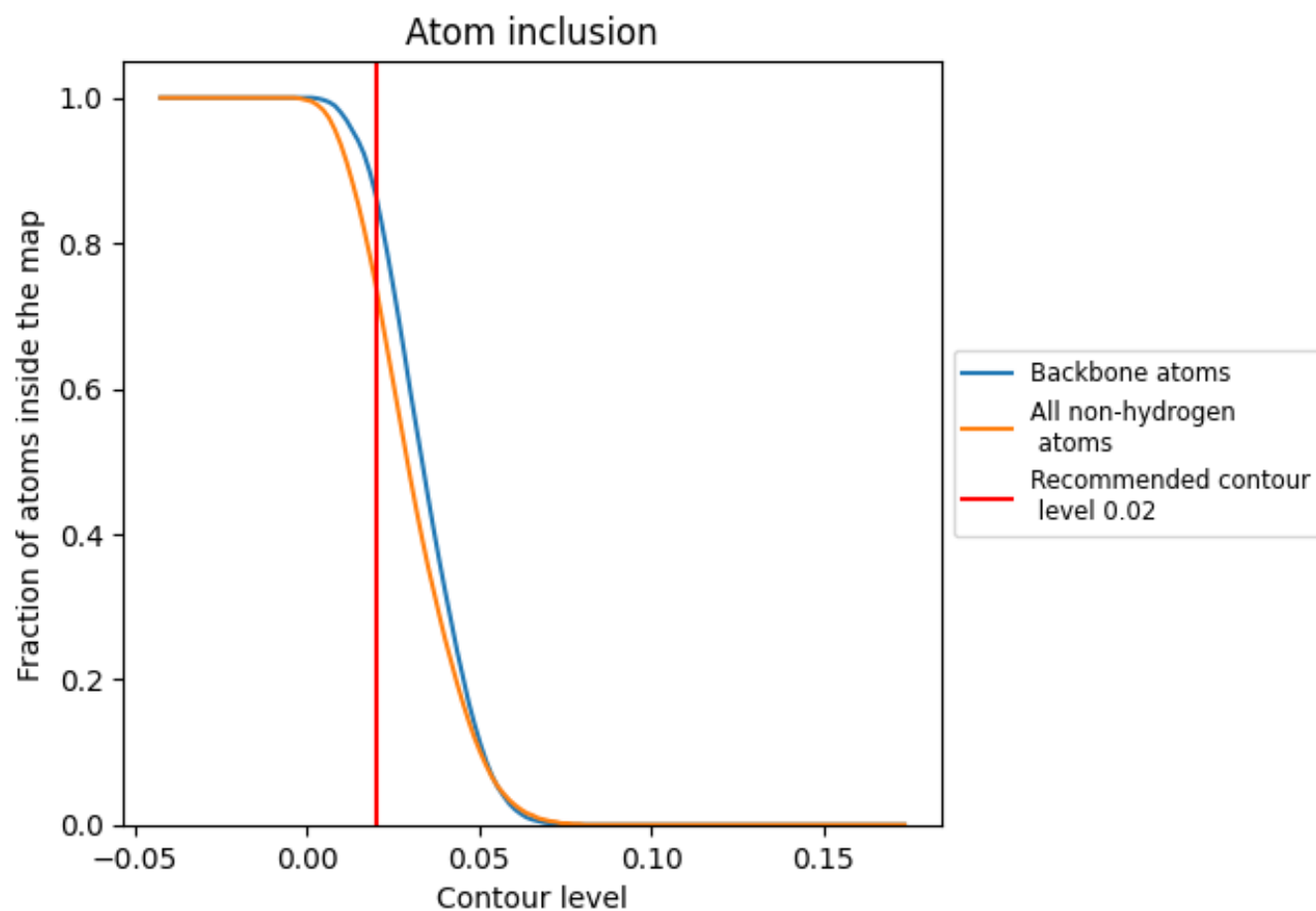
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 74% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7410	 0.3390
1	 0.8830	 0.3610
2	 0.8970	 0.3760
6	 0.9050	 0.3320
7	 0.6840	 0.3700
8	 0.3980	 0.2320
A	 0.7580	 0.3680
B	 0.6190	 0.3050
C	 0.8040	 0.4470
D	 0.8070	 0.4120
E	 0.7670	 0.3790
F	 0.7610	 0.3610
G	 0.7080	 0.3880
I	 0.7410	 0.3890
K	 0.6770	 0.2960
L	 0.8330	 0.4340
M	 0.7690	 0.3460
N	 0.7530	 0.4110
O	 0.7670	 0.3700
P	 0.7000	 0.4030
Q	 0.7990	 0.4310
S	 0.6840	 0.2910
V	 0.3040	 0.2010
W	 0.1450	 0.1650
Y	 0.7890	 0.4300
b	 0.6940	 0.3020
e	 0.6760	 0.4540
f	 0.8110	 0.4470
h	 0.7010	 0.3560
i	 0.7040	 0.3450
j	 0.7590	 0.4070
m	 0.8540	 0.2610
n	 0.6680	 0.2740
o	 0.6850	 0.2810
p	 0.6210	 0.3030



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Chain	Atom inclusion	Q-score
q	 0.0020	 0.0870
s	 0.7210	 0.3360
t	 0.6750	 0.2990
u	 0.3820	 0.1730
v	 0.3600	 0.2200
w	 0.2850	 0.1910
x	 0.8790	 0.3140
y	 0.3610	 0.1580
z	 0.7750	 0.3490