



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 11:44 AM UTC

PDB ID : 7BL5 / pdb_00007bl5
EMDB ID : EMD-12218
Title : pre-50S-ObgE particle
Authors : Hilal, T.; Nikolay, R.; Spahn, C.M.T.; Schmidt, S.
Deposited on : 2021-01-18
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

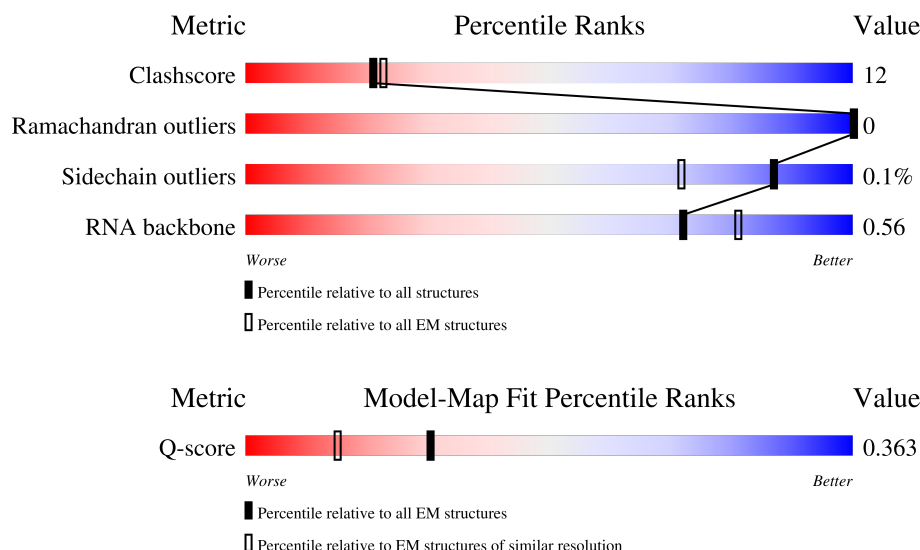
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	C	273	9% 71% 28% .
2	D	209	9% 69% 31%
3	E	201	19% 73% 27%

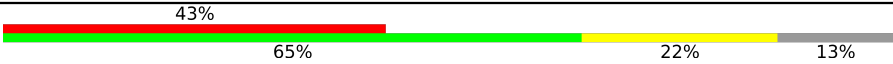
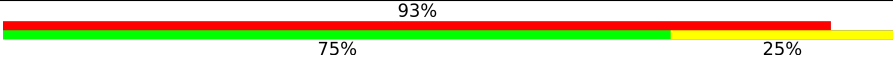
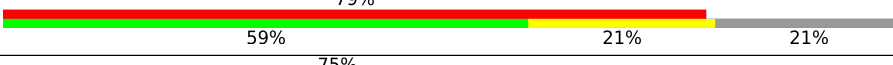
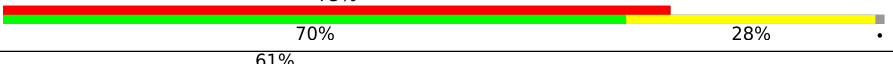
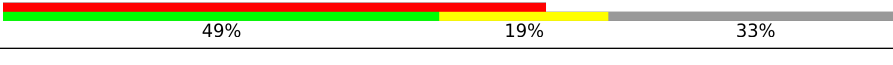
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Mol	Chain	Length	Quality of chain
4	G	177	
5	J	142	
6	L	144	
7	N	127	
8	O	117	
9	Q	118	
10	R	103	
11	S	110	
12	T	100	
13	U	104	
14	V	94	
15	W	85	
16	X	78	
17	Y	63	
18	Z	59	
19	0	57	
20	1	55	
21	2	46	
22	B	120	
23	I	142	
24	K	123	
25	P	115	
26	6	105	
27	7	326	
28	8	183	

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Mol	Chain	Length	Quality of chain
29	9	390	
30	M	136	
31	A	2919	
32	H	149	
33	e	165	
34	F	179	
35	b	70	

2 Entry composition

There are 39 unique types of molecules in this entry. The entry contains 98927 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 4 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	171	Total	C	N	O	S	0	0
			1281	806	235	238	2		

- Molecule 5 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 6 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 7 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 8 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	116	Total	C	N	O		0	0
			892	552	178	162			

- Molecule 9 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Q	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 10 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 11 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 12 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 13 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	U	102	Total	C	N	O		0	0
			779	492	146	141			

- Molecule 14 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 15 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	W	76	Total	C	N	O	S	0	0
			575	356	117	101	1		

- Molecule 16 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 17 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 18 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 19 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 20 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 21 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 22 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	B	119	Total	C	N	O	P	0	0
			2548	1135	466	829	118		

- Molecule 23 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 24 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 25 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	P	113	Total	C	N	O	S	0	0
			911	571	178	161	1		

- Molecule 26 is a protein called Ribosomal silencing factor RsfS.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	6	102	Total	C	N	O	S	0	0
			780	485	133	157	5		

- Molecule 27 is a protein called Ribosomal large subunit pseudouridine synthase D.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	7	317	Total	C	N	O	S	0	0
			2533	1593	471	457	12		

- Molecule 28 is a protein called UPF0307 protein YjgA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	8	157	Total	C	N	O	S	0	0
			1281	792	251	237	1		

- Molecule 29 is a protein called GTPase ObgE/CgtA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	9	338	Total	C	N	O	S	0	0
			2582	1626	453	490	13		

- Molecule 30 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 31 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	A	2913	Total	C	N	O	P	0	0
			62534	27897	11506	20218	2913		

- Molecule 32 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	H	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 33 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

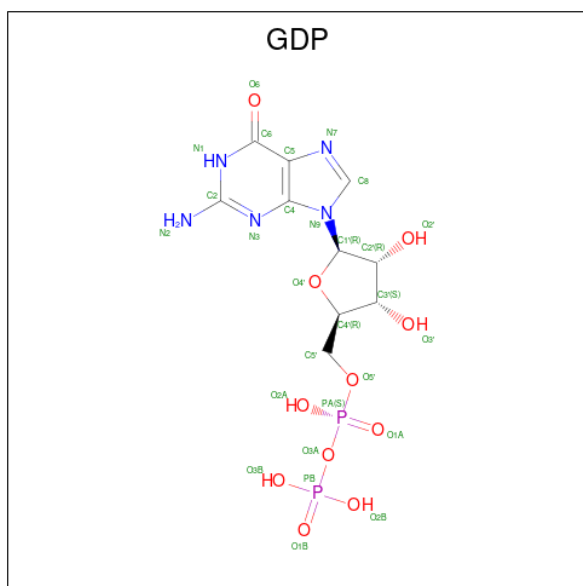
- Molecule 34 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	F	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 35 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b	47	Total	C	N	O	S	0	0
			364	227	64	67	6		

- Molecule 36 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
36	9	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	9	1	Total	Mg	0
			1	1	
37	A	1	Total	Mg	0
			1	1	

- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
38	b	1	Total	Zn	0
			1	1	

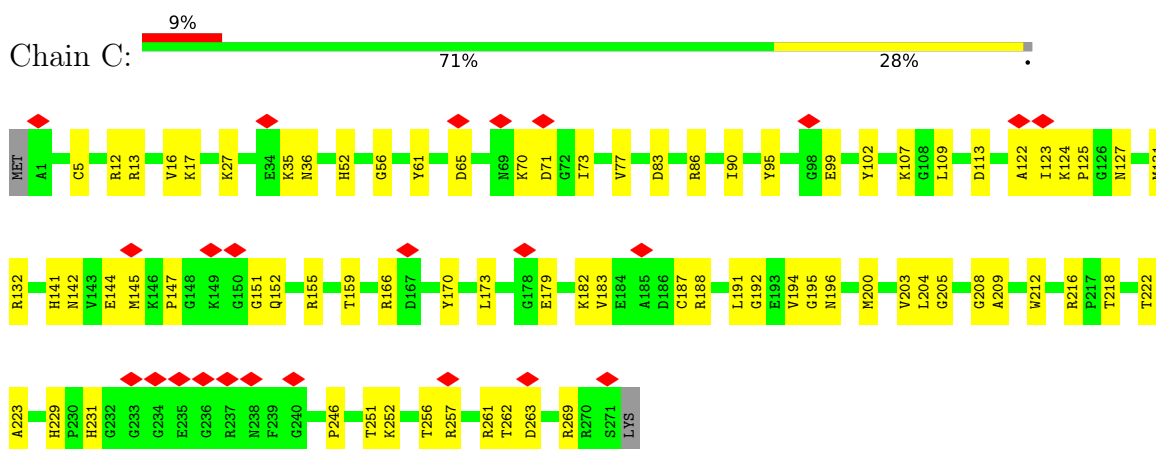
- Molecule 39 is water.

Mol	Chain	Residues	Atoms		AltConf
39	C	3	Total 3	O 3	0
39	D	1	Total 1	O 1	0
39	N	2	Total 2	O 2	0
39	S	1	Total 1	O 1	0
39	2	1	Total 1	O 1	0
39	B	1	Total 1	O 1	0
39	A	17	Total 17	O 17	0
39	F	1	Total 1	O 1	0

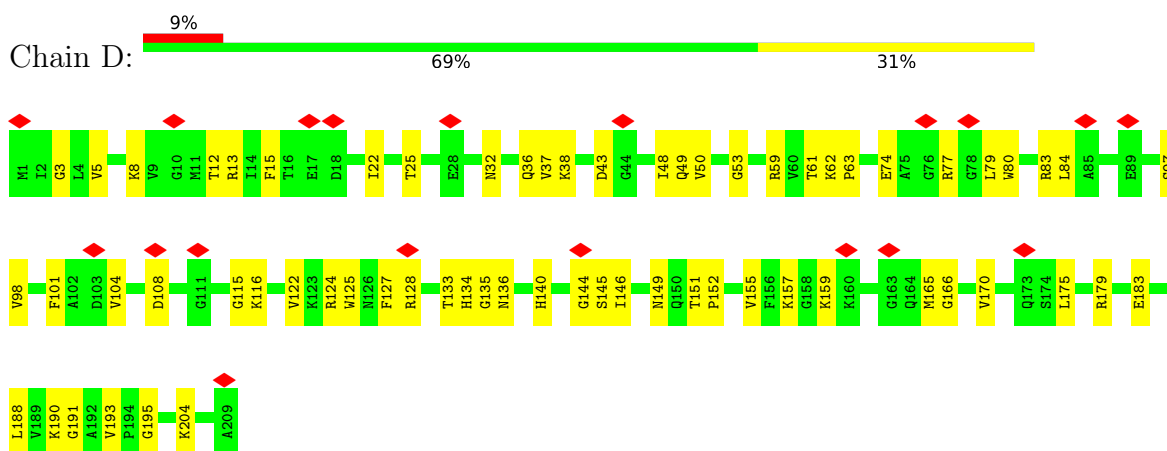
3 Residue-property plots

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

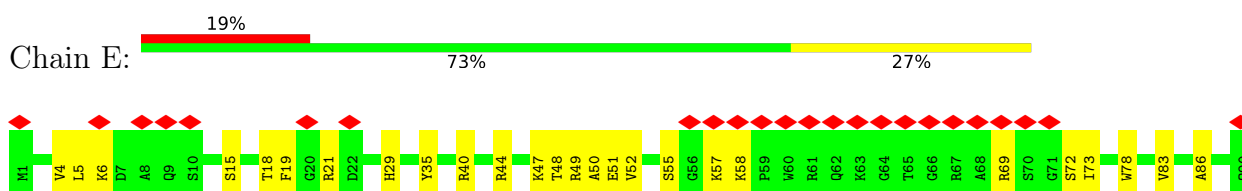
• Molecule 1: 50S ribosomal protein L2

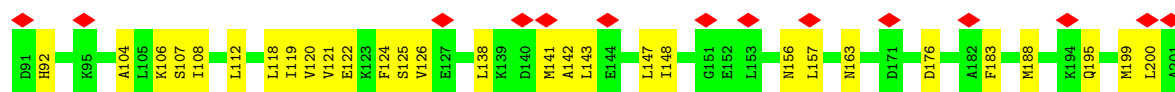


• Molecule 2: 50S ribosomal protein L3



• Molecule 3: 50S ribosomal protein L4

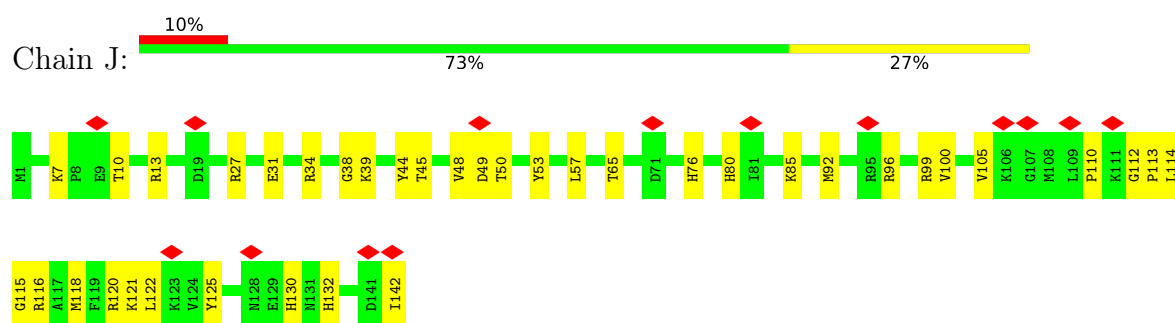




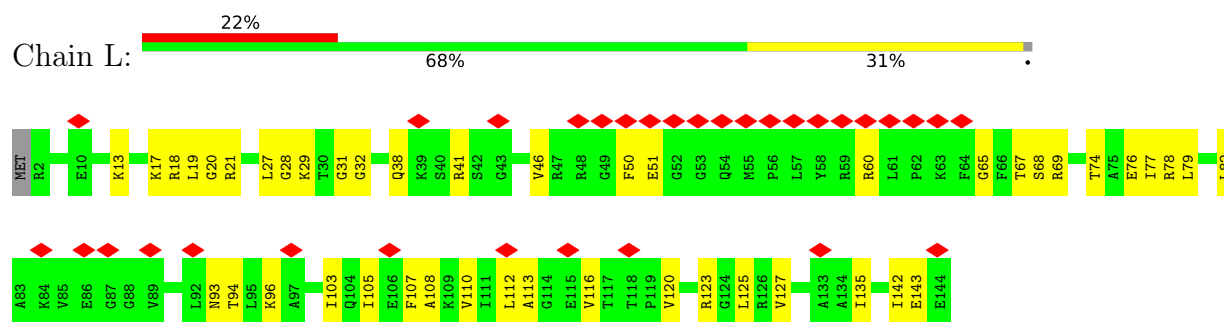
- Molecule 4: 50S ribosomal protein L6



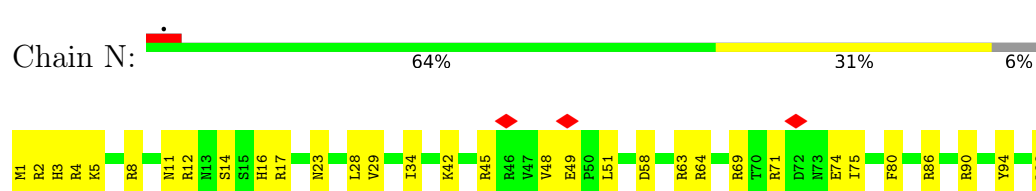
- Molecule 5: 50S ribosomal protein L13



- Molecule 6: 50S ribosomal protein L15

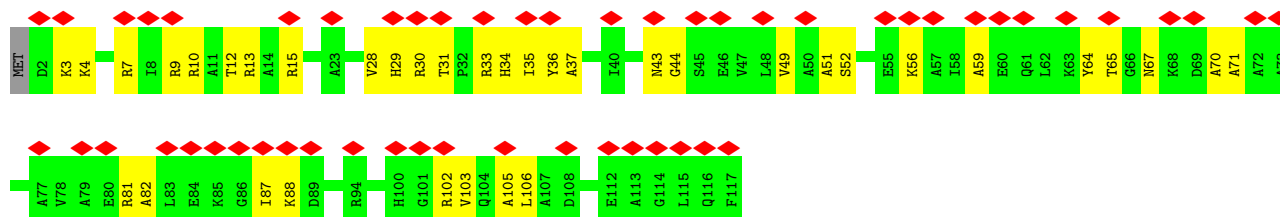


- Molecule 7: 50S ribosomal protein L17

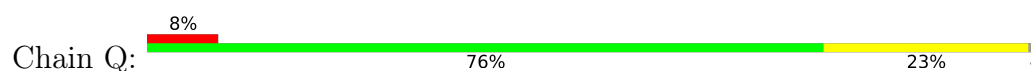




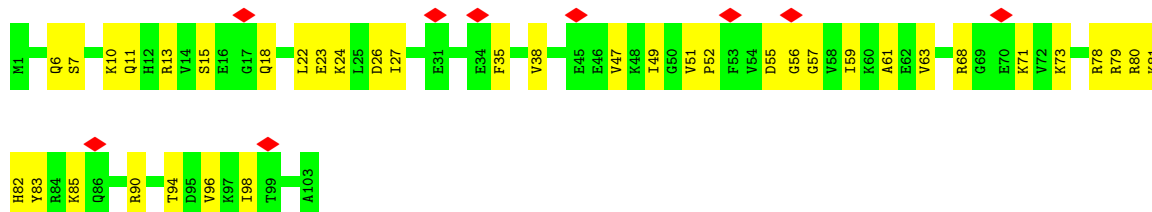
- Molecule 8: 50S ribosomal protein L18



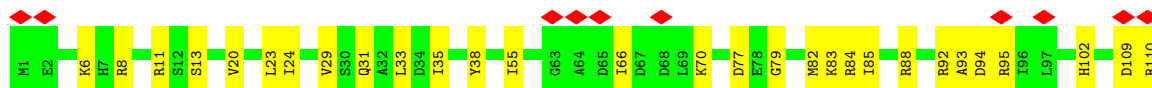
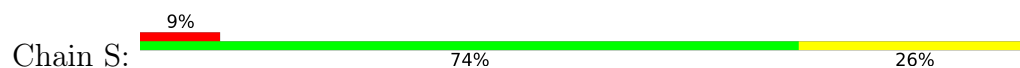
- Molecule 9: 50S ribosomal protein L20



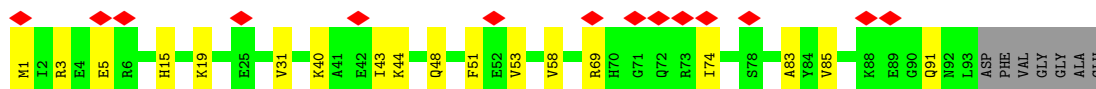
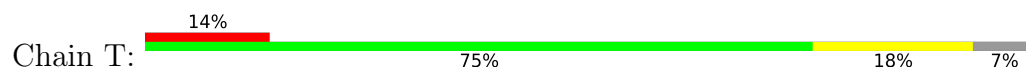
- Molecule 10: 50S ribosomal protein L21



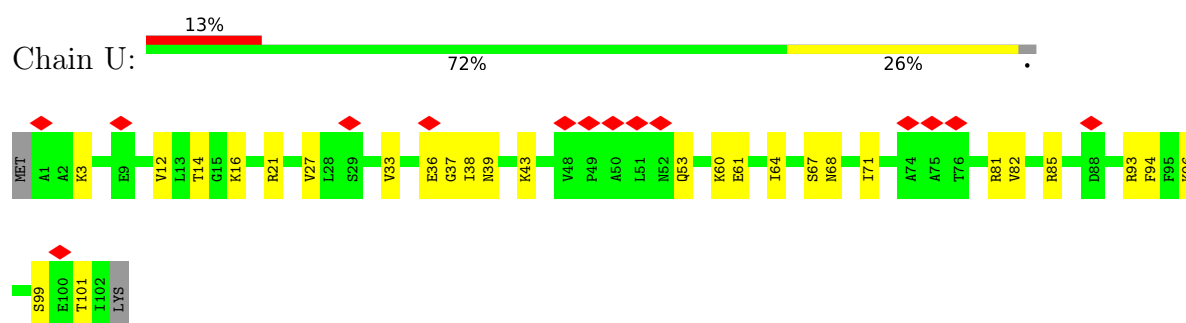
- Molecule 11: 50S ribosomal protein L22



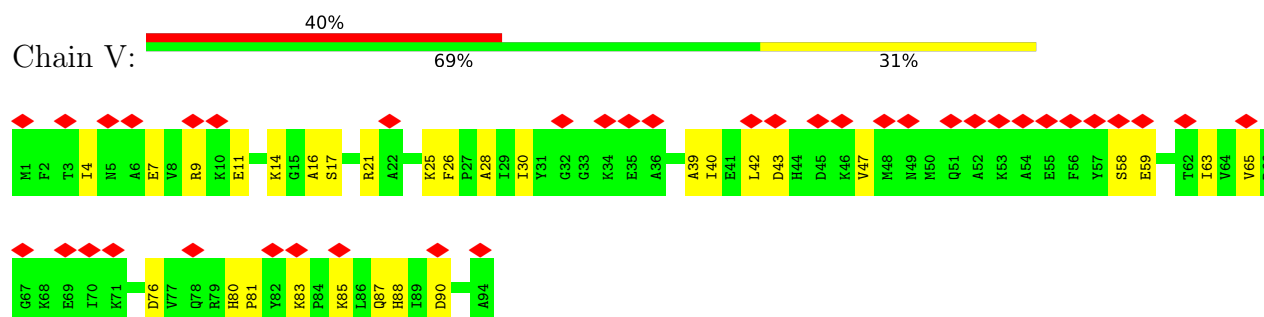
- Molecule 12: 50S ribosomal protein L23



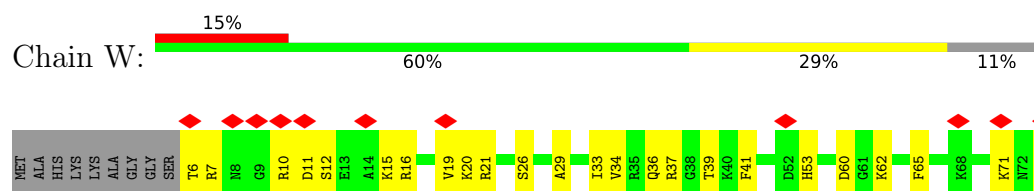
- Molecule 13: 50S ribosomal protein L24



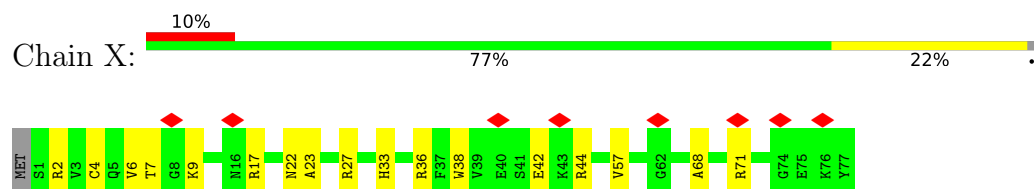
- Molecule 14: 50S ribosomal protein L25



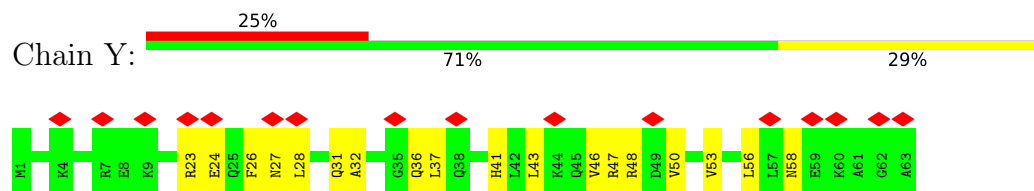
- Molecule 15: 50S ribosomal protein L27



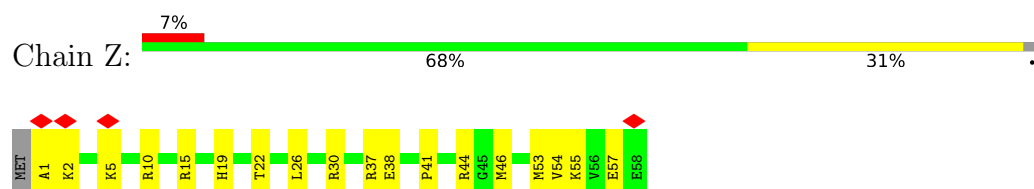
- Molecule 16: 50S ribosomal protein L28



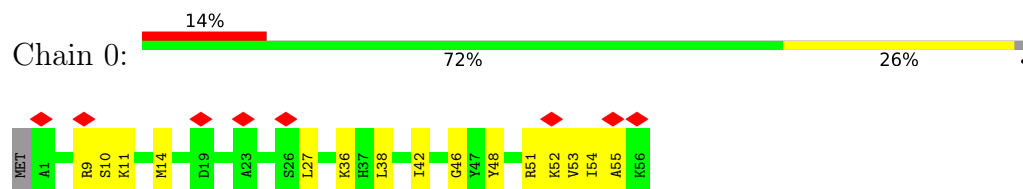
- Molecule 17: 50S ribosomal protein L29



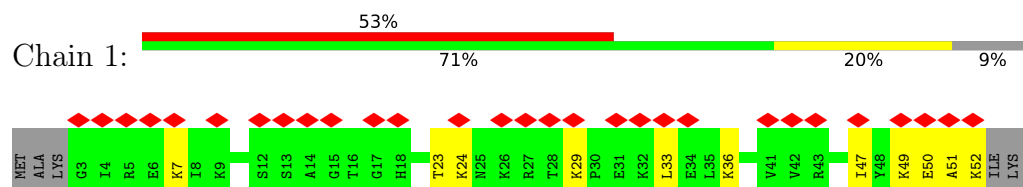
- Molecule 18: 50S ribosomal protein L30



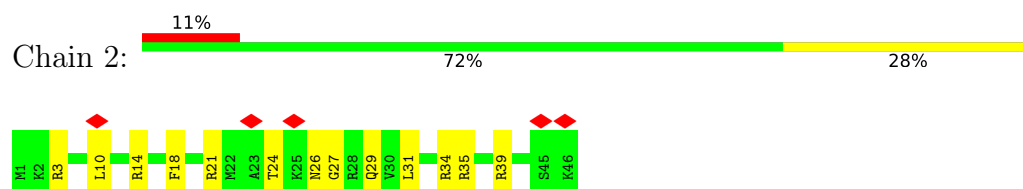
- Molecule 19: 50S ribosomal protein L32



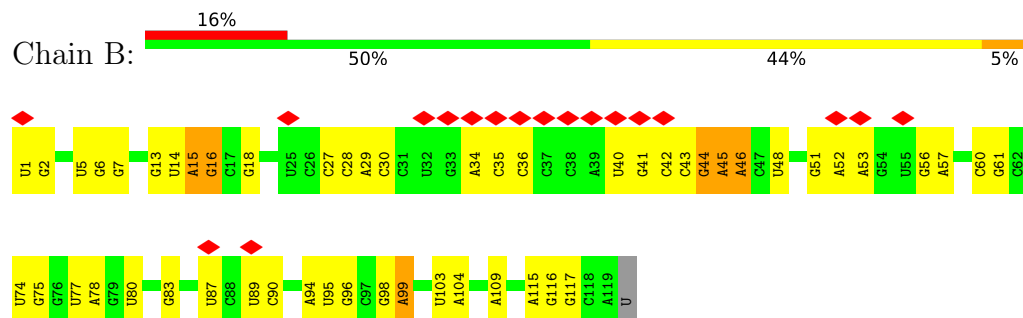
- Molecule 20: 50S ribosomal protein L33



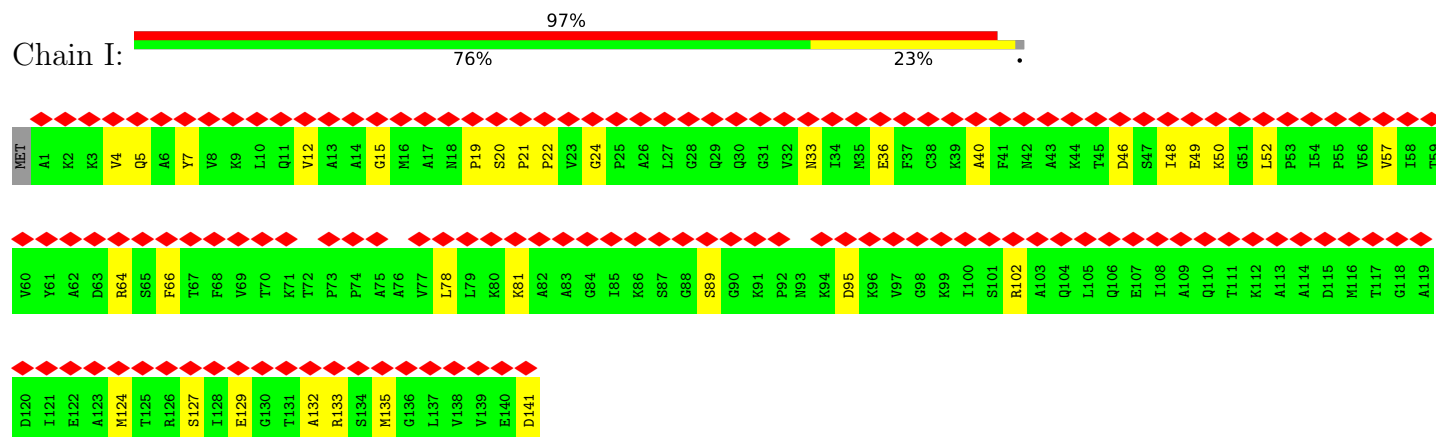
- Molecule 21: 50S ribosomal protein L34



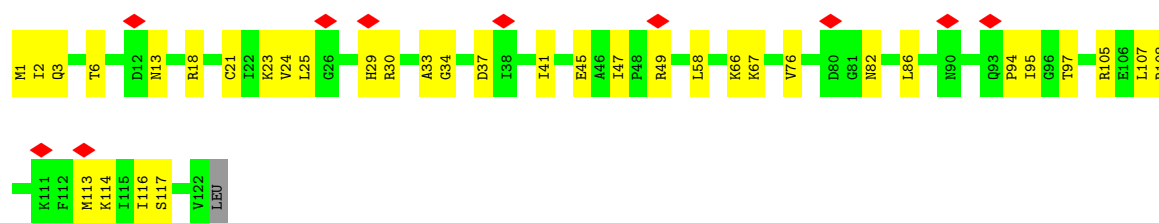
- Molecule 22: 5S ribosomal RNA



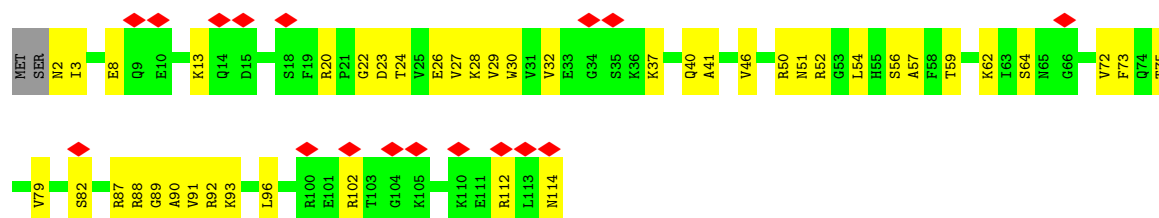
- Molecule 23: 50S ribosomal protein L11



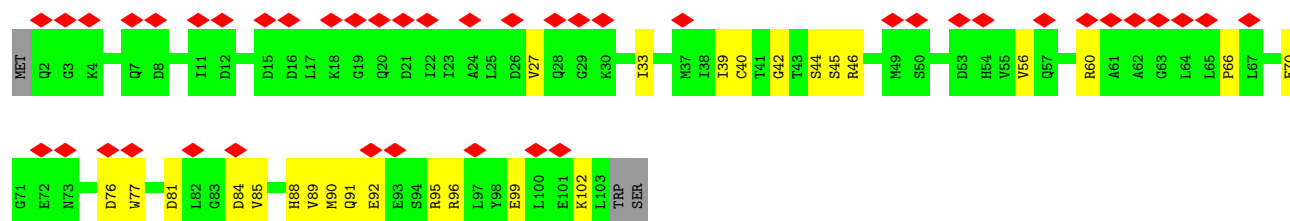
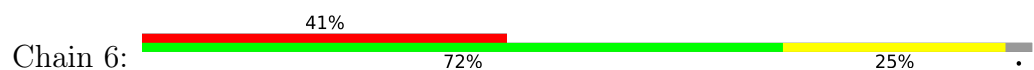
- Molecule 24: 50S ribosomal protein L14



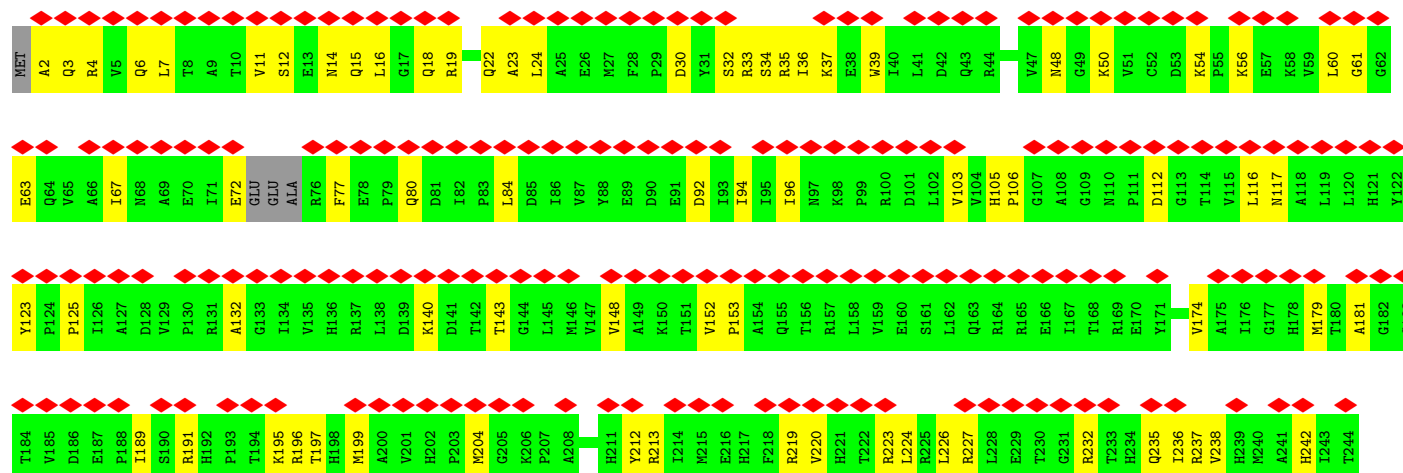
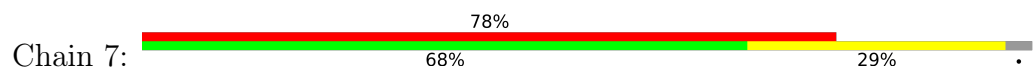
- Molecule 25: 50S ribosomal protein L19



- Molecule 26: Ribosomal silencing factor RsfS

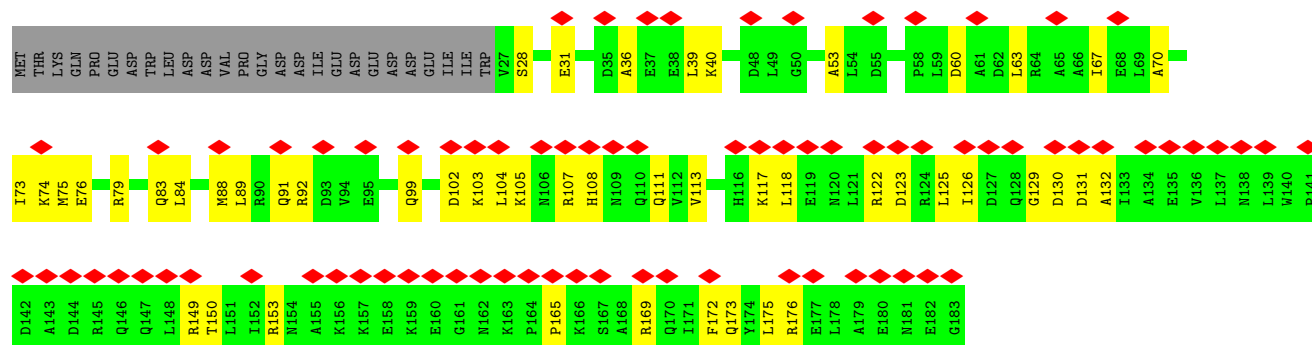
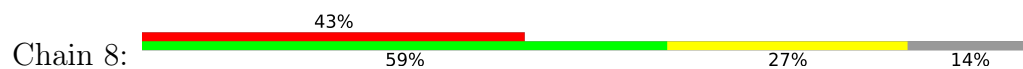


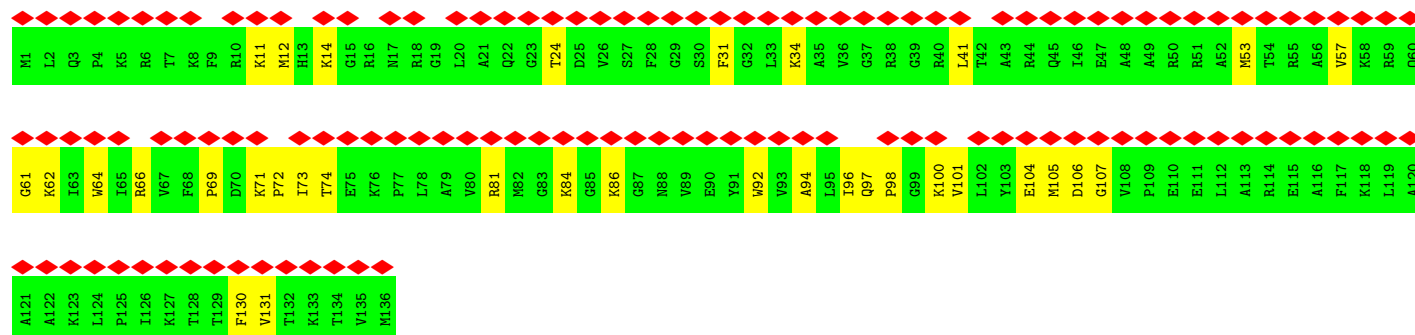
- Molecule 27: Ribosomal large subunit pseudouridine synthase D



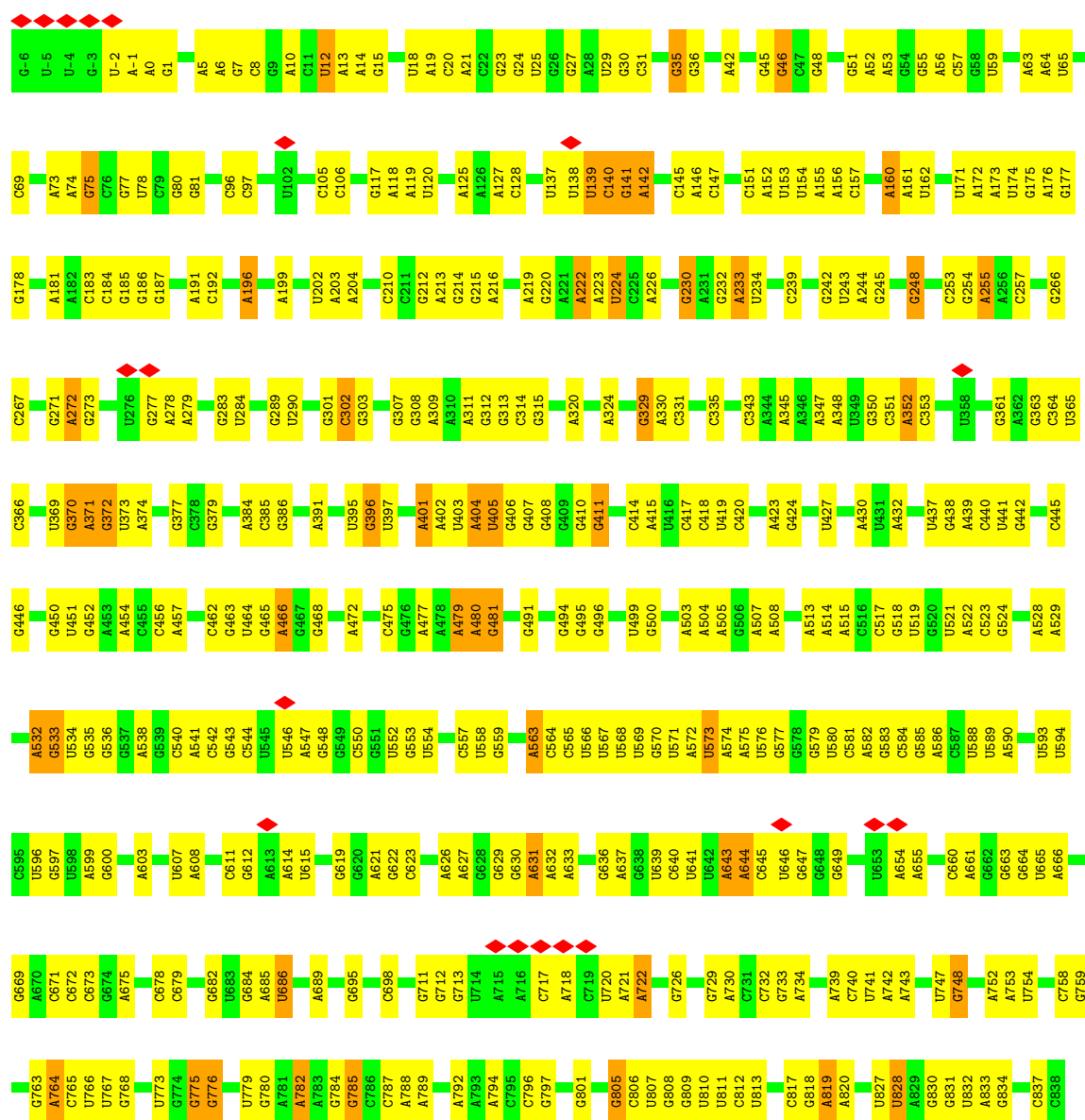


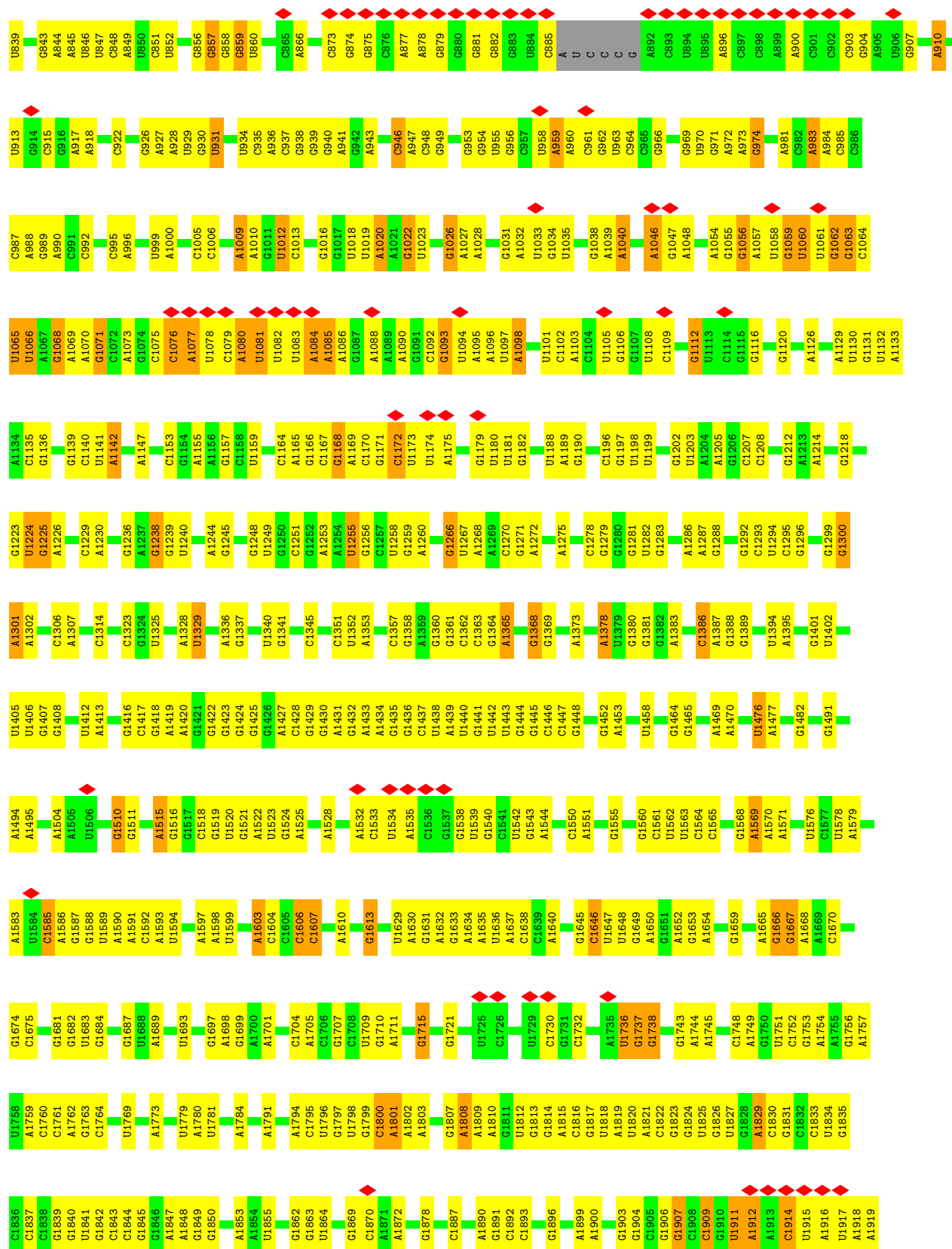
• Molecule 28: UPF0307 protein YjgA

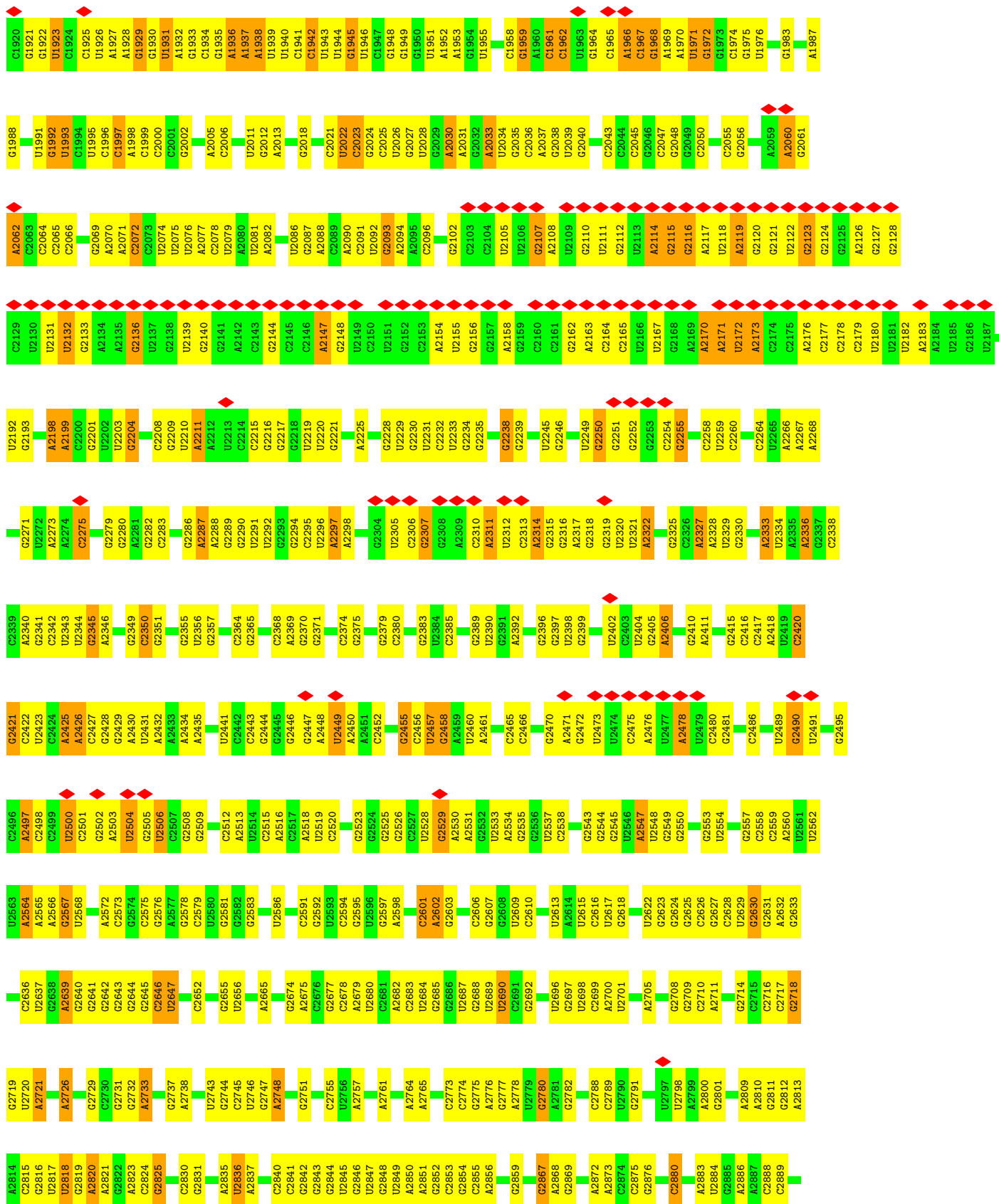


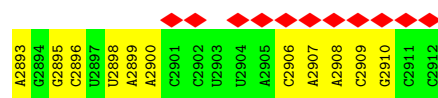


● Molecule 31: 23S ribosomal RNA

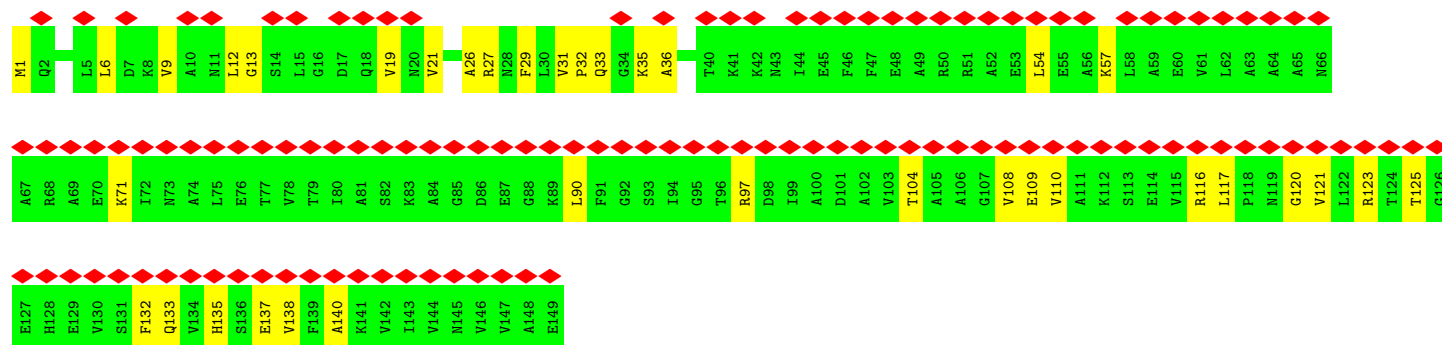
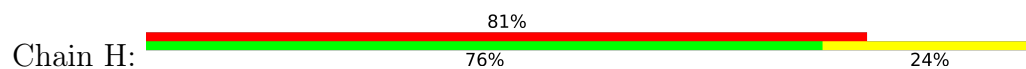




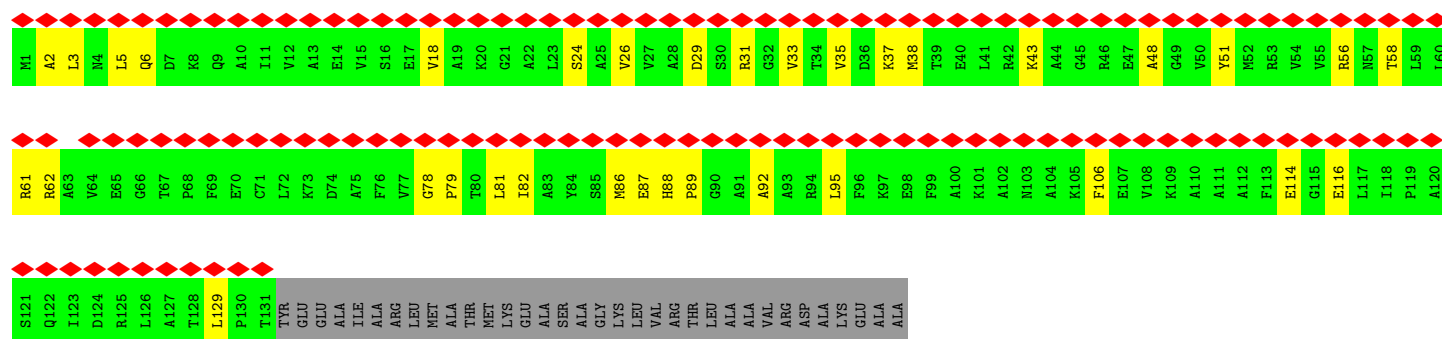
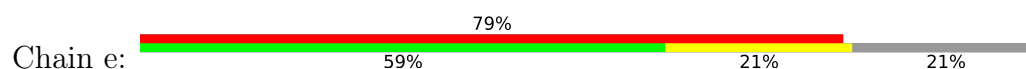




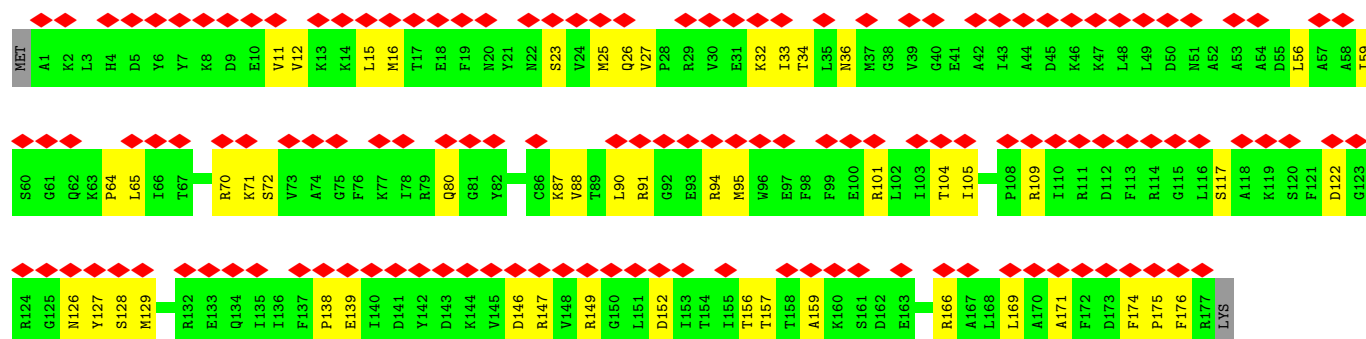
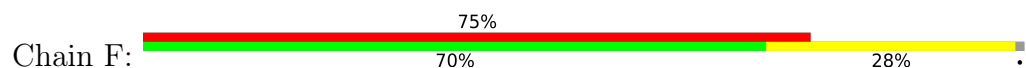
• Molecule 32: 50S ribosomal protein L9



• Molecule 33: 50S ribosomal protein L10



• Molecule 34: 50S ribosomal protein L5



• Molecule 35: 50S ribosomal protein L31



M1	K2	K3	D4	K8	Y9	E10	E11	I12	T13	A14	S15	C16	S17	C18	G19	N20	V21	N22	K23	I24	R25	S26	T27	V28	G29	H30	D31	L32	N33	L34	D35	V36	C37	S38	K39	C40	H41	P42	F43	F44	T45	G46	K47	G48	G49	G50	G51	G52	G53	G54	G55	G56	G57	G58	G59	G60	G61	G62	G63	G64	G65	G66	G67	G68	G69	G70	G71	G72	G73	G74	G75	G76	G77	G78	G79	G80	G81	G82	G83	G84	G85	G86	G87	G88	G89	G90	G91	G92	G93	G94	G95	G96	G97	G98	G99	G100	G101	G102	G103	G104	G105	G106	G107	G108	G109	G110	G111	G112	G113	G114	G115	G116	G117	G118	G119	G120	G121	G122	G123	G124	G125	G126	G127	G128	G129	G130	G131	G132	G133	G134	G135	G136	G137	G138	G139	G140	G141	G142	G143	G144	G145	G146	G147	G148	G149	G150	G151	G152	G153	G154	G155	G156	G157	G158	G159	G160	G161	G162	G163	G164	G165	G166	G167	G168	G169	G170	G171	G172	G173	G174	G175	G176	G177	G178	G179	G180	G181	G182	G183	G184	G185	G186	G187	G188	G189	G190	G191	G192	G193	G194	G195	G196	G197	G198	G199	G200	G201	G202	G203	G204	G205	G206	G207	G208	G209	G210	G211	G212	G213	G214	G215	G216	G217	G218	G219	G220	G221	G222	G223	G224	G225	G226	G227	G228	G229	G230	G231	G232	G233	G234	G235	G236	G237	G238	G239	G240	G241	G242	G243	G244	G245	G246	G247	G248	G249	G250	G251	G252	G253	G254	G255	G256	G257	G258	G259	G260	G261	G262	G263	G264	G265	G266	G267	G268	G269	G270	G271	G272	G273	G274	G275	G276	G277	G278	G279	G280	G281	G282	G283	G284	G285	G286	G287	G288	G289	G290	G291	G292	G293	G294	G295	G296	G297	G298	G299	G300	G301	G302	G303	G304	G305	G306	G307	G308	G309	G310	G311	G312	G313	G314	G315	G316	G317	G318	G319	G320	G321	G322	G323	G324	G325	G326	G327	G328	G329	G330	G331	G332	G333	G334	G335	G336	G337	G338	G339	G340	G341	G342	G343	G344	G345	G346	G347	G348	G349	G350	G351	G352	G353	G354	G355	G356	G357	G358	G359	G360	G361	G362	G363	G364	G365	G366	G367	G368	G369	G370	G371	G372	G373	G374	G375	G376	G377	G378	G379	G380	G381	G382	G383	G384	G385	G386	G387	G388	G389	G390	G391	G392	G393	G394	G395	G396	G397	G398	G399	G400	G401	G402	G403	G404	G405	G406	G407	G408	G409	G410	G411	G412	G413	G414	G415	G416	G417	G418	G419	G420	G421	G422	G423	G424	G425	G426	G427	G428	G429	G430	G431	G432	G433	G434	G435	G436	G437	G438	G439	G440	G441	G442	G443	G444	G445	G446	G447	G448	G449	G450	G451	G452	G453	G454	G455	G456	G457	G458	G459	G460	G461	G462	G463	G464	G465	G466	G467	G468	G469	G470	G471	G472	G473	G474	G475	G476	G477	G478	G479	G480	G481	G482	G483	G484	G485	G486	G487	G488	G489	G490	G491	G492	G493	G494	G495	G496	G497	G498	G499	G500	G501	G502	G503	G504	G505	G506	G507	G508	G509	G510	G511	G512	G513	G514	G515	G516	G517	G518	G519	G520	G521	G522	G523	G524	G525	G526	G527	G528	G529	G530	G531	G532	G533	G534	G535	G536	G537	G538	G539	G540	G541	G542	G543	G544	G545	G546	G547	G548	G549	G550	G551	G552	G553	G554	G555	G556	G557	G558	G559	G560	G561	G562	G563	G564	G565	G566	G567	G568	G569	G570	G571	G572	G573	G574	G575	G576	G577	G578	G579	G580	G581	G582	G583	G584	G585	G586	G587	G588	G589	G590	G591	G592	G593	G594	G595	G596	G597	G598	G599	G600	G601	G602	G603	G604	G605	G606	G607	G608	G609	G610	G611	G612	G613	G614	G615	G616	G617	G618	G619	G620	G621	G622	G623	G624	G625	G626	G627	G628	G629	G630	G631	G632	G633	G634	G635	G636	G637	G638	G639	G640	G641	G642	G643	G644	G645	G646	G647	G648	G649	G650	G651	G652	G653	G654	G655	G656	G657	G658	G659	G660	G661	G662	G663	G664	G665	G666	G667	G668	G669	G670	G671	G672	G673	G674	G675	G676	G677	G678	G679	G680	G681	G682	G683	G684	G685	G686	G687	G688	G689	G690	G691	G692	G693	G694	G695	G696	G697	G698	G699	G700	G701	G702	G703	G704	G705	G706	G707	G708	G709	G710	G711	G712	G713	G714	G715	G716	G717	G718	G719	G720	G721	G722	G723	G724	G725	G726	G727	G728	G729	G730	G731	G732	G733	G734	G735	G736	G737	G738	G739	G740	G741	G742	G743	G744	G745	G746	G747	G748	G749	G750	G751	G752	G753	G754	G755	G756	G757	G758	G759	G760	G761	G762	G763	G764	G765	G766	G767	G768	G769	G770	G771	G772	G773	G774	G775	G776	G777	G778	G779	G780	G781	G782	G783	G784	G785	G786	G787	G788	G789	G790	G791	G792	G793	G794	G795	G796	G797	G798	G799	G800	G801	G802	G803	G804	G805	G806	G807	G808	G809	G810	G811	G812	G813	G814	G815	G816	G817	G818	G819	G820	G821	G822	G823	G824	G825	G826	G827	G828	G829	G830	G831	G832	G833	G834	G835	G836	G837	G838	G839	G840	G841	G842	G843	G844	G845	G846	G847	G848	G849	G850	G851	G852	G853	G854	G855	G856	G857	G858	G859	G860	G861	G862	G863	G864	G865	G866	G867	G868	G869	G870	G871	G872	G873	G874	G875	G876	G877	G878	G879	G880	G881	G882	G883	G884	G885	G886	G887	G888	G889	G890	G891	G892	G893	G894	G895	G896	G897	G898	G899	G900	G901	G902	G903	G904	G905	G906	G907	G908	G909	G910	G911	G912	G913	G914	G915	G916	G917	G918	G919	G920	G921	G922	G923	G924	G925	G926	G927	G928	G929	G930	G931	G932	G933	G934	G935	G936	G937	G938	G939	G940	G941	G942	G943	G944	G945	G946	G947	G948	G949	G950	G951	G952	G953	G954	G955	G956	G957	G958	G959	G960	G961	G962	G963	G964	G965	G966	G967	G968	G969	G970	G971	G972	G973	G974	G975	G976	G977	G978	G979	G980	G981	G982	G983	G984	G985	G986	G987	G988	G989	G990	G991	G992	G993	G994	G995	G996	G997	G998	G999	G1000	G1001	G1002	G1003	G1004	G1005	G1006	G1007	G1008	G1009	G1010	G1011	G1012	G1013	G1014	G1015	G1016	G1017	G1018	G1019	G1020	G1021	G1022	G1023	G1024	G1025	G1026	G1027	G1028	G1029	G1030	G1031	G1032	G1033	G1034	G1035	G1036	G1037	G1038	G1039	G1040	G1041	G1042	G1043	G1044	G1045	G1046	G1047	G1048	G1049	G1050	G1051	G1052	G1053	G1054	G1055	G1056	G1057	G1058	G1059	G1060	G1061	G1062	G1063	G1064	G1065	G1066	G1067	G1068	G1069	G1070	G1071	G1072	G1073	G1074	G1075	G1076	G1077	G1078	G1079	G1080	G1081	G1082	G1083	G1084	G1085	G1086	G1087	G1088	G1089	G1090	G1091	G1092	G1093	G1094	G1095	G1096	G1097	G1098	G1099	G1100	G1101	G1102	G1103	G1104	G1105	G1106	G1107	G1108	G1109	G1110	G1111	G1112	G1113	G1114	G1115	G1116	G1117	G1118	G1119	G1120	G1121	G1122	G1123	G1124	G1125	G1126	G1127	G1128	G1129	G1130	G1131	G1132	G1133	G1134	G1135	G1136	G1137	G1138	G1139	G1140	G1141	G1142	G1143	G1144	G1145	G1146	G1147	G1148	G1149	G1150	G1151	G1152	G1153	G1154	G1155	G1156	G1157	G1158	G1159	G1160	G1161	G1162	G1163	G1164	G1165	G1166	G1167	G1168	G1169	G1170	G1171	G1172	G1173	G1174	G1175	G1176	G1177	G1178	G1179	G1180	G1181	G1182	G1183	G1184	G1185	G1186	G1187	G1188	G1189	G1190	G1191	G1192	G1193	G1194	G1195	G1196	G1197	G1198	G1199	G1200	G1201	G1202	G1203	G1204	G1205	G1206	G1207	G1208	G1209	G1210	G1211	G1212	G1213	G1214	G1215	G1216	G1217	G1218	G1219	G1220	G1221	G1222	G1223	G1224	G1225	G1226	G1227	G1228	G1229	G1230	G1231	G1232	G1233	G1234	G1235	G1236	G1237	G1238	G1239	G1240	G1241	G1242	G1243	G1244	G1245	G1246	G1247	G1248	G1249	G1250	G1251	G1252	G1253	G1254	G1255	G1256	G1257	G1258	G1259	G1260	G1261	G1262	G1263	G1264	G1265	G1266	G1267	G1268	G1269	G1270	G1271	G1272	G1273	G1274	G1275	G1276	G1277	G1278	G1279	G1280	G1281	G1282	G1283	G1284	G1285	G1286	G1287	G1288	G1289	G1290	G1291	G1292	G1293	G1294	G1295	G1296	G1297	G1298	G1299	G1300	G1301	G1302	G1303	G1304	G1305	G1306	G1307	G1308	G1309	G1310	G1311	G1312	G1313	G1314	G1315	G1316	G1317	G1318	G1319	G1320	G1321	G1322	G1323	G1324	G1325	G1326	G1327	G1328	G1329	G1330	G1331	G1332	G1333	G1334	G1335	G1336	G1337	G1338	G1339	G1340	G1341	G1342	G1343	G1344	G1345	G1346	G1347	G1348	G1349	G1350	G1351	G1352	G1353	G1354	G1355	G1356	G1357	G1358	G1359	G1360	G1361	G1362	G1363	G1364	G1365	G1366	G1367	G1368	G1369	G1370	G1371	G1372	G1373	G1374	G1375	G1376	G1377	G1378	G1379	G1380	G1381	G1382	G1383	G1384	G1385	G1386	G1387	G1388	G1389	G1390	G1391	G1392	G1393	G1394	G1395	G1396	G1397	G1398	G1399	G1400	G1401	G1402	G1403	G1404	G1405	G1406	G1407	G1408	G1409	G1410	G1411	G1412	G1413	G1414	G1415	G1416	G1417	G1418	G1419	G1420	G1421	G1422	G1423	G1424	G1425	G1426	G1427	G1428	G1429	G1430	G1431	G1432	G1433	G1434	G1435	G1436	G1437	G1438	G1439	G1440	G1441	G1442	G1443	G1444	G1445	G1446	G1447	G1448	G1449	G1450	G1451	G1452	G1453	G1454	G1455	G1456	G1457	G1458	G1459	G1460	G1461	G1462	G1463	G1464	G1465	G1466	G1467	G1468	G1469	G1470	G1471	G1472	G1473	G1474	G1475	G1476	G1477	G1478	G1479	G1480	G1481
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	22282	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	36000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	13.174	Depositor
Minimum map value	-5.976	Depositor
Average map value	0.034	Depositor
Map value standard deviation	0.789	Depositor
Recommended contour level	2.5	Depositor
Map size (Å)	334.8, 334.8, 334.8	wwPDB
Map dimensions	270, 270, 270	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.24, 1.24, 1.24	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, MG, 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	C	0.12	0/2121	0.33	0/2852
2	D	0.12	0/1586	0.35	0/2134
3	E	0.09	0/1571	0.28	0/2113
4	G	0.11	0/1301	0.31	0/1764
5	J	0.10	0/1152	0.28	0/1551
6	L	0.13	0/1054	0.44	0/1403
7	N	0.13	0/973	0.37	0/1301
8	O	0.11	0/902	0.32	0/1209
9	Q	0.10	0/960	0.30	0/1278
10	R	0.14	0/829	0.39	0/1107
11	S	0.11	0/864	0.30	0/1156
12	T	0.11	0/744	0.32	0/994
13	U	0.12	0/787	0.36	0/1051
14	V	0.12	0/766	0.38	0/1025
15	W	0.13	0/582	0.39	0/769
16	X	0.11	0/635	0.30	0/848
17	Y	0.12	0/510	0.41	0/677
18	Z	0.12	0/453	0.36	0/605
19	0	0.12	0/450	0.38	0/599
20	1	0.12	0/416	0.32	0/554
21	2	0.12	0/380	0.36	0/498
22	B	0.07	0/2847	0.16	0/4440
23	I	0.12	0/1046	0.37	0/1410
24	K	0.13	0/947	0.37	0/1268
25	P	0.11	0/923	0.34	0/1234
26	6	0.14	0/787	0.40	0/1062
27	7	0.12	0/2590	0.33	0/3513
28	8	0.12	0/1292	0.34	0/1727
29	9	0.12	0/2626	0.36	0/3542
30	M	0.12	0/1093	0.34	0/1460
31	A	0.08	0/70038	0.19	0/109262
32	H	0.11	0/1121	0.34	0/1515

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.11	0/1001	0.36	0/1350
34	F	0.12	0/1434	0.35	0/1926
35	b	0.11	0/371	0.30	0/496
All	All	0.09	0/107152	0.25	0/159693

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2082	0	2157	57	0
2	D	1565	0	1616	51	0
3	E	1552	0	1619	41	0
4	G	1281	0	1324	38	0
5	J	1129	0	1162	26	0
6	L	1045	0	1117	36	0
7	N	960	0	1000	34	0
8	O	892	0	923	26	0
9	Q	947	0	1022	24	0
10	R	816	0	839	28	0
11	S	857	0	922	23	0
12	T	738	0	807	15	0
13	U	779	0	834	19	0
14	V	753	0	780	22	0
15	W	575	0	589	20	0
16	X	625	0	655	12	0
17	Y	509	0	543	11	0
18	Z	449	0	491	13	0
19	0	444	0	461	11	0
20	1	409	0	440	9	0
21	2	377	0	418	10	0
22	B	2548	0	1292	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	I	1032	0	1088	23	0
24	K	938	0	1012	27	0
25	P	911	0	957	32	0
26	6	780	0	783	19	0
27	7	2533	0	2549	72	0
28	8	1281	0	1335	35	0
29	9	2582	0	2606	60	0
30	M	1074	0	1157	30	0
31	A	62534	0	31452	1171	0
32	H	1110	0	1148	25	0
33	e	988	0	1025	22	0
34	F	1410	0	1447	38	0
35	b	364	0	362	12	0
36	9	28	0	12	0	0
37	9	1	0	0	0	0
37	A	1	0	0	0	0
38	b	1	0	0	0	0
39	2	1	0	0	0	0
39	A	17	0	0	0	0
39	B	1	0	0	0	0
39	C	3	0	0	0	0
39	D	1	0	0	1	0
39	F	1	0	0	1	0
39	N	2	0	0	0	0
39	S	1	0	0	0	0
All	All	98927	0	67944	1915	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 12.

All (1915) 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)
31:A:1093:G:N2	31:A:1098:A:H62	1.48	1.12
31:A:377:G:H1	31:A:397:U:H3	1.04	0.97
31:A:713:G:H21	31:A:718:A:H62	1.12	0.95
31:A:196:A:H61	31:A:831:G:H21	1.14	0.95
31:A:1093:G:H21	31:A:1098:A:N6	1.64	0.94
31:A:1433:A:H61	31:A:1560:G:H1	1.06	0.94
31:A:2472:G:N2	31:A:2478:A:H62	1.66	0.94
31:A:1093:G:H21	31:A:1098:A:H62	0.98	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:196:A:H61	31:A:831:G:N2	1.67	0.93
31:A:1800:C:H42	31:A:1817:G:H22	1.15	0.93
22:B:78:A:H62	22:B:98:G:H21	0.92	0.92
31:A:711:G:H1	31:A:720:U:H3	1.15	0.91
22:B:78:A:H62	22:B:98:G:N2	1.68	0.90
31:A:1433:A:N6	31:A:1560:G:H1	1.70	0.90
31:A:2472:G:H21	31:A:2478:A:H62	0.98	0.90
11:S:92:ARG:HE	11:S:93:ALA:H	1.19	0.88
31:A:2455:G:H1	31:A:2497:A:H61	1.21	0.84
31:A:2472:G:H21	31:A:2478:A:N6	1.74	0.84
22:B:78:A:N6	22:B:98:G:H21	1.75	0.84
31:A:196:A:N6	31:A:831:G:H21	1.76	0.84
31:A:1932:A:H62	31:A:1968:G:H21	1.25	0.83
31:A:2294:G:N2	31:A:2338:C:O2	2.08	0.83
31:A:2526:G:H1	31:A:2537:U:H3	1.26	0.83
31:A:1800:C:H42	31:A:1817:G:N2	1.78	0.82
29:9:57:ILE:HD12	31:A:2529:G:H4'	1.62	0.81
31:A:954:G:H1	31:A:963:U:H3	0.83	0.81
31:A:1948:G:N2	31:A:1959:G:O6	2.13	0.81
31:A:1653:G:H21	31:A:2005:A:H62	1.26	0.81
29:9:47:MET:HB3	29:9:115:LEU:HB3	1.63	0.79
31:A:955:U:H3	31:A:962:G:H1	1.26	0.79
31:A:1800:C:N4	31:A:1817:G:H22	1.80	0.79
31:A:2747:G:H21	31:A:2757:A:H62	1.30	0.79
31:A:1287:A:N6	31:A:1649:G:O2'	2.13	0.79
31:A:2028:U:H3	31:A:2033:A:H62	1.27	0.79
3:E:21:ARG:HH22	3:E:106:LYS:HB3	1.47	0.78
4:G:151:ARG:HB2	4:G:161:VAL:HG12	1.66	0.77
34:F:117:SER:O	34:F:127:TYR:OH	2.03	0.77
27:7:18:GLN:HE22	27:7:23:ALA:HB2	1.49	0.77
35:b:11:GLU:HA	35:b:25:ARG:HH12	1.50	0.77
31:A:408:G:H1	31:A:419:U:H3	1.31	0.76
14:V:25:LYS:HG2	14:V:43:ASP:HA	1.67	0.76
23:I:124:MET:HA	23:I:127:SER:HB2	1.66	0.75
31:A:465:G:H21	31:A:684:G:H1'	1.48	0.75
31:A:698:C:O2'	31:A:734:A:N6	2.18	0.75
35:b:16:CYS:SG	35:b:18:CYS:HB2	2.27	0.75
25:P:59:THR:HG22	25:P:72:VAL:HG12	1.67	0.75
24:K:3:GLN:NE2	31:A:1666:G:N3	2.35	0.74
31:A:1282:U:H3	31:A:1286:A:H62	1.34	0.74
29:9:239:ARG:HH22	29:9:332:ILE:HG23	1.51	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:R:80:ARG:NH1	31:A:572:A:OP2	2.20	0.73
31:A:1597:A:H5''	31:A:1598:A:H5'	1.70	0.73
15:W:39:THR:HG21	31:A:2336:A:H61	1.52	0.73
6:L:41:ARG:NH1	31:A:807:U:OP2	2.21	0.73
31:A:713:G:N2	31:A:718:A:H62	1.85	0.73
31:A:1951:U:O2'	31:A:1953:A:N7	2.17	0.73
2:D:48:ILE:HG23	2:D:84:LEU:HD11	1.69	0.72
27:7:106:PRO:HD2	27:7:116:LEU:HD12	1.70	0.72
30:M:64:TRP:HB2	30:M:104:GLU:HB2	1.72	0.72
1:C:36:ASN:HB2	1:C:61:TYR:HB2	1.72	0.72
6:L:108:ALA:HB3	6:L:125:LEU:HD22	1.73	0.71
3:E:199:MET:HE2	3:E:200:LEU:HD22	1.71	0.71
29:9:207:LYS:HB3	29:9:329:MET:HE3	1.71	0.71
31:A:629:G:N3	31:A:639:U:O2'	2.24	0.71
31:A:1932:A:H62	31:A:1968:G:N2	1.89	0.71
31:A:981:A:HO2'	31:A:2036:C:HO2'	1.38	0.71
31:A:1961:C:H3'	31:A:1962:C:H5''	1.72	0.71
31:A:1992:G:N1	31:A:1996:C:O2	2.20	0.71
22:B:72:G:H21	22:B:104:A:H62	1.38	0.71
31:A:1948:G:H2'	31:A:1949:G:H8	1.56	0.71
33:e:2:ALA:HB3	33:e:6:GLN:HE22	1.55	0.71
31:A:1223:G:N2	31:A:1226:A:OP2	2.22	0.70
31:A:2601:C:N4	31:A:2603:G:O6	2.24	0.70
4:G:34:ARG:HG2	4:G:70:LEU:HD21	1.72	0.70
31:A:1779:U:OP2	31:A:1784:A:N6	2.24	0.70
30:M:11:LYS:HE2	30:M:73:ILE:HA	1.72	0.70
11:S:6:LYS:HE2	11:S:8:ARG:HH12	1.56	0.70
25:P:102:ARG:HH22	31:A:1754:A:H4'	1.56	0.70
31:A:1937:A:O2'	31:A:1966:A:N6	2.24	0.70
5:J:31:GLU:HG2	5:J:142:ILE:HG21	1.73	0.69
27:7:35:ARG:HH22	27:7:39:TRP:HE1	1.40	0.69
29:9:148:ASP:HB3	29:9:150:ARG:HH12	1.58	0.69
31:A:290:U:H3	31:A:350:G:H1	1.38	0.69
31:A:776:G:H1	31:A:2072:C:H5'	1.57	0.69
29:9:282:PHE:HE2	29:9:310:TYR:HB2	1.58	0.69
31:A:848:C:H2'	31:A:849:A:H8	1.57	0.68
31:A:1443:U:H2'	31:A:1444:G:H8	1.58	0.68
32:H:12:LEU:HD21	32:H:19:VAL:HG21	1.76	0.68
8:O:35:ILE:HD11	8:O:102:ARG:HH22	1.58	0.68
34:F:101:ARG:NH1	35:b:25:ARG:O	2.25	0.68
15:W:20:LYS:NZ	31:A:2355:G:O2'	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:B:40:U:H3	35:b:2:LYS:HG3	1.56	0.68
34:F:23:SER:HB3	34:F:26:GLN:HB2	1.75	0.68
27:7:34:SER:OG	31:A:1923:U:OP2	2.11	0.68
3:E:163:ASN:ND2	31:A:320:A:N3	2.42	0.67
6:L:96:LYS:NZ	6:L:105:ILE:O	2.27	0.67
8:O:13:ARG:HD3	31:A:2334:U:H1'	1.75	0.67
16:X:17:ARG:HE	16:X:23:ALA:HB2	1.59	0.67
31:A:2368:C:H2'	31:A:2369:A:H8	1.59	0.67
3:E:120:VAL:HG12	3:E:188:MET:HB2	1.74	0.67
5:J:39:LYS:NZ	31:A:1006:C:O3'	2.28	0.67
15:W:10:ARG:NH1	31:A:2280:G:O6	2.27	0.67
24:K:21:CYS:HA	24:K:41:ILE:HA	1.77	0.67
31:A:1102:C:H2'	31:A:1103:A:H8	1.58	0.67
31:A:2297:A:H2'	31:A:2298:A:H8	1.59	0.67
6:L:32:GLY:HA2	31:A:1190:G:H5''	1.75	0.67
31:A:1863:G:H4'	31:A:2411:A:H4'	1.77	0.67
31:A:212:G:H2'	31:A:213:A:C8	2.29	0.67
28:8:84:LEU:HG	28:8:88:MET:HE1	1.75	0.67
31:A:819:A:HO2'	31:A:837:C:HO2'	1.43	0.67
3:E:125:SER:HA	3:E:157:LEU:HD21	1.77	0.67
31:A:571:U:O2'	31:A:573:U:OP2	2.13	0.66
31:A:818:G:N1	31:A:1188:U:OP2	2.25	0.66
11:S:83:LYS:HZ3	11:S:95:ARG:HH11	1.41	0.66
31:A:1649:G:H2'	31:A:1650:A:H8	1.60	0.66
10:R:15:SER:H	10:R:18:GLN:HE22	1.42	0.66
31:A:13:A:O2'	31:A:15:G:N7	2.28	0.66
31:A:917:A:H5''	31:A:2268:A:H61	1.59	0.66
31:A:713:G:H21	31:A:718:A:N6	1.87	0.66
2:D:115:GLY:HA2	2:D:166:GLY:HA3	1.78	0.66
3:E:83:VAL:HB	3:E:86:ALA:HB2	1.77	0.66
5:J:13:ARG:NH2	5:J:49:ASP:O	2.28	0.66
1:C:208:GLY:HA2	31:A:764:A:H5'	1.78	0.66
2:D:122:VAL:HA	2:D:127:PHE:HB2	1.78	0.66
1:C:145:MET:HE3	1:C:152:GLN:HG2	1.78	0.65
1:C:151:GLY:O	1:C:155:ARG:NH1	2.29	0.65
11:S:77:ASP:HB2	11:S:102:HIS:HB2	1.77	0.65
17:Y:23:ARG:O	17:Y:27:ASN:ND2	2.29	0.65
2:D:149:ASN:HB2	31:A:2575:C:H5'	1.78	0.65
13:U:43:LYS:HE3	13:U:60:LYS:HE2	1.78	0.65
1:C:152:GLN:OE1	31:A:1818:U:N3	2.28	0.65
31:A:2144:G:O2'	31:A:2147:A:N6	2.28	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:V:58:SER:OG	14:V:59:GLU:OE1	2.13	0.65
31:A:574:A:N6	31:A:2034:U:OP1	2.29	0.65
31:A:2581:G:N2	31:A:2581:G:OP2	2.30	0.65
28:8:118:LEU:HD11	28:8:175:LEU:HB3	1.77	0.65
31:A:2297:A:H62	31:A:2319:G:H21	1.42	0.65
8:O:33:ARG:HH21	22:B:27:C:H3'	1.62	0.65
29:9:239:ARG:NH1	29:9:335:ASN:O	2.30	0.65
31:A:1528:A:N6	31:A:1543:G:O2'	2.29	0.65
7:N:11:ASN:ND2	31:A:1653:G:O6	2.30	0.65
31:A:2028:U:H3	31:A:2033:A:N6	1.94	0.65
33:e:3:LEU:HD12	33:e:5:LEU:H	1.62	0.65
1:C:131:MET:HE1	1:C:173:LEU:HD21	1.79	0.65
6:L:127:VAL:HG21	6:L:142:ILE:HD13	1.79	0.65
31:A:324:A:OP2	31:A:1205:A:N6	2.30	0.65
31:A:2506:U:H3	31:A:2583:G:H1	1.45	0.65
16:X:36:ARG:NH1	31:A:2199:A:OP1	2.29	0.65
27:7:219:ARG:HG3	27:7:220:VAL:HG13	1.79	0.65
29:9:116:LEU:HD21	29:9:119:LYS:HD3	1.79	0.65
8:O:9:ARG:NH2	31:A:2296:U:OP2	2.30	0.64
31:A:1791:A:N1	31:A:1829:A:H4'	2.13	0.64
31:A:1076:C:O2'	31:A:1077:A:N7	2.30	0.64
31:A:695:G:H1	31:A:767:U:H3	1.44	0.64
31:A:2656:U:O2	31:A:2665:A:N7	2.30	0.64
26:6:46:ARG:HB2	29:9:206:GLU:HG2	1.80	0.64
31:A:1105:U:H2'	31:A:1106:G:H8	1.62	0.64
31:A:1834:U:H5''	31:A:1835:G:H5'	1.80	0.64
27:7:84:LEU:HB3	27:7:96:ILE:HD11	1.79	0.64
15:W:16:ARG:NH1	31:A:2356:U:O3'	2.31	0.63
28:8:123:ASP:HA	28:8:126:ILE:HG22	1.80	0.63
31:A:1801:A:H5'	31:A:2203:U:H2'	1.81	0.63
4:G:94:ARG:HB2	4:G:105:SER:HB2	1.81	0.63
31:A:593:U:H3	31:A:664:G:H1	1.46	0.63
2:D:12:THR:HG22	2:D:13:ARG:H	1.63	0.63
4:G:3:VAL:HG21	31:A:2748:A:H5'	1.81	0.63
7:N:5:LYS:NZ	31:A:2000:C:OP1	2.31	0.63
6:L:20:GLY:H	6:L:28:GLY:HA2	1.62	0.63
29:9:96:VAL:HB	29:9:152:LEU:HD12	1.79	0.63
31:A:959:A:H2	31:A:2495:G:H21	1.47	0.63
31:A:2028:U:O4	31:A:2033:A:N7	2.31	0.63
9:Q:14:LYS:NZ	31:A:1218:G:OP2	2.27	0.63
31:A:55:G:H2'	31:A:56:A:H8	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:1826:G:O2'	31:A:1971:U:OP2	2.16	0.63
25:P:50:ARG:NH2	31:A:2683:C:OP1	2.31	0.63
31:A:59:U:H1'	31:A:73:A:H2'	1.80	0.63
31:A:1270:C:H5''	31:A:1271:G:H5'	1.81	0.63
31:A:1709:U:O2'	31:A:2859:G:N3	2.30	0.63
17:Y:31:GLN:HB3	17:Y:36:GLN:HB2	1.81	0.63
31:A:2229:U:H2'	31:A:2230:G:H8	1.64	0.63
31:A:2320:U:O2'	31:A:2322:A:N6	2.31	0.63
25:P:88:ARG:NH1	25:P:114:ASN:OXT	2.31	0.62
31:A:1754:A:N1	31:A:2716:C:O2'	2.32	0.62
29:9:17:GLY:HA3	29:9:40:GLY:H	1.64	0.62
31:A:371:A:H61	31:A:401:A:H3'	1.64	0.62
2:D:124:ARG:HA	2:D:165:MET:HE2	1.81	0.62
12:T:1:MET:N	31:A:142:A:N3	2.45	0.62
27:7:196:ARG:NE	31:A:1909:C:OP1	2.33	0.62
31:A:1288:G:OP2	31:A:1288:G:N2	2.32	0.62
31:A:1668:A:N3	31:A:1670:C:N4	2.48	0.62
31:A:160:A:N3	31:A:2208:C:O2'	2.31	0.62
10:R:6:GLN:HB3	10:R:11:GLN:HB3	1.82	0.62
21:2:29:GLN:NE2	31:A:210:C:OP1	2.33	0.62
28:8:107:ARG:NH2	31:A:1893:C:O2'	2.32	0.62
31:A:463:G:N2	31:A:466:A:OP2	2.26	0.62
31:A:629:G:H1'	31:A:639:U:H1'	1.80	0.62
31:A:1837:C:O2'	31:A:1927:A:N3	2.32	0.62
31:A:1447:C:O2'	31:A:1544:A:N3	2.28	0.62
5:J:92:MET:HE3	5:J:100:VAL:HG12	1.81	0.62
22:B:77:U:O2	22:B:99:A:N7	2.33	0.62
30:M:14:LYS:NZ	31:A:958:U:OP2	2.31	0.62
27:7:116:LEU:HD22	27:7:132:ALA:HB3	1.82	0.62
31:A:2692:G:N3	31:A:2847:U:O2'	2.33	0.61
1:C:159:THR:HG21	31:A:1819:A:H5''	1.82	0.61
7:N:74:GLU:OE2	31:A:1453:A:N6	2.32	0.61
13:U:81:ARG:NH1	31:A:301:G:OP2	2.32	0.61
26:6:99:GLU:OE2	26:6:102:LYS:NZ	2.29	0.61
31:A:955:U:O2	31:A:962:G:N2	2.32	0.61
19:0:46:GLY:HA3	19:0:55:ALA:HA	1.83	0.61
30:M:69:PRO:HA	30:M:94:ALA:HB2	1.81	0.61
31:A:279:A:H61	31:A:361:G:H2'	1.65	0.61
31:A:1932:A:N6	31:A:1968:G:H21	1.97	0.61
31:A:2136:G:N2	31:A:2156:G:O2'	2.33	0.61
31:A:220:G:H1	31:A:427:U:H3'	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:2374:C:N4	31:A:2375:G:O6	2.33	0.61
31:A:2855:C:H2'	31:A:2856:A:H8	1.65	0.61
8:O:30:ARG:NH2	22:B:48:U:OP2	2.33	0.61
29:9:59:TYR:OH	29:9:89:LYS:O	2.17	0.61
31:A:272:A:H2'	31:A:273:G:C8	2.35	0.61
3:E:6:LYS:HD2	3:E:119:ILE:HG23	1.82	0.61
7:N:106:ASP:OD2	31:A:1287:A:N6	2.34	0.61
23:I:46:ASP:HA	23:I:50:LYS:HD2	1.82	0.61
31:A:1224:U:H2'	31:A:1225:G:C2	2.34	0.61
34:F:32:LYS:NZ	34:F:34:THR:OG1	2.29	0.61
26:6:42:GLY:N	26:6:90:MET:O	2.32	0.61
31:A:494:G:H2'	31:A:495:G:H8	1.66	0.61
31:A:1056:G:H5'	31:A:1057:A:H5'	1.83	0.61
31:A:1407:G:H2'	31:A:1408:G:H8	1.64	0.61
31:A:2447:G:N2	31:A:2450:A:N7	2.46	0.61
2:D:108:ASP:N	2:D:204:LYS:O	2.30	0.61
33:e:26:VAL:HG21	33:e:114:GLU:HG2	1.81	0.61
31:A:2039:U:H2'	31:A:2040:G:C8	2.36	0.61
24:K:107:LEU:HB3	24:K:116:ILE:HD11	1.83	0.61
31:A:395:U:O2'	31:A:396:G:N7	2.30	0.61
34:F:33:ILE:HG12	34:F:95:MET:HG3	1.83	0.61
6:L:51:GLU:OE2	6:L:60:ARG:NH1	2.34	0.60
20:1:7:LYS:HG2	20:1:23:THR:HG22	1.83	0.60
3:E:18:THR:HG23	3:E:19:PHE:HD2	1.65	0.60
18:Z:55:LYS:NZ	18:Z:57:GLU:OE1	2.34	0.60
27:7:256:ARG:HB3	31:A:1945:G:H21	1.66	0.60
31:A:441:U:H2'	31:A:442:G:C8	2.36	0.60
31:A:2848:G:O2'	31:A:2867:G:N2	2.31	0.60
31:A:839:U:H3	31:A:939:G:H1	1.48	0.60
4:G:71:LEU:HD13	4:G:74:MET:HE3	1.83	0.60
10:R:35:PHE:HB2	10:R:59:ILE:HB	1.82	0.60
29:9:295:GLU:HA	29:9:298:LYS:HZ3	1.66	0.60
31:A:1830:C:H2'	31:A:1831:G:H8	1.66	0.60
4:G:106:LEU:HD13	4:G:151:ARG:HG2	1.82	0.60
28:8:53:ALA:HB1	28:8:104:LEU:HD11	1.83	0.60
31:A:935:C:H2'	31:A:936:A:H8	1.65	0.60
1:C:13:ARG:NH1	31:A:1693:U:O2'	2.35	0.60
1:C:71:ASP:OD2	1:C:188:ARG:NH1	2.32	0.60
11:S:83:LYS:O	11:S:84:ARG:NH2	2.33	0.60
25:P:92:ARG:NH1	31:A:2849:U:OP1	2.35	0.60
31:A:1592:C:H2'	31:A:1593:A:H8	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:1869:G:O2'	31:A:1872:A:N6	2.35	0.60
11:S:55:ILE:HG23	11:S:66:ILE:HD11	1.82	0.60
19:0:27:LEU:HD12	19:0:36:LYS:HB3	1.82	0.60
12:T:40:LYS:HZ1	12:T:58:VAL:HG12	1.67	0.60
31:A:1721:G:N1	31:A:1738:G:N7	2.50	0.60
22:B:5:U:OP1	22:B:61:G:O2'	2.19	0.60
31:A:1106:G:OP1	33:e:62:ARG:NH1	2.35	0.60
31:A:1825:U:H2'	31:A:1826:G:H8	1.67	0.60
31:A:1891:G:HO2'	31:A:2235:G:HO2'	1.50	0.60
31:A:2081:U:H2'	31:A:2082:A:H8	1.67	0.60
31:A:2131:U:H5'	31:A:2132:U:H5''	1.84	0.59
31:A:1386:C:H2'	31:A:1387:A:C8	2.36	0.59
11:S:109:ASP:OD1	11:S:110:ARG:N	2.35	0.59
12:T:19:LYS:NZ	31:A:1394:U:O2	2.35	0.59
31:A:369:U:OP1	31:A:403:U:O2'	2.19	0.59
31:A:1539:U:H2'	31:A:1540:G:H8	1.68	0.59
31:A:1633:G:N7	31:A:1635:A:N6	2.49	0.59
31:A:1299:G:N1	31:A:1640:A:OP2	2.32	0.59
4:G:94:ARG:HA	4:G:127:GLN:HE22	1.67	0.59
25:P:13:LYS:NZ	25:P:75:THR:O	2.32	0.59
25:P:22:GLY:H	25:P:46:VAL:HG13	1.68	0.59
31:A:1420:A:O2'	31:A:2211:A:N7	2.32	0.59
3:E:124:PHE:HE2	3:E:148:ILE:HD12	1.68	0.59
31:A:576:U:H2'	31:A:577:G:C8	2.37	0.59
31:A:594:U:H3	31:A:663:G:H1	1.50	0.59
31:A:2074:U:O2'	31:A:2597:G:N3	2.31	0.59
31:A:1164:C:HO2'	31:A:1224:U:H3	1.42	0.59
31:A:2289:G:O6	31:A:2343:U:O2	2.20	0.59
21:2:39:ARG:NH2	31:A:468:G:N7	2.49	0.59
29:9:244:LEU:HD11	29:9:283:ASN:HB2	1.83	0.59
31:A:2313:C:O2'	34:F:87:LYS:NZ	2.27	0.59
31:A:2643:G:H2'	31:A:2644:G:H8	1.68	0.59
5:J:44:TYR:HA	5:J:50:THR:HG21	1.85	0.59
6:L:13:LYS:NZ	31:A:1245:G:OP1	2.30	0.59
14:V:7:GLU:HA	14:V:65:VAL:HG23	1.83	0.59
31:A:741:U:H2'	31:A:742:A:H8	1.66	0.59
31:A:954:G:O6	31:A:963:U:O4	2.20	0.59
31:A:1629:U:O4	31:A:1630:A:N6	2.36	0.59
31:A:1907:G:O6	31:A:1923:U:O4	2.19	0.59
3:E:57:LYS:NZ	3:E:58:LYS:O	2.34	0.59
7:N:99:LYS:HA	7:N:111:ALA:HA	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:P:91:VAL:HG11	25:P:96:LEU:HD11	1.83	0.59
28:8:73:ILE:HD11	31:A:2396:G:H1'	1.85	0.59
31:A:1093:G:N2	31:A:1098:A:N6	2.30	0.59
31:A:1682:G:OP2	31:A:1699:G:N2	2.36	0.59
31:A:2116:G:O6	31:A:2171:A:N6	2.36	0.59
31:A:2655:G:N2	31:A:2665:A:OP2	2.35	0.59
23:I:78:LEU:HG	23:I:81:LYS:HE3	1.85	0.58
23:I:129:GLU:O	23:I:133:ARG:NH1	2.36	0.58
31:A:1606:C:HO2'	31:A:1607:C:P	2.26	0.58
15:W:36:GLN:HE22	15:W:41:PHE:HB2	1.67	0.58
27:7:12:SER:OG	27:7:14:ASN:OD1	2.18	0.58
31:A:910:A:N3	31:A:2264:C:O2'	2.31	0.58
16:X:42:GLU:HG3	16:X:44:ARG:HG2	1.85	0.58
31:A:1801:A:N6	31:A:2201:G:O2'	2.35	0.58
7:N:86:ARG:NE	7:N:117:ASP:OD2	2.36	0.58
27:7:191:ARG:NH2	27:7:196:ARG:O	2.37	0.58
31:A:1016:G:O6	31:A:1147:A:N6	2.37	0.58
31:A:1386:C:H2'	31:A:1387:A:H8	1.68	0.58
12:T:69:ARG:HB3	12:T:74:ILE:HA	1.85	0.58
31:A:105:C:H2'	31:A:106:C:C6	2.38	0.58
31:A:1300:G:H4'	31:A:1301:A:H5''	1.85	0.58
31:A:2036:C:H2'	31:A:2037:A:H8	1.68	0.58
9:Q:48:ASP:HA	9:Q:51:GLN:HB3	1.85	0.58
30:M:41:LEU:HG	30:M:96:ILE:HG13	1.85	0.58
31:A:1969:A:H2'	31:A:1972:G:H21	1.69	0.58
23:I:7:TYR:HB2	23:I:57:VAL:HG13	1.83	0.58
27:7:236:ILE:HD13	27:7:279:LEU:HD11	1.85	0.58
31:A:1196:C:H2'	31:A:1197:G:H8	1.69	0.58
31:A:1796:U:H2'	31:A:1797:G:H8	1.68	0.58
31:A:1197:G:N2	31:A:1249:U:O2'	2.37	0.58
31:A:1966:A:O2'	31:A:1967:C:O5'	2.22	0.58
15:W:10:ARG:NH2	31:A:2280:G:N7	2.51	0.58
24:K:114:LYS:N	26:6:70:GLU:OE1	2.37	0.58
30:M:11:LYS:HD3	30:M:74:THR:HG23	1.85	0.58
31:A:956:G:N2	31:A:960:A:OP2	2.37	0.58
31:A:2047:C:H2'	31:A:2048:G:H8	1.68	0.58
31:A:2297:A:N6	31:A:2319:G:H21	2.02	0.58
1:C:5:CYS:SG	1:C:17:LYS:NZ	2.76	0.57
30:M:81:ARG:NH1	31:A:2495:G:OP1	2.37	0.57
31:A:5:A:H2'	31:A:6:A:H8	1.69	0.57
31:A:220:G:H22	31:A:427:U:H2'	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:570:G:O2'	31:A:983:A:N1	2.36	0.57
31:A:1028:A:OP2	31:A:1126:A:N6	2.37	0.57
31:A:1429:G:H2'	31:A:1430:G:H8	1.69	0.57
31:A:1807:G:N2	31:A:1810:A:OP2	2.35	0.57
31:A:2420:C:H3'	31:A:2421:G:H5''	1.84	0.57
27:7:77:PHE:HB3	27:7:117:ASN:HD21	1.69	0.57
31:A:987:C:O2'	31:A:1000:A:N3	2.31	0.57
31:A:1681:G:OP2	31:A:1757:A:N6	2.37	0.57
31:A:1689:A:OP2	31:A:1698:A:N6	2.35	0.57
31:A:1864:U:OP1	31:A:2410:G:O2'	2.21	0.57
31:A:2039:U:H2'	31:A:2040:G:H8	1.69	0.57
31:A:2306:C:H5''	31:A:2307:G:H2'	1.86	0.57
13:U:3:LYS:NZ	13:U:82:VAL:O	2.38	0.57
28:8:28:SER:HB3	28:8:31:GLU:HB2	1.85	0.57
31:A:514:A:N3	31:A:581:C:O2'	2.34	0.57
22:B:1:U:H2'	22:B:2:G:H8	1.69	0.57
31:A:1295:C:H2'	31:A:1296:G:H8	1.68	0.57
31:A:213:A:H2'	31:A:214:G:C8	2.39	0.57
31:A:2815:C:H2'	31:A:2816:G:H8	1.69	0.57
1:C:269:ARG:NH2	31:A:1799:G:OP2	2.38	0.57
2:D:133:THR:OG1	31:A:1675:C:O2	2.23	0.57
5:J:114:LEU:HG	5:J:118:MET:HE1	1.87	0.57
30:M:105:MET:SD	30:M:106:ASP:N	2.78	0.57
31:A:1907:G:O6	31:A:1923:U:C4	2.58	0.57
33:e:92:ALA:HB1	33:e:129:LEU:HD22	1.85	0.57
6:L:96:LYS:HD3	6:L:103:ILE:HD12	1.87	0.57
27:7:140:LYS:HD3	31:A:1912:A:H4'	1.86	0.57
28:8:173:GLN:NE2	31:A:1850:G:OP1	2.37	0.57
31:A:1999:C:O2	31:A:2687:U:O2'	2.23	0.57
31:A:2737:G:H2'	31:A:2738:A:C8	2.40	0.57
31:A:2836:U:H2'	31:A:2837:A:H8	1.69	0.57
1:C:122:ALA:O	1:C:127:ASN:ND2	2.36	0.57
1:C:205:GLY:N	31:A:1791:A:O2'	2.30	0.57
3:E:29:HIS:NE2	31:A:1244:A:O2'	2.32	0.57
7:N:49:GLU:HG2	7:N:94:TYR:HB2	1.87	0.57
9:Q:89:ILE:HA	10:R:11:GLN:HE22	1.70	0.57
10:R:55:ASP:OD2	10:R:56:GLY:N	2.37	0.57
22:B:72:G:N2	22:B:104:A:H62	2.02	0.57
29:9:185:LYS:NZ	29:9:192:THR:O	2.38	0.57
31:A:272:A:H2'	31:A:273:G:H8	1.68	0.57
31:A:832:U:H2'	31:A:833:A:C8	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:2070:A:H2'	31:A:2071:A:H8	1.70	0.57
32:H:90:LEU:HD11	32:H:125:THR:HG23	1.86	0.57
1:C:205:GLY:H	31:A:1791:A:HO2'	1.49	0.57
9:Q:91:ARG:NH2	31:A:1153:C:OP1	2.38	0.57
31:A:219:A:N3	31:A:234:U:O2'	2.37	0.57
31:A:1589:U:H2'	31:A:1590:A:H8	1.70	0.57
31:A:2751:G:OP1	31:A:2751:G:N2	2.35	0.57
1:C:223:ALA:O	31:A:782:A:O2'	2.23	0.56
10:R:15:SER:H	10:R:18:GLN:NE2	2.03	0.56
21:2:24:THR:HG23	21:2:27:GLY:H	1.69	0.56
31:A:848:C:H2'	31:A:849:A:C8	2.40	0.56
31:A:1769:U:O2	31:A:1983:G:O6	2.22	0.56
9:Q:10:ARG:HH12	31:A:513:A:H1'	1.70	0.56
16:X:27:ARG:NH2	31:A:1365:A:OP1	2.33	0.56
29:9:157:MET:HG2	29:9:234:HIS:HA	1.88	0.56
5:J:118:MET:HA	5:J:121:LYS:HE2	1.87	0.56
25:P:20:ARG:NH2	31:A:2849:U:O4	2.38	0.56
30:M:11:LYS:NZ	30:M:12:MET:O	2.38	0.56
31:A:820:A:H2	31:A:943:A:H4'	1.70	0.56
31:A:2319:G:H1'	31:A:2320:U:H5	1.69	0.56
31:A:2557:G:H2'	31:A:2558:C:C6	2.39	0.56
2:D:59:ARG:NH2	31:A:2831:G:OP2	2.39	0.56
15:W:15:LYS:HD2	15:W:37:ARG:NH2	2.21	0.56
24:K:58:LEU:HD11	24:K:86:LEU:HD12	1.87	0.56
31:A:1275:A:OP2	31:A:1646:C:N4	2.37	0.56
6:L:79:LEU:HG	6:L:113:ALA:H	1.69	0.56
13:U:12:VAL:HG21	13:U:38:ILE:HG21	1.87	0.56
22:B:80:U:O2'	31:A:918:A:N3	2.38	0.56
5:J:45:THR:HB	5:J:48:VAL:HB	1.88	0.56
5:J:113:PRO:HB2	31:A:557:C:H5''	1.86	0.56
18:Z:37:ARG:HH12	31:A:929:U:H5'	1.71	0.56
31:A:1028:A:N3	31:A:2486:C:O2'	2.35	0.56
31:A:2594:C:H2'	31:A:2595:G:C8	2.40	0.56
22:B:57:A:C5	34:F:25:MET:HE1	2.41	0.56
31:A:391:A:O2'	31:A:410:G:OP1	2.22	0.56
31:A:1086:A:H1'	31:A:1103:A:H61	1.70	0.56
31:A:1164:C:H2'	31:A:1165:A:H8	1.71	0.56
31:A:2023:C:H2'	31:A:2024:G:H8	1.69	0.56
29:9:17:GLY:N	29:9:40:GLY:O	2.29	0.56
31:A:581:C:H2'	31:A:582:A:H8	1.71	0.56
31:A:1715:G:O2'	31:A:1743:G:O6	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:1927:A:H2'	31:A:1928:A:C8	2.41	0.56
33:e:58:THR:HG21	33:e:82:ILE:H	1.70	0.56
31:A:20:C:H2'	31:A:21:A:H8	1.71	0.56
31:A:2473:U:OP1	31:A:2475:C:N4	2.39	0.56
34:F:139:GLU:OE2	35:b:26:SER:OG	2.23	0.56
31:A:2626:C:H2'	31:A:2627:G:C8	2.42	0.55
1:C:179:GLU:OE2	1:C:269:ARG:NH1	2.39	0.55
4:G:85:LYS:NZ	4:G:129:GLU:OE1	2.33	0.55
6:L:74:THR:HG22	6:L:107:PHE:HB2	1.88	0.55
6:L:79:LEU:HD13	6:L:116:VAL:HB	1.89	0.55
11:S:24:ILE:HG22	11:S:35:ILE:HD11	1.88	0.55
31:A:779:U:O2	31:A:785:G:O6	2.25	0.55
31:A:1058:U:O4	31:A:1080:A:N6	2.39	0.55
1:C:257:ARG:HB2	31:A:1798:U:H5''	1.88	0.55
7:N:103:ARG:HE	7:N:108:ALA:HB3	1.71	0.55
31:A:1056:G:H21	31:A:1103:A:H62	1.54	0.55
8:O:43:ASN:OD1	8:O:44:GLY:N	2.39	0.55
27:7:35:ARG:HH12	27:7:39:TRP:CD1	2.25	0.55
31:A:596:U:H2'	31:A:597:G:H8	1.70	0.55
31:A:767:U:H2'	31:A:768:G:H8	1.72	0.55
31:A:1164:C:O2'	31:A:1224:U:N3	2.30	0.55
31:A:1834:U:O4	31:A:1900:A:N6	2.39	0.55
31:A:2120:G:H2'	31:A:2121:G:H8	1.71	0.55
1:C:86:ARG:NH2	31:A:1817:G:OP1	2.39	0.55
11:S:83:LYS:NZ	11:S:95:ARG:HH11	2.05	0.55
20:1:29:LYS:NZ	31:A:2286:G:OP1	2.39	0.55
20:1:50:GLU:OE1	20:1:52:LYS:NZ	2.39	0.55
28:8:74:LYS:HD3	28:8:75:MET:N	2.22	0.55
29:9:13:ALA:HB2	29:9:118:ALA:HB1	1.88	0.55
31:A:584:C:N4	31:A:585:G:O6	2.40	0.55
31:A:2233:U:H2'	31:A:2234:G:H8	1.70	0.55
33:e:24:SER:HB2	33:e:116:GLU:HG3	1.87	0.55
31:A:599:A:H2'	31:A:600:G:H8	1.71	0.55
31:A:1470:A:N6	31:A:1521:G:O2'	2.36	0.55
31:A:1830:C:H2'	31:A:1831:G:C8	2.41	0.55
31:A:1903:G:H2'	31:A:1904:G:H8	1.71	0.55
31:A:2743:U:OP2	31:A:2755:C:N4	2.37	0.55
4:G:132:LEU:HB3	4:G:140:ILE:HD11	1.88	0.55
5:J:38:GLY:HA3	5:J:50:THR:HG23	1.88	0.55
9:Q:22:GLY:HA2	31:A:18:U:O3'	2.06	0.55
24:K:13:ASN:ND2	24:K:97:THR:OG1	2.32	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:K:34:GLY:N	24:K:37:ASP:OD2	2.36	0.55
27:7:60:LEU:HD11	28:8:113:VAL:HB	1.88	0.55
31:A:2446:G:H21	31:A:2449:U:H3	1.54	0.55
32:H:104:THR:HG22	32:H:109:GLU:HA	1.88	0.55
33:e:33:VAL:HG12	33:e:35:VAL:H	1.72	0.55
6:L:79:LEU:HD11	6:L:112:LEU:HD12	1.89	0.55
9:Q:99:VAL:HG23	9:Q:100:PHE:HD1	1.72	0.55
14:V:28:ALA:HA	14:V:88:HIS:CE1	2.42	0.55
27:7:4:ARG:NH2	27:7:6:GLN:OE1	2.40	0.55
31:A:177:G:OP2	31:A:177:G:N2	2.20	0.55
31:A:2298:A:OP1	34:F:70:ARG:NH2	2.39	0.55
7:N:58:ASP:OD1	7:N:63:ARG:NH1	2.33	0.55
14:V:4:ILE:HG23	14:V:63:ILE:HD12	1.89	0.55
31:A:1911:U:H2'	31:A:1912:A:C8	2.42	0.55
22:B:60:C:H2'	22:B:61:G:H8	1.71	0.55
31:A:1604:C:O2'	31:A:1610:A:N1	2.33	0.55
31:A:1997:C:H2'	31:A:1998:A:H8	1.70	0.55
31:A:1432:G:H2'	31:A:1433:A:C8	2.42	0.54
34:F:109:ARG:HH12	34:F:138:PRO:HD3	1.70	0.54
4:G:37:ASN:HD21	4:G:63:GLN:HG3	1.71	0.54
8:O:56:LYS:HA	8:O:59:ALA:HB3	1.90	0.54
13:U:39:ASN:HB2	13:U:64:ILE:HD11	1.89	0.54
25:P:30:TRP:CD2	25:P:37:LYS:HE3	2.42	0.54
31:A:1649:G:H2'	31:A:1650:A:C8	2.41	0.54
31:A:2182:U:H2'	31:A:2183:A:H8	1.72	0.54
31:A:2329:U:H2'	31:A:2330:G:C8	2.42	0.54
31:A:2506:U:OP2	31:A:2576:G:N1	2.35	0.54
31:A:2731:G:H2'	31:A:2732:G:C8	2.42	0.54
1:C:132:ARG:HA	1:C:166:ARG:HH22	1.71	0.54
20:1:36:LYS:HB3	20:1:47:ILE:HD13	1.89	0.54
23:I:48:ILE:HG13	23:I:49:GLU:H	1.73	0.54
28:8:165:PRO:O	28:8:169:ARG:NH2	2.40	0.54
31:A:541:A:N6	31:A:553:G:O6	2.41	0.54
31:A:1687:G:H21	31:A:1701:A:H62	1.55	0.54
31:A:2070:A:H2'	31:A:2071:A:C8	2.43	0.54
31:A:2077:A:N3	31:A:2434:A:O2'	2.34	0.54
31:A:2576:G:O2'	31:A:2579:C:OP2	2.21	0.54
31:A:2747:G:N2	31:A:2757:A:H62	2.00	0.54
34:F:169:LEU:HD13	34:F:174:PHE:HB2	1.89	0.54
31:A:1855:U:H3	31:A:1887:C:H42	1.56	0.54
8:O:10:ARG:NH1	31:A:2295:C:OP1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:I:48:ILE:HG13	23:I:49:GLU:N	2.22	0.54
26:6:92:GLU:HA	26:6:95:ARG:HH12	1.73	0.54
31:A:31:C:O2'	31:A:1238:G:OP1	2.25	0.54
31:A:787:C:H5''	31:A:788:A:H5'	1.90	0.54
31:A:1736:U:H4'	31:A:1737:G:OP1	2.08	0.54
31:A:1833:C:O2'	31:A:1969:A:N1	2.35	0.54
31:A:2646:C:OP2	31:A:2732:G:O2'	2.26	0.54
33:e:33:VAL:HG21	33:e:106:PHE:HE2	1.73	0.54
11:S:11:ARG:NH2	31:A:1323:C:OP2	2.41	0.54
13:U:85:ARG:HH22	13:U:99:SER:HB3	1.72	0.54
31:A:1341:G:OP2	31:A:1394:U:O2'	2.24	0.54
31:A:2291:U:H1'	31:A:2374:C:H1'	1.89	0.54
2:D:62:LYS:HD3	31:A:2810:A:H4'	1.88	0.54
3:E:5:LEU:HD21	3:E:122:GLU:HB3	1.89	0.54
14:V:81:PRO:O	30:M:34:LYS:NZ	2.22	0.54
27:7:16:LEU:HD22	27:7:60:LEU:HD23	1.90	0.54
31:A:739:A:N3	31:A:740:C:N4	2.53	0.54
34:F:32:LYS:HE3	34:F:156:THR:HG21	1.90	0.54
4:G:43:LYS:NZ	4:G:51:PHE:O	2.35	0.54
31:A:-1:A:H2'	31:A:0:A:H8	1.73	0.54
3:E:44:ARG:NH2	31:A:1248:G:OP1	2.30	0.54
31:A:20:C:H2'	31:A:21:A:C8	2.43	0.54
31:A:956:G:O2'	31:A:959:A:N6	2.41	0.54
31:A:48:G:H22	31:A:177:G:P	2.31	0.53
31:A:155:A:H2'	31:A:156:A:H8	1.74	0.53
31:A:810:U:H5''	31:A:811:U:H5'	1.90	0.53
31:A:1296:G:OP1	31:A:2709:G:O2'	2.20	0.53
31:A:1510:G:H2'	31:A:1511:G:H8	1.74	0.53
2:D:157:LYS:HB3	5:J:80:HIS:HA	1.89	0.53
10:R:90:ARG:NH1	31:A:1223:G:OP2	2.41	0.53
12:T:19:LYS:NZ	31:A:1340:U:OP1	2.40	0.53
26:6:56:VAL:HG23	26:6:66:PRO:HG2	1.89	0.53
30:M:97:GLN:H	30:M:100:LYS:NZ	2.06	0.53
32:H:33:GLN:OE1	32:H:35:LYS:NZ	2.41	0.53
3:E:112:LEU:HB3	3:E:118:LEU:HB2	1.91	0.53
31:A:2119:A:H61	31:A:2167:U:H1'	1.73	0.53
1:C:141:HIS:ND1	1:C:192:GLY:O	2.30	0.53
12:T:53:VAL:HG13	12:T:91:GLN:HB3	1.90	0.53
27:7:37:LYS:NZ	31:A:1928:A:OP1	2.35	0.53
31:A:2500:U:O2'	31:A:2504:U:OP1	2.27	0.53
32:H:116:ARG:HB2	32:H:133:GLN:HG3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:82:LEU:HD13	6:L:120:VAL:HG11	1.89	0.53
9:Q:5:ARG:NH2	31:A:1251:C:OP2	2.41	0.53
22:B:42:C:H1'	34:F:65:LEU:HB3	1.91	0.53
28:8:105:LYS:O	28:8:107:ARG:NH1	2.42	0.53
29:9:167:MET:O	29:9:172:LYS:NZ	2.42	0.53
31:A:948:C:O2	31:A:984:A:O2'	2.27	0.53
31:A:1779:U:H5''	31:A:1780:A:H5''	1.91	0.53
2:D:145:SER:OG	31:A:2512:C:O2	2.26	0.53
3:E:21:ARG:NH2	3:E:106:LYS:HB3	2.20	0.53
3:E:121:VAL:HG21	3:E:124:PHE:HB2	1.90	0.53
24:K:24:VAL:HG13	24:K:30:ARG:HG3	1.89	0.53
31:A:729:G:O2'	31:A:763:G:H4'	2.08	0.53
31:A:741:U:H2'	31:A:742:A:C8	2.42	0.53
31:A:832:U:H2'	31:A:833:A:H8	1.73	0.53
34:F:128:SER:O	34:F:129:MET:HE2	2.08	0.53
8:O:28:VAL:HG12	8:O:37:ALA:HA	1.91	0.53
31:A:500:G:N1	31:A:503:A:OP2	2.33	0.53
31:A:780:G:N2	31:A:785:G:N7	2.57	0.53
31:A:1170:C:H2'	31:A:1171:G:H8	1.74	0.53
31:A:1358:G:O2'	31:A:1373:A:N6	2.40	0.53
31:A:69:C:O2	31:A:73:A:O2'	2.23	0.53
31:A:175:G:H2'	31:A:176:A:C8	2.44	0.53
31:A:475:C:O2	31:A:479:A:N6	2.40	0.53
31:A:581:C:H2'	31:A:582:A:C8	2.44	0.53
31:A:743:A:O2'	31:A:1659:G:OP1	2.26	0.53
31:A:934:U:H2'	31:A:935:C:H6	1.74	0.53
34:F:126:ASN:ND2	39:F:201:HOH:O	2.42	0.53
29:9:122:TRP:H	29:9:145:THR:HG1	1.55	0.53
31:A:926:G:H2'	31:A:927:A:H8	1.73	0.53
31:A:1168:G:O6	31:A:1181:U:O2	2.26	0.53
31:A:1520:U:H2'	31:A:1521:G:O4'	2.09	0.53
31:A:1800:C:N3	31:A:1817:G:N1	2.49	0.53
31:A:2136:G:H22	31:A:2156:G:H1'	1.73	0.53
31:A:2641:G:H2'	31:A:2642:G:C8	2.44	0.53
2:D:128:ARG:HH12	31:A:1995:U:H5''	1.74	0.53
29:9:6:GLU:HA	29:9:56:LEU:HD12	1.91	0.53
29:9:157:MET:O	29:9:237:ARG:NH1	2.41	0.53
29:9:203:MET:HE1	29:9:322:LYS:HE2	1.91	0.53
31:A:35:G:O2'	31:A:454:A:O4'	2.26	0.53
31:A:80:G:H2'	31:A:81:G:C8	2.44	0.53
31:A:445:C:H2'	31:A:446:G:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:664:G:O2'	31:A:940:G:OP1	2.17	0.53
31:A:1387:A:H2'	31:A:1388:G:H8	1.74	0.53
31:A:1438:U:H2'	31:A:1439:A:H8	1.74	0.53
3:E:147:LEU:HB2	3:E:183:PHE:HD2	1.74	0.52
16:X:4:CYS:HB3	16:X:9:LYS:H	1.73	0.52
25:P:23:ASP:OD1	25:P:89:GLY:N	2.43	0.52
30:M:34:LYS:HE2	30:M:131:VAL:HG11	1.91	0.52
31:A:589:U:H2'	31:A:590:A:H8	1.74	0.52
10:R:51:VAL:HB	10:R:52:PRO:HD3	1.90	0.52
11:S:85:ILE:HD11	11:S:93:ALA:HB1	1.91	0.52
22:B:13:G:O2'	22:B:15:A:OP2	2.22	0.52
31:A:239:C:HO2'	31:A:622:G:HO2'	1.53	0.52
31:A:2198:A:C4	32:H:29:PHE:HB2	2.44	0.52
7:N:12:ARG:HB3	7:N:16:HIS:HB3	1.91	0.52
8:O:12:THR:HA	8:O:15:ARG:HB2	1.91	0.52
10:R:71:LYS:HA	10:R:90:ARG:HG2	1.91	0.52
14:V:4:ILE:HD11	14:V:42:LEU:HD11	1.91	0.52
31:A:161:A:OP2	31:A:162:U:O2'	2.28	0.52
31:A:2076:U:OP2	31:A:2238:G:N2	2.41	0.52
31:A:2254:C:O2'	31:A:2255:G:O4'	2.27	0.52
31:A:2258:C:O2'	31:A:2427:C:OP2	2.26	0.52
1:C:52:HIS:HA	1:C:216:ARG:HB2	1.92	0.52
6:L:67:THR:HG21	31:A:244:A:H5''	1.91	0.52
14:V:26:PHE:HZ	14:V:47:VAL:HG11	1.73	0.52
16:X:2:ARG:NH2	31:A:1364:G:OP1	2.42	0.52
31:A:580:U:H2'	31:A:581:C:C6	2.44	0.52
31:A:1169:A:H2'	31:A:1170:C:C6	2.45	0.52
31:A:1447:C:H2'	31:A:1448:G:H8	1.73	0.52
31:A:1710:G:H2'	31:A:1711:A:C8	2.43	0.52
31:A:1752:C:H2'	31:A:1753:G:C8	2.44	0.52
31:A:2710:C:H2'	31:A:2711:A:C8	2.44	0.52
28:8:125:LEU:HD13	28:8:132:ALA:HB3	1.90	0.52
29:9:41:ASP:HB2	29:9:82:ARG:HG3	1.91	0.52
31:A:1417:C:HO2'	31:A:1587:G:HO2'	1.57	0.52
31:A:1590:A:H2'	31:A:1591:A:H8	1.74	0.52
31:A:2626:C:H2'	31:A:2627:G:H8	1.74	0.52
3:E:69:ARG:HH22	31:A:2060:A:H62	1.57	0.52
4:G:117:PRO:HG2	4:G:120:ILE:HD13	1.90	0.52
7:N:1:MET:HB2	7:N:3:HIS:CE1	2.44	0.52
15:W:15:LYS:HD2	15:W:37:ARG:HH22	1.74	0.52
31:A:1590:A:H2'	31:A:1591:A:C8	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:2294:G:N1	31:A:2338:C:N3	2.45	0.52
31:A:2705:A:O2'	31:A:2852:G:OP1	2.28	0.52
33:e:18:VAL:HA	33:e:86:MET:HE1	1.92	0.52
30:M:34:LYS:HG2	30:M:101:VAL:HG12	1.92	0.52
31:A:596:U:H2'	31:A:597:G:C8	2.45	0.52
31:A:833:A:H2'	31:A:834:G:C8	2.44	0.52
31:A:1060:U:C2	31:A:1062:G:H5''	2.44	0.52
31:A:1306:C:H2'	31:A:1307:A:H8	1.75	0.52
31:A:2641:G:H2'	31:A:2642:G:H8	1.72	0.52
31:A:2836:U:H2'	31:A:2837:A:C8	2.44	0.52
14:V:30:ILE:HG12	14:V:40:ILE:HD11	1.92	0.52
16:X:68:ALA:HA	16:X:71:ARG:HE	1.73	0.52
24:K:113:MET:HE1	26:6:81:ASP:HB3	1.92	0.52
27:7:60:LEU:HD22	28:8:117:LYS:HG2	1.91	0.52
31:A:242:G:N2	31:A:255:A:OP2	2.40	0.52
31:A:308:G:N2	31:A:477:A:N7	2.58	0.52
31:A:1592:C:H2'	31:A:1593:A:C8	2.43	0.52
31:A:2622:U:O2'	31:A:2825:G:N7	2.43	0.52
10:R:24:LYS:HA	10:R:94:THR:HG23	1.91	0.52
11:S:88:ARG:NH2	11:S:94:ASP:OD2	2.42	0.52
18:Z:37:ARG:NH1	31:A:928:A:O2'	2.43	0.52
25:P:90:ALA:HB2	25:P:112:ARG:HA	1.91	0.52
29:9:189:TYR:CE2	29:9:192:THR:HA	2.45	0.52
31:A:1229:C:H2'	31:A:1230:A:C8	2.44	0.52
31:A:2398:U:H2'	31:A:2399:G:C8	2.44	0.52
25:P:24:THR:HB	25:P:87:ARG:H	1.74	0.52
29:9:167:MET:HG3	29:9:168:PRO:HD2	1.92	0.52
31:A:1736:U:H2'	31:A:1737:G:N3	2.24	0.52
31:A:2508:G:H2'	31:A:2509:G:H8	1.75	0.52
7:N:3:HIS:CD2	31:A:2820:A:H4'	2.44	0.51
13:U:37:GLY:N	13:U:61:GLU:OE2	2.43	0.51
15:W:73:ARG:NH2	31:A:2333:A:OP2	2.42	0.51
23:I:36:GLU:HB3	23:I:66:PHE:HE1	1.74	0.51
24:K:66:LYS:N	24:K:82:ASN:OD1	2.41	0.51
25:P:30:TRP:CE3	25:P:37:LYS:HE3	2.45	0.51
31:A:948:C:H2'	31:A:949:G:C8	2.45	0.51
31:A:1063:G:H2'	31:A:1064:C:H6	1.76	0.51
31:A:2192:U:H2'	31:A:2193:G:H8	1.76	0.51
31:A:2398:U:H2'	31:A:2399:G:H8	1.75	0.51
34:F:11:VAL:HG22	34:F:171:ALA:HB1	1.92	0.51
34:F:147:ARG:O	34:F:149:ARG:NH1	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:110:VAL:HB	6:L:127:VAL:HG12	1.93	0.51
6:L:123:ARG:HG3	6:L:143:GLU:HB2	1.92	0.51
7:N:17:ARG:NH2	31:A:2002:G:OP1	2.30	0.51
8:O:31:THR:HB	8:O:34:HIS:O	2.10	0.51
27:7:123:TYR:CE2	27:7:125:PRO:HG2	2.45	0.51
31:A:184:C:H2'	31:A:185:G:C8	2.45	0.51
31:A:1637:A:H2'	31:A:1638:C:C6	2.44	0.51
2:D:140:HIS:NE2	39:D:301:HOH:O	2.35	0.51
4:G:17:LYS:HB3	4:G:24:THR:HB	1.92	0.51
4:G:21:GLN:NE2	4:G:38:ASP:OD1	2.39	0.51
24:K:114:LYS:HD2	26:6:77:TRP:CD1	2.45	0.51
31:A:302:C:H2'	31:A:303:G:H8	1.75	0.51
31:A:1170:C:N4	31:A:1171:G:O6	2.43	0.51
31:A:2595:G:N2	31:A:2598:A:OP2	2.32	0.51
31:A:2645:G:OP2	31:A:2645:G:N2	2.25	0.51
27:7:189:ILE:HD11	27:7:199:MET:HG3	1.91	0.51
31:A:809:G:H2'	31:A:810:U:C6	2.45	0.51
31:A:1606:C:O2'	31:A:1607:C:O5'	2.28	0.51
31:A:1958:C:H2'	31:A:1959:G:N7	2.26	0.51
34:F:36:ASN:HB3	34:F:152:ASP:HB2	1.93	0.51
24:K:86:LEU:HB3	24:K:95:ILE:HD12	1.92	0.51
28:8:102:ASP:HB3	28:8:108:HIS:HB2	1.93	0.51
31:A:45:G:H5'	31:A:46:G:H5'	1.93	0.51
24:K:76:VAL:H	25:P:72:VAL:HG22	1.76	0.51
27:7:282:THR:HA	27:7:299:ALA:HB3	1.93	0.51
31:A:438:G:H2'	31:A:439:A:H8	1.76	0.51
31:A:1387:A:H5'	31:A:1469:A:H1'	1.92	0.51
31:A:2310:C:H2'	31:A:2311:A:H4'	1.93	0.51
31:A:2812:G:H2'	31:A:2813:A:C8	2.45	0.51
1:C:56:GLY:HA2	1:C:212:TRP:HA	1.92	0.51
27:7:32:SER:HB3	31:A:1923:U:H5'	1.91	0.51
31:A:248:G:O2'	31:A:2432:A:OP1	2.27	0.51
31:A:720:U:H2'	31:A:721:A:H8	1.75	0.51
31:A:962:G:H2'	31:A:963:U:C6	2.45	0.51
31:A:1683:U:H2'	31:A:1684:G:C8	2.45	0.51
31:A:2313:C:H2'	31:A:2314:A:C8	2.45	0.51
19:0:42:ILE:HG22	19:0:48:TYR:HB2	1.93	0.51
31:A:222:A:H2	31:A:233:A:H4'	1.75	0.51
31:A:437:U:H2'	31:A:438:G:H8	1.75	0.51
31:A:819:A:N7	31:A:1188:U:O4	2.44	0.51
31:A:1080:A:H4'	31:A:1081:U:OP1	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:2036:C:H2'	31:A:2037:A:C8	2.46	0.51
31:A:2447:G:O4'	31:A:2501:C:N4	2.38	0.51
31:A:2656:U:C2	31:A:2665:A:N7	2.79	0.51
31:A:2687:U:H2'	31:A:2688:G:O4'	2.11	0.51
6:L:77:ILE:HD13	6:L:108:ALA:HB1	1.93	0.51
6:L:110:VAL:O	6:L:110:VAL:HG12	2.11	0.51
31:A:1282:U:O4	31:A:1286:A:N7	2.43	0.51
31:A:1681:G:N2	31:A:1763:G:OP2	2.36	0.51
33:e:37:LYS:HE3	33:e:38:MET:HE3	1.93	0.51
34:F:147:ARG:H	34:F:149:ARG:HH12	1.59	0.51
1:C:35:LYS:NZ	31:A:1353:A:O3'	2.44	0.51
8:O:33:ARG:O	8:O:65:THR:OG1	2.27	0.51
31:A:937:C:H2'	31:A:938:G:H8	1.75	0.51
31:A:1441:G:H2'	31:A:1442:U:C6	2.46	0.51
31:A:1563:U:H2'	31:A:1564:C:C6	2.46	0.51
31:A:2616:C:H2'	31:A:2617:U:H6	1.75	0.51
31:A:2853:C:N4	31:A:2854:G:O6	2.44	0.51
1:C:209:ALA:HA	1:C:212:TRP:CE2	2.46	0.50
11:S:6:LYS:NZ	31:A:495:G:OP1	2.43	0.50
15:W:11:ASP:OD2	15:W:12:SER:N	2.42	0.50
24:K:105:ARG:NH2	25:P:32:VAL:O	2.44	0.50
25:P:28:LYS:HD3	25:P:82:SER:HB3	1.93	0.50
27:7:3:GLN:HB3	27:7:72:GLU:H	1.76	0.50
30:M:84:LYS:N	31:A:2275:C:O2	2.35	0.50
31:A:686:U:H2'	31:A:788:A:N1	2.26	0.50
31:A:1539:U:H2'	31:A:1540:G:C8	2.45	0.50
31:A:1631:G:H21	31:A:1635:A:H62	1.59	0.50
31:A:2898:U:H2'	31:A:2899:A:C8	2.46	0.50
4:G:4:ALA:HA	4:G:68:ARG:HD3	1.93	0.50
31:A:6:A:H2'	31:A:7:G:H8	1.76	0.50
31:A:633:A:O2'	31:A:2404:U:OP1	2.25	0.50
31:A:1351:C:HO2'	31:A:1571:A:HO2'	1.54	0.50
4:G:29:ASN:HB3	4:G:78:VAL:HA	1.92	0.50
5:J:65:THR:OG1	31:A:1141:U:OP2	2.29	0.50
10:R:61:ALA:HA	10:R:98:ILE:HA	1.93	0.50
31:A:962:G:H2'	31:A:963:U:H6	1.77	0.50
31:A:1437:C:HO2'	31:A:1516:G:HO2'	1.48	0.50
31:A:2417:C:H2'	31:A:2418:A:C8	2.47	0.50
1:C:155:ARG:HD3	31:A:1818:U:H2'	1.94	0.50
18:Z:15:ARG:HG2	18:Z:53:MET:HE1	1.92	0.50
31:A:117:G:OP2	31:A:119:A:O2'	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:457:A:N7	31:A:472:A:N6	2.59	0.50
31:A:711:G:N2	31:A:720:U:O2	2.30	0.50
31:A:1841:U:H2'	31:A:1842:G:H8	1.76	0.50
31:A:2086:U:H2'	31:A:2087:G:C8	2.47	0.50
31:A:2220:U:H2'	31:A:2221:G:H8	1.76	0.50
10:R:63:VAL:HG22	10:R:96:VAL:HG12	1.92	0.50
14:V:14:LYS:HZ1	22:B:98:G:H22	1.60	0.50
16:X:6:VAL:HG13	16:X:7:THR:HG23	1.94	0.50
26:6:84:ASP:OD1	26:6:85:VAL:N	2.44	0.50
28:8:74:LYS:HD3	28:8:76:GLU:H	1.75	0.50
31:A:155:A:H2'	31:A:156:A:C8	2.46	0.50
31:A:643:A:H2'	31:A:644:A:C4	2.46	0.50
31:A:1368:G:H2'	31:A:1369:G:H8	1.77	0.50
31:A:1844:C:H2'	31:A:1845:G:C8	2.47	0.50
31:A:1936:A:H4'	31:A:1937:A:O5'	2.10	0.50
31:A:2290:G:H2'	31:A:2291:U:C6	2.46	0.50
8:O:3:LYS:HG3	8:O:7:ARG:HH12	1.76	0.50
15:W:65:PHE:HD1	31:A:857:G:H5'	1.76	0.50
22:B:60:C:H2'	22:B:61:G:C8	2.46	0.50
24:K:18:ARG:HB3	24:K:45:GLU:HB3	1.93	0.50
31:A:640:C:N4	31:A:649:G:O6	2.44	0.50
31:A:1266:G:N2	31:A:2013:A:OP2	2.33	0.50
31:A:2698:U:H2'	31:A:2699:C:C6	2.47	0.50
31:A:2898:U:H2'	31:A:2899:A:H8	1.77	0.50
1:C:194:VAL:HG22	1:C:195:GLY:H	1.76	0.50
8:O:64:TYR:OH	22:B:51:G:N2	2.44	0.50
9:Q:47:ARG:NH1	9:Q:48:ASP:OD1	2.45	0.50
11:S:82:MET:N	11:S:82:MET:SD	2.85	0.50
29:9:47:MET:HA	29:9:47:MET:HE2	1.94	0.50
31:A:55:G:H2'	31:A:56:A:C8	2.44	0.50
31:A:640:C:H2'	31:A:641:U:C6	2.47	0.50
31:A:1165:A:H2'	31:A:1166:G:H8	1.75	0.50
31:A:1380:G:H2'	31:A:1381:G:H8	1.77	0.50
31:A:1437:C:H2'	31:A:1438:U:H6	1.77	0.50
31:A:1442:U:H2'	31:A:1443:U:C6	2.47	0.50
31:A:1928:A:H2'	31:A:1929:G:C4	2.46	0.50
34:F:175:PRO:HB3	35:b:43:PHE:CD1	2.46	0.50
24:K:47:ILE:HG22	24:K:49:ARG:H	1.77	0.50
26:6:40:CYS:HB2	26:6:89:VAL:HG12	1.94	0.50
2:D:3:GLY:HA3	2:D:204:LYS:HG2	1.94	0.50
8:O:36:TYR:HA	8:O:52:SER:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:9:1:MET:HG3	29:9:54:ASN:HD21	1.77	0.50
29:9:301:ALA:O	29:9:306:TRP:N	2.37	0.50
30:M:66:ARG:NH1	30:M:104:GLU:OE2	2.45	0.50
31:A:414:C:H2'	31:A:415:A:C8	2.47	0.50
31:A:742:A:H2'	31:A:743:A:H8	1.76	0.50
31:A:1518:C:H2'	31:A:1519:G:C8	2.47	0.50
15:W:33:ILE:HG22	15:W:34:VAL:HG23	1.94	0.49
21:2:34:ARG:NE	21:2:39:ARG:HD2	2.27	0.49
23:I:33:ASN:HB3	23:I:64:ARG:HH22	1.75	0.49
27:7:267:PHE:O	27:7:270:THR:OG1	2.27	0.49
31:A:5:A:H2'	31:A:6:A:C8	2.46	0.49
31:A:828:U:H4'	31:A:831:G:N1	2.27	0.49
31:A:931:U:O2	31:A:1167:C:O2'	2.30	0.49
31:A:1825:U:H2'	31:A:1826:G:C8	2.47	0.49
31:A:2219:U:O2'	32:H:97:ARG:NH2	2.44	0.49
27:7:18:GLN:NE2	27:7:23:ALA:HB2	2.25	0.49
27:7:179:MET:HE1	27:7:245:HIS:CD2	2.47	0.49
31:A:926:G:H2'	31:A:927:A:C8	2.47	0.49
31:A:2489:U:H3'	31:A:2490:G:H8	1.76	0.49
3:E:141:MET:HE1	3:E:143:LEU:HD12	1.95	0.49
10:R:10:LYS:NZ	10:R:23:GLU:OE2	2.42	0.49
21:2:10:LEU:HD11	21:2:14:ARG:HH11	1.77	0.49
31:A:6:A:H2'	31:A:7:G:C8	2.47	0.49
31:A:18:U:H2'	31:A:19:A:C8	2.46	0.49
31:A:711:G:H2'	31:A:712:G:H8	1.76	0.49
31:A:742:A:H2'	31:A:743:A:C8	2.47	0.49
31:A:833:A:H2'	31:A:834:G:H8	1.77	0.49
31:A:1278:C:H2'	31:A:1279:G:H8	1.76	0.49
31:A:1589:U:H2'	31:A:1590:A:C8	2.47	0.49
31:A:1814:G:OP2	31:A:1815:A:O2'	2.26	0.49
31:A:1890:A:H3'	31:A:1891:G:H8	1.78	0.49
31:A:2594:C:H2'	31:A:2595:G:H8	1.77	0.49
2:D:97:SER:OG	2:D:98:VAL:N	2.46	0.49
7:N:48:VAL:HA	7:N:51:LEU:HD12	1.93	0.49
9:Q:48:ASP:O	9:Q:52:ARG:N	2.45	0.49
13:U:3:LYS:O	13:U:93:ARG:NH2	2.45	0.49
17:Y:24:GLU:O	17:Y:28:LEU:HB3	2.11	0.49
26:6:76:ASP:HA	26:6:91:GLN:HE22	1.78	0.49
31:A:1704:C:H2'	31:A:1705:A:C8	2.48	0.49
31:A:2699:C:H2'	31:A:2700:A:C8	2.48	0.49
3:E:104:ALA:O	3:E:107:SER:OG	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:34:ARG:HG3	5:J:39:LYS:HE3	1.94	0.49
10:R:68:ARG:NH1	10:R:90:ARG:HB2	2.27	0.49
18:Z:53:MET:HG3	18:Z:54:VAL:HG23	1.94	0.49
22:B:70:C:H2'	22:B:71:C:H6	1.78	0.49
31:A:1019:U:OP1	31:A:1035:U:O2'	2.24	0.49
31:A:1800:C:O2	31:A:1817:G:O6	2.31	0.49
31:A:2291:U:H2'	31:A:2292:U:C6	2.48	0.49
31:A:2848:G:HO2'	31:A:2867:G:H22	1.57	0.49
2:D:136:ASN:OD1	31:A:2579:C:O2'	2.29	0.49
29:9:69:ARG:NH1	29:9:72:ASN:OD1	2.46	0.49
31:A:1164:C:H2'	31:A:1165:A:C8	2.47	0.49
7:N:3:HIS:HD2	31:A:2820:A:H4'	1.77	0.49
10:R:7:SER:HB3	10:R:22:LEU:HD11	1.94	0.49
31:A:139:U:O2'	31:A:141:G:N2	2.39	0.49
31:A:521:U:H2'	31:A:522:A:H8	1.78	0.49
31:A:582:A:H2'	31:A:583:G:H8	1.78	0.49
31:A:1387:A:H2'	31:A:1388:G:C8	2.47	0.49
31:A:2855:C:H2'	31:A:2856:A:C8	2.47	0.49
13:U:71:ILE:HD13	13:U:82:VAL:HB	1.95	0.49
22:B:116:G:H2'	22:B:117:G:H8	1.78	0.49
24:K:108:ARG:HH21	26:6:33:ILE:HG22	1.77	0.49
27:7:92:ASP:OD1	27:7:288:HIS:NE2	2.46	0.49
31:A:175:G:H2'	31:A:176:A:H8	1.77	0.49
31:A:665:U:H2'	31:A:666:A:H8	1.78	0.49
31:A:1229:C:H2'	31:A:1230:A:H8	1.76	0.49
31:A:2319:G:H4'	31:A:2320:U:H5'	1.95	0.49
31:A:2515:C:H2'	31:A:2516:A:H8	1.77	0.49
31:A:2773:C:H2'	31:A:2774:C:H6	1.78	0.49
26:6:60:ARG:HH12	31:A:2652:C:H5''	1.78	0.49
31:A:660:C:H2'	31:A:661:A:H8	1.78	0.49
31:A:946:C:H2'	31:A:947:A:C8	2.48	0.49
31:A:948:C:H2'	31:A:949:G:H8	1.78	0.49
31:A:1266:G:O2'	31:A:2012:G:O6	2.23	0.49
31:A:2314:A:H2'	31:A:2315:G:C8	2.48	0.49
31:A:2364:C:H2'	31:A:2365:G:O4'	2.13	0.49
33:e:56:ARG:HD3	33:e:81:LEU:HD11	1.94	0.49
21:2:34:ARG:HE	21:2:39:ARG:HD2	1.77	0.49
31:A:154:U:H2'	31:A:155:A:H8	1.78	0.49
31:A:462:C:N4	31:A:463:G:O6	2.46	0.49
31:A:733:G:N2	31:A:734:A:N7	2.61	0.49
31:A:1564:C:H2'	31:A:1565:C:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:F:56:LEU:HA	34:F:59:ILE:HG22	1.95	0.49
4:G:70:LEU:HD23	4:G:74:MET:HE2	1.94	0.48
4:G:85:LYS:NZ	4:G:86:LEU:O	2.46	0.48
8:O:67:ASN:OD1	8:O:70:ALA:N	2.31	0.48
15:W:26:SER:HA	15:W:62:LYS:HA	1.94	0.48
31:A:1808:A:H3'	31:A:1809:A:C8	2.48	0.48
31:A:1932:A:H2'	31:A:1933:G:O4'	2.13	0.48
31:A:2564:A:C2	31:A:2647:U:H4'	2.48	0.48
4:G:142:GLN:HE22	31:A:2761:A:H1'	1.78	0.48
27:7:286:LEU:HD12	27:7:297:TRP:HZ3	1.78	0.48
31:A:-1:A:H2'	31:A:0:A:C8	2.48	0.48
31:A:370:G:OP1	31:A:423:A:N6	2.46	0.48
31:A:851:C:H2'	31:A:852:U:C6	2.47	0.48
31:A:858:G:H3'	31:A:859:G:C8	2.49	0.48
31:A:1286:A:N6	31:A:1329:U:O2	2.46	0.48
31:A:2139:U:H2'	31:A:2140:G:H8	1.78	0.48
31:A:2528:U:O2'	31:A:2530:A:OP1	2.26	0.48
31:A:213:A:H2'	31:A:214:G:H8	1.79	0.48
31:A:969:G:H2'	31:A:970:U:C6	2.48	0.48
31:A:1071:G:N2	31:A:1090:A:N7	2.61	0.48
31:A:1437:C:H2'	31:A:1438:U:C6	2.48	0.48
31:A:2370:G:H2'	31:A:2371:G:C8	2.48	0.48
34:F:176:PHE:HD2	35:b:47:LYS:HZ2	1.60	0.48
2:D:116:LYS:HB2	2:D:165:MET:HB2	1.95	0.48
2:D:179:ARG:HB2	2:D:188:LEU:HD12	1.95	0.48
4:G:154:GLU:OE1	4:G:159:LYS:N	2.39	0.48
6:L:17:LYS:HB3	6:L:27:LEU:HD11	1.94	0.48
6:L:38:GLN:HG3	31:A:805:G:H5''	1.96	0.48
24:K:2:ILE:HB	24:K:33:ALA:HB3	1.93	0.48
29:9:96:VAL:HG12	29:9:154:LEU:HD23	1.95	0.48
31:A:64:A:H2'	31:A:65:U:H6	1.78	0.48
31:A:1357:C:H2'	31:A:1358:G:O4'	2.13	0.48
31:A:2297:A:H62	31:A:2319:G:N2	2.10	0.48
31:A:2564:A:O2'	31:A:2565:A:O4'	2.22	0.48
31:A:2639:A:H2'	31:A:2640:G:O4'	2.13	0.48
6:L:29:LYS:HD3	10:R:82:HIS:CD2	2.49	0.48
11:S:8:ARG:HG2	11:S:102:HIS:CE1	2.49	0.48
24:K:29:HIS:NE2	31:A:2547:A:H4'	2.28	0.48
27:7:35:ARG:HA	27:7:35:ARG:HH11	1.78	0.48
31:A:373:U:H2'	31:A:374:A:H8	1.78	0.48
31:A:858:G:O2'	31:A:2268:A:N3	2.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:1532:A:H2'	31:A:1533:C:C6	2.48	0.48
31:A:1636:U:O2'	31:A:1760:C:O2	2.30	0.48
31:A:1948:G:H2'	31:A:1949:G:C8	2.42	0.48
5:J:7:LYS:HB2	5:J:10:THR:HG22	1.95	0.48
7:N:8:ARG:HG2	31:A:1652:A:OP1	2.13	0.48
9:Q:89:ILE:HD11	9:Q:93:ILE:HB	1.94	0.48
22:B:103:U:H2'	22:B:104:A:H8	1.79	0.48
31:A:363:G:H2'	31:A:364:C:C6	2.48	0.48
31:A:1796:U:H2'	31:A:1797:G:C8	2.48	0.48
31:A:2074:U:H2'	31:A:2075:U:H6	1.77	0.48
34:F:166:ARG:NH2	34:F:169:LEU:HD11	2.28	0.48
1:C:65:ASP:N	1:C:102:TYR:O	2.36	0.48
2:D:8:LYS:NZ	2:D:195:GLY:O	2.35	0.48
15:W:29:ALA:N	15:W:60:ASP:OD1	2.44	0.48
31:A:223:A:N1	31:A:407:G:O2'	2.46	0.48
31:A:813:U:O2'	31:A:1225:G:O2'	2.20	0.48
33:e:88:HIS:HB2	33:e:89:PRO:HD3	1.94	0.48
6:L:65:GLY:HA2	31:A:631:A:H1'	1.96	0.48
29:9:47:MET:SD	29:9:90:VAL:HG21	2.53	0.48
31:A:314:C:H2'	31:A:315:G:C8	2.49	0.48
31:A:419:U:H2'	31:A:420:C:C6	2.48	0.48
31:A:660:C:H2'	31:A:661:A:C8	2.47	0.48
31:A:1683:U:H2'	31:A:1684:G:H8	1.78	0.48
31:A:2489:U:H3'	31:A:2490:G:C8	2.49	0.48
2:D:25:THR:HG21	2:D:193:VAL:HG22	1.94	0.48
2:D:37:VAL:HG22	2:D:48:ILE:HG22	1.93	0.48
31:A:48:G:N2	31:A:177:G:OP2	2.47	0.48
31:A:1018:U:O2'	31:A:1120:G:N2	2.39	0.48
31:A:1085:A:H1'	31:A:1105:U:H1'	1.94	0.48
31:A:2623:G:H2'	31:A:2624:G:C8	2.48	0.48
1:C:144:GLU:HB2	1:C:187:CYS:HB2	1.95	0.48
2:D:13:ARG:HD2	2:D:15:PHE:CZ	2.49	0.48
2:D:59:ARG:NH2	31:A:2830:C:H3'	2.29	0.48
4:G:2:ARG:HA	4:G:5:LYS:HG2	1.96	0.48
4:G:137:LYS:HB3	31:A:2746:U:H4'	1.96	0.48
23:I:20:SER:HA	23:I:24:GLY:HA2	1.96	0.48
25:P:40:GLN:NE2	25:P:41:ALA:O	2.47	0.48
31:A:499:U:H2'	31:A:500:G:O4'	2.13	0.48
31:A:566:U:H2'	31:A:567:U:C6	2.49	0.48
31:A:2291:U:O2'	31:A:2374:C:O2	2.29	0.48
31:A:2907:A:H2'	31:A:2908:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:F:157:THR:HG22	34:F:159:ALA:H	1.77	0.48
2:D:53:GLY:HA3	2:D:77:ARG:HG3	1.96	0.47
22:B:14:U:OP2	22:B:70:C:O2'	2.28	0.47
31:A:552:U:H2'	31:A:553:G:H8	1.78	0.47
32:H:71:LYS:HB3	32:H:108:VAL:HG21	1.96	0.47
18:Z:10:ARG:HG3	18:Z:53:MET:HA	1.95	0.47
27:7:2:ALA:N	27:7:72:GLU:O	2.47	0.47
31:A:1287:A:H2'	31:A:1288:G:C4	2.50	0.47
31:A:1447:C:H2'	31:A:1448:G:C8	2.48	0.47
31:A:2231:U:H2'	31:A:2232:C:C6	2.48	0.47
4:G:156:TYR:CZ	31:A:2531:A:H5''	2.49	0.47
23:I:15:GLY:HA2	23:I:50:LYS:HB3	1.96	0.47
24:K:114:LYS:O	24:K:117:SER:OG	2.27	0.47
27:7:24:LEU:HB2	27:7:36:ILE:HD13	1.97	0.47
29:9:38:ASP:OD2	29:9:129:ARG:NH1	2.46	0.47
30:M:14:LYS:O	30:M:71:LYS:NZ	2.41	0.47
31:A:1744:A:H3'	31:A:1745:A:H8	1.80	0.47
31:A:2081:U:H2'	31:A:2082:A:C8	2.49	0.47
31:A:2458:G:O2'	31:A:2461:A:N6	2.47	0.47
8:O:88:LYS:HD2	8:O:88:LYS:N	2.29	0.47
9:Q:69:ARG:NH1	31:A:1012:U:OP2	2.41	0.47
17:Y:43:LEU:HA	17:Y:46:VAL:HG12	1.96	0.47
23:I:52:LEU:HD11	23:I:81:LYS:HE2	1.96	0.47
31:A:796:C:H2'	31:A:797:G:C8	2.49	0.47
31:A:1351:C:O2'	31:A:1571:A:O2'	2.22	0.47
31:A:1443:U:H2'	31:A:1444:G:C8	2.43	0.47
31:A:2086:U:H2'	31:A:2087:G:H8	1.80	0.47
31:A:2674:G:H2'	31:A:2675:A:C8	2.49	0.47
32:H:117:LEU:HD23	32:H:120:GLY:HA2	1.96	0.47
1:C:99:GLU:OE2	31:A:1491:G:O2'	2.31	0.47
24:K:25:LEU:HD22	31:A:2562:U:H4'	1.96	0.47
31:A:1022:G:N7	31:A:1140:C:N4	2.62	0.47
31:A:1569:A:H2'	31:A:1570:A:C8	2.48	0.47
31:A:1823:G:H2'	31:A:1824:G:H8	1.78	0.47
31:A:2329:U:H2'	31:A:2330:G:H8	1.78	0.47
8:O:71:ALA:HB3	8:O:105:ALA:HB3	1.97	0.47
14:V:17:SER:O	14:V:21:ARG:HG2	2.14	0.47
28:8:149:ARG:HD2	28:8:149:ARG:HA	1.71	0.47
31:A:675:A:N3	31:A:2443:C:O2'	2.46	0.47
31:A:1939:U:O2	31:A:1939:U:H2'	2.15	0.47
31:A:2107:G:H2'	31:A:2108:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:256:THR:HG1	31:A:1803:A:HO2'	1.59	0.47
8:O:49:VAL:HG21	8:O:82:ALA:HB2	1.96	0.47
14:V:80:HIS:HB2	14:V:87:GLN:HE22	1.80	0.47
19:O:10:SER:O	19:O:14:MET:HG3	2.15	0.47
22:B:95:U:H2'	22:B:96:G:H8	1.80	0.47
24:K:2:ILE:O	24:K:33:ALA:N	2.45	0.47
25:P:8:GLU:HG2	25:P:54:LEU:HD22	1.97	0.47
31:A:371:A:N6	31:A:402:A:OP2	2.47	0.47
31:A:579:G:H2'	31:A:580:U:C6	2.50	0.47
31:A:1054:A:OP1	33:e:31:ARG:NH2	2.43	0.47
31:A:1092:C:H2'	31:A:1093:G:C8	2.49	0.47
31:A:1239:G:H2'	31:A:1240:U:O4'	2.14	0.47
31:A:1406:U:H2'	31:A:1407:G:C8	2.50	0.47
31:A:1931:U:H2'	31:A:1932:A:C8	2.50	0.47
31:A:2289:G:H2'	31:A:2290:G:H8	1.79	0.47
31:A:2699:C:H2'	31:A:2700:A:H8	1.79	0.47
33:e:87:GLU:HG2	33:e:95:LEU:HD12	1.97	0.47
4:G:22:VAL:HG12	4:G:35:THR:HG22	1.95	0.47
18:Z:19:HIS:O	18:Z:22:THR:OG1	2.30	0.47
23:I:40:ALA:HB3	23:I:66:PHE:CZ	2.50	0.47
31:A:414:C:O3'	31:A:1878:G:N2	2.48	0.47
31:A:441:U:H2'	31:A:442:G:H8	1.77	0.47
31:A:1278:C:H2'	31:A:1279:G:C8	2.49	0.47
31:A:2677:G:H2'	31:A:2678:C:C6	2.50	0.47
2:D:83:ARG:HH11	31:A:2637:U:H5''	1.80	0.47
2:D:183:GLU:CD	2:D:183:GLU:H	2.22	0.47
3:E:48:THR:O	3:E:52:VAL:HG23	2.15	0.47
23:I:102:ARG:HB3	23:I:141:ASP:HA	1.96	0.47
28:8:107:ARG:NH2	31:A:1893:C:H4'	2.30	0.47
31:A:12:U:O2	31:A:2626:C:H4'	2.15	0.47
31:A:630:G:N2	31:A:633:A:OP2	2.42	0.47
31:A:881:G:H2'	31:A:882:G:H8	1.79	0.47
31:A:1363:C:O2'	31:A:1809:A:N3	2.42	0.47
31:A:1645:G:H5''	31:A:1646:C:H5'	1.96	0.47
5:J:34:ARG:HA	5:J:39:LYS:HE3	1.97	0.47
7:N:2:ARG:HH21	31:A:2821:A:N6	2.13	0.47
7:N:58:ASP:HA	7:N:80:PHE:HD1	1.79	0.47
14:V:81:PRO:HA	30:M:24:THR:HG23	1.96	0.47
29:9:281:VAL:HG12	29:9:311:TYR:HB2	1.97	0.47
31:A:2027:G:H2'	31:A:2028:U:C6	2.49	0.47
1:C:77:VAL:HG11	1:C:109:LEU:HD11	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:W:37:ARG:O	15:W:53:HIS:ND1	2.46	0.46
21:2:3:ARG:NH2	31:A:1613:G:O2'	2.39	0.46
27:7:219:ARG:HH22	27:7:261:LYS:HB3	1.80	0.46
29:9:8:SER:O	29:9:63:LYS:NZ	2.44	0.46
31:A:629:G:H2'	31:A:630:G:C8	2.50	0.46
31:A:987:C:H2'	31:A:988:A:O4'	2.15	0.46
31:A:2092:U:OP2	32:H:27:ARG:NH2	2.48	0.46
31:A:2314:A:H2'	31:A:2315:G:H8	1.80	0.46
34:F:122:ASP:OD1	34:F:126:ASN:HB2	2.15	0.46
35:b:28:VAL:HG11	35:b:32:LEU:HD13	1.96	0.46
5:J:7:LYS:HG2	31:A:538:A:H4'	1.97	0.46
7:N:71:ARG:HA	7:N:71:ARG:HD2	1.74	0.46
17:Y:47:ARG:HH22	17:Y:48:ARG:HH12	1.64	0.46
17:Y:50:VAL:HA	17:Y:53:VAL:HG12	1.97	0.46
20:1:33:LEU:HD11	31:A:2286:G:N7	2.30	0.46
22:B:18:G:H1	22:B:65:U:H3	1.62	0.46
31:A:1418:G:N1	31:A:1579:A:OP2	2.46	0.46
1:C:83:ASP:HB2	1:C:90:ILE:HG12	1.96	0.46
3:E:21:ARG:HH12	3:E:106:LYS:CB	2.28	0.46
3:E:106:LYS:HG3	3:E:200:LEU:HD12	1.96	0.46
13:U:16:LYS:N	31:A:329:G:O6	2.49	0.46
18:Z:26:LEU:HD23	18:Z:46:MET:HE2	1.96	0.46
19:0:11:LYS:HA	19:0:14:MET:HE2	1.96	0.46
31:A:404:A:H4'	31:A:405:U:O5'	2.15	0.46
31:A:1394:U:H5'	31:A:1603:A:H4'	1.96	0.46
31:A:1432:G:H2'	31:A:1433:A:H8	1.79	0.46
31:A:2425:A:H4'	31:A:2426:A:O5'	2.14	0.46
31:A:2710:C:H2'	31:A:2711:A:H8	1.80	0.46
2:D:155:VAL:HG21	31:A:2618:G:H21	1.80	0.46
4:G:23:ILE:HD12	4:G:71:LEU:HD11	1.97	0.46
4:G:41:GLU:CD	4:G:54:ARG:HE	2.23	0.46
5:J:76:HIS:CE1	5:J:85:LYS:HB2	2.50	0.46
18:Z:5:LYS:HB3	18:Z:57:GLU:HB2	1.97	0.46
28:8:70:ALA:O	28:8:73:ILE:HG22	2.15	0.46
31:A:56:A:H2'	31:A:57:C:C6	2.51	0.46
31:A:558:U:H2'	31:A:559:G:C8	2.50	0.46
31:A:720:U:H2'	31:A:721:A:C8	2.50	0.46
31:A:1843:C:H2'	31:A:1844:C:C6	2.50	0.46
29:9:125:LEU:HD12	29:9:129:ARG:HG2	1.97	0.46
31:A:414:C:H1'	31:A:1864:U:H1'	1.98	0.46
31:A:438:G:H2'	31:A:439:A:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:608:A:OP2	31:A:619:G:N1	2.38	0.46
31:A:698:C:HO2'	31:A:734:A:H61	1.58	0.46
31:A:1998:A:H2'	31:A:1999:C:C6	2.51	0.46
31:A:2245:U:H5''	31:A:2246:G:H5'	1.97	0.46
2:D:61:THR:HB	2:D:63:PRO:HD2	1.97	0.46
3:E:69:ARG:NH1	31:A:1255:U:OP2	2.48	0.46
7:N:29:VAL:HG11	7:N:75:ILE:HG23	1.96	0.46
17:Y:41:HIS:CG	31:A:96:C:H4'	2.50	0.46
31:A:19:A:H2'	31:A:20:C:H6	1.81	0.46
31:A:966:G:H4'	31:A:2271:G:H22	1.81	0.46
31:A:1131:G:O2'	31:A:2025:C:O2'	2.23	0.46
31:A:2470:G:H2'	31:A:2471:A:C8	2.51	0.46
24:K:94:PRO:HG2	24:K:114:LYS:HE3	1.97	0.46
28:8:122:ARG:HD2	28:8:172:PHE:HD1	1.81	0.46
28:8:150:THR:HA	28:8:153:ARG:HD2	1.98	0.46
31:A:532:A:N1	31:A:2035:G:N2	2.63	0.46
31:A:796:C:H2'	31:A:797:G:H8	1.81	0.46
34:F:101:ARG:HG3	34:F:105:ILE:HD11	1.97	0.46
14:V:11:GLU:OE1	14:V:16:ALA:HB2	2.15	0.46
22:B:72:G:H21	22:B:104:A:N6	2.11	0.46
23:I:4:VAL:C	23:I:5:GLN:HG3	2.41	0.46
27:7:80:GLN:HB2	27:7:112:ASP:HB2	1.98	0.46
31:A:345:A:N3	31:A:347:A:N6	2.64	0.46
31:A:1532:A:N6	31:A:1540:G:O6	2.49	0.46
31:A:2643:G:H2'	31:A:2644:G:C8	2.48	0.46
31:A:2906:C:H2'	31:A:2907:A:H8	1.81	0.46
1:C:52:HIS:CD2	1:C:218:THR:HA	2.51	0.46
6:L:68:SER:O	6:L:69:ARG:HG2	2.16	0.46
29:9:8:SER:HB3	29:9:153:LEU:HD13	1.96	0.46
31:A:589:U:H2'	31:A:590:A:C8	2.51	0.46
31:A:671:C:H2'	31:A:672:C:C6	2.50	0.46
31:A:851:C:H2'	31:A:852:U:H6	1.79	0.46
31:A:1423:G:H2'	31:A:1424:G:H8	1.79	0.46
31:A:1906:G:O6	31:A:1929:G:N2	2.49	0.46
31:A:2123:G:H2'	31:A:2124:G:H8	1.81	0.46
31:A:2455:G:H1	31:A:2497:A:N6	2.01	0.46
31:A:2567:G:H2'	31:A:2568:U:C6	2.50	0.46
1:C:107:LYS:HA	1:C:195:GLY:HA2	1.98	0.46
1:C:124:LYS:HG3	1:C:125:PRO:HD2	1.97	0.46
6:L:68:SER:HB3	31:A:632:A:H5''	1.97	0.46
10:R:47:VAL:HG12	10:R:49:ILE:HG12	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Z:30:ARG:NH2	31:A:1159:U:OP1	2.48	0.46
19:0:53:VAL:HG12	19:0:54:ILE:HG12	1.97	0.46
27:7:152:VAL:N	27:7:153:PRO:HD2	2.31	0.46
31:A:1424:G:H2'	31:A:1425:G:C8	2.51	0.46
31:A:1709:U:H2'	31:A:1710:G:C8	2.51	0.46
31:A:2037:A:H2'	31:A:2038:G:H8	1.81	0.46
31:A:2078:C:H2'	31:A:2079:U:C6	2.51	0.46
31:A:2259:U:H2'	31:A:2260:C:H6	1.81	0.46
31:A:2327:A:H2'	31:A:2328:A:C8	2.51	0.46
33:e:38:MET:HE2	33:e:38:MET:HA	1.97	0.46
31:A:414:C:H2'	31:A:415:A:H8	1.81	0.45
31:A:582:A:H2'	31:A:583:G:C8	2.51	0.45
31:A:1141:U:H4'	31:A:1142:A:O4'	2.15	0.45
31:A:1258:U:H2'	31:A:1259:G:C8	2.51	0.45
31:A:1281:G:H2'	31:A:1282:U:H6	1.82	0.45
31:A:1388:G:H2'	31:A:1389:G:C8	2.50	0.45
31:A:2732:G:H5''	31:A:2733:A:O4'	2.15	0.45
1:C:200:MET:HG3	31:A:1820:U:C2	2.51	0.45
7:N:103:ARG:NH1	31:A:1287:A:N7	2.64	0.45
9:Q:46:TYR:HA	9:Q:49:ARG:NH1	2.31	0.45
10:R:73:LYS:HD2	10:R:73:LYS:HA	1.79	0.45
14:V:25:LYS:HZ3	14:V:25:LYS:HB2	1.81	0.45
20:1:29:LYS:NZ	31:A:2287:A:OP1	2.39	0.45
28:8:91:GLN:NE2	28:8:92:ARG:HE	2.15	0.45
31:A:154:U:H2'	31:A:155:A:C8	2.50	0.45
31:A:184:C:H2'	31:A:185:G:H8	1.81	0.45
31:A:570:G:H2'	31:A:2030:A:N7	2.31	0.45
31:A:903:C:H2'	31:A:904:G:C8	2.51	0.45
31:A:1167:C:H2'	31:A:1168:G:C8	2.51	0.45
31:A:1550:C:H2'	31:A:1551:A:H8	1.80	0.45
31:A:1839:G:C2	31:A:1840:G:C8	3.04	0.45
31:A:2120:G:H2'	31:A:2121:G:C8	2.50	0.45
31:A:2457:U:O2	31:A:2495:G:N1	2.45	0.45
2:D:32:ASN:HB3	2:D:50:VAL:HG21	1.98	0.45
2:D:151:THR:HB	2:D:152:PRO:HD3	1.97	0.45
18:Z:41:PRO:HA	18:Z:44:ARG:HB2	1.99	0.45
31:A:137:U:H2'	31:A:140:C:N3	2.31	0.45
31:A:174:U:H2'	31:A:175:G:C8	2.51	0.45
31:A:314:C:H2'	31:A:315:G:H8	1.81	0.45
31:A:569:U:H2'	31:A:570:G:O4'	2.16	0.45
31:A:866:A:H61	31:A:913:U:H1'	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:1405:U:H2'	31:A:1406:U:C6	2.51	0.45
31:A:1751:U:H2'	31:A:1752:C:C6	2.52	0.45
31:A:2006:C:O2'	31:A:2823:A:N3	2.46	0.45
31:A:2071:A:H2'	31:A:2072:C:C6	2.51	0.45
31:A:2250:G:OP1	31:A:2275:C:N4	2.39	0.45
31:A:2841:C:H2'	31:A:2842:G:C8	2.52	0.45
4:G:88:LEU:HD22	4:G:95:ALA:HB2	1.98	0.45
4:G:148:ARG:HD3	4:G:163:TYR:CE1	2.51	0.45
14:V:76:ASP:H	14:V:90:ASP:HB2	1.81	0.45
25:P:93:LYS:NZ	31:A:1754:A:N7	2.63	0.45
27:7:30:ASP:OD1	27:7:30:ASP:N	2.47	0.45
31:A:935:C:H2'	31:A:936:A:C8	2.48	0.45
31:A:964:C:O2'	31:A:2273:A:N3	2.42	0.45
31:A:971:G:H2'	31:A:972:A:O4'	2.16	0.45
31:A:1435:G:H2'	31:A:1436:G:H8	1.82	0.45
31:A:2543:G:H2'	31:A:2544:G:C8	2.51	0.45
31:A:2642:G:H2'	31:A:2643:G:H8	1.81	0.45
31:A:2788:C:H2'	31:A:2789:C:C6	2.52	0.45
1:C:142:ASN:OD1	1:C:151:GLY:HA2	2.17	0.45
2:D:49:GLN:HG2	2:D:79:LEU:HD11	1.97	0.45
26:6:44:SER:OG	26:6:45:SER:N	2.50	0.45
31:A:7:G:H2'	31:A:8:C:C6	2.52	0.45
31:A:302:C:H2'	31:A:303:G:C8	2.52	0.45
31:A:534:U:H2'	31:A:535:G:C8	2.51	0.45
31:A:563:A:H2'	31:A:564:C:C6	2.51	0.45
31:A:671:C:H2'	31:A:672:C:H6	1.81	0.45
31:A:776:G:N1	31:A:2072:C:H5'	2.29	0.45
31:A:1406:U:H2'	31:A:1407:G:H8	1.82	0.45
31:A:1630:A:H2'	31:A:1631:G:O4'	2.17	0.45
31:A:1995:U:H3'	31:A:1996:C:H2'	1.98	0.45
31:A:2841:C:H2'	31:A:2842:G:H8	1.81	0.45
31:A:2895:G:H2'	31:A:2896:C:C6	2.52	0.45
1:C:27:LYS:NZ	31:A:1568:G:N7	2.62	0.45
18:Z:2:LYS:HE2	18:Z:2:LYS:HA	1.98	0.45
28:8:111:GLN:NE2	28:8:111:GLN:O	2.50	0.45
31:A:1408:G:H1	31:A:1594:U:H3	1.64	0.45
31:A:1441:G:H2'	31:A:1442:U:H6	1.81	0.45
31:A:2465:C:H2'	31:A:2466:C:C6	2.51	0.45
31:A:2625:G:H2'	31:A:2626:C:C6	2.52	0.45
31:A:2818:U:H2'	31:A:2819:G:C8	2.52	0.45
32:H:54:LEU:HA	32:H:57:LYS:HG2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:F:104:THR:HA	35:b:38:SER:HB3	1.98	0.45
1:C:123:ILE:HG23	1:C:191:LEU:HD21	1.97	0.45
1:C:261:ARG:HE	1:C:262:THR:HG23	1.80	0.45
7:N:23:ASN:ND2	31:A:1294:U:O2	2.50	0.45
8:O:51:ALA:HB2	8:O:81:ARG:HD2	1.99	0.45
10:R:26:ASP:O	10:R:27:ILE:HD13	2.16	0.45
19:O:51:ARG:HD2	19:O:52:LYS:N	2.30	0.45
22:B:16:G:N2	22:B:69:G:H1'	2.31	0.45
26:6:40:CYS:O	26:6:90:MET:N	2.49	0.45
31:A:406:G:H2'	31:A:407:G:H8	1.81	0.45
31:A:807:U:H2'	31:A:808:G:H8	1.82	0.45
31:A:1407:G:H2'	31:A:1408:G:C8	2.49	0.45
31:A:1429:G:H2'	31:A:1430:G:C8	2.50	0.45
31:A:1433:A:N1	31:A:1560:G:N2	2.52	0.45
31:A:1992:G:N2	31:A:1996:C:O2'	2.50	0.45
31:A:2093:G:H21	31:A:2198:A:N6	2.14	0.45
31:A:2405:G:O2'	31:A:2411:A:N6	2.50	0.45
31:A:2543:G:H21	31:A:2646:C:H5''	1.81	0.45
4:G:148:ARG:HA	4:G:161:VAL:HG13	1.98	0.45
13:U:67:SER:OG	31:A:335:C:O2	2.21	0.45
27:7:22:GLN:HE21	27:7:33:ARG:HD3	1.82	0.45
27:7:226:LEU:HD21	27:7:236:ILE:HD11	1.97	0.45
27:7:238:VAL:O	27:7:242:HIS:N	2.47	0.45
31:A:970:U:O2	31:A:984:A:O2'	2.30	0.45
31:A:1464:G:H2'	31:A:1465:G:C8	2.51	0.45
31:A:1997:C:H2'	31:A:1998:A:C8	2.49	0.45
31:A:2064:C:H2'	31:A:2065:C:C6	2.52	0.45
31:A:2399:G:O6	31:A:2418:A:N6	2.49	0.45
31:A:2708:G:H2'	31:A:2709:G:H8	1.81	0.45
31:A:2868:A:H2'	31:A:2869:G:C8	2.52	0.45
32:H:26:ALA:O	32:H:31:VAL:HG22	2.16	0.45
3:E:55:SER:HB3	31:A:468:G:H5''	1.98	0.45
29:9:167:MET:HB3	29:9:170:ALA:HB2	1.98	0.45
31:A:145:C:H2'	31:A:146:A:C8	2.52	0.45
31:A:685:A:O2'	31:A:773:U:O4	2.30	0.45
31:A:1281:G:H2'	31:A:1282:U:C6	2.51	0.45
31:A:1295:C:H2'	31:A:1296:G:C8	2.51	0.45
31:A:1363:C:H2'	31:A:1364:G:H8	1.82	0.45
31:A:2179:C:H2'	31:A:2180:U:C6	2.52	0.45
31:A:2591:C:H2'	31:A:2592:G:H8	1.81	0.45
31:A:2845:U:H2'	31:A:2846:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:18:THR:HG23	3:E:19:PHE:CD2	2.48	0.45
7:N:98:LEU:O	7:N:112:TYR:N	2.35	0.45
11:S:88:ARG:NH1	31:A:748:G:OP2	2.50	0.45
27:7:275:ASP:OD2	31:A:1914:C:H5'	2.17	0.45
30:M:66:ARG:HG3	30:M:101:VAL:HG23	1.99	0.45
31:A:35:G:H1'	31:A:454:A:N3	2.32	0.45
31:A:289:G:H2'	31:A:290:U:C6	2.52	0.45
31:A:766:U:H2'	31:A:767:U:C6	2.52	0.45
31:A:1417:C:H2'	31:A:1418:G:O4'	2.17	0.45
31:A:2025:C:H2'	31:A:2026:U:C6	2.52	0.45
31:A:2074:U:H2'	31:A:2075:U:C6	2.52	0.45
34:F:72:SER:HB2	34:F:80:GLN:N	2.32	0.45
34:F:91:ARG:HA	34:F:95:MET:SD	2.57	0.45
2:D:133:THR:HG23	2:D:134:HIS:CD2	2.52	0.44
5:J:53:TYR:CE1	5:J:121:LYS:HG2	2.52	0.44
5:J:125:TYR:OH	5:J:132:HIS:NE2	2.46	0.44
6:L:18:ARG:HG2	6:L:21:ARG:HG3	1.99	0.44
7:N:2:ARG:HA	7:N:5:LYS:HD2	1.98	0.44
13:U:14:THR:OG1	13:U:68:ASN:OD1	2.34	0.44
22:B:28:C:H2'	22:B:29:A:C8	2.52	0.44
27:7:212:TYR:HA	27:7:226:LEU:HB2	1.98	0.44
27:7:288:HIS:CG	27:7:289:PRO:HD2	2.53	0.44
31:A:-2:U:H2'	31:A:-1:A:C8	2.51	0.44
31:A:226:A:H5'	31:A:257:C:H4'	1.99	0.44
31:A:419:U:H2'	31:A:420:C:H6	1.82	0.44
31:A:521:U:H2'	31:A:522:A:C8	2.52	0.44
31:A:1129:A:O2'	31:A:2515:C:O2	2.31	0.44
31:A:1188:U:H2'	31:A:1189:A:H8	1.82	0.44
31:A:1442:U:H2'	31:A:1443:U:H6	1.82	0.44
31:A:2696:U:H2'	31:A:2697:G:H8	1.81	0.44
31:A:2875:C:H2'	31:A:2876:G:H8	1.83	0.44
34:F:64:PRO:HB3	34:F:88:VAL:HB	1.97	0.44
34:F:71:LYS:HB3	34:F:71:LYS:HE2	1.84	0.44
5:J:27:ARG:HH21	31:A:1141:U:H5''	1.82	0.44
28:8:103:LYS:HD2	28:8:111:GLN:HB2	1.99	0.44
29:9:187:ALA:N	29:9:192:THR:HG21	2.32	0.44
31:A:19:A:H2'	31:A:20:C:C6	2.52	0.44
31:A:1306:C:H41	31:A:1606:C:H2'	1.82	0.44
31:A:1427:A:N6	31:A:1571:A:OP2	2.40	0.44
31:A:1469:A:OP2	31:A:1522:A:N6	2.39	0.44
31:A:1802:A:H2'	31:A:1803:A:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:2163:A:OP1	31:A:2170:A:O2'	2.35	0.44
31:A:2674:G:H2'	31:A:2675:A:H8	1.82	0.44
31:A:2875:C:H2'	31:A:2876:G:C8	2.52	0.44
2:D:5:VAL:HG11	2:D:80:TRP:CZ3	2.52	0.44
2:D:101:PHE:HD1	2:D:104:VAL:HG21	1.82	0.44
3:E:195:GLN:OE1	3:E:195:GLN:HA	2.17	0.44
4:G:59:ASP:N	4:G:59:ASP:OD1	2.48	0.44
5:J:120:ARG:NE	31:A:2780:G:OP1	2.41	0.44
25:P:27:VAL:HG21	25:P:73:PHE:HE2	1.82	0.44
27:7:179:MET:HE1	27:7:245:HIS:CG	2.52	0.44
28:8:130:ASP:OD1	28:8:131:ASP:N	2.51	0.44
29:9:22:SER:H	29:9:127:ASN:ND2	2.15	0.44
30:M:62:LYS:HE2	31:A:874:G:H5'	1.98	0.44
30:M:97:GLN:HG2	30:M:98:PRO:HD2	1.98	0.44
31:A:1038:G:H2'	31:A:1039:A:C8	2.52	0.44
31:A:1131:G:HO2'	31:A:2025:C:HO2'	1.52	0.44
31:A:1538:G:H2'	31:A:1539:U:C6	2.52	0.44
31:A:2064:C:H2'	31:A:2065:C:H6	1.82	0.44
31:A:2176:A:H2'	31:A:2177:C:C6	2.53	0.44
31:A:2406:A:OP1	31:A:2411:A:N6	2.51	0.44
31:A:2679:A:H2'	31:A:2680:U:C6	2.52	0.44
33:e:78:GLY:N	33:e:79:PRO:HD2	2.31	0.44
2:D:170:VAL:HG11	31:A:2679:A:H5'	2.00	0.44
3:E:40:ARG:HE	3:E:92:HIS:CG	2.35	0.44
7:N:90:ARG:NH2	31:A:2880:C:O2'	2.50	0.44
10:R:80:ARG:NH2	31:A:571:U:OP1	2.46	0.44
31:A:202:U:H2'	31:A:203:A:O4'	2.17	0.44
31:A:1684:G:O6	31:A:1705:A:N6	2.50	0.44
31:A:1853:A:N3	31:A:2233:U:O2'	2.42	0.44
31:A:1938:A:C6	31:A:1939:U:H5	2.36	0.44
31:A:2091:C:H5''	32:H:27:ARG:HH12	1.83	0.44
31:A:2431:U:N3	31:A:2434:A:OP2	2.38	0.44
31:A:2800:A:H3'	31:A:2801:G:H5'	2.00	0.44
2:D:83:ARG:NH1	31:A:2637:U:H5''	2.32	0.44
16:X:38:TRP:CD1	32:H:32:PRO:HA	2.53	0.44
23:I:132:ALA:O	23:I:133:ARG:HD3	2.17	0.44
24:K:6:THR:HA	31:A:1667:G:OP1	2.17	0.44
27:7:48:ASN:HD21	27:7:63:GLU:HG2	1.83	0.44
27:7:174:VAL:HG11	27:7:308:LEU:HD21	2.00	0.44
29:9:187:ALA:H	29:9:192:THR:HG21	1.83	0.44
29:9:247:ILE:HD11	29:9:282:PHE:CD1	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:523:C:H2'	31:A:524:G:C8	2.52	0.44
31:A:934:U:H2'	31:A:935:C:C6	2.52	0.44
31:A:1561:C:H2'	31:A:1562:U:C6	2.53	0.44
31:A:1791:A:C2	31:A:1829:A:H4'	2.53	0.44
31:A:1802:A:H2'	31:A:1803:A:C8	2.52	0.44
31:A:2350:C:H2'	31:A:2351:G:O4'	2.17	0.44
31:A:2606:C:H2'	31:A:2607:G:C8	2.52	0.44
33:e:29:ASP:HB2	33:e:56:ARG:HH12	1.82	0.44
20:1:7:LYS:NZ	31:A:2421:G:OP2	2.37	0.44
22:B:116:G:H2'	22:B:117:G:C8	2.52	0.44
23:I:89:SER:HA	23:I:135:MET:HE3	2.00	0.44
27:7:112:ASP:N	27:7:112:ASP:OD1	2.50	0.44
27:7:181:ALA:HB3	29:9:150:ARG:HE	1.82	0.44
31:A:1444:G:H2'	31:A:1445:G:H8	1.82	0.44
31:A:2037:A:H2'	31:A:2038:G:C8	2.52	0.44
31:A:2123:G:O6	31:A:2176:A:N6	2.50	0.44
31:A:2720:U:C2	31:A:2721:A:C8	3.06	0.44
1:C:170:TYR:HD2	1:C:182:LYS:HG2	1.82	0.44
9:Q:46:TYR:HA	9:Q:49:ARG:HH12	1.82	0.44
12:T:58:VAL:HG13	12:T:85:VAL:HG22	2.00	0.44
15:W:21:ARG:HB2	15:W:33:ILE:HG23	2.00	0.44
25:P:27:VAL:HG21	25:P:73:PHE:CE2	2.53	0.44
27:7:50:LYS:HB2	27:7:50:LYS:HE2	1.78	0.44
27:7:213:ARG:O	27:7:224:LEU:HB2	2.18	0.44
29:9:13:ALA:HB1	29:9:120:GLY:HA2	1.99	0.44
31:A:0:A:H2'	31:A:1:G:C8	2.53	0.44
31:A:244:A:H2'	31:A:245:G:O4'	2.17	0.44
31:A:1361:G:H2'	31:A:1362:C:H6	1.82	0.44
31:A:1438:U:H2'	31:A:1439:A:C8	2.53	0.44
31:A:1524:G:H2'	31:A:1525:A:H8	1.82	0.44
31:A:2215:C:H2'	31:A:2216:G:C8	2.52	0.44
31:A:2266:A:H4'	31:A:2267:A:N3	2.33	0.44
31:A:2313:C:H4'	34:F:87:LYS:HZ2	1.83	0.44
31:A:2623:G:H2'	31:A:2624:G:H8	1.81	0.44
32:H:121:VAL:O	32:H:123:ARG:HG3	2.18	0.44
7:N:28:LEU:HA	7:N:34:ILE:HG23	1.99	0.44
7:N:64:ARG:NH2	31:A:2851:A:O2'	2.51	0.44
24:K:23:LYS:HD2	24:K:23:LYS:HA	1.79	0.44
30:M:61:GLY:HA2	30:M:107:GLY:HA3	1.99	0.44
31:A:481:G:N1	31:A:507:A:H1'	2.33	0.44
31:A:532:A:H4'	31:A:533:G:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:685:A:C2	31:A:787:C:H1'	2.53	0.44
31:A:1031:G:H2'	31:A:1032:A:C8	2.53	0.44
31:A:1435:G:H2'	31:A:1436:G:C8	2.53	0.44
31:A:1632:A:H2'	31:A:1633:G:C4	2.52	0.44
31:A:2154:A:H2'	31:A:2155:U:C6	2.53	0.44
31:A:2480:C:H2'	31:A:2481:G:O4'	2.18	0.44
31:A:2696:U:H2'	31:A:2697:G:C8	2.53	0.44
1:C:231:HIS:HE1	31:A:1825:U:H4'	1.83	0.44
2:D:59:ARG:HH22	31:A:2830:C:H3'	1.83	0.44
4:G:66:THR:HG22	31:A:2748:A:H1'	2.00	0.44
8:O:103:VAL:HA	8:O:106:LEU:HD12	1.99	0.44
26:6:92:GLU:OE2	26:6:96:ARG:NH2	2.48	0.44
27:7:35:ARG:HH12	27:7:39:TRP:NE1	2.16	0.44
27:7:223:ARG:HD2	27:7:309:ILE:HG21	2.00	0.44
29:9:164:MET:HE1	29:9:172:LYS:HG2	2.00	0.44
31:A:540:C:N4	31:A:541:A:H62	2.16	0.44
31:A:1068:G:O6	31:A:1069:A:N6	2.50	0.44
31:A:1095:A:H2'	31:A:1096:A:C8	2.52	0.44
31:A:1562:U:H2'	31:A:1563:U:C6	2.53	0.44
31:A:2627:G:N2	31:A:2777:G:OP2	2.51	0.44
35:b:12:ILE:HD11	35:b:26:SER:HB3	2.00	0.44
35:b:28:VAL:HG21	35:b:32:LEU:HD13	1.99	0.44
1:C:5:CYS:SG	1:C:12:ARG:NH2	2.91	0.43
23:I:46:ASP:N	23:I:46:ASP:OD1	2.51	0.43
25:P:26:GLU:OE1	25:P:26:GLU:HA	2.18	0.43
26:6:46:ARG:CZ	26:6:46:ARG:HA	2.48	0.43
29:9:22:SER:H	29:9:127:ASN:HD21	1.65	0.43
31:A:177:G:H3'	31:A:178:G:H8	1.83	0.43
31:A:2349:G:O6	31:A:2369:A:N6	2.51	0.43
31:A:2543:G:H2'	31:A:2544:G:H8	1.82	0.43
13:U:43:LYS:NZ	31:A:480:A:OP2	2.48	0.43
14:V:21:ARG:HH21	14:V:87:GLN:HA	1.82	0.43
21:2:18:PHE:HZ	21:2:35:ARG:HH22	1.67	0.43
31:A:576:U:H2'	31:A:577:G:H8	1.82	0.43
31:A:874:G:H2'	31:A:875:G:H8	1.83	0.43
31:A:1361:G:H2'	31:A:1362:C:C6	2.53	0.43
31:A:1464:G:H2'	31:A:1465:G:H8	1.83	0.43
31:A:1794:A:H2'	31:A:1795:C:C6	2.53	0.43
31:A:2047:C:H2'	31:A:2048:G:C8	2.51	0.43
31:A:2443:C:H2'	31:A:2444:G:C8	2.53	0.43
31:A:2595:G:N2	31:A:2597:G:H3'	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:2824:C:OP2	31:A:2825:G:N2	2.51	0.43
5:J:57:LEU:HD21	5:J:130:HIS:HB3	2.00	0.43
10:R:38:VAL:HG11	10:R:57:GLY:HA3	2.01	0.43
22:B:70:C:H2'	22:B:71:C:C6	2.53	0.43
25:P:51:ASN:O	31:A:2845:U:H5''	2.18	0.43
31:A:18:U:H2'	31:A:19:A:H8	1.83	0.43
31:A:30:G:O2'	31:A:1214:A:N3	2.43	0.43
31:A:440:C:H2'	31:A:441:U:H6	1.83	0.43
31:A:528:A:H2'	31:A:529:A:H5''	2.00	0.43
31:A:1422:G:H1	31:A:1576:U:H3	1.66	0.43
31:A:1542:U:H2'	31:A:1543:G:O4'	2.18	0.43
31:A:2564:A:H2	31:A:2647:U:H4'	1.83	0.43
1:C:204:LEU:HB3	1:C:209:ALA:HB3	2.00	0.43
11:S:20:VAL:HG23	11:S:23:LEU:HD12	2.00	0.43
30:M:11:LYS:HG2	30:M:86:LYS:HE2	2.00	0.43
31:A:64:A:H2'	31:A:65:U:C6	2.52	0.43
31:A:928:A:H2'	31:A:929:U:C6	2.53	0.43
31:A:1022:G:N2	31:A:1023:U:O4	2.50	0.43
31:A:1380:G:H2'	31:A:1381:G:C8	2.54	0.43
31:A:1437:C:O2'	31:A:1516:G:O2'	2.24	0.43
31:A:1637:A:H2'	31:A:1638:C:H6	1.81	0.43
3:E:4:VAL:HG22	3:E:6:LYS:H	1.83	0.43
6:L:13:LYS:HE3	31:A:661:A:H4'	1.99	0.43
6:L:78:ARG:HG2	6:L:113:ALA:HB3	2.00	0.43
12:T:51:PHE:O	12:T:53:VAL:HG23	2.18	0.43
27:7:94:ILE:N	27:7:148:VAL:O	2.51	0.43
31:A:52:A:H2'	31:A:53:A:C8	2.54	0.43
31:A:77:G:H2'	31:A:78:U:C6	2.54	0.43
31:A:224:U:O4	31:A:232:G:N2	2.51	0.43
31:A:347:A:H2'	31:A:348:A:C8	2.54	0.43
31:A:363:G:H2'	31:A:364:C:H6	1.84	0.43
31:A:717:C:H3'	31:A:718:A:H8	1.84	0.43
31:A:971:G:OP1	31:A:989:G:N1	2.52	0.43
31:A:1065:U:C4	31:A:1066:U:H1'	2.52	0.43
31:A:1102:C:H2'	31:A:1103:A:C8	2.46	0.43
31:A:1412:U:H2'	31:A:1413:A:C8	2.53	0.43
31:A:1839:G:C8	31:A:1927:A:C6	3.06	0.43
31:A:2328:A:H2'	31:A:2329:U:C6	2.52	0.43
31:A:2379:G:H2'	31:A:2380:C:C6	2.54	0.43
34:F:36:ASN:HA	34:F:87:LYS:HG3	2.01	0.43
3:E:21:ARG:HH12	3:E:106:LYS:HB2	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:25:ILE:HD13	4:G:74:MET:SD	2.58	0.43
9:Q:46:TYR:OH	31:A:992:C:OP1	2.30	0.43
11:S:29:VAL:O	11:S:33:LEU:HG	2.19	0.43
21:2:26:ASN:CG	31:A:682:G:H5'	2.43	0.43
24:K:6:THR:HG23	31:A:1666:G:H4'	2.01	0.43
27:7:204:MET:HG2	27:7:204:MET:O	2.19	0.43
30:M:62:LYS:NZ	31:A:873:C:O3'	2.37	0.43
31:A:1524:G:H2'	31:A:1525:A:C8	2.53	0.43
31:A:1987:A:H2'	31:A:1988:G:C8	2.53	0.43
31:A:2717:C:H2'	31:A:2718:G:O4'	2.19	0.43
31:A:2788:C:O2'	31:A:2809:A:N3	2.47	0.43
1:C:147:PRO:O	31:A:2204:G:O2'	2.34	0.43
13:U:94:PHE:HA	13:U:101:THR:HA	2.00	0.43
19:0:53:VAL:HG12	19:0:54:ILE:N	2.34	0.43
22:B:45:A:H3'	22:B:46:A:C8	2.54	0.43
23:I:19:PRO:HG2	23:I:22:PRO:HG2	1.99	0.43
25:P:62:LYS:HZ2	25:P:64:SER:HB2	1.83	0.43
30:M:53:MET:O	30:M:57:VAL:HG22	2.18	0.43
31:A:23:G:H2'	31:A:24:G:C8	2.54	0.43
31:A:36:G:N3	31:A:450:G:O2'	2.52	0.43
31:A:1259:G:H2'	31:A:1260:A:C8	2.53	0.43
31:A:2297:A:H2'	31:A:2298:A:C8	2.48	0.43
31:A:2342:C:H2'	31:A:2343:U:O4'	2.18	0.43
34:F:15:LEU:HD23	34:F:27:VAL:HG12	2.00	0.43
2:D:25:THR:OG1	2:D:191:GLY:O	2.36	0.43
3:E:35:TYR:HE1	3:E:176:ASP:HB3	1.83	0.43
3:E:124:PHE:CE2	3:E:148:ILE:HD12	2.52	0.43
7:N:14:SER:OG	31:A:2690:U:OP1	2.32	0.43
14:V:9:ARG:HD3	14:V:39:ALA:HB1	2.00	0.43
30:M:12:MET:HB3	30:M:72:PRO:HD2	2.01	0.43
30:M:73:ILE:H	30:M:92:TRP:HE3	1.67	0.43
31:A:541:A:H2'	31:A:542:C:C6	2.54	0.43
31:A:1170:C:H2'	31:A:1171:G:C8	2.53	0.43
31:A:1207:C:H2'	31:A:1208:C:C6	2.53	0.43
31:A:1434:A:H2'	31:A:1435:G:H8	1.84	0.43
31:A:1759:A:H1'	31:A:2711:A:C2	2.54	0.43
3:E:50:ALA:HB2	31:A:801:G:C8	2.54	0.43
3:E:126:VAL:O	3:E:156:ASN:ND2	2.52	0.43
4:G:151:ARG:HD3	4:G:151:ARG:HA	1.75	0.43
11:S:13:SER:OG	31:A:1266:G:O6	2.23	0.43
12:T:44:LYS:O	12:T:48:GLN:HG2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:W:71:LYS:HD2	15:W:71:LYS:HA	1.82	0.43
19:O:9:ARG:NH2	31:A:517:C:OP2	2.47	0.43
20:1:24:LYS:NZ	20:1:51:ALA:O	2.52	0.43
31:A:191:A:H2'	31:A:192:C:C6	2.54	0.43
31:A:563:A:C6	31:A:2018:G:C5	3.07	0.43
31:A:732:C:H2'	31:A:733:G:O4'	2.18	0.43
31:A:1862:G:H2'	31:A:1863:G:H8	1.83	0.43
31:A:2192:U:H2'	31:A:2193:G:C8	2.53	0.43
31:A:2340:A:H2'	31:A:2341:G:H8	1.84	0.43
31:A:2632:A:H2'	31:A:2633:G:C8	2.54	0.43
31:A:2854:G:H2'	31:A:2855:C:C6	2.54	0.43
3:E:73:ILE:HA	3:E:78:TRP:CE3	2.54	0.43
6:L:76:GLU:OE2	31:A:636:G:N2	2.47	0.43
6:L:93:ASN:O	6:L:94:THR:OG1	2.35	0.43
13:U:21:ARG:NH1	13:U:21:ARG:HA	2.34	0.43
13:U:53:GLN:H	13:U:53:GLN:CD	2.27	0.43
16:X:17:ARG:HA	16:X:17:ARG:HD3	1.90	0.43
22:B:103:U:H2'	22:B:104:A:C8	2.54	0.43
28:8:63:LEU:O	28:8:67:ILE:HG12	2.19	0.43
31:A:523:C:H5''	31:A:540:C:O2'	2.18	0.43
31:A:974:G:O2'	31:A:989:G:N2	2.52	0.43
31:A:1079:C:H41	31:A:1080:A:N6	2.17	0.43
31:A:1094:U:H2'	31:A:1095:A:H8	1.83	0.43
31:A:1431:A:H2'	31:A:1432:G:C8	2.54	0.43
31:A:1821:A:H2'	31:A:1822:C:H6	1.83	0.43
31:A:1942:C:O2'	31:A:1943:U:H3'	2.18	0.43
31:A:1944:U:H5'	31:A:1945:G:H3'	2.00	0.43
31:A:2114:A:H3'	31:A:2115:G:H8	1.84	0.43
31:A:2282:G:N2	31:A:2390:U:O2	2.48	0.43
32:H:132:PHE:HB2	32:H:140:ALA:HB3	2.01	0.43
32:H:135:HIS:ND1	32:H:137:GLU:HG2	2.34	0.43
2:D:38:LYS:HD3	2:D:43:ASP:OD2	2.19	0.42
2:D:133:THR:HG21	31:A:1993:U:H4'	2.01	0.42
4:G:68:ARG:O	4:G:72:ASN:N	2.40	0.42
9:Q:6:GLY:HA3	31:A:29:U:H4'	2.00	0.42
9:Q:21:LYS:HE2	9:Q:21:LYS:HB2	1.88	0.42
11:S:79:GLY:HA3	11:S:102:HIS:HD2	1.84	0.42
12:T:3:ARG:NH2	12:T:5:GLU:OE2	2.52	0.42
12:T:51:PHE:HE2	17:Y:26:PHE:HZ	1.67	0.42
14:V:80:HIS:HB2	14:V:85:LYS:HB3	2.01	0.42
27:7:232:ARG:HB2	27:7:235:GLN:HG2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:172:A:H2'	31:A:173:A:C8	2.54	0.42
31:A:411:G:OP2	31:A:2406:A:O2'	2.29	0.42
31:A:963:U:H2'	31:A:964:C:C6	2.54	0.42
31:A:1687:G:N2	31:A:1701:A:H62	2.16	0.42
31:A:2011:U:H2'	31:A:2012:G:O4'	2.19	0.42
31:A:2811:G:H2'	31:A:2812:G:C8	2.54	0.42
32:H:27:ARG:HH21	32:H:27:ARG:HG3	1.84	0.42
1:C:70:LYS:HE2	1:C:95:TYR:CD2	2.53	0.42
9:Q:58:GLN:NE2	31:A:1009:A:N3	2.68	0.42
20:1:49:LYS:O	20:1:50:GLU:HG3	2.19	0.42
29:9:74:ALA:HB3	29:9:78:CYS:HB3	2.01	0.42
31:A:25:U:H3	31:A:515:A:N6	2.17	0.42
31:A:145:C:H2'	31:A:146:A:H8	1.82	0.42
31:A:518:G:H2'	31:A:519:U:C6	2.54	0.42
31:A:1020:A:OP1	31:A:1034:G:N2	2.41	0.42
31:A:1363:C:H2'	31:A:1364:G:C8	2.54	0.42
31:A:1405:U:H2'	31:A:1406:U:H6	1.84	0.42
31:A:2544:G:H2'	31:A:2545:G:C8	2.55	0.42
31:A:2868:A:H2'	31:A:2869:G:H8	1.85	0.42
34:F:90:LEU:HD12	34:F:94:ARG:HB3	2.01	0.42
3:E:40:ARG:HE	3:E:92:HIS:CD2	2.37	0.42
6:L:46:VAL:HB	6:L:50:PHE:HB3	2.01	0.42
17:Y:48:ARG:NH2	31:A:75:G:H4'	2.34	0.42
22:B:74:U:H2'	22:B:75:G:O4'	2.19	0.42
25:P:50:ARG:O	25:P:57:ALA:N	2.38	0.42
27:7:35:ARG:HG2	31:A:1923:U:P	2.59	0.42
29:9:306:TRP:NE1	29:9:308:ASP:HB2	2.34	0.42
31:A:1046:A:H4'	33:e:61:ARG:HB3	2.00	0.42
31:A:1084:A:H2'	31:A:1085:A:H5''	2.01	0.42
31:A:2460:U:H2'	31:A:2461:A:C8	2.54	0.42
34:F:146:ASP:OD1	34:F:149:ARG:NH1	2.52	0.42
3:E:49:ARG:NH1	3:E:72:SER:OG	2.52	0.42
25:P:29:VAL:HG23	25:P:79:VAL:HG12	2.01	0.42
28:8:60:ASP:OD2	28:8:92:ARG:NH1	2.52	0.42
29:9:170:ALA:O	29:9:283:ASN:ND2	2.52	0.42
31:A:464:U:H2'	31:A:465:G:O4'	2.19	0.42
31:A:753:A:H2'	31:A:754:U:H6	1.84	0.42
31:A:843:G:H2'	31:A:844:A:C8	2.54	0.42
31:A:1841:U:C2	31:A:1842:G:C8	3.07	0.42
31:A:2389:G:H5''	31:A:2390:U:O4'	2.19	0.42
31:A:2630:G:H2'	31:A:2631:G:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:2632:A:H2'	31:A:2633:G:H8	1.83	0.42
31:A:2637:U:O4	31:A:2776:A:N7	2.52	0.42
31:A:2840:C:H2'	31:A:2841:C:H6	1.84	0.42
31:A:2899:A:H2'	31:A:2900:A:C8	2.54	0.42
32:H:12:LEU:HD23	32:H:12:LEU:O	2.18	0.42
34:F:12:VAL:HG22	34:F:16:MET:HE3	2.01	0.42
34:F:36:ASN:CG	34:F:87:LYS:HE3	2.44	0.42
1:C:145:MET:HA	1:C:183:VAL:HG21	2.01	0.42
5:J:96:ARG:HG2	5:J:99:ARG:HB2	2.02	0.42
9:Q:107:ALA:HA	9:Q:110:GLU:OE2	2.20	0.42
12:T:40:LYS:HG2	31:A:1599:U:P	2.59	0.42
27:7:92:ASP:OD2	27:7:92:ASP:N	2.53	0.42
29:9:136:ARG:NH2	29:9:136:ARG:HB3	2.34	0.42
29:9:169:ASN:HB3	29:9:190:PRO:HA	2.01	0.42
31:A:1412:U:H2'	31:A:1413:A:H8	1.84	0.42
31:A:2065:C:H1'	31:A:2449:U:N3	2.35	0.42
31:A:2123:G:H2'	31:A:2124:G:C8	2.54	0.42
31:A:2229:U:H2'	31:A:2230:G:C8	2.49	0.42
31:A:2537:U:H2'	31:A:2538:C:C6	2.55	0.42
31:A:2630:G:H2'	31:A:2631:G:C8	2.54	0.42
31:A:2906:C:H2'	31:A:2907:A:C8	2.55	0.42
32:H:135:HIS:HB3	32:H:138:VAL:HB	2.01	0.42
1:C:263:ASP:OD1	1:C:263:ASP:N	2.53	0.42
2:D:144:GLY:HA2	31:A:2578:G:H1'	2.01	0.42
10:R:79:ARG:O	10:R:81:LYS:HG2	2.19	0.42
27:7:19:ARG:NH1	27:7:22:GLN:HE22	2.17	0.42
28:8:36:ALA:O	28:8:40:LYS:HG2	2.20	0.42
31:A:96:C:H2'	31:A:97:C:C6	2.53	0.42
31:A:565:C:H2'	31:A:566:U:C6	2.55	0.42
31:A:1139:G:H2'	31:A:1140:C:C6	2.54	0.42
31:A:2062:A:H62	31:A:2503:A:H62	1.67	0.42
31:A:2628:C:O2'	31:A:2782:G:OP1	2.31	0.42
31:A:2737:G:H2'	31:A:2738:A:H8	1.84	0.42
33:e:29:ASP:HB2	33:e:56:ARG:NH1	2.35	0.42
35:b:8:LYS:HD3	35:b:8:LYS:HA	1.86	0.42
1:C:196:ASN:OD1	1:C:196:ASN:N	2.52	0.42
6:L:38:GLN:OE1	31:A:831:G:O2'	2.35	0.42
10:R:83:TYR:OH	10:R:85:LYS:HE3	2.19	0.42
22:B:83:G:O6	22:B:94:A:N6	2.52	0.42
23:I:12:VAL:HG11	23:I:22:PRO:HB3	2.01	0.42
27:7:199:MET:N	27:7:253:TYR:OH	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:186:G:H2'	31:A:187:G:H8	1.84	0.42
31:A:307:G:N2	31:A:309:A:H3'	2.35	0.42
31:A:365:U:H2'	31:A:366:C:C6	2.54	0.42
31:A:599:A:H2'	31:A:600:G:C8	2.51	0.42
31:A:953:G:O2'	31:A:2266:A:OP2	2.32	0.42
31:A:1224:U:H2'	31:A:1225:G:N3	2.34	0.42
31:A:1352:U:H1'	31:A:1570:A:H2	1.84	0.42
31:A:1431:A:H2'	31:A:1432:G:H8	1.84	0.42
31:A:1515:A:H3'	31:A:1516:G:H8	1.85	0.42
31:A:1926:U:H3	31:A:1929:G:H22	1.68	0.42
31:A:2294:G:H2'	31:A:2295:C:H6	1.84	0.42
31:A:2523:G:O2'	31:A:2764:A:O2'	2.34	0.42
31:A:2547:A:H2'	31:A:2548:U:H6	1.85	0.42
32:H:104:THR:HG22	32:H:110:VAL:H	1.84	0.42
33:e:43:LYS:HE2	33:e:43:LYS:HB3	1.88	0.42
1:C:155:ARG:HB2	31:A:1818:U:H2'	2.02	0.42
1:C:251:THR:HG22	1:C:252:LYS:N	2.35	0.42
2:D:175:LEU:HD22	2:D:190:LYS:O	2.20	0.42
3:E:104:ALA:O	3:E:108:ILE:HG12	2.20	0.42
7:N:1:MET:HE2	7:N:3:HIS:CE1	2.55	0.42
7:N:42:LYS:NZ	31:A:2817:U:OP1	2.53	0.42
13:U:36:GLU:HA	13:U:61:GLU:OE1	2.20	0.42
22:B:95:U:H2'	22:B:96:G:C8	2.55	0.42
27:7:19:ARG:HH11	27:7:22:GLN:HE22	1.68	0.42
29:9:29:ILE:HD12	29:9:30:PRO:HD2	2.01	0.42
31:A:-2:U:H2'	31:A:-1:A:H8	1.85	0.42
31:A:174:U:H2'	31:A:175:G:H8	1.84	0.42
31:A:678:C:H2'	31:A:679:C:H6	1.84	0.42
31:A:1054:A:H2'	31:A:1055:G:C8	2.54	0.42
31:A:1108:U:H2'	31:A:1109:C:C6	2.55	0.42
31:A:1196:C:C2	31:A:1197:G:C8	3.07	0.42
31:A:1494:A:H2'	31:A:1495:A:C8	2.55	0.42
31:A:1812:U:H2'	31:A:1813:G:C8	2.55	0.42
31:A:2286:G:H4'	31:A:2287:A:N3	2.35	0.42
31:A:2368:C:H2'	31:A:2369:A:C8	2.47	0.42
31:A:2685:G:H21	31:A:2726:A:N6	2.17	0.42
31:A:2774:C:H2'	31:A:2775:G:O4'	2.19	0.42
31:A:2909:C:H2'	31:A:2910:G:C8	2.54	0.42
2:D:124:ARG:HD3	2:D:125:TRP:CZ3	2.54	0.42
4:G:154:GLU:HG2	4:G:156:TYR:H	1.85	0.42
10:R:68:ARG:HH22	10:R:90:ARG:HD3	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:S:70:LYS:HB3	11:S:70:LYS:HE3	1.85	0.42
14:V:17:SER:HB3	14:V:21:ARG:HH12	1.82	0.42
30:M:71:LYS:HE3	30:M:71:LYS:HB3	1.79	0.42
30:M:86:LYS:HZ2	31:A:955:U:H5''	1.85	0.42
31:A:1401:G:H2'	31:A:1402:U:C6	2.55	0.42
31:A:1843:C:H2'	31:A:1844:C:H6	1.84	0.42
31:A:1848:A:H2'	31:A:1849:G:O4'	2.20	0.42
3:E:47:LYS:HG2	3:E:51:GLU:HG3	2.02	0.42
6:L:135:ILE:HG21	6:L:142:ILE:HD11	2.02	0.42
9:Q:56:PHE:CZ	31:A:536:G:H4'	2.55	0.42
11:S:38:TYR:HB3	19:O:38:LEU:HD11	2.01	0.42
14:V:30:ILE:HG12	14:V:40:ILE:CD1	2.50	0.42
14:V:80:HIS:CE1	14:V:83:LYS:HG3	2.54	0.42
22:B:115:A:H2'	22:B:116:G:C8	2.55	0.42
25:P:52:ARG:HG2	31:A:2845:U:H4'	2.02	0.42
28:8:99:GLN:HE21	28:8:99:GLN:HB3	1.73	0.42
29:9:25:ARG:HB2	31:A:2452:C:H5'	2.01	0.42
31:A:151:C:H2'	31:A:152:A:H8	1.85	0.42
31:A:203:A:H3'	31:A:204:A:H8	1.84	0.42
31:A:462:C:H2'	31:A:463:G:C8	2.55	0.42
31:A:563:A:H2'	31:A:564:C:H6	1.85	0.42
31:A:632:A:H2'	31:A:633:A:C8	2.54	0.42
31:A:758:C:H2'	31:A:759:G:C8	2.54	0.42
31:A:881:G:H2'	31:A:882:G:C8	2.54	0.42
31:A:1171:G:H2'	31:A:1172:C:H6	1.85	0.42
31:A:1417:C:O2'	31:A:1587:G:O2'	2.32	0.42
31:A:1704:C:H2'	31:A:1705:A:H8	1.84	0.42
31:A:2396:G:C2	31:A:2397:G:C8	3.08	0.42
2:D:74:GLU:OE1	2:D:74:GLU:HA	2.19	0.41
7:N:69:ARG:C	7:N:71:ARG:H	2.28	0.41
10:R:78:ARG:NH1	31:A:990:A:N1	2.68	0.41
18:Z:1:ALA:HB3	18:Z:38:GLU:HB3	2.02	0.41
22:B:6:G:H2'	22:B:7:G:H8	1.85	0.41
31:A:171:U:H2'	31:A:172:A:C8	2.55	0.41
31:A:373:U:O2'	31:A:423:A:N3	2.48	0.41
31:A:523:C:H2'	31:A:524:G:H8	1.85	0.41
31:A:721:A:H2'	31:A:722:A:H8	1.85	0.41
31:A:1440:U:H2'	31:A:1441:G:C8	2.55	0.41
31:A:2090:A:N6	31:A:2230:G:O6	2.53	0.41
31:A:2415:G:H2'	31:A:2416:C:C6	2.55	0.41
32:H:6:LEU:HD13	32:H:36:ALA:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:T:40:LYS:HA	12:T:40:LYS:HD2	1.81	0.41
15:W:19:VAL:HA	15:W:34:VAL:HG22	2.01	0.41
23:I:95:ASP:OD1	23:I:95:ASP:N	2.53	0.41
25:P:51:ASN:HA	25:P:56:SER:HB3	2.02	0.41
27:7:11:VAL:HG13	27:7:61:GLY:HA2	2.02	0.41
31:A:1710:G:H2'	31:A:1711:A:H8	1.84	0.41
31:A:2745:C:H2'	31:A:2746:U:C6	2.55	0.41
31:A:2888:C:H2'	31:A:2889:C:C6	2.55	0.41
1:C:222:THR:HG23	31:A:1826:G:OP1	2.21	0.41
22:B:34:A:H2	22:B:44:G:H8	1.68	0.41
27:7:32:SER:HB3	31:A:1923:U:OP1	2.21	0.41
31:A:226:A:H1'	31:A:230:G:N2	2.35	0.41
31:A:351:C:H2'	31:A:352:A:C8	2.55	0.41
31:A:739:A:H1'	31:A:740:C:H5	1.84	0.41
31:A:1748:C:H2'	31:A:1749:A:C8	2.56	0.41
31:A:1794:A:H2'	31:A:1795:C:H6	1.84	0.41
31:A:2228:G:H2'	31:A:2229:U:C6	2.56	0.41
31:A:2294:G:H2'	31:A:2295:C:C6	2.56	0.41
31:A:2296:U:O2'	31:A:2320:U:O4	2.37	0.41
31:A:2519:U:H5'	31:A:2567:G:H21	1.86	0.41
31:A:2907:A:H2'	31:A:2908:A:H8	1.85	0.41
1:C:16:VAL:HB	1:C:203:VAL:HG12	2.02	0.41
15:W:41:PHE:HB3	15:W:76:ILE:HG12	2.02	0.41
17:Y:32:ALA:HB2	17:Y:37:LEU:HD23	2.02	0.41
27:7:237:ARG:HH22	27:7:252:VAL:HB	1.85	0.41
29:9:161:ASP:H	29:9:210:VAL:HG23	1.85	0.41
29:9:258:ASN:HA	29:9:261:ILE:HG12	2.03	0.41
30:M:97:GLN:NE2	30:M:98:PRO:O	2.53	0.41
31:A:253:C:H2'	31:A:254:G:O4'	2.20	0.41
31:A:523:C:H1'	31:A:554:U:H1'	2.01	0.41
31:A:947:A:H2'	31:A:948:C:C6	2.55	0.41
31:A:1510:G:H2'	31:A:1511:G:C8	2.53	0.41
31:A:1561:C:H2'	31:A:1562:U:H6	1.85	0.41
31:A:2557:G:H2'	31:A:2558:C:H6	1.84	0.41
33:e:48:ALA:HB3	33:e:51:TYR:CE1	2.55	0.41
3:E:138:LEU:O	3:E:142:ALA:N	2.54	0.41
7:N:4:ARG:HD3	7:N:4:ARG:HA	1.84	0.41
12:T:43:ILE:HD11	12:T:83:ALA:HB1	2.02	0.41
25:P:2:ASN:HB2	31:A:2876:G:H5''	2.01	0.41
27:7:54:LYS:HE2	27:7:54:LYS:HB2	1.80	0.41
27:7:54:LYS:HG3	27:7:56:LYS:HG2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:146:A:H2'	31:A:147:C:C6	2.54	0.41
31:A:689:A:N3	31:A:779:U:O2'	2.43	0.41
31:A:806:C:H2'	31:A:807:U:C6	2.56	0.41
31:A:877:A:O2'	31:A:900:A:N6	2.53	0.41
31:A:2172:U:H4'	31:A:2173:A:H5'	2.03	0.41
31:A:2642:G:H2'	31:A:2643:G:C8	2.56	0.41
31:A:2719:G:H4'	31:A:2846:G:H4'	2.02	0.41
31:A:2854:G:H2'	31:A:2855:C:H6	1.85	0.41
32:H:117:LEU:HD12	32:H:117:LEU:HA	1.97	0.41
4:G:104:LEU:HB3	4:G:106:LEU:HG	2.00	0.41
5:J:110:PRO:O	5:J:115:GLY:HA3	2.20	0.41
9:Q:54:ARG:HD3	31:A:1155:A:H5''	2.01	0.41
31:A:775:G:C5	31:A:794:A:C8	3.09	0.41
31:A:1026:G:H2'	31:A:1027:A:H8	1.85	0.41
31:A:1360:G:C8	31:A:1361:G:C8	3.08	0.41
31:A:1519:G:H2'	31:A:1520:U:C6	2.55	0.41
31:A:1952:A:N6	31:A:1953:A:N1	2.69	0.41
31:A:2087:G:H2'	31:A:2088:A:H8	1.85	0.41
31:A:2209:G:OP2	31:A:2210:U:O2'	2.34	0.41
31:A:2515:C:H2'	31:A:2516:A:C8	2.54	0.41
31:A:2850:A:N7	31:A:2868:A:O2'	2.49	0.41
1:C:229:HIS:CD2	1:C:246:PRO:HB3	2.56	0.41
9:Q:57:ARG:HA	9:Q:60:TRP:CE3	2.55	0.41
9:Q:90:ASP:CG	10:R:11:GLN:HE21	2.28	0.41
10:R:13:ARG:HG2	10:R:13:ARG:HH11	1.85	0.41
13:U:27:VAL:HG23	13:U:33:VAL:HG22	2.03	0.41
24:K:1:MET:HG3	24:K:67:LYS:HG2	2.03	0.41
25:P:3:ILE:HD12	25:P:3:ILE:HA	1.92	0.41
28:8:176:ARG:NH2	31:A:1850:G:H5'	2.35	0.41
31:A:1446:C:H2'	31:A:1447:C:C6	2.55	0.41
31:A:1826:G:H2'	31:A:1827:U:C6	2.56	0.41
31:A:1837:C:H2'	31:A:1899:A:H61	1.84	0.41
31:A:1975:G:H2'	31:A:1976:U:O4'	2.20	0.41
31:A:2065:C:H2'	31:A:2066:C:C6	2.56	0.41
2:D:79:LEU:HD12	2:D:80:TRP:N	2.35	0.41
8:O:29:HIS:CE1	8:O:36:TYR:HB2	2.55	0.41
23:I:20:SER:HB3	23:I:21:PRO:HD3	2.03	0.41
28:8:79:ARG:O	28:8:83:GLN:HG2	2.20	0.41
28:8:123:ASP:OD1	28:8:123:ASP:N	2.53	0.41
31:A:152:A:N6	31:A:175:G:O6	2.53	0.41
31:A:417:C:H2'	31:A:418:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:579:G:H2'	31:A:580:U:H6	1.85	0.41
31:A:817:C:O2'	31:A:839:U:H5''	2.20	0.41
31:A:929:U:H2'	31:A:930:G:C8	2.56	0.41
31:A:947:A:C6	31:A:971:G:N1	2.88	0.41
31:A:1005:C:H2'	31:A:1006:C:C6	2.55	0.41
31:A:1048:A:H1'	31:A:1112:G:N2	2.35	0.41
31:A:1063:G:H2'	31:A:1064:C:C6	2.54	0.41
31:A:2815:C:H2'	31:A:2816:G:C8	2.53	0.41
32:H:1:MET:N	32:H:21:VAL:O	2.54	0.41
6:L:19:LEU:HB2	6:L:31:GLY:HA3	2.03	0.41
6:L:78:ARG:HH11	31:A:626:A:N6	2.18	0.41
22:B:63:C:H2'	22:B:64:G:C8	2.56	0.41
23:I:5:GLN:NE2	23:I:7:TYR:HB3	2.36	0.41
27:7:7:LEU:HB2	27:7:67:ILE:HB	2.02	0.41
27:7:103:VAL:HG22	27:7:105:HIS:H	1.86	0.41
27:7:199:MET:O	27:7:238:VAL:HG11	2.21	0.41
27:7:246:PRO:HB2	27:7:254:GLY:HA2	2.02	0.41
29:9:158:LEU:HD23	29:9:198:LEU:HD13	2.03	0.41
31:A:23:G:H2'	31:A:24:G:H8	1.86	0.41
31:A:42:A:N6	31:A:438:G:O6	2.54	0.41
31:A:152:A:H2'	31:A:153:U:C6	2.56	0.41
31:A:672:C:H2'	31:A:673:C:C6	2.56	0.41
31:A:807:U:H2'	31:A:808:G:C8	2.55	0.41
31:A:817:C:H2'	31:A:818:G:O4'	2.21	0.41
31:A:999:U:H2'	31:A:1000:A:H8	1.86	0.41
31:A:1040:A:N6	31:A:1116:G:O6	2.54	0.41
31:A:1139:G:H2'	31:A:1140:C:H6	1.85	0.41
31:A:1171:G:H2'	31:A:1172:C:C6	2.56	0.41
31:A:1267:U:H2'	31:A:1268:A:H8	1.85	0.41
31:A:1292:G:H2'	31:A:1293:C:C6	2.56	0.41
31:A:1469:A:H2'	31:A:1470:A:H8	1.85	0.41
31:A:1476:U:H2'	31:A:1477:A:H8	1.86	0.41
31:A:1562:U:H2'	31:A:1563:U:H6	1.86	0.41
31:A:1697:G:OP2	31:A:1698:A:O2'	2.38	0.41
31:A:1707:G:C8	31:A:1756:G:C5	3.09	0.41
31:A:1826:G:H2'	31:A:1827:U:H6	1.85	0.41
31:A:2216:G:H2'	31:A:2217:G:C8	2.56	0.41
31:A:2355:G:H2'	31:A:2356:U:C6	2.56	0.41
31:A:2533:U:H2'	31:A:2534:A:O4'	2.21	0.41
31:A:2601:C:H5'	31:A:2602:A:OP2	2.20	0.41
31:A:2678:C:H2'	31:A:2679:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:2700:A:H2'	31:A:2701:U:C6	2.56	0.41
6:L:41:ARG:NE	31:A:806:C:OP2	2.35	0.41
16:X:33:HIS:HE1	31:A:2229:U:O2	2.04	0.41
22:B:1:U:H2'	22:B:2:G:C8	2.53	0.41
27:7:195:LYS:HG2	27:7:197:THR:HG22	2.02	0.41
28:8:39:LEU:HD21	28:8:89:LEU:HD22	2.02	0.41
31:A:56:A:H2'	31:A:57:C:H6	1.85	0.41
31:A:156:A:H2'	31:A:157:C:C6	2.56	0.41
31:A:171:U:H2'	31:A:172:A:H8	1.86	0.41
31:A:494:G:H2'	31:A:495:G:C8	2.51	0.41
31:A:669:G:N1	31:A:801:G:O6	2.54	0.41
31:A:758:C:H2'	31:A:759:G:H8	1.86	0.41
31:A:1522:A:H4'	31:A:1524:G:C8	2.56	0.41
31:A:1666:G:HO2'	31:A:1667:G:P	2.44	0.41
31:A:1821:A:H2'	31:A:1822:C:C6	2.56	0.41
31:A:1892:C:H2'	31:A:1893:C:O4'	2.20	0.41
31:A:2559:C:H2'	31:A:2560:A:H8	1.86	0.41
2:D:22:ILE:O	2:D:22:ILE:HG13	2.20	0.40
8:O:33:ARG:NH2	22:B:27:C:H3'	2.34	0.40
8:O:87:ILE:HG13	8:O:88:LYS:N	2.36	0.40
26:6:27:VAL:O	26:6:27:VAL:HG12	2.21	0.40
26:6:39:ILE:HD13	26:6:88:HIS:HB2	2.02	0.40
29:9:157:MET:SD	29:9:237:ARG:HG2	2.60	0.40
31:A:127:A:H5''	31:A:128:C:O4'	2.21	0.40
31:A:283:G:H2'	31:A:284:U:C6	2.56	0.40
31:A:1198:U:H2'	31:A:1199:U:H6	1.86	0.40
31:A:1283:G:H1'	31:A:1329:U:O2	2.21	0.40
31:A:1336:A:H2'	31:A:1337:G:C8	2.56	0.40
31:A:1588:G:H2'	31:A:1589:U:C6	2.57	0.40
31:A:1928:A:H2'	31:A:1929:G:N9	2.36	0.40
31:A:2022:U:O2'	31:A:2617:U:H5'	2.20	0.40
31:A:2747:G:H21	31:A:2757:A:N6	2.08	0.40
2:D:135:GLY:HA2	31:A:743:A:OP1	2.21	0.40
2:D:146:ILE:HA	2:D:159:LYS:NZ	2.36	0.40
3:E:15:SER:HB3	3:E:18:THR:HG22	2.02	0.40
7:N:45:ARG:HE	7:N:45:ARG:HB2	1.76	0.40
13:U:96:LYS:HB3	13:U:96:LYS:HE2	1.89	0.40
16:X:57:VAL:HG22	31:A:372:G:H2'	2.04	0.40
17:Y:56:LEU:C	17:Y:58:ASN:H	2.28	0.40
21:2:21:ARG:HG3	21:2:31:LEU:HD11	2.02	0.40
27:7:143:THR:O	27:7:280:HIS:HA	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:8:99:GLN:O	28:8:103:LYS:HG2	2.21	0.40
28:8:129:GLY:O	28:8:149:ARG:NH1	2.54	0.40
31:A:312:G:C2	31:A:313:G:N7	2.89	0.40
31:A:379:G:N1	31:A:396:G:O6	2.55	0.40
31:A:611:C:H2'	31:A:612:G:O4'	2.22	0.40
31:A:856:G:O6	31:A:922:C:N4	2.55	0.40
31:A:1059:G:H1	31:A:1079:C:N4	2.20	0.40
31:A:1845:G:N1	31:A:1896:G:C6	2.89	0.40
31:A:2287:A:N7	31:A:2289:G:C8	2.89	0.40
31:A:2405:G:N1	31:A:2411:A:OP2	2.55	0.40
31:A:2549:G:H2'	31:A:2550:G:H8	1.86	0.40
31:A:2899:A:H2'	31:A:2900:A:H8	1.86	0.40
32:H:9:VAL:H	32:H:13:GLY:CA	2.34	0.40
1:C:70:LYS:HE3	1:C:73:ILE:HD13	2.03	0.40
1:C:77:VAL:HG12	1:C:113:ASP:H	1.86	0.40
2:D:115:GLY:N	31:A:2821:A:OP2	2.45	0.40
5:J:105:VAL:HG11	5:J:122:LEU:HD22	2.03	0.40
7:N:45:ARG:O	7:N:49:GLU:HB2	2.21	0.40
12:T:15:HIS:HB3	12:T:31:VAL:HG12	2.04	0.40
19:0:14:MET:HB3	31:A:2045:C:H4'	2.02	0.40
25:P:62:LYS:NZ	25:P:64:SER:HB2	2.36	0.40
29:9:27:LYS:HE3	29:9:27:LYS:HB2	1.89	0.40
29:9:219:GLU:HG3	29:9:261:ILE:HD12	2.03	0.40
31:A:309:A:H1'	31:A:329:G:C4	2.56	0.40
31:A:678:C:H2'	31:A:679:C:C6	2.56	0.40
31:A:1287:A:H61	31:A:1649:G:HO2'	1.57	0.40
31:A:1761:C:H2'	31:A:1762:A:O4'	2.21	0.40
31:A:1839:G:N3	31:A:1839:G:H2'	2.36	0.40
31:A:2319:G:H1'	31:A:2320:U:C5	2.53	0.40
31:A:2345:G:H4'	31:A:2346:A:H3'	2.03	0.40
31:A:2591:C:H2'	31:A:2592:G:C8	2.55	0.40
1:C:124:LYS:HE2	1:C:124:LYS:HB2	1.93	0.40
8:O:30:ARG:HA	8:O:35:ILE:HD12	2.04	0.40
11:S:31:GLN:HA	11:S:31:GLN:OE1	2.22	0.40
15:W:6:THR:O	15:W:7:ARG:HG2	2.20	0.40
27:7:213:ARG:HH22	27:7:227:ARG:HG3	1.87	0.40
30:M:31:PHE:HB3	30:M:130:PHE:CE1	2.57	0.40
31:A:152:A:H2'	31:A:153:U:H6	1.86	0.40
31:A:183:C:H1'	31:A:432:A:H2	1.86	0.40
31:A:243:U:H2'	31:A:244:A:C8	2.56	0.40
31:A:622:G:H2'	31:A:623:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:1388:G:H2'	31:A:1389:G:H8	1.86	0.40
31:A:1809:A:H2'	31:A:1810:A:C8	2.55	0.40
31:A:1974:C:H2'	31:A:1975:G:C8	2.57	0.40
31:A:2553:G:C2	31:A:2583:G:H1'	2.57	0.40
31:A:2843:G:H2'	31:A:2844:G:H8	1.85	0.40
2:D:5:VAL:H	2:D:32:ASN:HD21	1.68	0.40
4:G:72:ASN:HA	4:G:75:VAL:HG22	2.04	0.40
4:G:162:ARG:HB2	4:G:166:GLU:OE2	2.22	0.40
5:J:112:GLY:O	5:J:116:ARG:NE	2.52	0.40
8:O:4:LYS:HA	8:O:7:ARG:CZ	2.52	0.40
9:Q:57:ARG:O	9:Q:61:ILE:HG12	2.21	0.40
29:9:196:PRO:HG3	29:9:234:HIS:CE1	2.57	0.40
31:A:372:G:N2	31:A:401:A:OP2	2.47	0.40
31:A:607:U:H2'	31:A:608:A:H8	1.86	0.40
31:A:954:G:N2	31:A:963:U:O2	2.43	0.40
31:A:1130:U:N3	31:A:2025:C:OP1	2.40	0.40
31:A:1202:G:H2'	31:A:1203:U:O4'	2.22	0.40
31:A:1328:A:H4'	31:A:1329:U:H5	1.87	0.40
31:A:1378:A:O2'	31:A:1380:G:N7	2.55	0.40
31:A:1433:A:H2'	31:A:1434:A:C8	2.57	0.40
31:A:1585:C:H2'	31:A:1586:A:O4'	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	269/273 (98%)	252 (94%)	17 (6%)	0	100	100
2	D	207/209 (99%)	197 (95%)	10 (5%)	0	100	100
3	E	199/201 (99%)	195 (98%)	4 (2%)	0	100	100
4	G	169/177 (96%)	163 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	J	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
6	L	141/144 (98%)	119 (84%)	22 (16%)	0	100	100
7	N	118/127 (93%)	111 (94%)	7 (6%)	0	100	100
8	O	114/117 (97%)	111 (97%)	3 (3%)	0	100	100
9	Q	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
10	R	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
11	S	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
12	T	91/100 (91%)	82 (90%)	9 (10%)	0	100	100
13	U	100/104 (96%)	90 (90%)	10 (10%)	0	100	100
14	V	92/94 (98%)	92 (100%)	0	0	100	100
15	W	74/85 (87%)	70 (95%)	4 (5%)	0	100	100
16	X	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
17	Y	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
18	Z	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
19	0	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
20	1	48/55 (87%)	47 (98%)	1 (2%)	0	100	100
21	2	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
23	I	139/142 (98%)	116 (84%)	23 (16%)	0	100	100
24	K	120/123 (98%)	111 (92%)	9 (8%)	0	100	100
25	P	111/115 (96%)	107 (96%)	4 (4%)	0	100	100
26	6	100/105 (95%)	94 (94%)	6 (6%)	0	100	100
27	7	313/326 (96%)	304 (97%)	9 (3%)	0	100	100
28	8	155/183 (85%)	152 (98%)	3 (2%)	0	100	100
29	9	336/390 (86%)	312 (93%)	24 (7%)	0	100	100
30	M	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
32	H	147/149 (99%)	135 (92%)	12 (8%)	0	100	100
33	e	129/165 (78%)	113 (88%)	16 (12%)	0	100	100
34	F	175/179 (98%)	168 (96%)	7 (4%)	0	100	100
35	b	45/70 (64%)	41 (91%)	4 (9%)	0	100	100
All	All	4280/4545 (94%)	4035 (94%)	245 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	216/218 (99%)	216 (100%)	0	100	100
2	D	164/164 (100%)	163 (99%)	1 (1%)	78	81
3	E	165/165 (100%)	165 (100%)	0	100	100
4	G	133/138 (96%)	133 (100%)	0	100	100
5	J	116/116 (100%)	116 (100%)	0	100	100
6	L	102/103 (99%)	102 (100%)	0	100	100
7	N	100/103 (97%)	100 (100%)	0	100	100
8	O	86/87 (99%)	86 (100%)	0	100	100
9	Q	89/90 (99%)	89 (100%)	0	100	100
10	R	84/84 (100%)	84 (100%)	0	100	100
11	S	93/93 (100%)	93 (100%)	0	100	100
12	T	80/84 (95%)	80 (100%)	0	100	100
13	U	83/85 (98%)	83 (100%)	0	100	100
14	V	78/78 (100%)	78 (100%)	0	100	100
15	W	56/63 (89%)	56 (100%)	0	100	100
16	X	67/68 (98%)	66 (98%)	1 (2%)	57	72
17	Y	55/55 (100%)	55 (100%)	0	100	100
18	Z	48/49 (98%)	48 (100%)	0	100	100
19	0	47/48 (98%)	47 (100%)	0	100	100
20	1	45/49 (92%)	45 (100%)	0	100	100
21	2	38/38 (100%)	38 (100%)	0	100	100
23	I	109/110 (99%)	109 (100%)	0	100	100
24	K	103/104 (99%)	103 (100%)	0	100	100
25	P	98/100 (98%)	98 (100%)	0	100	100
26	6	88/91 (97%)	88 (100%)	0	100	100
27	7	274/282 (97%)	273 (100%)	1 (0%)	84	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	8	135/161 (84%)	135 (100%)	0	100	100
29	9	273/321 (85%)	272 (100%)	1 (0%)	84	84
30	M	109/109 (100%)	109 (100%)	0	100	100
32	H	114/114 (100%)	114 (100%)	0	100	100
33	e	100/123 (81%)	100 (100%)	0	100	100
34	F	148/150 (99%)	148 (100%)	0	100	100
35	b	43/62 (69%)	43 (100%)	0	100	100
All	All	3539/3705 (96%)	3535 (100%)	4 (0%)	87	90

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	36	GLN
16	X	22	ASN
27	7	15	GLN
29	9	143	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	14	HIS
1	C	20	ASN
1	C	52	HIS
2	D	173	GLN
3	E	115	GLN
4	G	115	GLN
4	G	127	GLN
5	J	76	HIS
7	N	11	ASN
7	N	73	ASN
8	O	100	HIS
10	R	11	GLN
10	R	18	GLN
10	R	82	HIS
11	S	15	GLN
13	U	44	HIS
19	0	18	HIS
25	P	11	GLN

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Mol	Chain	Res	Type
26	6	28	GLN
26	6	91	GLN
27	7	3	GLN
27	7	18	GLN
27	7	22	GLN
27	7	117	ASN
27	7	155	GLN
27	7	235	GLN
27	7	239	HIS
28	8	147	GLN
29	9	52	ASN
29	9	113	GLN
29	9	234	HIS
32	H	133	GLN
33	e	9	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	B	118/120 (98%)	18 (15%)	0
31	A	2911/2919 (99%)	474 (16%)	17 (0%)
All	All	3029/3039 (99%)	492 (16%)	17 (0%)

All (492) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
22	B	15	A
22	B	16	G
22	B	30	C
22	B	35	C
22	B	36	C
22	B	41	G
22	B	43	C
22	B	44	G
22	B	45	A
22	B	46	A
22	B	52	A
22	B	53	A
22	B	56	G
22	B	87	U
22	B	89	U

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Mol	Chain	Res	Type
22	B	90	C
22	B	99	A
22	B	109	A
31	A	10	A
31	A	12	U
31	A	14	A
31	A	27	G
31	A	35	G
31	A	46	G
31	A	51	G
31	A	63	A
31	A	74	A
31	A	75	G
31	A	118	A
31	A	120	U
31	A	125	A
31	A	138	U
31	A	139	U
31	A	140	C
31	A	141	G
31	A	142	A
31	A	160	A
31	A	181	A
31	A	196	A
31	A	199	A
31	A	215	G
31	A	216	A
31	A	222	A
31	A	224	U
31	A	230	G
31	A	233	A
31	A	248	G
31	A	255	A
31	A	266	G
31	A	267	C
31	A	272	A
31	A	277	G
31	A	278	A
31	A	302	C
31	A	311	A
31	A	329	G
31	A	330	A

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Mol	Chain	Res	Type
31	A	331	C
31	A	343	C
31	A	352	A
31	A	353	C
31	A	370	G
31	A	371	A
31	A	372	G
31	A	384	A
31	A	385	C
31	A	386	G
31	A	396	G
31	A	401	A
31	A	404	A
31	A	405	U
31	A	411	G
31	A	424	G
31	A	430	A
31	A	451	U
31	A	452	G
31	A	456	C
31	A	466	A
31	A	480	A
31	A	481	G
31	A	491	G
31	A	496	G
31	A	504	A
31	A	505	A
31	A	508	A
31	A	532	A
31	A	533	G
31	A	543	G
31	A	544	C
31	A	546	U
31	A	547	A
31	A	548	G
31	A	550	C
31	A	563	A
31	A	568	U
31	A	573	U
31	A	575	A
31	A	586	A
31	A	588	U

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Mol	Chain	Res	Type
31	A	603	A
31	A	614	A
31	A	615	U
31	A	621	A
31	A	627	A
31	A	631	A
31	A	637	A
31	A	643	A
31	A	644	A
31	A	645	C
31	A	646	U
31	A	647	G
31	A	654	A
31	A	655	A
31	A	686	U
31	A	722	A
31	A	726	G
31	A	730	A
31	A	747	U
31	A	748	G
31	A	752	A
31	A	764	A
31	A	765	C
31	A	775	G
31	A	776	G
31	A	782	A
31	A	784	G
31	A	785	G
31	A	789	A
31	A	792	A
31	A	805	G
31	A	812	C
31	A	819	A
31	A	827	U
31	A	828	U
31	A	830	G
31	A	845	A
31	A	846	U
31	A	847	U
31	A	857	G
31	A	859	G
31	A	860	U

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Mol	Chain	Res	Type
31	A	878	A
31	A	879	G
31	A	885	C
31	A	896	A
31	A	907	G
31	A	910	A
31	A	915	C
31	A	931	U
31	A	941	A
31	A	946	C
31	A	959	A
31	A	961	C
31	A	973	A
31	A	974	G
31	A	983	A
31	A	985	C
31	A	995	C
31	A	996	A
31	A	1009	A
31	A	1010	A
31	A	1012	U
31	A	1013	C
31	A	1020	A
31	A	1022	G
31	A	1026	G
31	A	1033	U
31	A	1040	A
31	A	1046	A
31	A	1047	G
31	A	1056	G
31	A	1059	G
31	A	1060	U
31	A	1061	U
31	A	1062	G
31	A	1063	G
31	A	1065	U
31	A	1066	U
31	A	1068	G
31	A	1070	A
31	A	1071	G
31	A	1073	A
31	A	1075	C

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Mol	Chain	Res	Type
31	A	1077	A
31	A	1078	U
31	A	1080	A
31	A	1081	U
31	A	1082	U
31	A	1083	U
31	A	1084	A
31	A	1085	A
31	A	1088	A
31	A	1093	G
31	A	1097	U
31	A	1098	A
31	A	1101	U
31	A	1112	G
31	A	1132	U
31	A	1133	A
31	A	1135	C
31	A	1136	G
31	A	1142	A
31	A	1157	G
31	A	1168	G
31	A	1172	C
31	A	1173	U
31	A	1174	U
31	A	1175	A
31	A	1179	G
31	A	1180	U
31	A	1182	G
31	A	1212	G
31	A	1225	G
31	A	1236	G
31	A	1238	G
31	A	1253	A
31	A	1255	U
31	A	1256	G
31	A	1266	G
31	A	1272	A
31	A	1300	G
31	A	1301	A
31	A	1302	A
31	A	1314	C
31	A	1325	U

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Mol	Chain	Res	Type
31	A	1329	U
31	A	1345	C
31	A	1365	A
31	A	1368	G
31	A	1378	A
31	A	1383	A
31	A	1386	C
31	A	1395	A
31	A	1416	G
31	A	1419	A
31	A	1428	C
31	A	1452	G
31	A	1458	U
31	A	1476	U
31	A	1482	G
31	A	1504	A
31	A	1510	G
31	A	1515	A
31	A	1523	U
31	A	1534	U
31	A	1535	A
31	A	1555	G
31	A	1569	A
31	A	1578	U
31	A	1583	A
31	A	1585	C
31	A	1603	A
31	A	1607	C
31	A	1613	G
31	A	1634	A
31	A	1646	C
31	A	1647	U
31	A	1648	U
31	A	1654	A
31	A	1665	A
31	A	1667	G
31	A	1674	G
31	A	1715	G
31	A	1730	C
31	A	1732	C
31	A	1736	U
31	A	1737	G

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Mol	Chain	Res	Type
31	A	1738	G
31	A	1764	C
31	A	1773	A
31	A	1781	U
31	A	1800	C
31	A	1801	A
31	A	1808	A
31	A	1816	C
31	A	1829	A
31	A	1847	A
31	A	1870	C
31	A	1907	G
31	A	1909	C
31	A	1911	U
31	A	1912	A
31	A	1914	C
31	A	1915	U
31	A	1916	A
31	A	1917	U
31	A	1918	A
31	A	1919	A
31	A	1921	G
31	A	1922	G
31	A	1923	U
31	A	1925	C
31	A	1929	G
31	A	1930	G
31	A	1931	U
31	A	1934	C
31	A	1935	G
31	A	1936	A
31	A	1937	A
31	A	1938	A
31	A	1940	U
31	A	1941	C
31	A	1942	C
31	A	1945	G
31	A	1946	U
31	A	1955	U
31	A	1959	G
31	A	1961	C
31	A	1962	C

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Mol	Chain	Res	Type
31	A	1964	G
31	A	1965	C
31	A	1966	A
31	A	1967	C
31	A	1968	G
31	A	1970	A
31	A	1971	U
31	A	1972	G
31	A	1991	U
31	A	1992	G
31	A	1993	U
31	A	1997	C
31	A	2021	C
31	A	2022	U
31	A	2023	C
31	A	2030	A
31	A	2031	A
31	A	2033	A
31	A	2043	C
31	A	2050	C
31	A	2055	C
31	A	2056	G
31	A	2060	A
31	A	2061	G
31	A	2062	A
31	A	2069	G
31	A	2072	C
31	A	2093	G
31	A	2094	A
31	A	2096	C
31	A	2102	G
31	A	2105	U
31	A	2107	G
31	A	2110	G
31	A	2111	U
31	A	2112	G
31	A	2114	A
31	A	2115	G
31	A	2116	G
31	A	2117	A
31	A	2118	U
31	A	2119	A

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Mol	Chain	Res	Type
31	A	2122	U
31	A	2123	G
31	A	2126	A
31	A	2128	G
31	A	2132	U
31	A	2133	G
31	A	2136	G
31	A	2147	A
31	A	2148	G
31	A	2158	A
31	A	2162	G
31	A	2164	C
31	A	2165	C
31	A	2170	A
31	A	2171	A
31	A	2172	U
31	A	2173	A
31	A	2178	C
31	A	2198	A
31	A	2199	A
31	A	2204	G
31	A	2211	A
31	A	2225	A
31	A	2238	G
31	A	2239	G
31	A	2250	G
31	A	2251	G
31	A	2252	G
31	A	2255	G
31	A	2275	C
31	A	2279	G
31	A	2283	C
31	A	2287	A
31	A	2288	A
31	A	2297	A
31	A	2305	U
31	A	2307	G
31	A	2312	U
31	A	2314	A
31	A	2316	G
31	A	2317	A
31	A	2318	G

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Mol	Chain	Res	Type
31	A	2321	U
31	A	2322	A
31	A	2325	G
31	A	2327	A
31	A	2333	A
31	A	2336	A
31	A	2344	U
31	A	2345	G
31	A	2350	C
31	A	2357	G
31	A	2383	G
31	A	2385	C
31	A	2392	A
31	A	2402	U
31	A	2406	A
31	A	2420	C
31	A	2421	G
31	A	2422	C
31	A	2423	U
31	A	2425	A
31	A	2426	A
31	A	2428	G
31	A	2429	G
31	A	2430	A
31	A	2435	A
31	A	2441	U
31	A	2448	A
31	A	2449	U
31	A	2455	G
31	A	2456	C
31	A	2457	U
31	A	2458	G
31	A	2476	A
31	A	2478	A
31	A	2490	G
31	A	2491	U
31	A	2497	A
31	A	2498	C
31	A	2500	U
31	A	2502	G
31	A	2504	U
31	A	2505	G

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Mol	Chain	Res	Type
31	A	2506	U
31	A	2513	A
31	A	2518	A
31	A	2520	C
31	A	2525	G
31	A	2529	G
31	A	2535	G
31	A	2547	A
31	A	2554	U
31	A	2564	A
31	A	2566	A
31	A	2567	G
31	A	2572	A
31	A	2573	C
31	A	2586	U
31	A	2601	C
31	A	2602	A
31	A	2609	U
31	A	2610	C
31	A	2613	U
31	A	2615	U
31	A	2629	U
31	A	2630	G
31	A	2636	C
31	A	2639	A
31	A	2646	C
31	A	2647	U
31	A	2682	A
31	A	2684	U
31	A	2689	U
31	A	2690	U
31	A	2714	G
31	A	2718	G
31	A	2721	A
31	A	2726	A
31	A	2729	G
31	A	2733	A
31	A	2744	G
31	A	2748	A
31	A	2765	A
31	A	2778	A
31	A	2780	G

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Mol	Chain	Res	Type
31	A	2791	G
31	A	2798	U
31	A	2818	U
31	A	2820	A
31	A	2825	G
31	A	2835	A
31	A	2836	U
31	A	2867	G
31	A	2872	A
31	A	2873	A
31	A	2880	C
31	A	2883	A
31	A	2884	U
31	A	2886	A
31	A	2893	A

All (17) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
31	A	271	G
31	A	404	A
31	A	479	A
31	A	995	C
31	A	1070	A
31	A	1076	C
31	A	1080	A
31	A	1224	U
31	A	1606	C
31	A	1666	G
31	A	1736	U
31	A	1914	C
31	A	1936	A
31	A	2127	G
31	A	2249	U
31	A	2311	A
31	A	2425	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
36	GDP	9	1001	37	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	GDP	9	1001	37	-	3/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	9	1001	GDP	C5-C4	3.18	1.47	1.38
36	9	1001	GDP	C6-N1	-2.41	1.34	1.38
36	9	1001	GDP	C5-N7	-2.04	1.35	1.39

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	9	1001	GDP	C5-C4-N3	-6.18	118.55	128.39
36	9	1001	GDP	C2-N3-C4	5.05	121.01	112.30
36	9	1001	GDP	N9-C4-N3	4.53	135.01	125.95
36	9	1001	GDP	C6-C5-N7	3.26	136.23	130.29
36	9	1001	GDP	C4-C5-N7	-2.64	106.48	110.67
36	9	1001	GDP	O6-C6-C5	-2.09	121.03	126.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	9	1001	GDP	C3'-C2'-C1'	2.07	105.37	101.46

There are no chirality outliers.

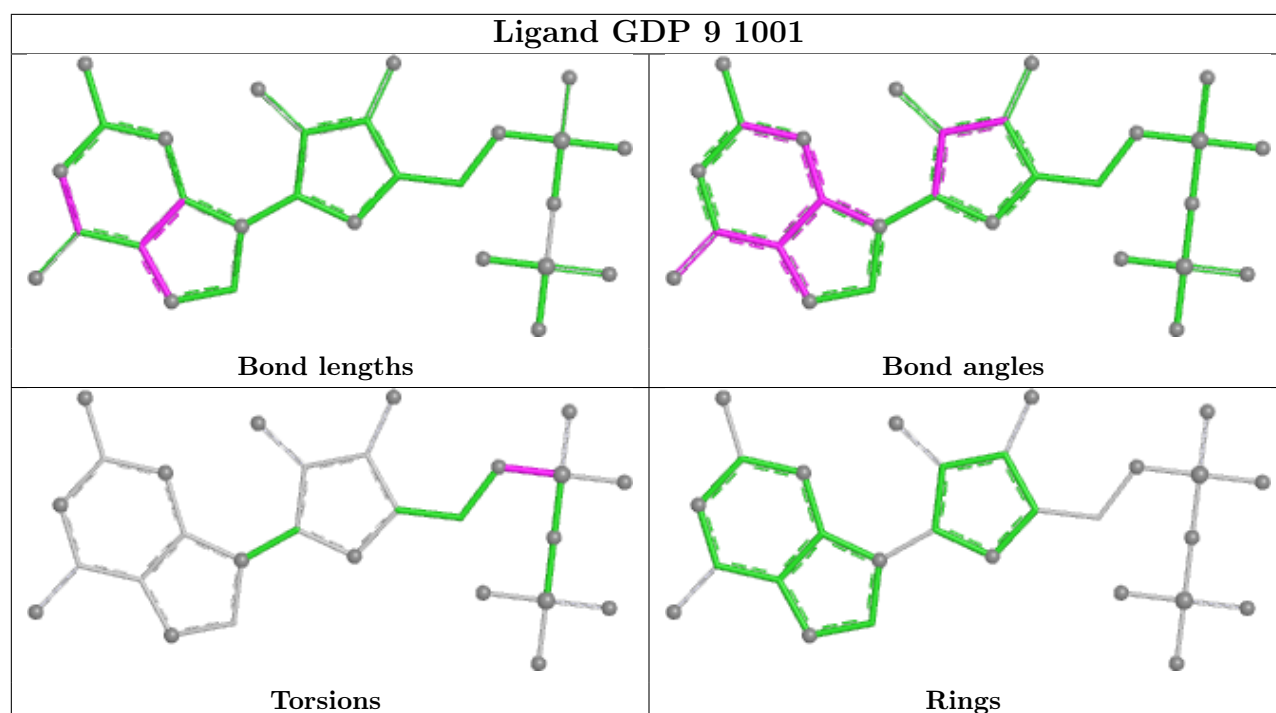
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
36	9	1001	GDP	C5'-O5'-PA-O3A
36	9	1001	GDP	C5'-O5'-PA-O1A
36	9	1001	GDP	C5'-O5'-PA-O2A

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

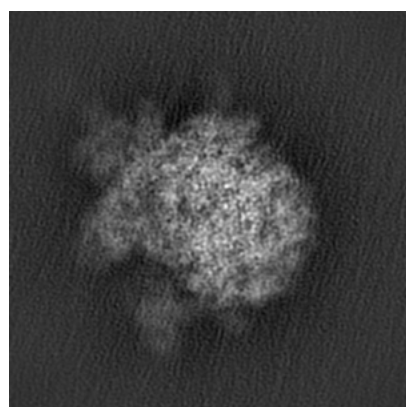
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12218. These allow visual inspection of the internal detail of the map and identification of artifacts.

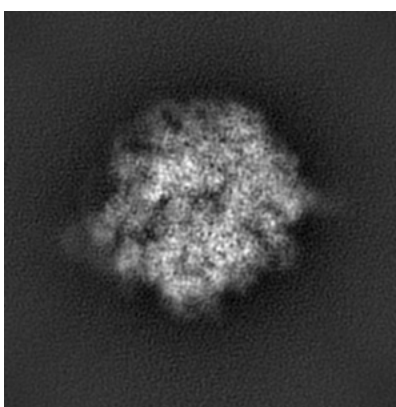
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

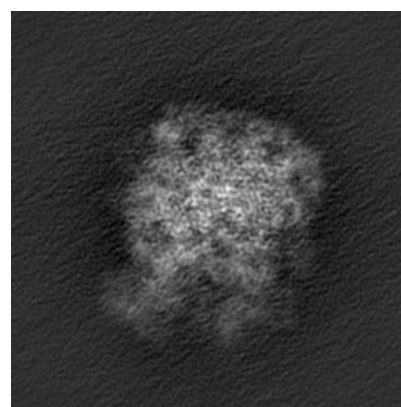
6.1.1 Primary map



X



Y

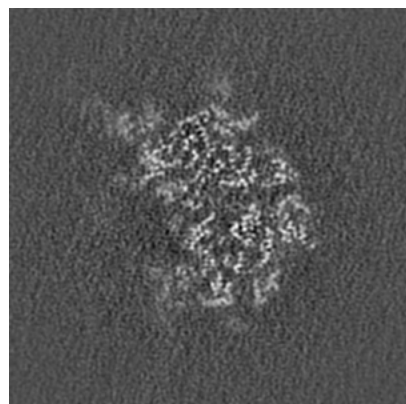


Z

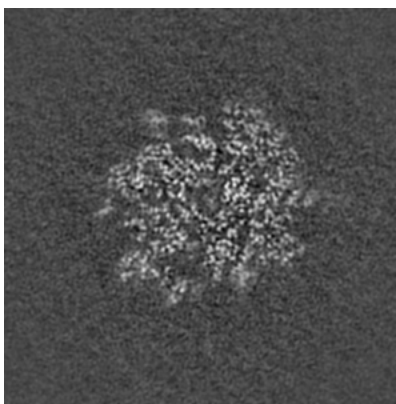
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

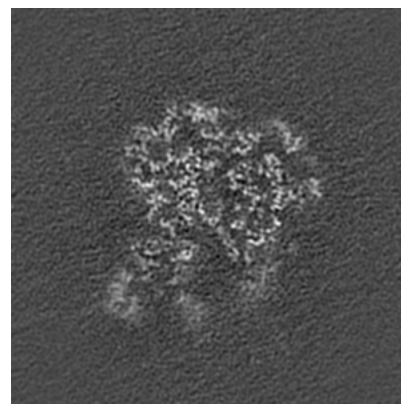
6.2.1 Primary map



X Index: 135



Y Index: 135

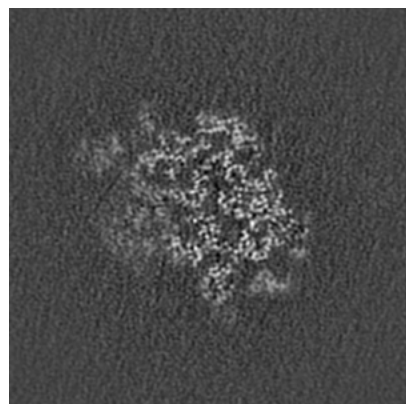


Z Index: 135

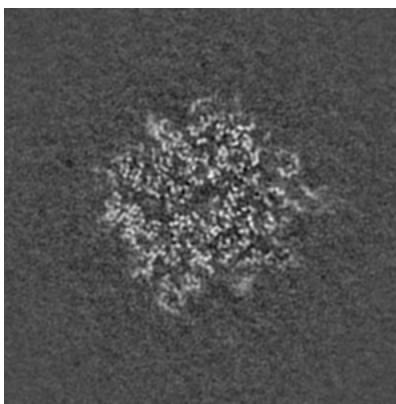
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

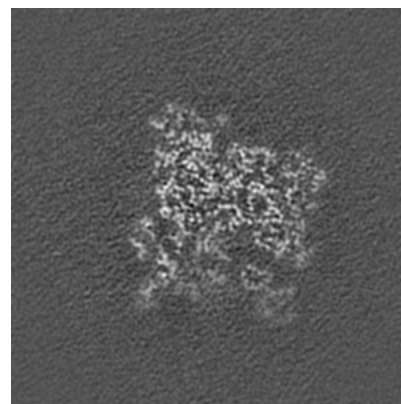
6.3.1 Primary map



X Index: 157



Y Index: 142

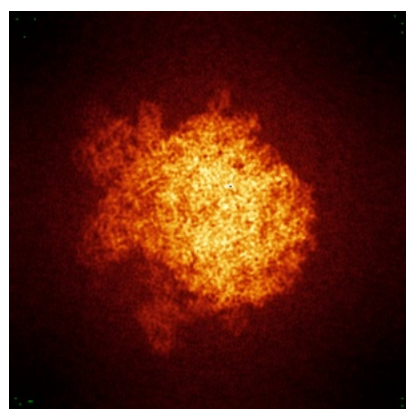


Z Index: 151

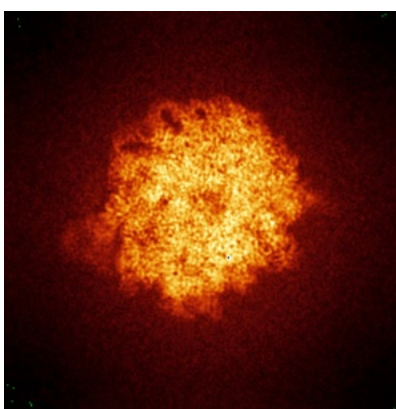
The images above show the largest variance slices of the map in three orthogonal directions.

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

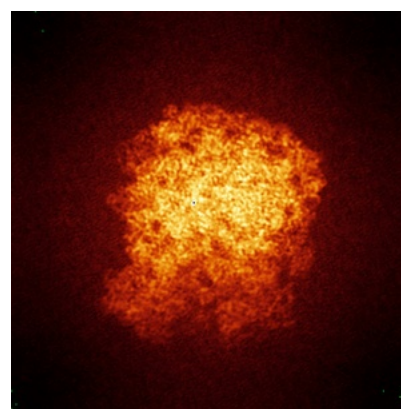
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

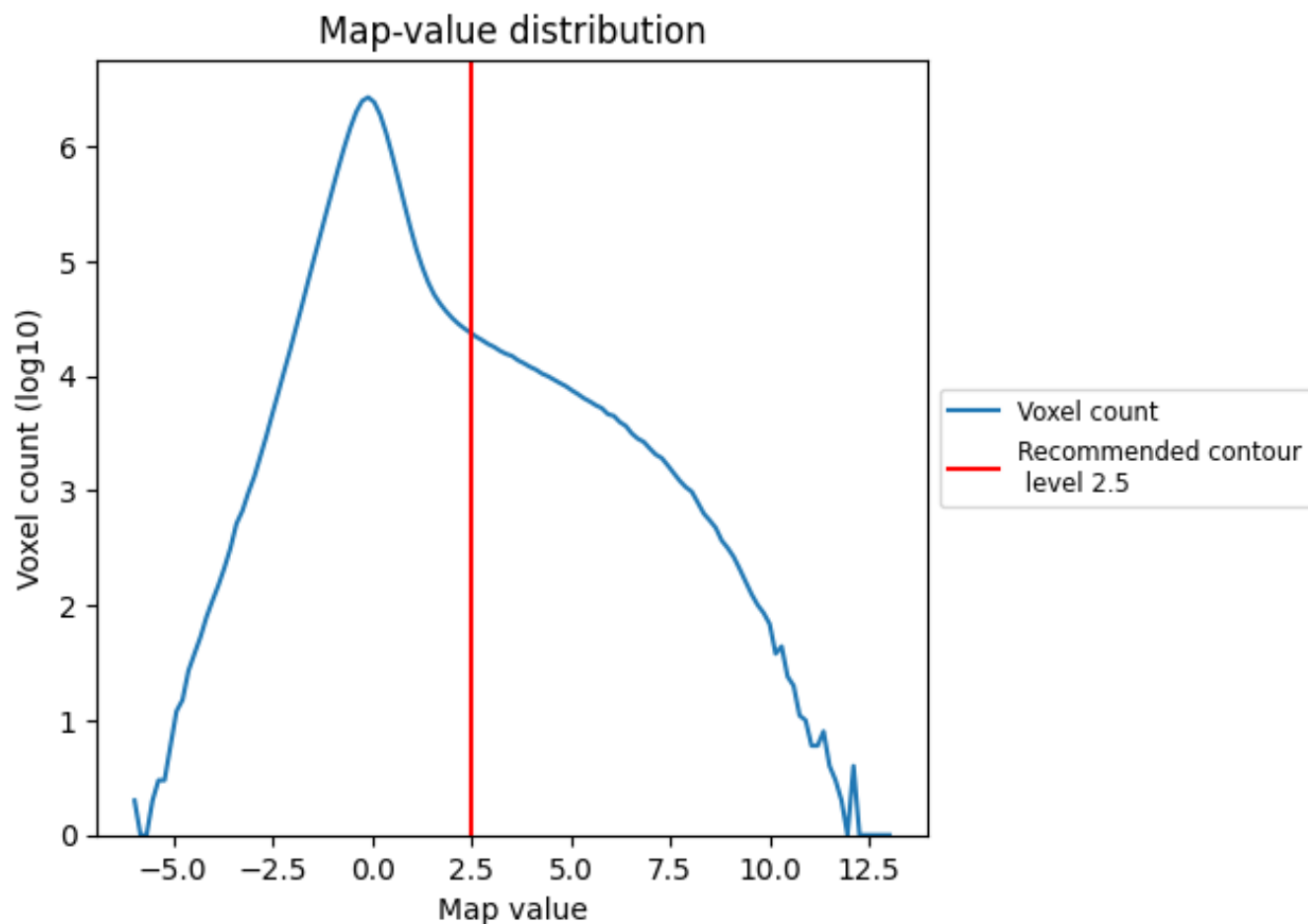
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

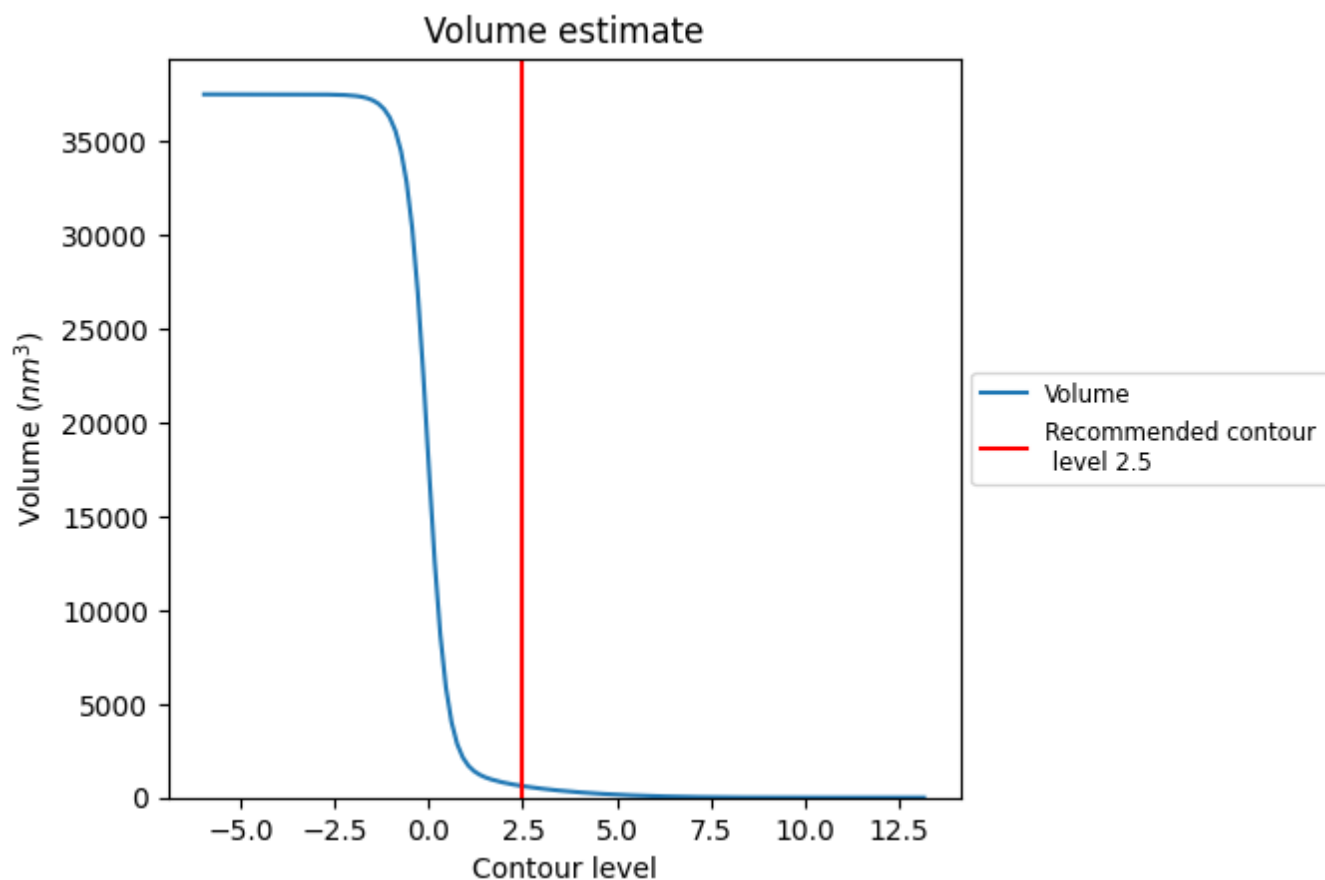
This section contains the results of statistical analysis of the map.

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.

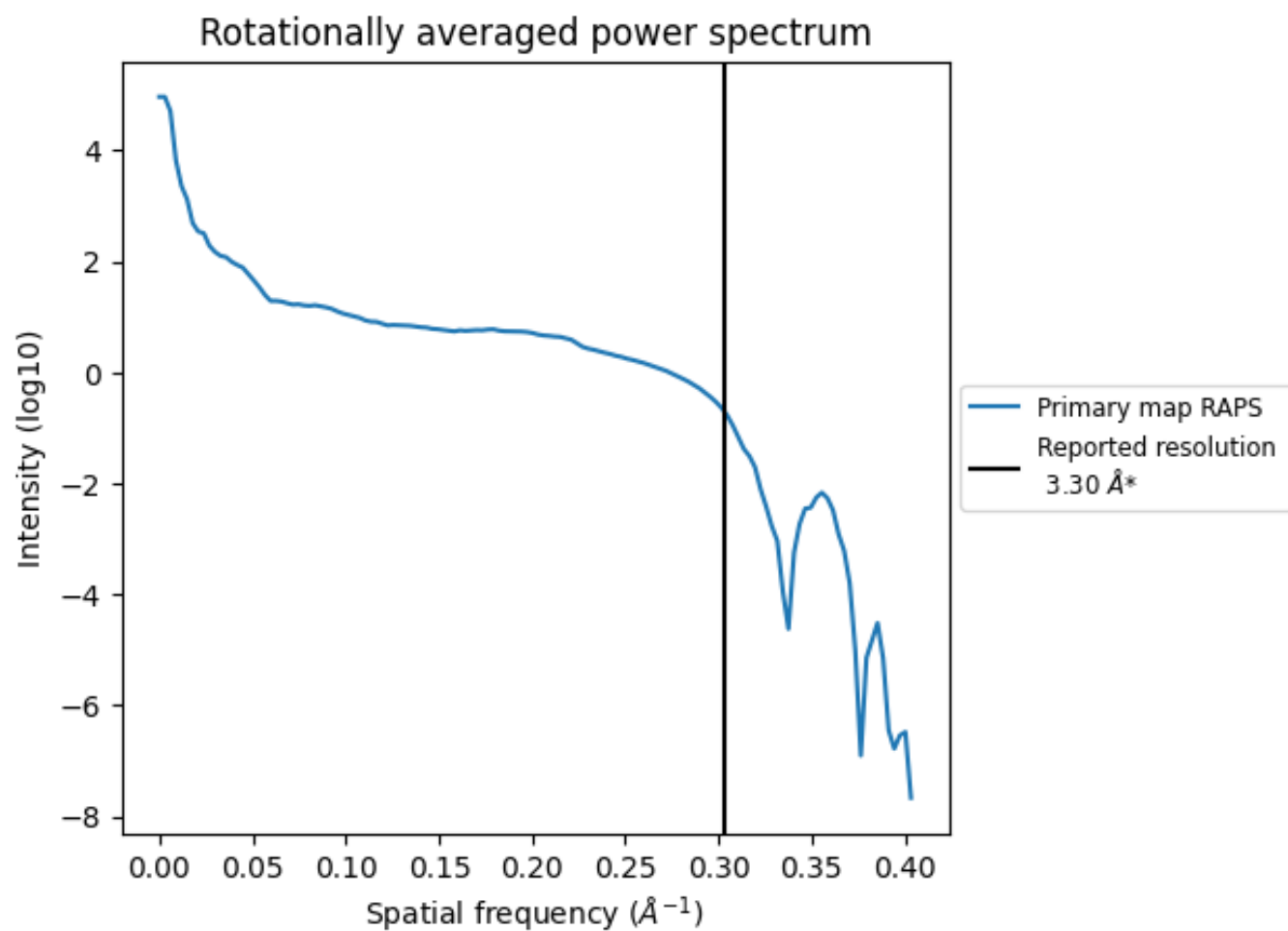
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 613 nm^3 ; this corresponds to an approximate mass of 554 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 ⓘ

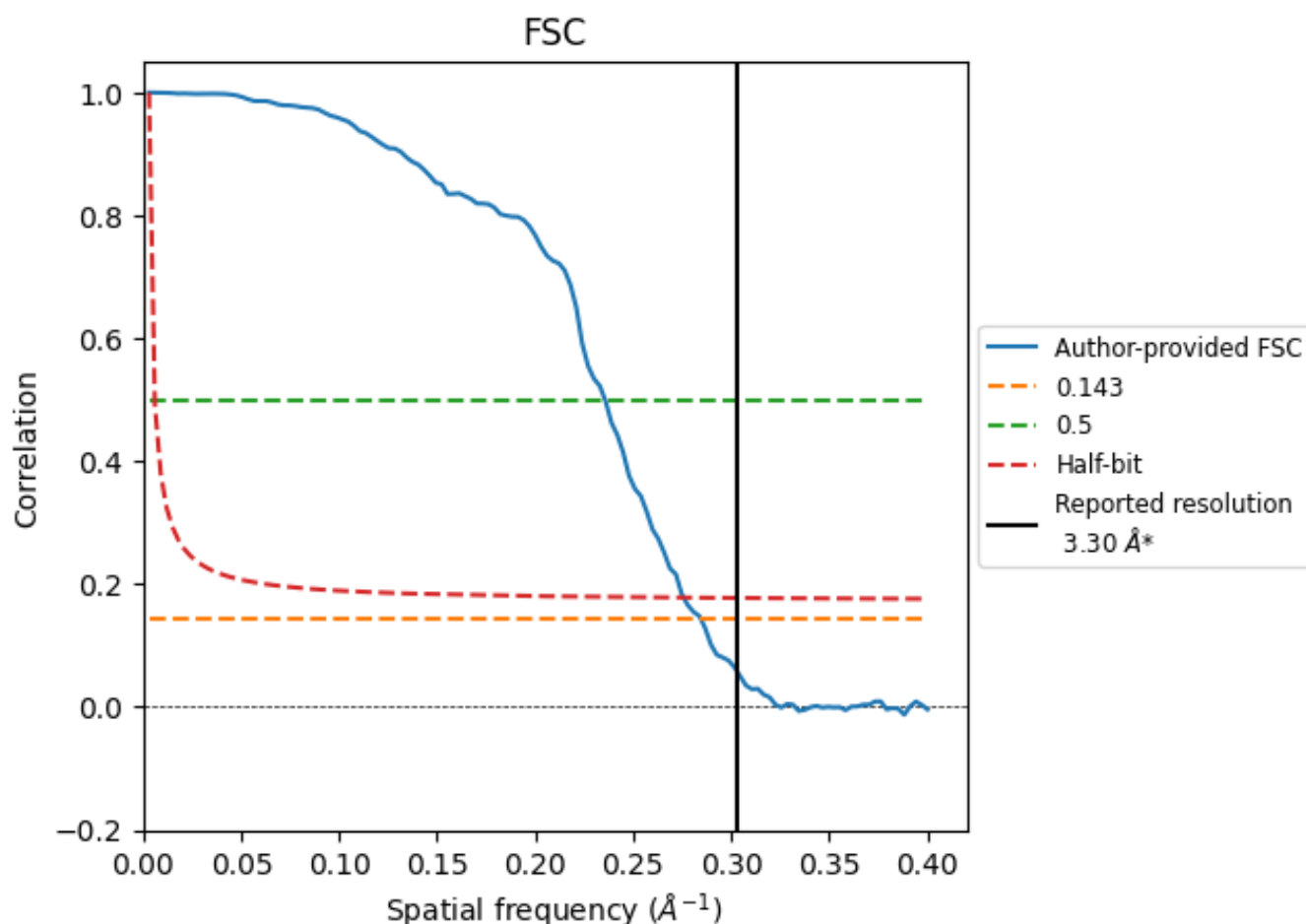


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

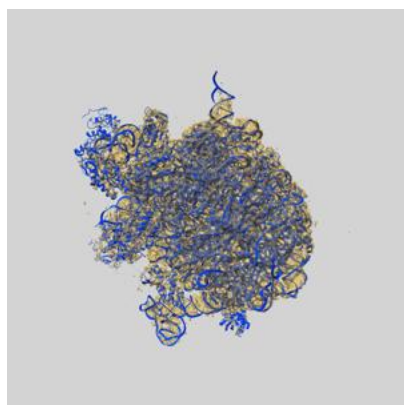
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.51	4.24	3.63
Unmasked-calculated*	-	-	-

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

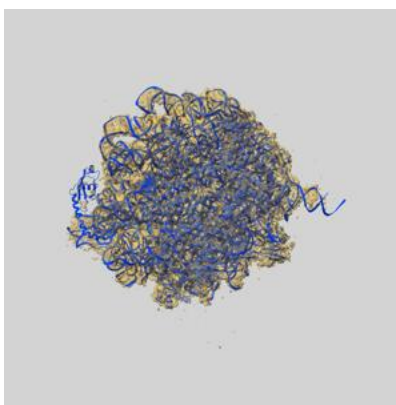
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12218 and PDB model 7BL5. Per-residue inclusion information can be found in section [3](#) on page [12](#).

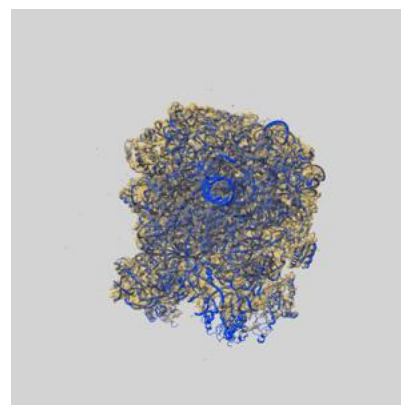
9.1 Map-model overlay [i](#)



X



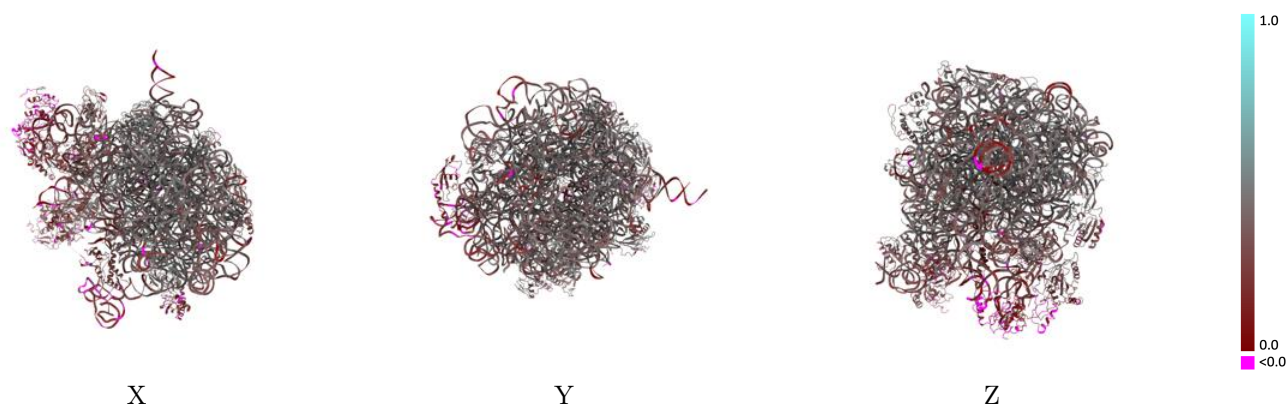
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

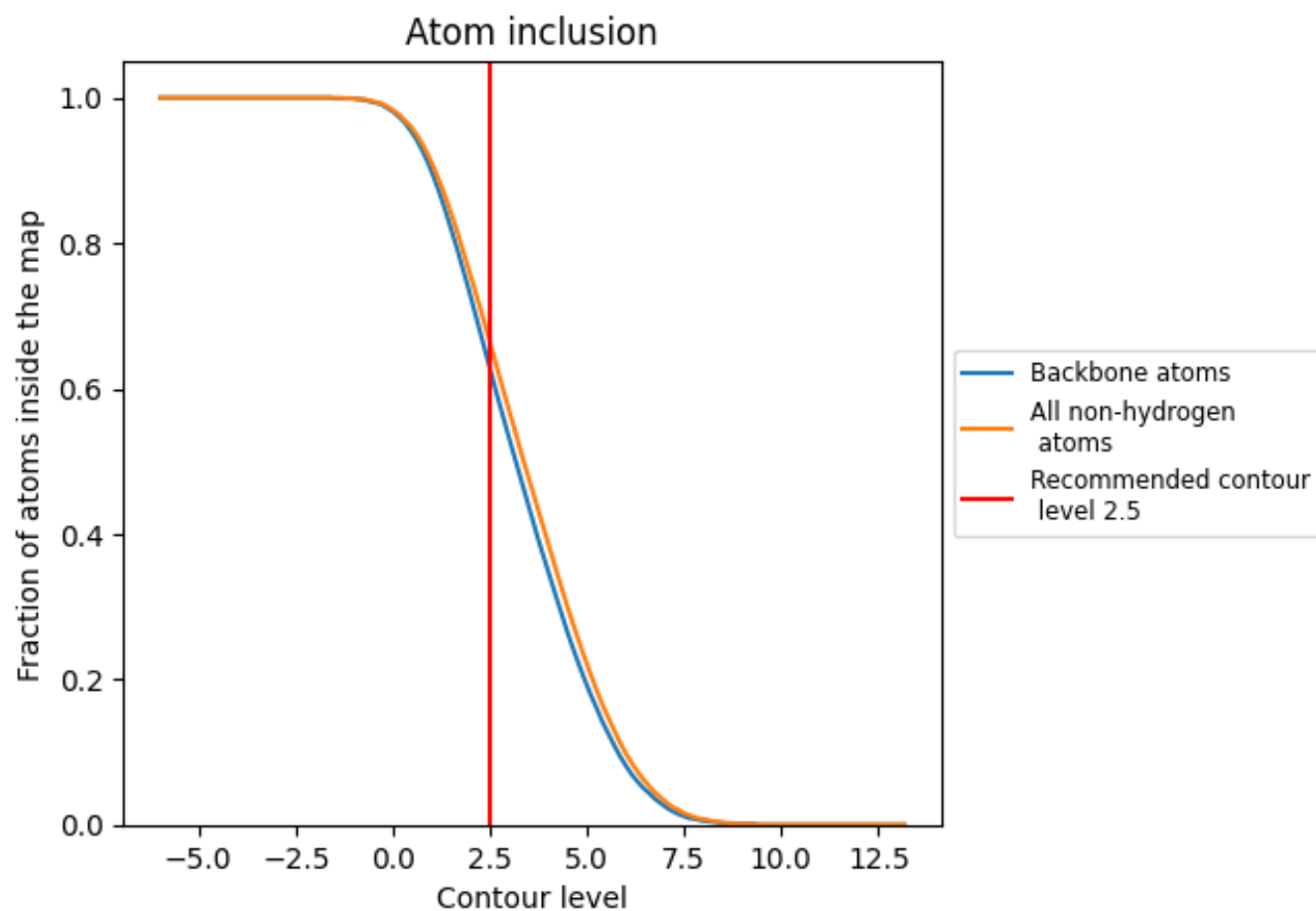


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 66% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6640	 0.3630
0	 0.6470	 0.4120
1	 0.3540	 0.3060
2	 0.6650	 0.4390
6	 0.4120	 0.3080
7	 0.2520	 0.2880
8	 0.3920	 0.3140
9	 0.3890	 0.3330
A	 0.7730	 0.3750
B	 0.6600	 0.3140
C	 0.6770	 0.4390
D	 0.6660	 0.4400
E	 0.5830	 0.3860
F	 0.2420	 0.2380
G	 0.4300	 0.3270
H	 0.1590	 0.1980
I	 0.0440	 0.0980
J	 0.6640	 0.4410
K	 0.6470	 0.4360
L	 0.5570	 0.3700
M	 0.1360	 0.2670
N	 0.6970	 0.4440
O	 0.4370	 0.3040
P	 0.6470	 0.4240
Q	 0.6720	 0.4340
R	 0.6610	 0.4270
S	 0.6720	 0.4340
T	 0.6150	 0.4050
U	 0.6150	 0.4020
V	 0.4490	 0.3160
W	 0.6080	 0.4200
X	 0.6640	 0.4450
Y	 0.5730	 0.3310
Z	 0.6640	 0.4210
b	 0.0910	 0.1770
e	 0.0240	 0.0660

