



Full wwPDB EM Validation Report ⓘ

Mar 24, 2026 – 11:51 PM UTC

PDB ID : 5JCS / pdb_00005jcs
EMDB ID : EMD-3199
Title : CRYO-EM STRUCTURE OF THE RIX1-REA1 PRE-60S PARTICLE
Authors : Barrio-Garcia, C.; Thoms, M.; Flemming, D.; Kater, L.; Berninghausen, O.;
Bassler, J.; Beckmann, R.; Hurt, E.
Deposited on : 2016-04-15
Resolution : 9.50 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

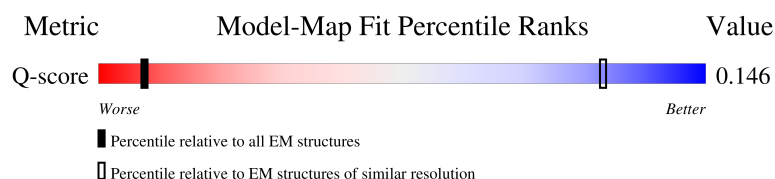
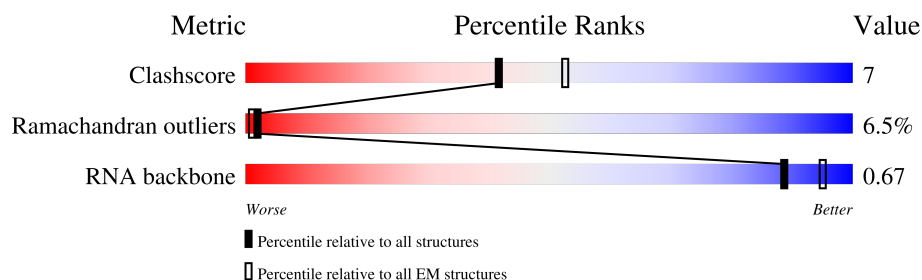
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 9.50 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	234 (9.00 - 10.00)

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	A	254	
2	c	105	
3	B	387	
4	d	113	

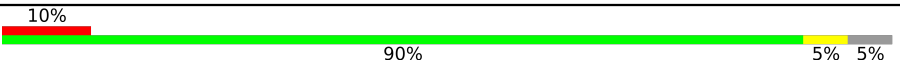
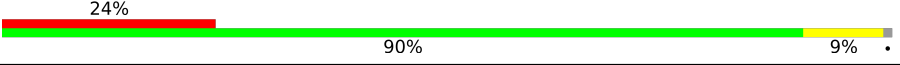
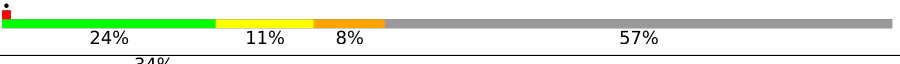
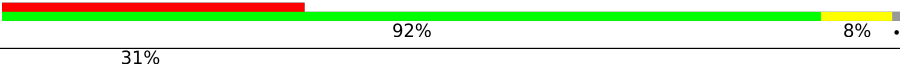
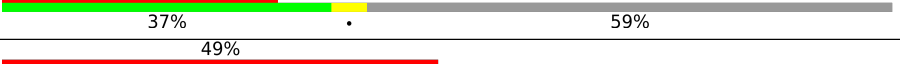
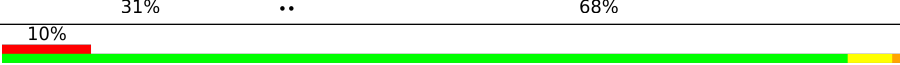
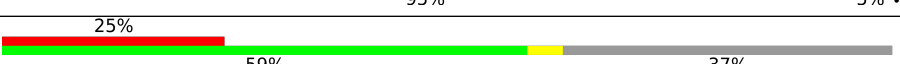
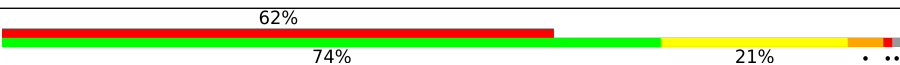
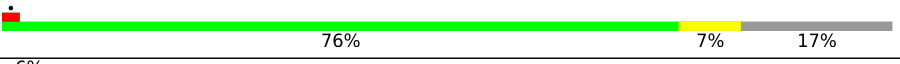
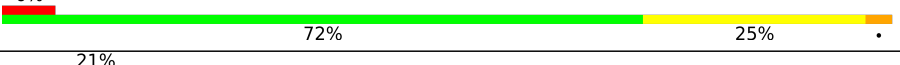
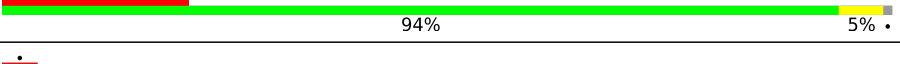
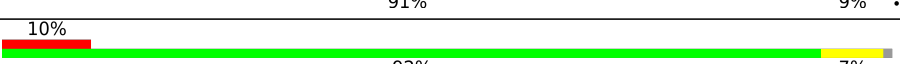
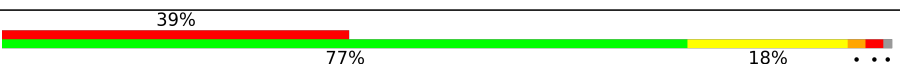
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Mol	Chain	Length	Quality of chain
5	C	362	
6	e	130	
7	D	297	
8	f	107	
9	E	176	
10	g	121	
11	F	244	
12	h	120	
13	G	256	
14	i	100	
15	H	191	
16	j	88	
17	I	217	
18	k	78	
19	J	174	
20	l	51	
21	K	165	
22	m	245	
23	L	199	
24	n	236	
25	M	138	
26	o	647	
27	N	204	
28	p	92	
29	O	199	

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Mol	Chain	Length	Quality of chain
30	q	515	
31	P	184	
32	r	767	
33	Q	186	
34	s	4910	
35	R	189	
36	t	199	
37	S	172	
38	u	593	
39	T	160	
40	x	3396	
41	U	121	
42	y	158	
43	V	137	
44	z	121	
45	X	142	
46	Y	127	
47	Z	136	
48	a	149	

2 Entry composition

There are 48 unique types of molecules in this entry. The entry contains 118855 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 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	252	Total	C	N	O	0	0
			1007	504	252	251		

- Molecule 2 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	c	97	Total	C	N	O	0	0
			387	194	97	96		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	B	386	Total	C	N	O	0	0
			1543	772	386	385		

- Molecule 4 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	d	109	Total	C	N	O	0	0
			435	218	109	108		

- Molecule 5 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	C	361	Total	C	N	O	0	0
			1443	722	361	360		

- Molecule 6 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	e	127	Total	C	N	O	0	0
			507	254	127	126		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	D	296	Total	C	N	O	0	0
			1183	592	296	295		

- Molecule 8 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	f	106	Total	C	N	O	0	0
			423	212	106	105		

- Molecule 9 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	E	156	Total	C	N	O	0	0
			622	312	156	154		

- Molecule 10 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	g	112	Total	C	N	O	0	0
			447	224	112	111		

- Molecule 11 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	F	222	Total	C	N	O	0	0
			887	444	222	221		

- Molecule 12 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	h	119	Total	C	N	O	0	0
			475	238	119	118		

- Molecule 13 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	G	233	Total	C	N	O	0	0
			931	466	233	232		

- Molecule 14 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	i	99	Total	C	N	O	0	0
			395	198	99	98		

- Molecule 15 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	H	191	Total	C	N	O	0	0
			763	382	191	190		

- Molecule 16 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	j	87	Total	C	N	O	0	0
			347	174	87	86		

- Molecule 17 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	I	217	Total	C	N	O	0	0
			867	434	217	216		

- Molecule 18 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	k	77	Total	C	N	O	0	0
			307	154	77	76		

- Molecule 19 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	J	169	Total	C	N	O	0	0
			675	338	169	168		

- Molecule 20 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	l	50	Total	C	N	O	0	0
			199	100	50	49		

- Molecule 21 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	K	127	Total	C	N	O	0	0
			507	254	127	126		

- Molecule 22 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	m	224	Total	C	N	O	0	0
			895	448	224	223		

- Molecule 23 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	L	193	Total	C	N	O	0	0
			771	386	193	192		

- Molecule 24 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	n	212	Total	C	N	O	0	0
			847	424	212	211		

- Molecule 25 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	M	136	Total	C	N	O	0	0
			543	272	136	135		

- Molecule 26 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	o	347	Total	C	N	O	0	0
			1387	694	347	346		

- Molecule 27 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	N	203	Total	C	N	O	0	0
			811	406	203	202		

- Molecule 28 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	p	91	Total	C	N	O	0	0
			363	182	91	90		

- Molecule 29 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	O	197	Total	C	N	O	0	0
			787	394	197	196		

- Molecule 30 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	q	488	Total	C	N	O	0	0
			1951	976	488	487		

- Molecule 31 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	P	183	Total	C	N	O	0	0
			731	366	183	182		

- Molecule 32 is a protein called Protein SDA1.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	r	333	Total	C	N	O	0	0
			1304	666	333	305		

- Molecule 33 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	Q	185	Total	C	N	O	0	0
			739	370	185	184		

- Molecule 34 is a protein called Midasin.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	s	2003	Total	C	N	O	0	0
			8007	4006	2003	1998		

- Molecule 35 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	R	188	Total	C	N	O	0	0
			751	376	188	187		

- Molecule 36 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	t	63	Total	C	N	O	0	0
			251	126	63	62		

- Molecule 37 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	S	172	Total	C	N	O	0	0
			687	344	172	171		

- Molecule 38 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	u	373	Total	C	N	O	0	0
			1491	746	373	372		

- Molecule 39 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	T	159	Total	C	N	O	0	0
			635	318	159	158		

- Molecule 40 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	x	3394	Total	C	N	O	P	0	0
			72570	32410	13042	23725	3393		

- Molecule 41 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	U	100	Total	C	N	O	0	0
			399	200	100	99		

- Molecule 42 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	y	158	Total	C	N	O	P	0	0
			3350	1500	586	1107	157		

- Molecule 43 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	V	136	Total	C	N	O	0	0
			543	272	136	135		

- Molecule 44 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	z	121	Total	C	N	O	P	0	0
			2576	1152	461	843	120		

- Molecule 45 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	X	121	Total	C	N	O	0	0
			483	242	121	120		

- Molecule 46 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	Y	126	Total	C	N	O	0	0
			503	252	126	125		

- Molecule 47 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	Z	135	Total	C	N	O	0	0
			539	270	135	134		

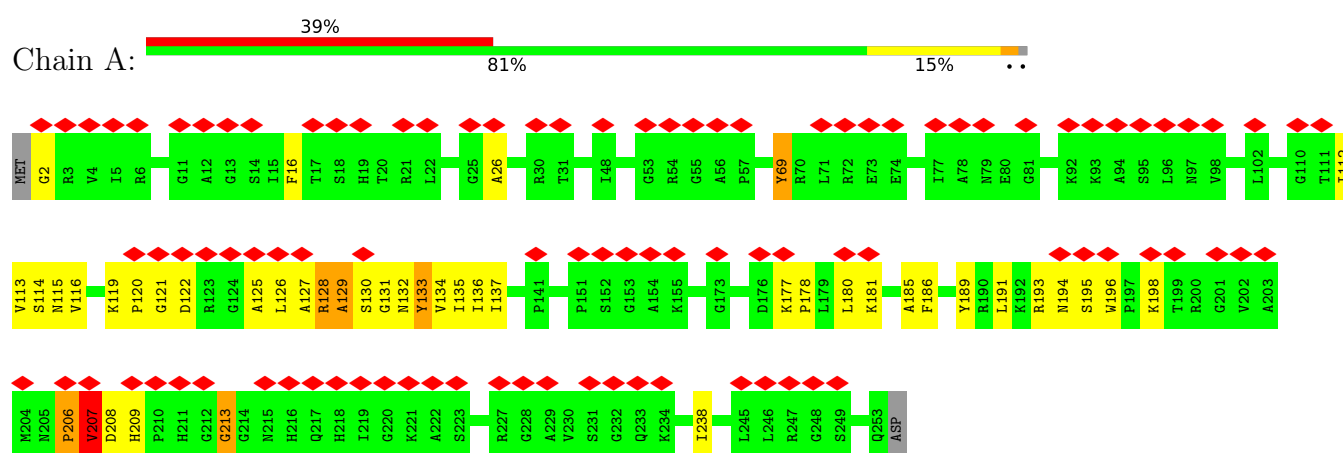
- Molecule 48 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	a	148	Total	C	N	O	0	0
			591	296	148	147		

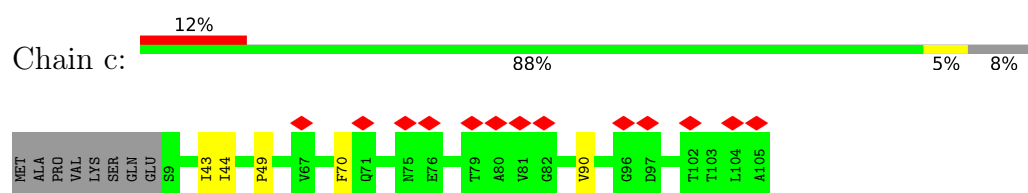
3 Residue-property plots

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.

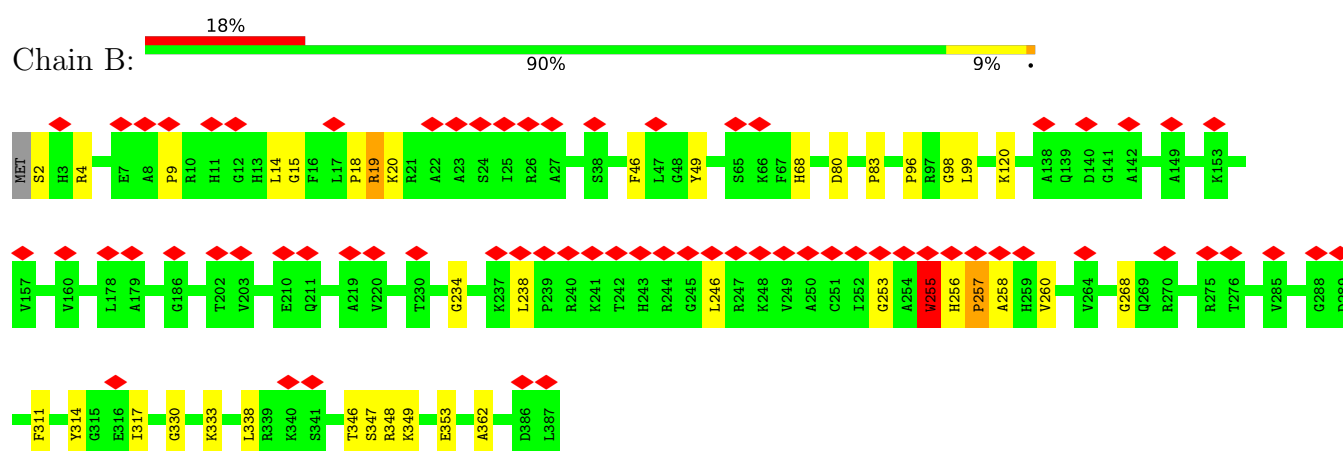
• Molecule 1: 60S ribosomal protein L2-A



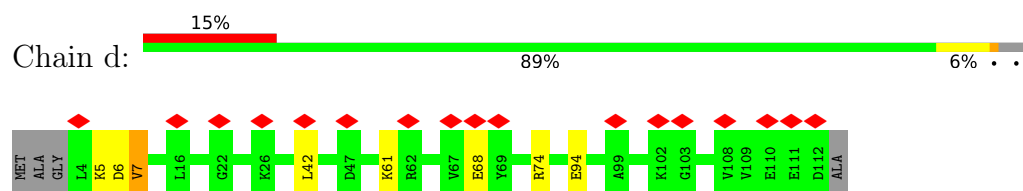
• Molecule 2: 60S ribosomal protein L30



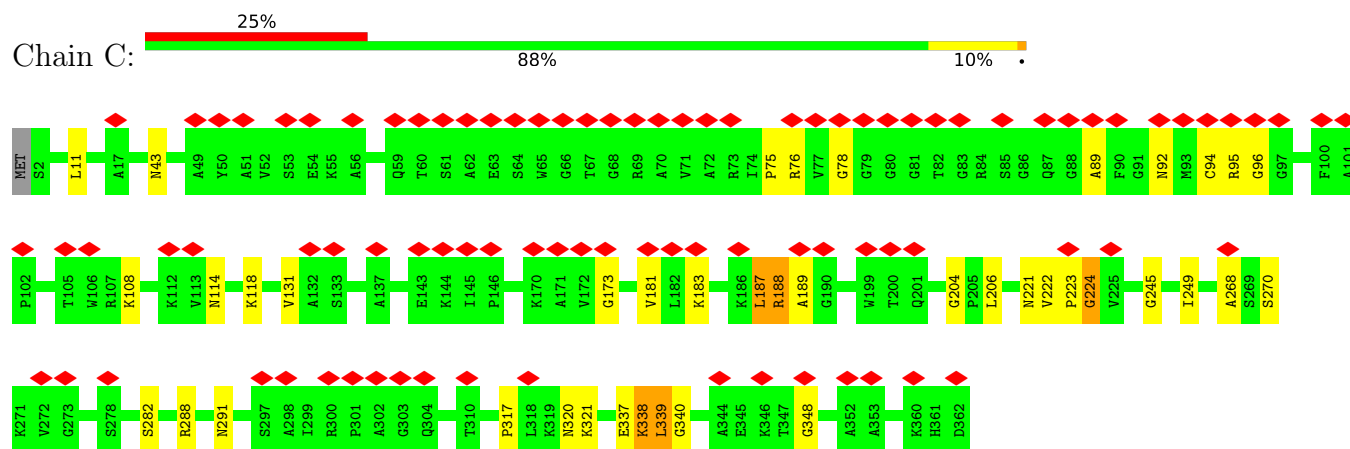
• Molecule 3: 60S ribosomal protein L3



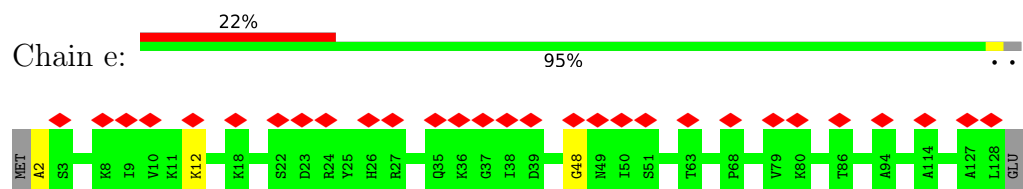
- Molecule 4: 60S ribosomal protein L31-A



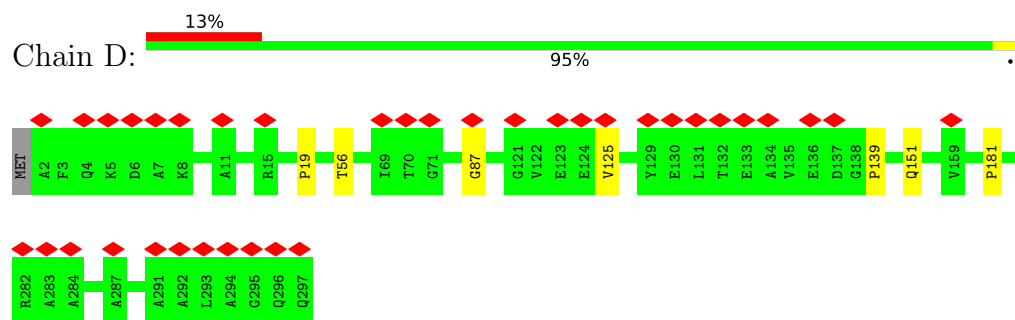
- Molecule 5: 60S ribosomal protein L4-A



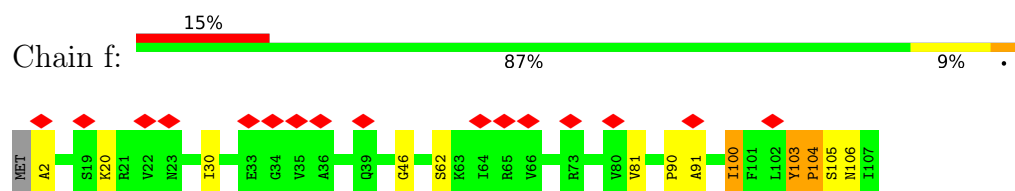
- Molecule 6: 60S ribosomal protein L32



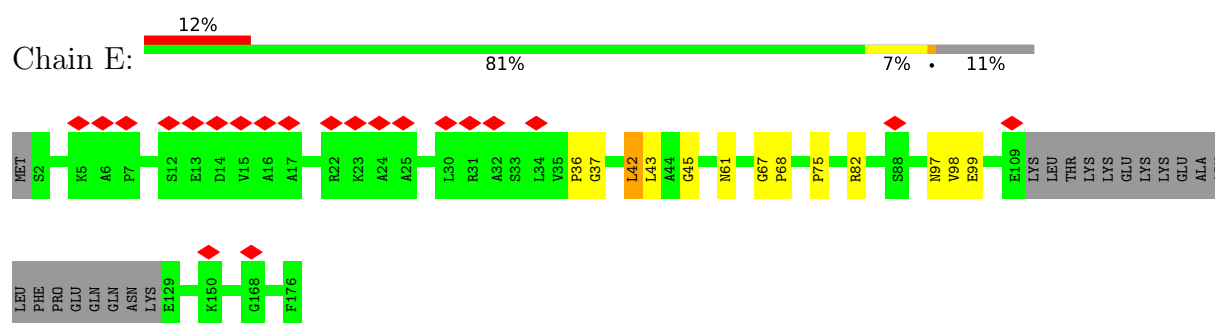
- Molecule 7: 60S ribosomal protein L5



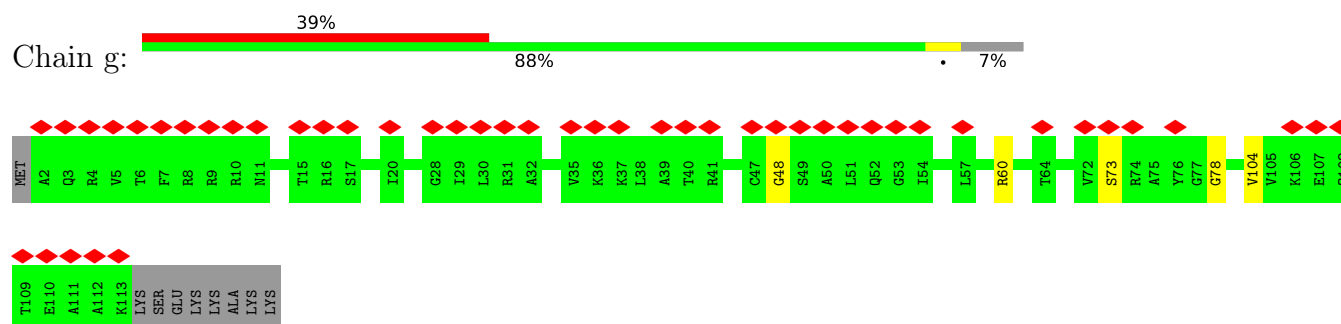
- Molecule 8: 60S ribosomal protein L33-A



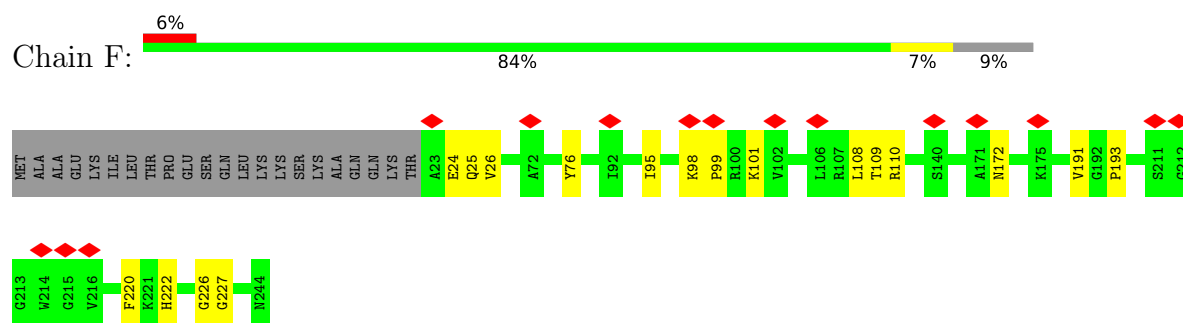
- Molecule 9: 60S ribosomal protein L6-A



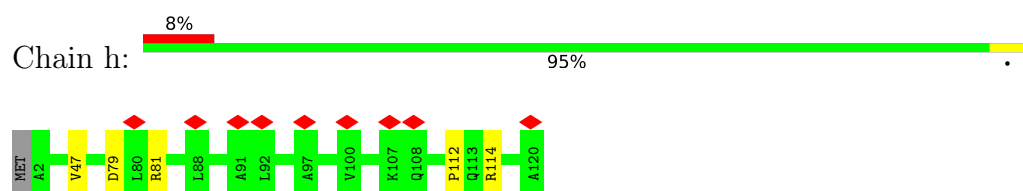
- Molecule 10: 60S ribosomal protein L34-A



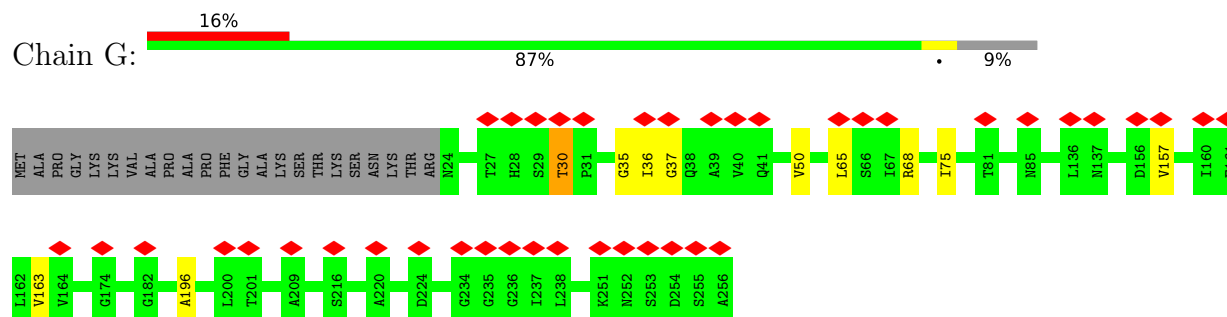
- Molecule 11: 60S ribosomal protein L7-A



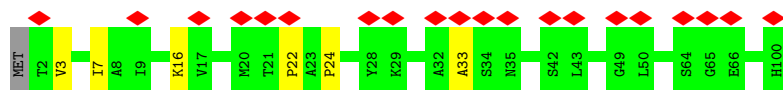
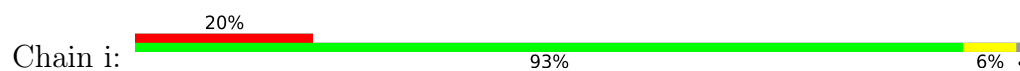
- Molecule 12: 60S ribosomal protein L35-A



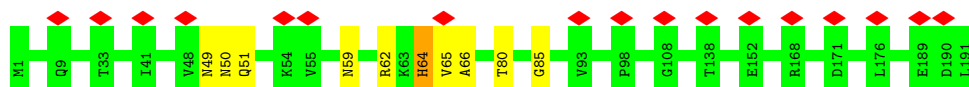
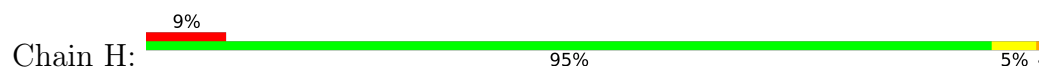
- Molecule 13: 60S ribosomal protein L8-A



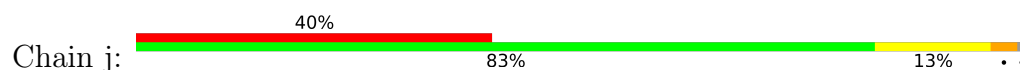
- Molecule 14: 60S ribosomal protein L36-A



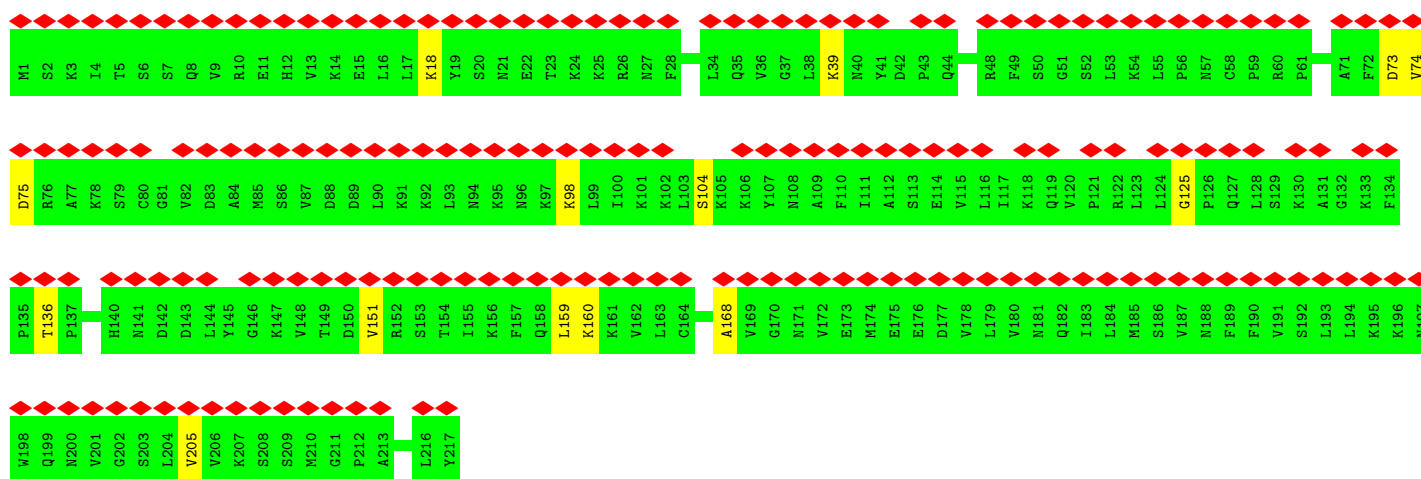
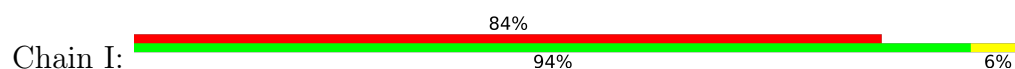
- Molecule 15: 60S ribosomal protein L9-A



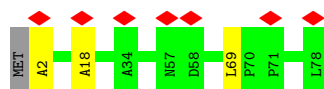
- Molecule 16: 60S ribosomal protein L37-A



- Molecule 17: 60S ribosomal protein L1-A

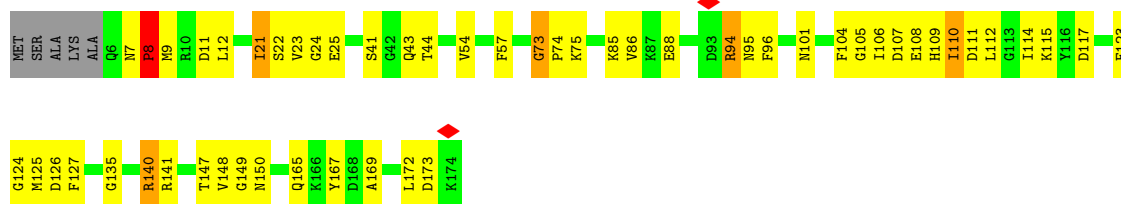


- Molecule 18: 60S ribosomal protein L38



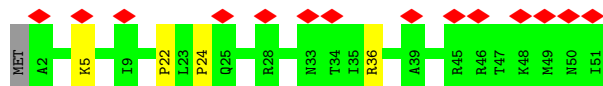
- Molecule 19: 60S ribosomal protein L11-A

Chain J:  66% 28% . . .



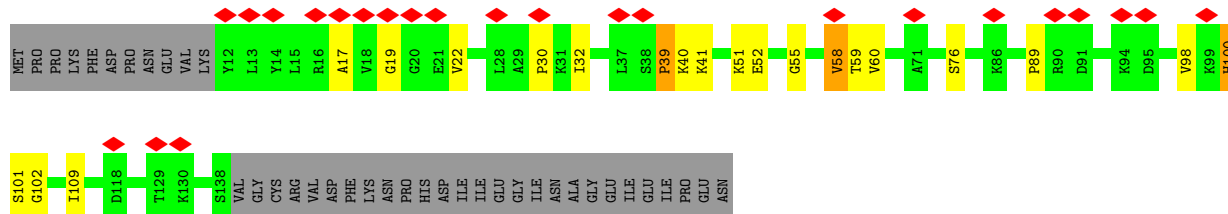
- Molecule 20: 60S ribosomal protein L39

Chain I:  27% 90% 8% .



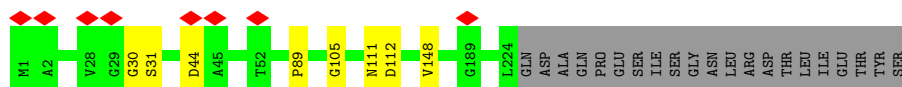
- Molecule 21: 60S ribosomal protein L12-A

Chain K:  15% 64% 11% . 23%



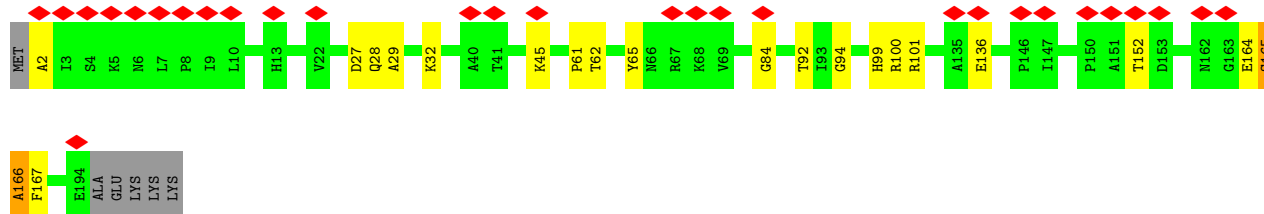
- Molecule 22: Eukaryotic translation initiation factor 6

Chain m:  88% 9%



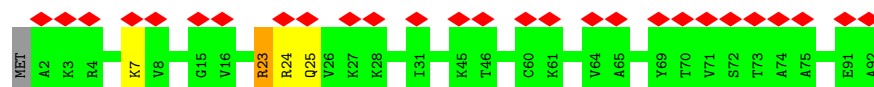
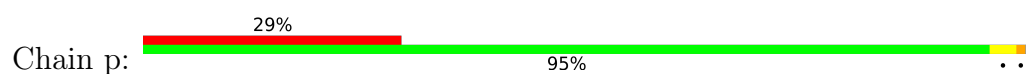
- Molecule 23: 60S ribosomal protein L13-A

Chain L:  15% 86% 10% . .

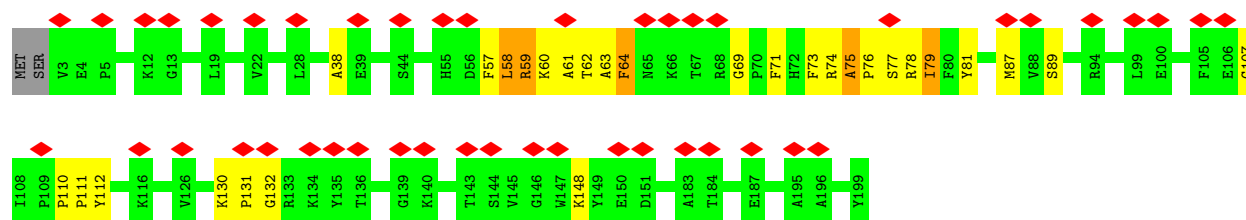
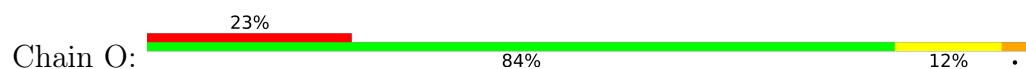


- Molecule 24: Ribosome assembly factor MRT4

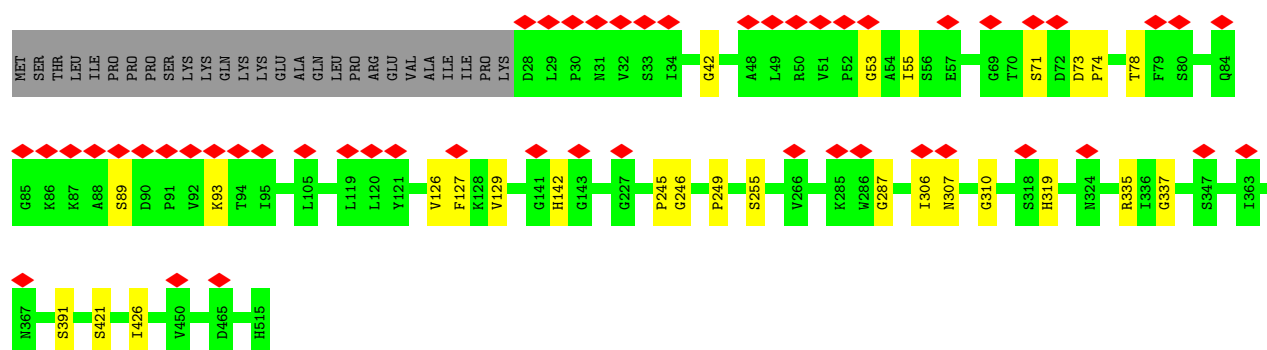
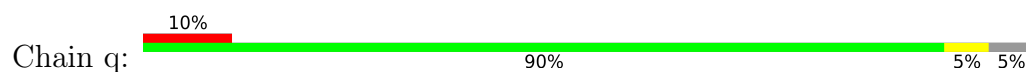
Chain n:  86% 10%



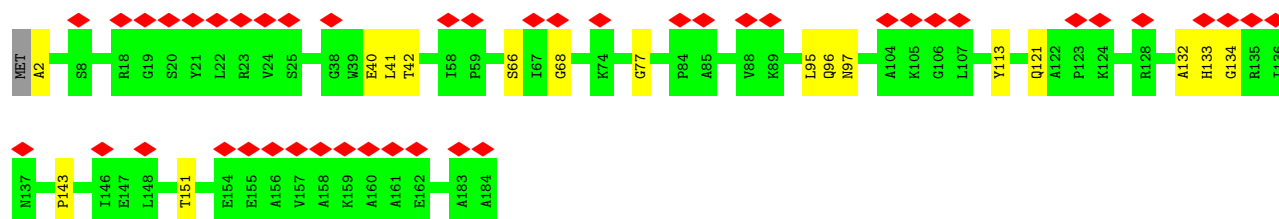
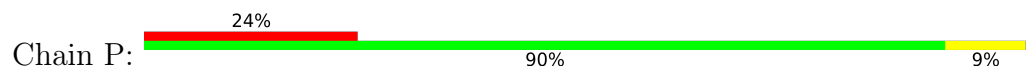
- Molecule 29: 60S ribosomal protein L16-A



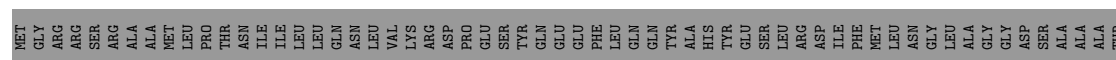
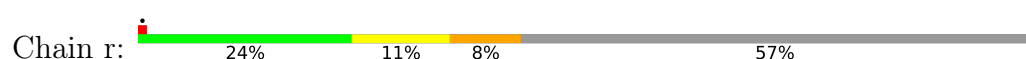
- Molecule 30: Ribosome assembly protein 4



- Molecule 31: 60S ribosomal protein L17-A



- Molecule 32: Protein SDA1



E863	P864	I865	K866	A867	H868	P869	D870	F871	R872	I873	F874	S815	A816	M817	N818	P819	A880	T881	D882	V883	G884	K885	D886	D887	L888	P889	M890	G891	I892	R893	S894	R895	F896	T897	E898	I899	Y900	V901	H902	S903	F904	E905	R906	D907	I908	D910	L911	L912	S913	K917	K921	Y922	S923	V924	S925	D926					
L743	W744	N745	E746	A747	W748	F749	M750	A751	Q752	S753	L754	L755	K756	L757	T758	N759	T760	E761	N762	E763	N764	E765	N766	A767	K768	K769	K770	K771	R772	R773	L774	N775	T776	H777	E778	K779	K780	L781	L782	L783	D784	K785	M786	A787	D788	F789	N790	D791	R792	V793	K794	K795	F796	E797	A798	Q799	S800	S801	S802		
I803	E804	N805	S806	F807	V808	P809	N810	F811	V812	E813	G814	S815	L816	V817	K818	T819	I820	R821	A822	G823	E824	W825	L826	L827	L828	D829	E830	N831	R832	L833	A834	T835	A836	D837	T838	L839	E840	S841	I842	S843	D844	L845	L846	T847	E848	P849	D850	S851	R852	S853	I854	L855	L856	S857	E858	K859	G860	D861	A862		
T683	E684	T685	G686	D687	L688	L689	G690	G691	Y692	K693	P694	VAL	ASN	SER	K698	T699	V700	A701	V702	P703	I704	Q705	E706	N707	F708	E709	T710	L711	F712	N713	A714	T715	F716	S717	L718	K719	K720	N721	E722	K723	F724	H725	K726	H727	L728	H729	R730	C731	F732	K733	N734	N735	Q736	W737	K738	N739	V740	V741	K742		
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D546	S547	I548	F549	S550	E551	D554	C555	F556	A557	G558	A559	I560	G561	P568	I569	I570	I573	S576	D578	I579	A580	S581	S582	R583	I584	S585	L586	F587	L588	T589	Q590	H591	V592	P593	T594	L595	E596	N597	L598	D599	D600	S601	I602	K603	I604	G605	R606	A607	V608	L609	L610	K611	E612	K613							
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G421	F422	Q423	L424	I425	S426	T427	V428	R429	I430	N431	D432	A433	H434	Q435	K436	D437	S438	S439	N440	K441	I442	Y443	N444	L445	N446	M447	I448	G449	M450	R451	I452	W453	N454	V455	I456	E459	D465	L466	T467	H468	I469	L470	A471	Q472	K473	F474	P475	I476	L477	T478	N479	L480	I481	P482	K483	L484	I485				
K361	P362	G363	T364	F365	E366	W367	R368	A369	G370	V371	L372	A373	T374	A375	V376	K377	E378	G379	R380	W381	V382	L383	I384	E385	D386	I387	D388	K389	A390	P391	T392	D393	V394	L395	S396	I397	L398	L399	S400	L401	L402	E403	K404	R405	E406	L407	T408	I409	P410	S411	R412	G413	E414	T415	V416	K417	A418	A419	N420		
L301	G302	R303	K304	I305	Q306	N307	S308	T309	P310	I311	N312	L313	I314	G315	K316	A317	G318	S319	G320	K321	T322	F323	L324	I325	N326	E327	L328	S329	K330	Y331	N332	G333	C334	H335	D336	S337	I338	V339	K340	I341	H342	L343	G344	E345	Q346	T347	D348	A349	K350	L351	L352	I353	G354	T355	Y356	T357	S358	G359	D360		
PRO	GLU	CYS	PHE	THR	ILE	GLU	LYS	ASP	SER	GLY	THR	PRO	GLN	ASP	ASP	LEU	SER	THR	VAL	ALA	SER	ILE	CYS	VAL	ILE	VAL	PRO	GLY	GLN	ASP	GLY	THR	ILE	LYS	VAL	PHE	THR	PRO	LEU	T287	F288	V289	P290	T291	H292	K293	T294	V295	S296	S297	L298	Q300									
LYS	VAL	SER	LEU	THR	GLN	ASP	GLY	THR	LYS	LEU	ASP	VAL	VAL	PHE	THR	LYS	LYS	LYS	THR	ASP	ARG	ASP	THR	TYR	ARG	LYS	THR	TYR	GLY	ASP	ILE	GLY	THR	ASP	VAL	GLU	ASN	ILE	GLU	THR	ASP	GLY	THR	ILE	LYS	ASN	GLN	VAL	ASN	PHE	SER	VAL	ILE	PHE	LEU	PRO	THR	ALA	GLY		
HIS	VAL	PHE	LEU	TYR	ARG	LEU	ASP	GLU	VAL	VAL	VAL	ALA	ASN	GLN	ARG	TRP	ILE	ILE	ALA	ASP	MET	LEU	LEU	ILE	ILE	ASP	ASP	PRO	MET	VAL	ALA	LEU	ASP	GLU	ASN	ILE	GLU	THR	ASP	GLY	THR	ILE	LYS	ASN	GLN	GLU	VAL	THR	ILE	ILE	THR	ALA	GLY								
LEU	GLN	ASN	PRO	SER	LEU	THR	LYS	MET	PHE	THR	LYS	LEU	ASP	ASP	TYR	ARG	LYS	LYS	ASP	HIS	ASP	VAL	ASP	THR	TYR	ARG	LYS	THR	ILE	LYS	LYS	ASP	ALA	LEU	GLU	ASN	ILE	GLU	THR	ASP	GLY	THR	ILE	LYS	ASN	GLN	VAL	THR	ILE	ILE	THR	ALA	GLY								

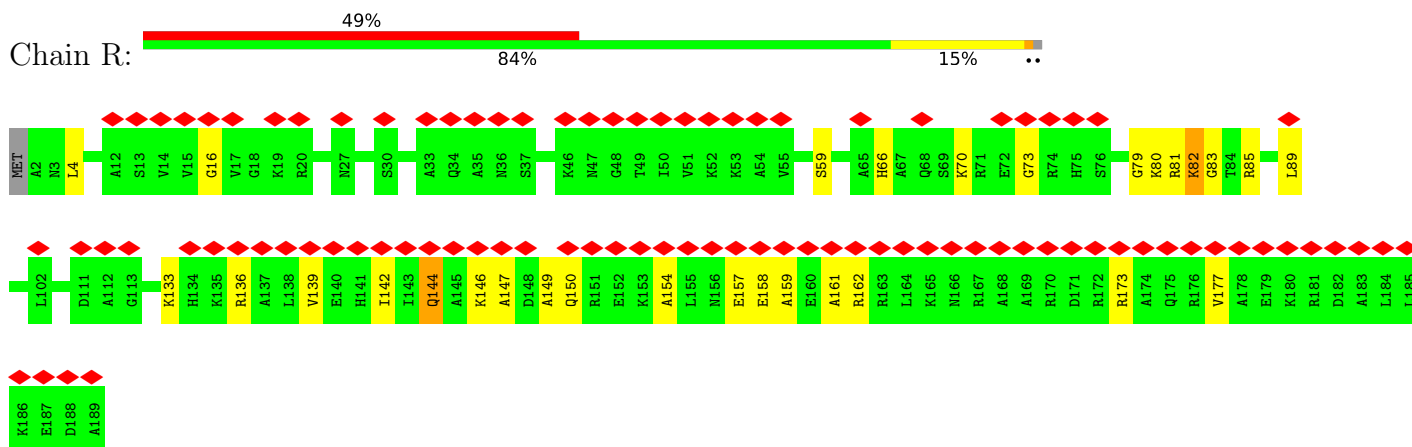
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K1753	T1754	S1755	L1756	I1757	A1761	N1762	I1763	T1764	G1765	N1766	K1767	L1768	T1769	R1770	I1771	N1772	L1773	S1774	E1775	Q1776	D1777	T1778	L1779	V1780	D1781	L1782	F1783	G1784	A1785	D1786	A1787	P1788	G1789	E1790	R1791	S1792	G1793	E1794	F1795	L1796	W1797	H1798	D1799	A1800	P1801	F1802	L1803	K1807	K1808	G1809	V1812	L1813	L1814	D1815	E1816				
G1681	D1682	L1684	GLU	LEU	GLN	GLN	ILE	THR	GLU	ASN	GLU	ILE	THR	GLN	ASP	GLU	GLN	VAL	GLY	MET	PHE	LYS	ILE	ARG	PHE	PRO	ASP	ALA	GLN	SER	SER	SER	PHE	N1720	L1721	T1722	A1723	T1726	V1734	R1735	A1736	M1737	Q1738	V1739	H1740	I1743	S1748	V1751	G1752	G1680									
G1599	K1600	K1601	L1602	G1603	G1604	G1605	N1606	A1607	T1608	S1609	G1610	V1611	I1612	S1613	L1614	L1618	A1619	N1625	K1626	V1627	F1628	P1629	Q1640	G1641	A1642	S1643	A1649	L1650	G1651	T1652	N1653	N1654	T1655	A1656	Y1657	L1658	A1659	E1660	N1661	E1662	N1663	D1664	L1665	K1666	S1667	L1668	R1669	T1670	E1671	C1672	I1673	I1674	Q1675	C1680					
S1522	S1523	D1524	S1525	L1526	V1527	T1528	A1529	S1530	F1533	Q1534	F1535	F1536	A1537	T1538	M1539	G1542	G1543	D1544	Y1545	G1546	K1547	K1548	E1549	L1550	S1551	P1552	A1553	P1564	S1565	M1566	E1567	D1568	V1572	M1573	M1574	I1575	S1577	S1578	R1579	L1580	L1581	E1582	D1583	L1584	K1585	D1586	V1592	K1593	F1594	S1595	E1596	W1597	F1598						
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A1394	H1395	Q1396	N1397	T1398	E1399	T1400	G1401	D1402	I1403	L1404	G1405	A1406	Q1407	R1408	P1409	V1410	R1411	N1412	R1413	S1414	E1415	I1416	Q1417	Y1418	K1419	L1420	I1421	K1422	S1423	L1424	K1425	T1426	A1427	L1428	N1429	I1430	A1431	N1432	D1433	Q1434	D1435	V1436	D1437	L1438	K1439	E1440	L1441	L1442	Q1443	L1444	Y1445	S1446	K1447	S1448	D1449	N1450	K1451	N1452	I1453
L1271	A1282	V1283	G1284	Y1285	L1295	L1296	A1297	E1298	R1299	C1300	R1301	T1302	E1305	K1306	L1313	V1319	K1320	L1321	D1322	M1323	ASP	GLN	TYR	TYR	ALA	SER	LEU	GLU	ASP	LYS	SER	LEU	GLU	ALA	ILE	GLY	SER	VAL	THR	T1344	K1361	E1362	G1371	R1387	E1388	L1389	T1390	T1391	L1392	N1393									
H1185	P1186	D1187	F1188	L1189	L1190	Q1194	N1195	P1196	P1197	G1198	I1199	Y1200	G1201	G1202	R1203	K1204	I1205	L1206	S1207	R1208	A1209	R1213	I1222	D1225	E1233	K1234	C1235	A1238	Y1241	V1248	Y1249	L1252	S1253	I1254	E1255	R1256	S1257	A1258	S1259	R1260	L1261	F1262	E1263	Q1264	K1265	N1266	S1267	F1268	A1269	V1181	V1182	H1183	P1184						
Y1118	L1119	G1120	T1121	Y1122	V1123	T1124	D1125	L1126	T1127	G1128	K1129	L1130	S1131	F1132	K1133	E1134	G1135	V1136	L1137	V1138	E1139	A1140	L1141	R1142	K1143	D1150	L1154	A1155	P1156	T1157	D1158	V1159	L1160	E1161	A1162	L1163	N1164	R1165	L1166	L1167	D1168	D1169	N1170	R1171	E1172	L1173	F1174	I1175	P1176	E1177	T1178	Q1179	E1180	V1181	V1182	H1183	P1184		
SER	PRO	GLY	PRO	ASP	TYR	VAL	GLN	PHE	LYS	THR	TYR	LYS	GLY	PRO	ASN	THR	ILE	GLN	GLN	ALA	HIS	Y1055	I1056	I1057	K1063	R1070	A1071	T1072	S1073	G1074	P1075	R1076	F1077	T1085	S1086	S1087	G1088	K1089	R1090	S1091	M1092	G1101	R1106	I1107	E1111	L1115	Q1116	E1117											
E927	W928	Y929	G930	H931	D932	P933	A934	K942	S953	K956	P957	S960	T965	L969	V970	Y971	T972	D973	Y974	Y977	Y978	S991	F992	L995	K999	I1003	L1004	K1005	P1006	K1010	L1013	G1014	R1015	L1016	K1017	M1018	V1019	K1020	S1021	I1022	M1023	S1024	GLN	THR	PRO	PRO													





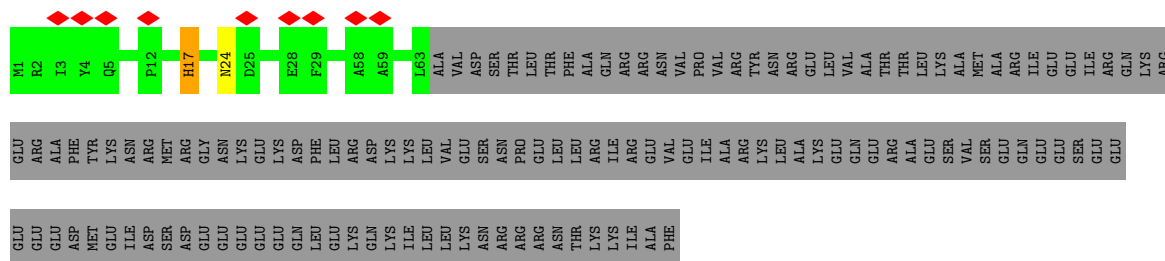
[illegible]

- Molecule 35: 60S ribosomal protein L19-A

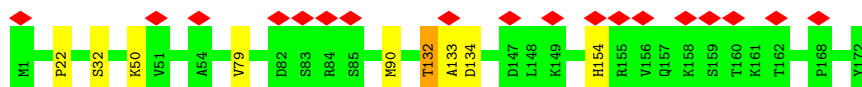
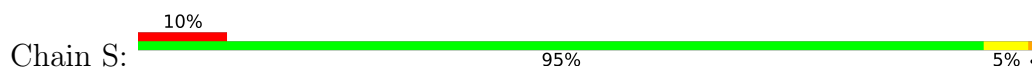


- Molecule 36: Ribosome biogenesis protein RLP24

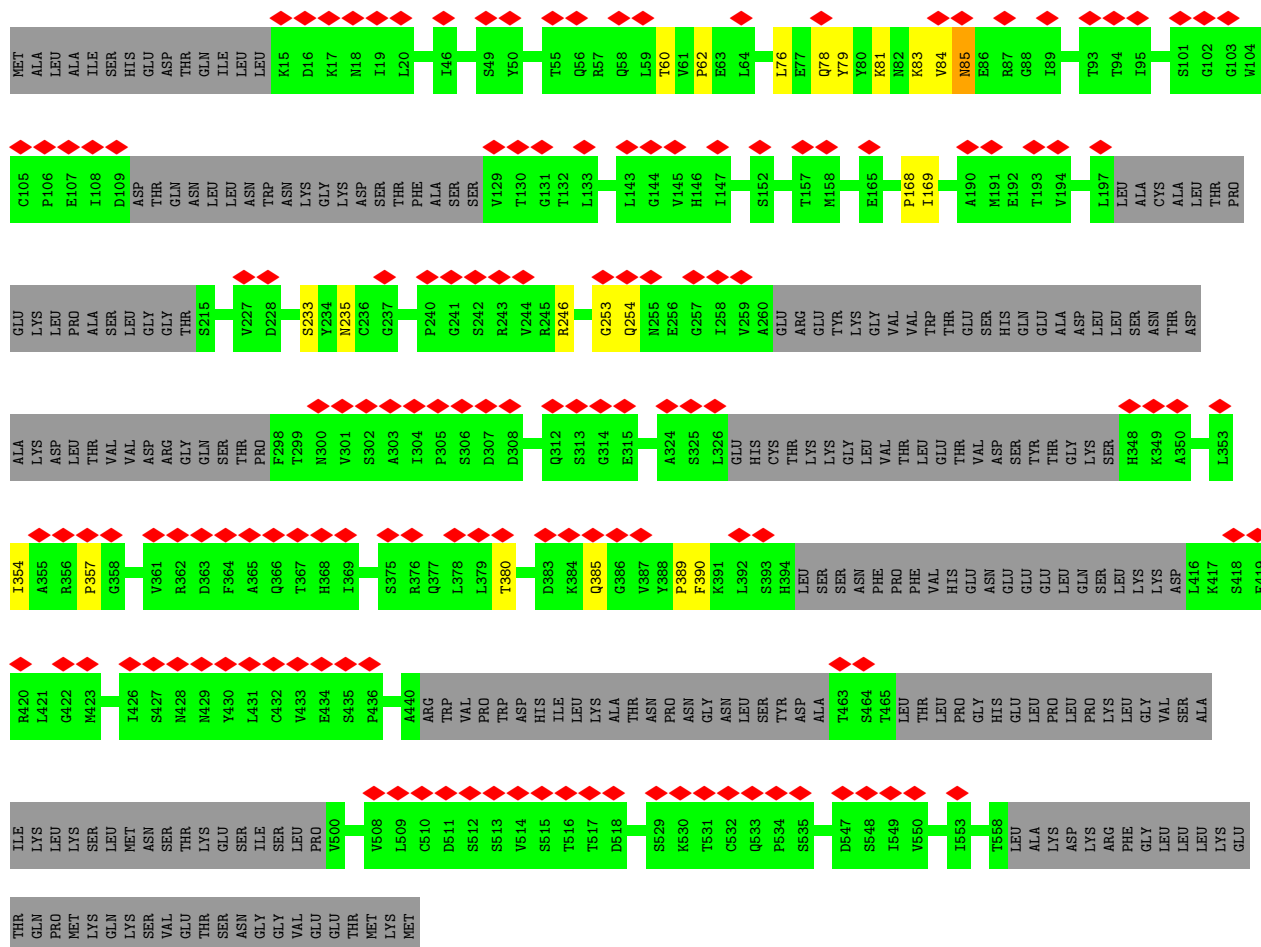




• Molecule 37: 60S ribosomal protein L20-A

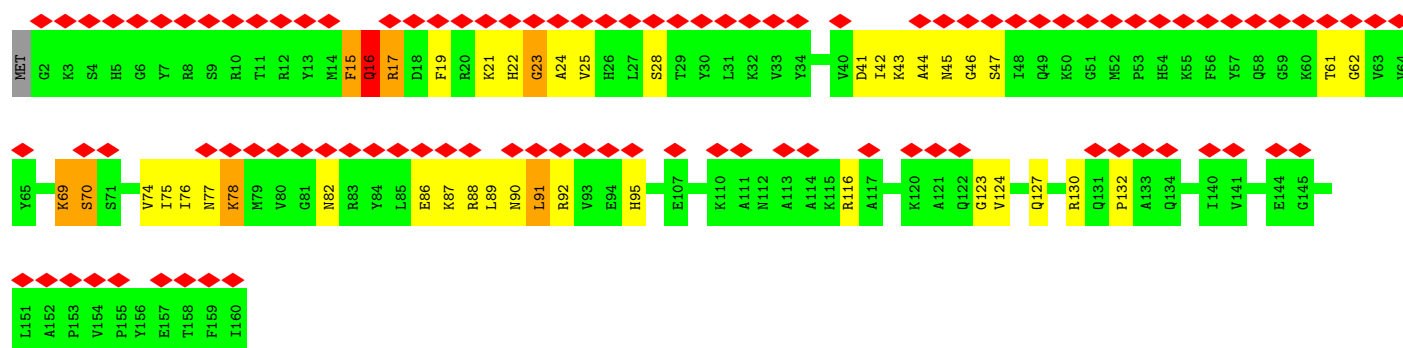


• Molecule 38: Probable metalloprotease ARX1



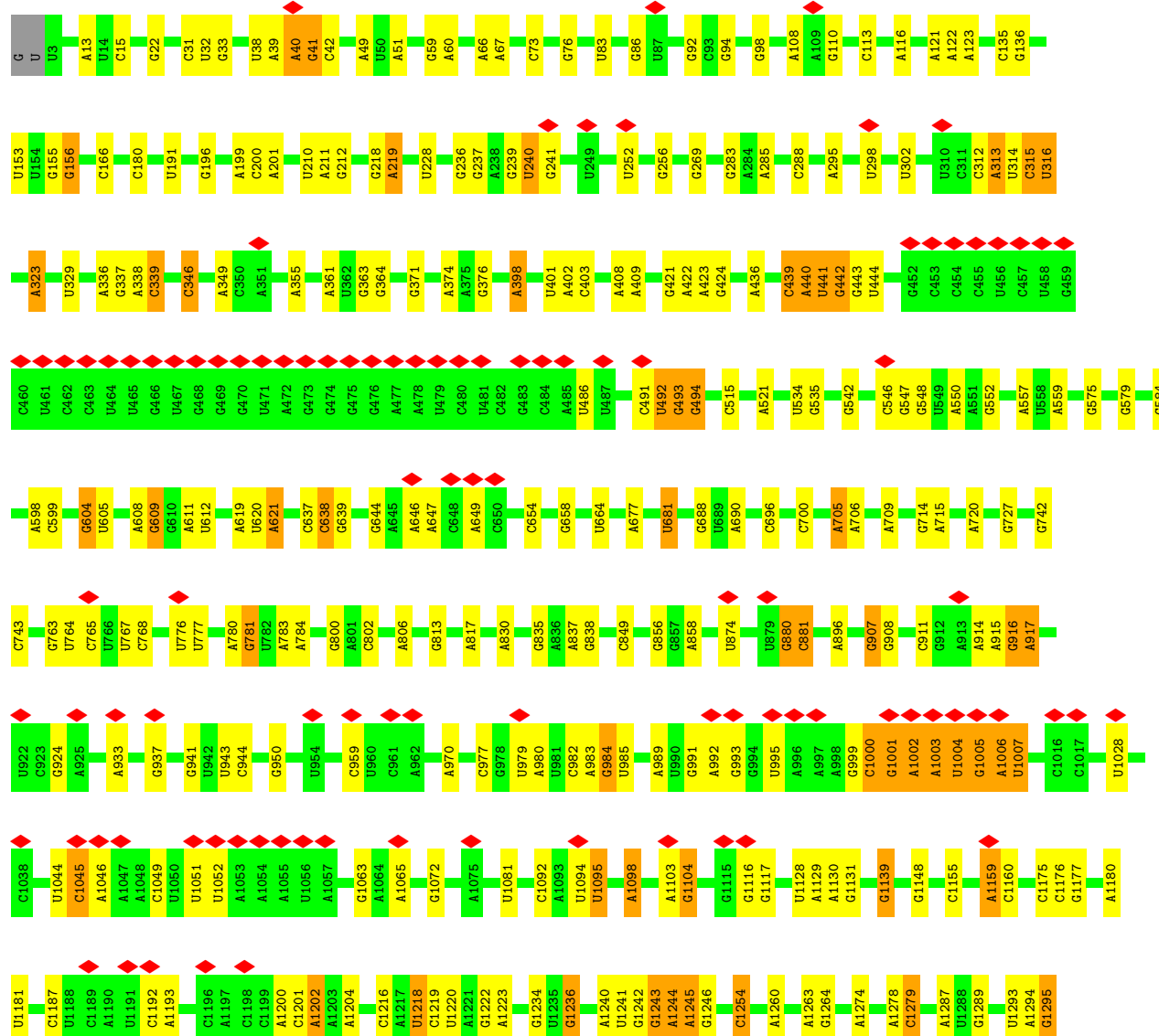
• Molecule 39: 60S ribosomal protein L21-A

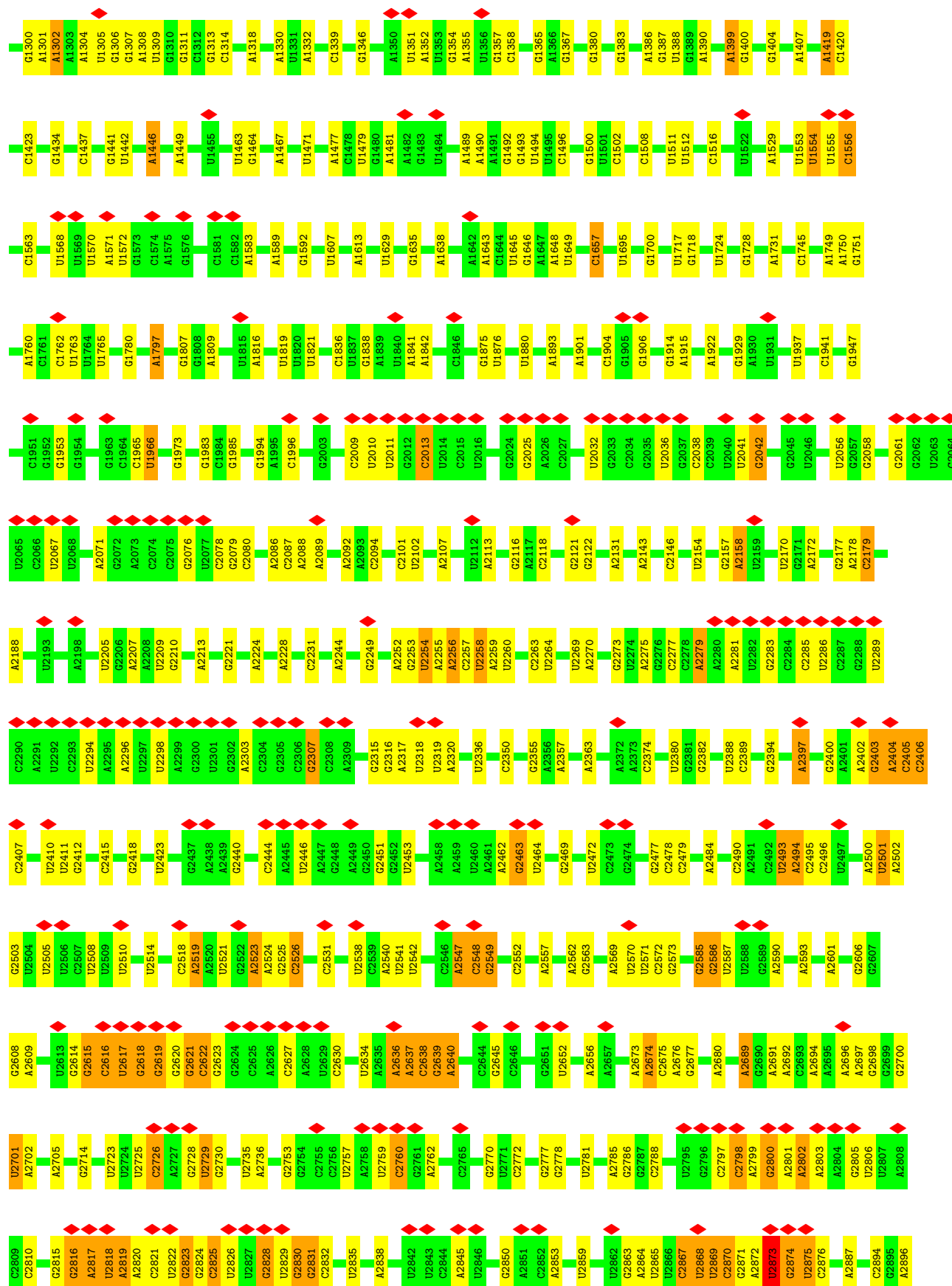
Chain T: 

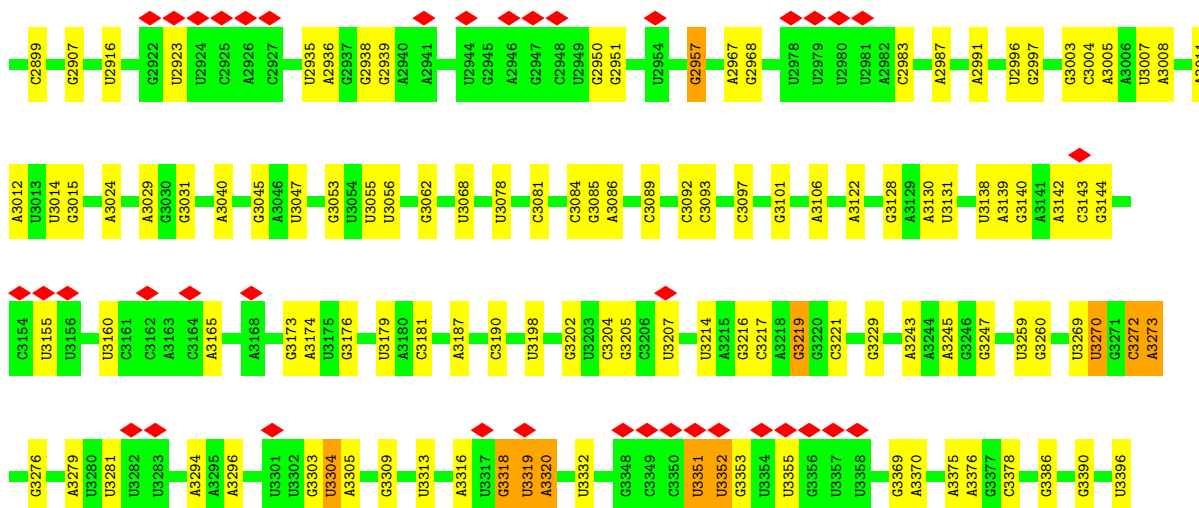


• Molecule 40: 25S ribosomal RNA

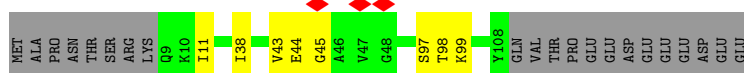
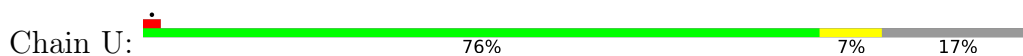
Chain x: 







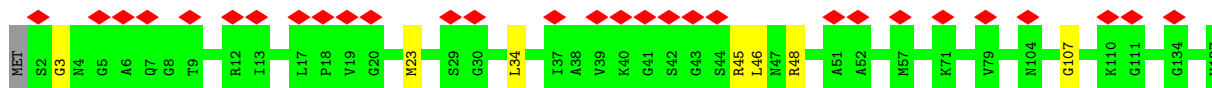
• Molecule 41: 60S ribosomal protein L22-A



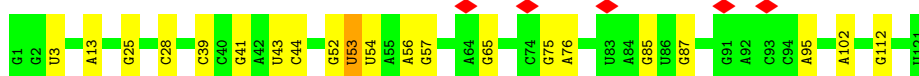
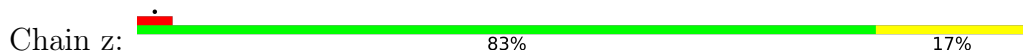
• Molecule 42: 5.8S ribosomal RNA



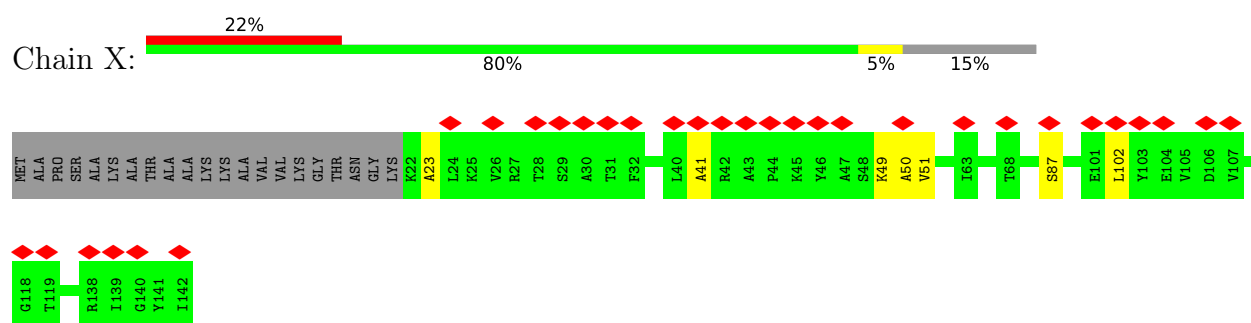
• Molecule 43: 60S ribosomal protein L23-A



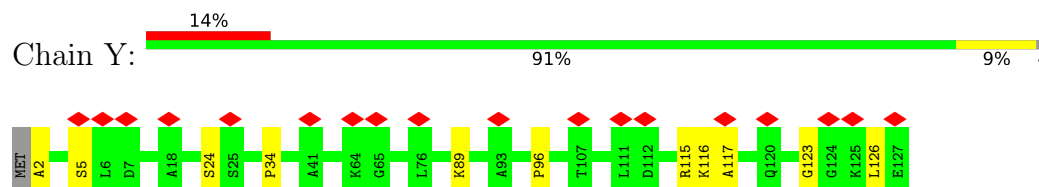
• Molecule 44: 5S ribosomal RNA



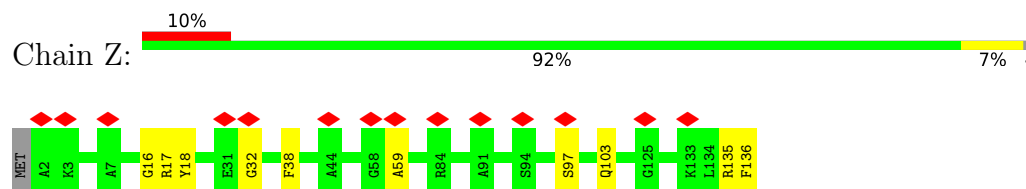
• Molecule 45: 60S ribosomal protein L25



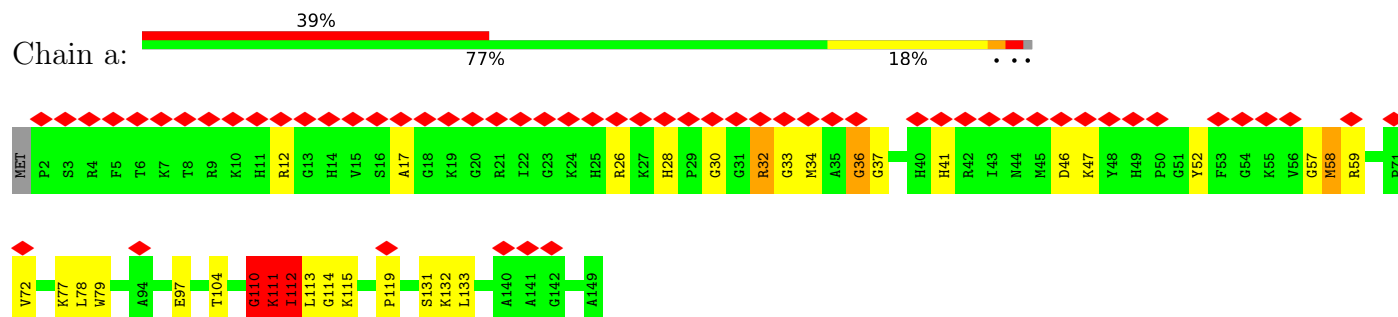
- Molecule 46: 60S ribosomal protein L26-A



- Molecule 47: 60S ribosomal protein L27-A



- Molecule 48: 60S ribosomal protein L28



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15749	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	TVIPS TEMCAM-F816 (8k x 8k)	Depositor
Maximum map value	1.479	Depositor
Minimum map value	-0.721	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.045	Depositor
Recommended contour level	0.3	Depositor
Map size ($\text{\AA}$)	827.6, 827.6, 827.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.069, 2.069, 2.069	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.61	2/1006 (0.2%)	1.01	3/1256 (0.2%)
2	c	0.29	0/386	0.81	0/481
3	B	0.33	0/1542	0.94	3/1926 (0.2%)
4	d	0.31	0/434	0.91	0/541
5	C	0.34	0/1442	0.91	1/1801 (0.1%)
6	e	0.29	0/506	0.85	0/631
7	D	0.31	0/1182	0.86	0/1476
8	f	0.86	1/422 (0.2%)	1.33	4/526 (0.8%)
9	E	0.80	5/620 (0.8%)	1.59	8/772 (1.0%)
10	g	0.28	0/446	0.86	0/556
11	F	0.34	0/886	0.94	2/1106 (0.2%)
12	h	0.30	0/474	0.91	0/591
13	G	0.32	0/930	0.86	0/1161
14	i	0.29	0/394	0.83	0/491
15	H	0.28	0/762	0.86	0/951
16	j	0.89	1/346 (0.3%)	1.07	4/431 (0.9%)
17	I	0.33	0/866	0.89	0/1081
18	k	0.35	0/306	0.94	2/381 (0.5%)
19	J	0.91	0/674	1.55	6/841 (0.7%)
20	l	0.30	0/198	0.90	0/246
21	K	0.35	0/506	0.94	0/631
22	m	0.30	0/894	0.86	0/1116
23	L	0.33	0/770	0.92	0/961
24	n	0.31	0/846	0.91	0/1056
25	M	0.29	0/542	0.86	0/676
26	o	0.97	11/1386 (0.8%)	1.42	25/1731 (1.4%)
27	N	0.35	0/810	0.97	1/1011 (0.1%)
28	p	0.28	0/362	0.81	0/451
29	O	0.36	0/786	1.10	2/981 (0.2%)
30	q	1.54	0/1950	1.62	25/2436 (1.0%)
31	P	0.30	0/730	0.88	0/911
32	r	0.90	1/1276 (0.1%)	1.68	31/1553 (2.0%)
33	Q	0.31	0/738	0.85	0/921
34	s	0.50	14/8001 (0.2%)	0.99	28/9992 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	R	0.36	0/750	0.98	1/936 (0.1%)
36	t	0.53	0/250	1.01	0/311
37	S	0.30	0/686	0.91	0/856
38	u	1.56	0/1483	1.57	12/1840 (0.7%)
39	T	0.77	4/634 (0.6%)	1.17	5/791 (0.6%)
40	x	0.15	2/81221 (0.0%)	0.40	170/126638 (0.1%)
41	U	0.32	0/398	0.95	0/496
42	y	0.06	0/3743	0.06	0/5828
43	V	0.37	0/542	0.92	0/676
44	z	0.06	0/2880	0.05	0/4487
45	X	0.30	0/482	0.85	0/601
46	Y	0.30	0/502	0.87	0/626
47	Z	0.31	0/538	0.89	0/671
48	a	1.27	5/590 (0.8%)	1.12	6/736 (0.8%)
All	All	0.39	46/128118 (0.0%)	0.65	339/187166 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
3	B	0	2
8	f	0	2
9	E	0	1
19	J	0	1
26	o	0	1
32	r	0	3
34	s	0	11
36	t	0	1
39	T	0	3
48	a	0	1
All	All	0	27

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	a	111	LYS	N-CA	22.03	1.74	1.46
48	a	110	GLY	C-N	16.68	1.57	1.33
16	j	39	TYR	C-O	-13.49	1.06	1.24
8	f	100	ILE	C-N	12.64	1.50	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	o	44	ALA	CA-C	11.40	1.68	1.52
9	E	67	GLY	CA-C	-10.96	1.36	1.51
26	o	120	GLN	CA-C	10.25	1.64	1.52
34	s	1480	ILE	CA-C	10.18	1.62	1.53
39	T	16	GLN	N-CA	9.60	1.58	1.46
32	r	111	GLU	C-N	9.27	1.46	1.33
34	s	859	LYS	CA-C	-8.89	1.40	1.52
48	a	112	ILE	N-CA	-8.69	1.35	1.46
1	A	207	VAL	N-CA	8.43	1.56	1.46
34	s	2362	ALA	CA-C	-7.82	1.47	1.52
26	o	118	PHE	N-CA	7.59	1.55	1.46
26	o	120	GLN	C-O	7.42	1.32	1.23
26	o	118	PHE	CA-C	7.36	1.62	1.52
39	T	17	ARG	CA-C	-7.31	1.43	1.52
26	o	44	ALA	N-CA	7.22	1.55	1.46
34	s	2362	ALA	C-O	7.18	1.36	1.25
9	E	67	GLY	C-N	7.04	1.41	1.33
34	s	630	ASN	CA-C	-7.00	1.43	1.52
26	o	44	ALA	C-O	6.96	1.32	1.24
34	s	1480	ILE	C-N	6.91	1.41	1.33
26	o	56	GLY	C-O	6.80	1.33	1.23
26	o	247	ARG	CA-C	6.78	1.61	1.52
34	s	1479	LEU	C-N	6.60	1.39	1.33
39	T	15	PHE	CA-C	6.16	1.61	1.52
34	s	1409	PRO	CA-C	-6.04	1.43	1.52
34	s	2361	LEU	C-O	-6.04	1.17	1.24
34	s	576	SER	C-N	6.02	1.41	1.33
40	x	2638	C	O3'-P	-5.98	1.52	1.61
34	s	2362	ALA	C-N	-5.88	1.25	1.33
9	E	68	PRO	CA-C	5.74	1.59	1.52
34	s	2363	ALA	C-O	-5.72	1.16	1.24
1	A	207	VAL	CA-C	5.71	1.59	1.52
26	o	247	ARG	N-CA	5.57	1.53	1.46
34	s	1015	ARG	C-N	5.49	1.41	1.33
34	s	630	ASN	C-N	5.43	1.41	1.33
40	x	2781	U	O3'-P	-5.43	1.53	1.61
9	E	43	LEU	CA-C	5.25	1.59	1.52
48	a	111	LYS	CA-C	-5.25	1.45	1.52
48	a	110	GLY	CA-C	5.22	1.59	1.51
9	E	82	ARG	CA-C	-5.09	1.47	1.53
39	T	16	GLN	CA-C	5.05	1.59	1.52
26	o	143	LEU	C-O	-5.01	1.17	1.24

All (339) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	s	858	GLU	O-C-N	-25.52	88.65	122.59
9	E	67	GLY	CA-C-N	-20.95	96.46	120.13
9	E	67	GLY	C-N-CA	-20.95	96.46	120.13
40	x	494	G	C4'-C3'-O3'	17.76	136.04	109.40
40	x	2870	C	C4'-C3'-O3'	17.26	135.28	109.40
40	x	2403	G	C4'-C3'-O3'	-15.79	89.32	113.00
40	x	2617	U	C4'-C3'-O3'	-15.74	85.79	109.40
40	x	2874	G	C4'-C3'-O3'	-15.55	89.67	113.00
32	r	88	ILE	N-CA-C	-15.40	96.72	110.74
40	x	440	A	P-O5'-C5'	15.15	143.62	120.90
40	x	2637	A	C4'-C3'-O3'	-15.10	90.34	113.00
40	x	2319	U	C2'-C3'-O3'	-14.89	91.36	113.70
29	O	59	ARG	N-CA-C	14.62	128.39	110.41
34	s	1015	ARG	O-C-N	-14.62	106.44	121.93
40	x	494	G	P-O5'-C5'	14.51	142.66	120.90
8	f	100	ILE	O-C-N	-14.28	106.41	122.69
40	x	2873	U	P-O5'-C5'	14.18	142.16	120.90
40	x	2873	U	C5'-C4'-C3'	14.07	137.10	116.00
40	x	2638	C	P-O3'-C3'	-13.79	99.52	120.20
40	x	1000	C	C4'-C3'-O3'	13.71	129.96	109.40
40	x	2819	A	C4'-C3'-O3'	13.47	133.21	113.00
40	x	2867	C	C4'-C3'-O3'	13.45	133.17	113.00
40	x	1001	G	C4'-C3'-O3'	13.31	129.37	109.40
9	E	67	GLY	N-CA-C	-13.15	85.50	112.34
40	x	442	G	C4'-C3'-O3'	13.14	132.72	113.00
38	u	389	PRO	N-CA-C	12.79	130.34	114.35
40	x	2873	U	C5'-C4'-O4'	-12.71	90.73	109.80
40	x	2873	U	C2'-C3'-O3'	12.33	132.19	113.70
40	x	2874	G	O5'-C5'-C4'	12.28	129.91	111.50
32	r	306	LEU	N-CA-C	-12.13	96.60	111.40
32	r	442	ALA	N-CA-C	-12.09	95.64	111.24
32	r	421	ASN	N-CA-C	-12.08	97.62	111.03
40	x	1001	G	C2'-C3'-O3'	-12.03	91.45	109.50
40	x	2638	C	C4'-C3'-O3'	11.78	130.68	113.00
40	x	1218	U	P-O5'-C5'	11.59	138.28	120.90
40	x	1002	A	P-O5'-C5'	11.40	138.00	120.90
40	x	2259	A	C4'-C3'-O3'	11.23	129.84	113.00
48	a	110	GLY	CA-C-O	-11.02	101.40	120.57
40	x	1130	A	C4'-C3'-O3'	11.01	129.52	113.00
19	J	54	VAL	N-CA-C	10.97	120.29	111.62
5	C	187	LEU	N-CA-C	-10.88	96.17	110.53
40	x	1554	U	C4'-C3'-O3'	10.59	125.29	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	x	2254	U	C4'-C3'-O3'	10.58	128.87	113.00
40	x	2587	U	C4'-C3'-O3'	-10.56	97.16	113.00
26	o	247	ARG	N-CA-C	10.54	133.26	110.80
40	x	2319	U	C4'-C3'-O3'	10.28	128.41	113.00
26	o	119	GLY	CA-C-N	10.26	139.56	122.33
26	o	119	GLY	C-N-CA	10.26	139.56	122.33
40	x	2256	A	C4'-C3'-O3'	-10.21	97.69	113.00
40	x	2617	U	C2'-C3'-O3'	10.08	124.63	109.50
19	J	7	ASN	CA-C-N	10.06	132.42	119.84
19	J	7	ASN	C-N-CA	10.06	132.42	119.84
40	x	2869	U	C2'-C3'-O3'	10.02	128.73	113.70
40	x	315	C	C2'-C3'-O3'	9.81	128.42	113.70
32	r	540	LEU	N-CA-C	-9.76	100.60	111.14
48	a	110	GLY	CA-C-N	9.71	140.08	121.54
48	a	110	GLY	C-N-CA	9.71	140.08	121.54
40	x	2817	A	C4'-C3'-O3'	-9.70	98.44	113.00
26	o	119	GLY	O-C-N	9.60	135.18	122.70
32	r	694	LEU	N-CA-C	-9.52	100.86	111.14
40	x	2585	G	C4'-C3'-O3'	-9.51	95.13	109.40
40	x	2639	G	P-O5'-C5'	9.51	135.16	120.90
26	o	237	MET	N-CA-C	-9.45	95.86	111.37
40	x	2638	C	C2'-C3'-O3'	-9.45	99.53	113.70
40	x	983	A	C4'-C3'-O3'	-9.44	95.24	109.40
32	r	464	LEU	N-CA-C	-9.39	100.69	113.18
40	x	2616	C	C4'-C3'-O3'	-9.34	98.98	113.00
40	x	1131	G	O4'-C4'-C3'	-9.31	94.69	104.00
40	x	315	C	P-O5'-C5'	-9.07	107.30	120.90
34	s	1408	ARG	CA-C-N	9.06	131.17	119.84
34	s	1408	ARG	C-N-CA	9.06	131.17	119.84
34	s	630	ASN	CA-C-N	-9.04	104.27	121.54
34	s	630	ASN	C-N-CA	-9.04	104.27	121.54
40	x	440	A	C4'-C3'-O3'	-8.95	99.58	113.00
34	s	1480	ILE	N-CA-C	8.92	120.03	107.37
40	x	2816	G	C2'-C3'-O3'	-8.91	96.14	109.50
40	x	2874	G	P-O5'-C5'	-8.90	107.54	120.90
40	x	1130	A	O3'-P-O5'	8.90	117.35	104.00
32	r	631	ALA	N-CA-C	-8.68	101.77	111.14
40	x	2404	A	C5'-C4'-C3'	8.65	128.17	115.20
39	T	16	GLN	N-CA-C	8.58	129.08	110.80
40	x	2818	U	O4'-C4'-C3'	-8.57	95.43	104.00
40	x	2210	G	C4'-C3'-O3'	8.52	125.78	113.00
40	x	2586	G	C4'-C3'-O3'	8.46	125.69	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	255	TRP	CA-C-N	8.46	130.13	120.06
3	B	255	TRP	C-N-CA	8.46	130.13	120.06
39	T	16	GLN	CA-C-N	8.46	137.69	121.54
39	T	16	GLN	C-N-CA	8.46	137.69	121.54
40	x	313	A	P-O3'-C3'	-8.39	107.62	120.20
30	q	55	ILE	N-CA-C	8.38	120.25	108.93
40	x	313	A	O3'-P-O5'	8.31	116.47	104.00
9	E	68	PRO	N-CA-C	-8.30	97.02	110.55
26	o	44	ALA	N-CA-C	8.25	128.37	110.80
40	x	2873	U	P-O3'-C3'	8.18	132.47	120.20
32	r	294	GLN	N-CA-C	-8.17	102.32	111.14
34	s	1479	LEU	O-C-N	-8.16	113.67	123.29
32	r	127	LEU	N-CA-C	-8.09	102.42	111.07
26	o	117	LYS	CA-C-N	8.07	136.96	121.54
26	o	117	LYS	C-N-CA	8.07	136.96	121.54
40	x	494	G	O5'-C5'-C4'	-8.07	99.60	111.70
40	x	2639	G	O5'-C5'-C4'	-7.98	99.53	111.50
32	r	150	ILE	N-CA-C	-7.97	102.67	110.72
40	x	494	G	C2'-C3'-O3'	-7.97	97.55	109.50
40	x	1003	A	C4'-C3'-O3'	-7.97	101.05	113.00
40	x	1002	A	O5'-C5'-C4'	-7.96	99.56	111.50
40	x	1219	C	C2'-C3'-O3'	-7.92	101.81	113.70
32	r	650	LEU	N-CA-C	-7.92	102.23	111.03
40	x	440	A	O5'-C5'-C4'	-7.91	99.63	111.50
40	x	440	A	O5'-P-OP2	7.89	131.68	108.00
40	x	2316	G	C4'-C3'-O3'	7.89	124.83	113.00
32	r	398	ARG	N-CA-C	-7.88	102.38	110.97
40	x	1003	A	O3'-P-O5'	-7.87	92.20	104.00
40	x	2256	A	C2'-C3'-O3'	7.78	125.36	113.70
40	x	2209	U	C2'-C3'-O3'	7.74	121.12	109.50
40	x	1218	U	O5'-C5'-C4'	-7.73	99.90	111.50
40	x	2870	C	C2'-C3'-O3'	-7.71	97.94	109.50
30	q	287	GLY	CA-C-N	7.71	130.01	120.22
30	q	287	GLY	C-N-CA	7.71	130.01	120.22
32	r	278	SER	N-CA-C	-7.70	102.82	111.14
34	s	582	SER	CA-C-N	7.69	130.59	120.28
34	s	582	SER	C-N-CA	7.69	130.59	120.28
40	x	443	G	C4'-C3'-O3'	7.69	124.54	113.00
26	o	148	ALA	N-CA-C	-7.68	102.84	111.14
16	j	38	GLY	O-C-N	-7.63	112.78	122.70
30	q	306	ILE	N-CA-C	7.63	118.22	110.82
40	x	2617	U	P-O5'-C5'	7.59	132.28	120.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	x	315	C	C5'-C4'-O4'	-7.58	98.43	109.80
38	u	385	GLN	N-CA-C	7.54	119.14	111.07
26	o	120	GLN	N-CA-C	7.54	122.03	108.69
40	x	442	G	C2'-C3'-O3'	-7.46	102.51	113.70
40	x	985	U	C4'-C3'-O3'	-7.43	101.86	113.00
40	x	2207	A	C4'-C3'-O3'	7.43	124.14	113.00
38	u	253	GLY	N-CA-C	7.42	121.47	112.49
26	o	93	ILE	N-CA-C	-7.41	103.34	112.76
40	x	2818	U	O5'-C5'-C4'	7.41	122.61	111.50
27	N	97	SER	N-CA-C	7.40	119.78	107.20
40	x	2868	U	C2'-C3'-O3'	-7.36	102.65	113.70
32	r	86	GLN	N-CA-C	-7.35	102.87	111.03
40	x	2640	A	P-O5'-C5'	-7.29	109.96	120.90
40	x	1131	G	C2'-C3'-O3'	-7.29	102.77	113.70
40	x	493	G	O3'-P-O5'	7.29	114.93	104.00
40	x	2318	U	C2'-C3'-O3'	-7.27	102.80	113.70
32	r	115	LEU	N-CA-C	-7.26	103.08	112.23
26	o	47	MET	N-CA-C	-7.23	103.40	111.28
40	x	493	G	C2'-C3'-O3'	-7.21	102.89	113.70
40	x	2585	G	P-O5'-C5'	7.17	131.66	120.90
32	r	147	GLU	N-CA-C	-7.14	103.58	111.36
40	x	2818	U	O3'-P-O5'	7.14	114.70	104.00
40	x	2615	G	C4'-C3'-O3'	7.13	123.69	113.00
40	x	2405	C	O5'-C5'-C4'	-7.04	101.15	111.70
34	s	630	ASN	N-CA-C	-7.03	95.82	110.80
40	x	2404	A	O5'-C5'-C4'	7.03	122.25	111.70
32	r	542	LYS	N-CA-C	-7.00	103.65	111.28
40	x	440	A	O5'-P-OP1	-6.96	87.12	108.00
40	x	2258	U	C4'-C3'-O3'	6.96	123.43	113.00
32	r	152	SER	N-CA-C	-6.96	103.31	111.03
40	x	443	G	O3'-P-O5'	6.91	114.36	104.00
40	x	444	U	P-O5'-C5'	6.85	131.18	120.90
38	u	60	THR	CA-C-N	-6.85	115.93	120.24
38	u	60	THR	C-N-CA	-6.85	115.93	120.24
19	J	101	ASN	N-CA-C	-6.83	99.85	109.69
19	J	21	ILE	N-CA-C	6.81	117.55	106.72
40	x	2823	G	C4'-C3'-O3'	-6.79	102.81	113.00
39	T	25	VAL	N-CA-C	-6.76	105.93	112.29
40	x	1555	U	C4'-C3'-O3'	6.76	123.14	113.00
34	s	578	ASP	N-CA-C	-6.67	96.60	110.80
40	x	2874	G	C2'-C3'-O3'	-6.64	103.74	113.70
32	r	222	ALA	N-CA-C	-6.64	103.97	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	o	120	GLN	CA-C-O	6.62	128.43	120.28
26	o	239	SER	N-CA-C	-6.62	103.76	110.97
34	s	1480	ILE	O-C-N	-6.61	115.38	122.45
1	A	177	LYS	CA-C-N	6.58	128.07	119.84
1	A	177	LYS	C-N-CA	6.58	128.07	119.84
30	q	42	GLY	N-CA-C	-6.58	106.85	115.47
32	r	227	ARG	N-CA-C	-6.58	104.10	111.28
40	x	2320	A	C2'-C3'-O3'	-6.56	103.86	113.70
40	x	2563	G	C4'-C3'-O3'	-6.54	103.19	113.00
40	x	1130	A	C2'-C3'-O3'	-6.53	103.90	113.70
40	x	1000	C	C2'-C3'-O3'	-6.53	99.70	109.50
32	r	129	GLU	N-CA-C	-6.48	97.00	110.80
26	o	94	SER	N-CA-C	-6.46	97.04	110.80
40	x	2820	A	C2'-C3'-O3'	-6.45	104.03	113.70
40	x	2270	A	C2'-C3'-O3'	-6.44	99.84	109.50
40	x	2618	G	O5'-C5'-C4'	-6.39	102.11	111.70
30	q	255	SER	CA-C-N	6.39	129.48	120.28
30	q	255	SER	C-N-CA	6.39	129.48	120.28
40	x	2818	U	N1-C1'-C2'	-6.38	102.44	112.00
40	x	441	U	O5'-C5'-C4'	-6.37	101.95	111.50
40	x	2639	G	C4'-C3'-O3'	6.35	122.53	113.00
34	s	1019	VAL	CA-C-N	6.34	133.64	121.54
34	s	1019	VAL	C-N-CA	6.34	133.64	121.54
40	x	1004	U	C5'-C4'-C3'	6.32	125.49	116.00
26	o	43	ARG	CA-C-N	6.31	133.60	121.54
26	o	43	ARG	C-N-CA	6.31	133.60	121.54
40	x	1131	G	P-O5'-C5'	6.29	130.33	120.90
40	x	2403	G	O3'-P-O5'	-6.28	94.58	104.00
40	x	2406	C	C4'-C3'-O3'	-6.28	103.59	113.00
40	x	2403	G	P-O3'-C3'	6.27	129.61	120.20
26	o	56	GLY	CA-C-O	6.23	126.80	120.45
40	x	1219	C	C4'-C3'-O3'	6.23	122.34	113.00
40	x	441	U	C4'-C3'-O3'	6.21	122.32	113.00
40	x	2818	U	OP2-P-O3'	-6.18	89.47	108.00
30	q	319	HIS	CA-C-N	6.17	129.70	120.31
30	q	319	HIS	C-N-CA	6.17	129.70	120.31
40	x	2616	C	C2'-C3'-O3'	6.17	122.95	113.70
34	s	630	ASN	CA-C-O	-6.16	111.70	120.51
32	r	425	ARG	N-CA-C	-6.16	104.26	110.97
35	R	133	LYS	O-C-N	6.15	127.81	121.79
40	x	2403	G	N9-C1'-C2'	6.13	121.19	112.00
38	u	246	ARG	CA-C-N	6.12	128.85	120.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	u	246	ARG	C-N-CA	6.12	128.85	120.35
9	E	82	ARG	N-CA-C	-6.11	103.34	111.96
32	r	479	ASN	N-CA-C	-6.09	104.55	111.07
40	x	2865	U	C4'-C3'-O3'	6.09	122.14	113.00
40	x	2819	A	O5'-C5'-C4'	-6.08	102.37	111.50
40	x	2825	C	C5'-C4'-C3'	6.07	125.10	116.00
40	x	2400	G	C4'-C3'-O3'	-6.06	103.91	113.00
40	x	2586	G	O4'-C4'-C3'	6.05	110.05	104.00
16	j	40	PRO	N-CA-C	-6.05	106.30	113.86
30	q	307	ASN	N-CA-C	-6.05	104.75	111.71
30	q	337	GLY	CA-C-N	6.04	129.50	120.31
30	q	337	GLY	C-N-CA	6.04	129.50	120.31
40	x	2320	A	C5'-C4'-C3'	6.03	125.04	116.00
26	o	241	TYR	N-CA-C	6.02	117.52	111.07
40	x	2818	U	C2'-C3'-O3'	-6.00	104.70	113.70
40	x	2405	C	O3'-P-O5'	-6.00	95.01	104.00
40	x	2637	A	C2'-C3'-O3'	6.00	122.69	113.70
16	j	5	THR	CA-C-N	-5.99	112.16	120.25
16	j	5	THR	C-N-CA	-5.99	112.16	120.25
30	q	74	PRO	N-CA-C	-5.99	101.79	111.14
8	f	104	PRO	CA-C-N	5.96	132.92	121.54
8	f	104	PRO	C-N-CA	5.96	132.92	121.54
38	u	62	PRO	N-CA-C	5.93	121.35	113.40
40	x	2586	G	C2'-C3'-O3'	5.93	122.59	113.70
40	x	493	G	C4'-C3'-O3'	5.93	121.89	113.00
40	x	2209	U	C4'-C3'-O3'	-5.84	100.65	109.40
40	x	1216	C	C4'-C3'-O3'	-5.83	104.25	113.00
40	x	2146	C	P-O3'-C3'	-5.83	111.46	120.20
30	q	78	THR	N-CA-C	-5.78	100.47	109.72
34	s	859	LYS	CA-C-N	-5.76	111.71	121.85
34	s	859	LYS	C-N-CA	-5.76	111.71	121.85
32	r	543	TRP	N-CA-C	-5.76	104.92	111.14
1	A	189	TYR	N-CA-C	-5.76	103.53	110.44
40	x	2819	A	O5'-P-OP2	5.75	125.26	108.00
48	a	111	LYS	N-CA-C	5.75	123.04	110.80
40	x	2869	U	P-O5'-C5'	5.73	129.50	120.90
40	x	1554	U	P-O3'-C3'	5.73	128.79	120.20
19	J	110	ILE	N-CA-C	-5.72	104.98	113.39
40	x	2876	C	C4'-C3'-O3'	-5.71	100.83	109.40
34	s	906	ARG	N-CA-C	-5.68	106.25	112.72
40	x	1220	U	C2'-C3'-O3'	-5.67	101.00	109.50
40	x	439	C	O3'-P-O5'	5.66	112.49	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	x	1003	A	N9-C1'-C2'	-5.66	103.52	112.00
26	o	157	ILE	N-CA-C	5.65	121.10	109.34
40	x	2315	G	C4'-C3'-O3'	5.62	121.44	113.00
48	a	111	LYS	CA-C-N	-5.62	111.85	121.97
48	a	111	LYS	C-N-CA	-5.62	111.85	121.97
40	x	2864	A	C2'-C3'-O3'	-5.59	105.31	113.70
40	x	2863	G	C4'-C3'-O3'	-5.58	104.63	113.00
30	q	426	ILE	N-CA-C	-5.58	100.37	108.17
8	f	106	ASN	N-CA-C	-5.57	105.11	111.07
40	x	2869	U	C4'-C3'-O3'	-5.54	104.69	113.00
40	x	2269	U	C4'-C3'-O3'	5.53	117.70	109.40
30	q	310	GLY	N-CA-C	-5.53	106.02	115.08
38	u	253	GLY	CA-C-N	5.52	132.09	121.54
38	u	253	GLY	C-N-CA	5.52	132.09	121.54
40	x	1002	A	C4'-C3'-O3'	-5.52	104.72	113.00
9	E	43	LEU	N-CA-C	5.51	119.72	112.89
40	x	2868	U	P-O5'-C5'	-5.51	112.63	120.90
26	o	92	LYS	O-C-N	5.51	127.96	122.12
30	q	335	ARG	CA-C-N	5.51	129.76	120.29
30	q	335	ARG	C-N-CA	5.51	129.76	120.29
40	x	2618	G	P-O5'-C5'	5.51	129.16	120.90
34	s	591	HIS	CA-C-N	5.47	124.71	120.33
34	s	591	HIS	C-N-CA	5.47	124.71	120.33
40	x	313	A	C4'-C3'-O3'	5.46	117.59	109.40
40	x	2207	A	C2'-C3'-O3'	-5.46	105.51	113.70
40	x	2873	U	O4'-C4'-C3'	-5.46	98.54	104.00
40	x	2617	U	N1-C1'-C2'	-5.45	105.82	114.00
32	r	128	LYS	N-CA-C	-5.45	106.70	113.19
40	x	2269	U	P-O5'-C5'	5.44	129.06	120.90
30	q	391	SER	CA-C-N	5.42	128.55	120.31
30	q	391	SER	C-N-CA	5.42	128.55	120.31
30	q	142	HIS	CA-C-N	5.42	127.10	120.22
30	q	142	HIS	C-N-CA	5.42	127.10	120.22
34	s	592	VAL	CA-C-O	-5.42	115.06	118.69
40	x	2875	U	C4'-C3'-O3'	5.42	121.13	113.00
40	x	1220	U	C4'-C3'-O3'	-5.40	101.30	109.40
40	x	1218	U	C4'-C3'-O3'	5.36	121.04	113.00
39	T	69	LYS	N-CA-C	-5.34	104.35	111.24
30	q	53	GLY	N-CA-C	-5.33	107.17	113.99
40	x	2819	A	N9-C1'-C2'	5.33	119.99	112.00
40	x	2319	U	C5'-C4'-O4'	5.32	117.78	109.80
34	s	1465	ARG	N-CA-C	-5.32	99.47	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	u	233	SER	CA-C-N	-5.32	113.21	120.44
38	u	233	SER	C-N-CA	-5.32	113.21	120.44
34	s	1467	SER	CA-C-N	5.30	131.67	121.54
34	s	1467	SER	C-N-CA	5.30	131.67	121.54
40	x	439	C	C4'-C3'-O3'	-5.30	105.05	113.00
40	x	1005	G	P-O5'-C5'	5.30	128.84	120.90
40	x	1004	U	P-O5'-C5'	5.29	128.84	120.90
40	x	2871	G	C4'-C3'-O3'	5.29	120.93	113.00
40	x	1128	U	C2'-C3'-O3'	-5.29	105.77	113.70
40	x	1005	G	O5'-C5'-C4'	-5.26	103.60	111.50
32	r	419	VAL	N-CA-C	5.26	115.20	107.15
9	E	42	LEU	CA-C-N	5.25	130.33	121.14
9	E	42	LEU	C-N-CA	5.25	130.33	121.14
40	x	2319	U	O4'-C4'-C3'	-5.24	98.76	104.00
40	x	2868	U	O5'-C5'-C4'	5.24	119.36	111.50
40	x	442	G	P-O5'-C5'	-5.23	113.06	120.90
32	r	256	VAL	N-CA-C	-5.20	105.31	110.62
40	x	999	G	C4'-C3'-O3'	-5.20	105.20	113.00
32	r	149	LEU	N-CA-C	5.19	117.84	111.82
26	o	117	LYS	N-CA-C	5.18	117.68	109.96
26	o	46	TYR	N-CA-C	-5.17	105.72	111.36
32	r	478	VAL	N-CA-C	-5.16	105.50	110.72
34	s	2362	ALA	CA-C-O	-5.14	116.03	119.68
40	x	1556	C	C2'-C3'-O3'	-5.14	101.79	109.50
40	x	984	G	C4'-C3'-O3'	5.13	117.10	109.40
18	k	69	LEU	CA-C-N	5.12	123.40	119.66
18	k	69	LEU	C-N-CA	5.12	123.40	119.66
30	q	421	SER	CA-C-N	5.12	128.09	120.31
30	q	421	SER	C-N-CA	5.12	128.09	120.31
26	o	118	PHE	N-CA-C	5.11	121.68	110.80
34	s	1409	PRO	O-C-N	5.11	129.53	122.64
40	x	2825	C	C4'-C3'-O3'	5.11	120.66	113.00
34	s	591	HIS	N-CA-C	-5.10	101.49	108.38
40	x	1554	U	C2'-C3'-O3'	-5.10	101.85	109.50
40	x	2270	A	O5'-C5'-C4'	5.09	119.33	111.70
32	r	113	LYS	N-CA-C	-5.05	106.97	113.23
40	x	1000	C	O3'-P-O5'	5.04	111.56	104.00
40	x	2817	A	P-O3'-C3'	5.04	127.76	120.20
3	B	257	PRO	N-CA-C	-5.04	102.09	112.47
40	x	2865	U	C2'-C3'-O3'	-5.04	106.15	113.70
40	x	2869	U	O4'-C4'-C3'	5.03	109.03	104.00
11	F	95	ILE	CA-C-N	5.03	123.33	119.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	F	95	ILE	C-N-CA	5.03	123.33	119.66
29	O	58	LEU	N-CA-C	5.03	121.51	110.80
26	o	242	ALA	N-CA-C	-5.03	105.80	111.28

There are no chirality outliers.

All (27) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	198	LYS	Peptide
3	B	255	TRP	Peptide
3	B	256	HIS	Peptide
9	E	42	LEU	Mainchain
19	J	8	PRO	Peptide
39	T	16	GLN	Mainchain
39	T	23	GLY	Peptide
39	T	86	GLU	Peptide
48	a	111	LYS	Peptide
8	f	100	ILE	Mainchain
8	f	103	TYR	Peptide
26	o	43	ARG	Mainchain
32	r	111	GLU	Mainchain
32	r	461	GLU	Peptide
32	r	462	ILE	Peptide
34	s	1015	ARG	Mainchain
34	s	1018	ASN	Peptide
34	s	1466	ASP	Peptide
34	s	1479	LEU	Mainchain
34	s	576	SER	Peptide,Mainchain
34	s	578	ASP	Peptide
34	s	628	PHE	Peptide
34	s	858	GLU	Mainchain
34	s	859	LYS	Peptide
34	s	903	SER	Peptide
36	t	17	HIS	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1007	0	310	59	0
2	c	387	0	113	2	0
3	B	1543	0	433	32	0
4	d	435	0	114	3	0
5	C	1443	0	399	24	0
6	e	507	0	135	1	0
7	D	1183	0	325	1	0
8	f	423	0	117	3	0
9	E	622	0	160	3	0
10	g	447	0	121	0	0
11	F	887	0	241	6	0
12	h	475	0	118	1	0
13	G	931	0	242	2	0
14	i	395	0	109	0	0
15	H	763	0	215	3	0
16	j	347	0	104	6	0
17	I	867	0	230	8	0
18	k	307	0	79	1	0
19	J	675	0	191	68	0
20	l	199	0	47	0	0
21	K	507	0	140	19	0
22	m	895	0	257	0	0
23	L	771	0	199	21	0
24	n	847	0	224	2	0
25	M	543	0	145	2	0
26	o	1387	0	358	58	0
27	N	811	0	221	11	0
28	p	363	0	108	1	0
29	O	787	0	214	30	0
30	q	1951	0	540	16	0
31	P	731	0	197	8	0
32	r	1304	0	332	114	0
33	Q	739	0	205	4	0
34	s	8007	0	2136	1	0
35	R	751	0	203	32	0
36	t	251	0	68	0	0
37	S	687	0	175	3	0
38	u	1491	0	399	8	0
39	T	635	0	174	58	0
40	x	72570	0	36462	692	0
41	U	399	0	109	2	0
42	y	3350	0	1696	21	0
43	V	543	0	162	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	z	2576	0	1304	28	0
45	X	483	0	121	1	0
46	Y	503	0	134	3	0
47	Z	539	0	144	3	0
48	a	591	0	176	89	0
All	All	118855	0	50406	1065	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 7.

All (1065) 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)
21:K:100:HIS:C	30:q:246:GLY:CA	1.79	1.54
40:x:705:A:H2	48:a:110:GLY:C	1.03	1.52
48:a:111:LYS:N	48:a:111:LYS:CA	1.74	1.50
23:L:2:ALA:CA	48:a:33:GLY:N	1.74	1.49
40:x:705:A:C2	48:a:110:GLY:C	1.89	1.47
19:J:124:GLY:HA3	40:x:2674:A:N3	1.13	1.46
1:A:132:ASN:CA	40:x:2177:G:O2'	1.68	1.41
40:x:705:A:C2	48:a:111:LYS:N	1.89	1.41
40:x:1129:A:C8	40:x:2828:G:N2	1.90	1.40
40:x:1129:A:C1'	40:x:2828:G:H21	1.34	1.37
26:o:92:LYS:O	26:o:96:ALA:CA	1.70	1.37
40:x:1129:A:C8	40:x:2828:G:C2	2.15	1.35
19:J:124:GLY:CA	40:x:2674:A:N3	1.89	1.35
40:x:1129:A:N9	40:x:2828:G:N2	1.72	1.34
40:x:705:A:H2	48:a:111:LYS:N	1.23	1.32
26:o:236:GLU:O	26:o:239:SER:N	1.62	1.31
40:x:714:G:H2'	48:a:110:GLY:C	1.55	1.30
40:x:1129:A:C1'	40:x:2828:G:N2	1.94	1.29
19:J:22:SER:N	40:x:2675:C:H42	1.31	1.26
29:O:74:ARG:O	40:x:3007:U:C5'	1.83	1.25
26:o:92:LYS:O	26:o:96:ALA:N	1.69	1.24
21:K:100:HIS:C	30:q:246:GLY:HA2	1.48	1.23
40:x:714:G:H2'	48:a:111:LYS:N	1.50	1.23
21:K:100:HIS:O	30:q:246:GLY:CA	1.81	1.23
26:o:91:TYR:O	26:o:94:SER:N	1.71	1.23
39:T:46:GLY:N	40:x:993:G:OP1	1.73	1.21
40:x:2618:G:N2	40:x:2823:G:H5'	1.56	1.20
40:x:41:G:O4'	48:a:37:GLY:HA2	1.38	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:J:22:SER:H	40:x:2675:C:N4	1.37	1.20
21:K:100:HIS:O	30:q:246:GLY:N	1.72	1.20
40:x:2617:U:O2'	40:x:2824:G:C8	1.94	1.18
21:K:100:HIS:CA	30:q:246:GLY:HA3	1.74	1.18
23:L:2:ALA:CA	48:a:33:GLY:CA	2.23	1.17
40:x:41:G:H5'	48:a:37:GLY:CA	1.74	1.16
40:x:714:G:N3	48:a:111:LYS:N	1.94	1.15
40:x:1129:A:O4'	40:x:2828:G:N2	1.78	1.14
29:O:74:ARG:CA	40:x:3008:A:P	2.36	1.13
26:o:29:THR:CA	40:x:1302:A:H61	1.62	1.12
29:O:71:PHE:CA	40:x:2382:G:O2'	1.97	1.11
40:x:67:A:O2'	40:x:315:C:H1'	1.48	1.11
35:R:146:LYS:O	40:x:2092:A:C2	2.03	1.11
27:N:96:ARG:N	40:x:32:U:OP1	1.83	1.10
39:T:44:ALA:CA	40:x:992:A:OP1	1.98	1.10
40:x:2404:A:OP1	40:x:2405:C:N4	1.84	1.10
26:o:224:ILE:CA	26:o:237:MET:CA	2.30	1.09
40:x:714:G:C8	48:a:110:GLY:HA3	1.87	1.09
19:J:141:ARG:CA	44:z:43:U:O3'	2.01	1.09
19:J:140:ARG:C	44:z:43:U:H4'	1.78	1.08
39:T:62:GLY:N	39:T:75:ILE:H	1.51	1.07
29:O:74:ARG:C	40:x:3007:U:H5''	1.80	1.07
19:J:22:SER:CA	40:x:2676:A:N6	2.17	1.07
1:A:129:ALA:N	40:x:2158:A:O2'	1.86	1.07
21:K:100:HIS:C	30:q:246:GLY:HA3	1.62	1.07
1:A:130:SER:C	40:x:2157:G:H21	1.61	1.07
21:K:100:HIS:O	30:q:246:GLY:HA2	1.44	1.07
40:x:714:G:C4	48:a:111:LYS:N	2.23	1.06
29:O:74:ARG:O	40:x:3007:U:H5''	0.89	1.06
39:T:43:LYS:O	39:T:95:HIS:CA	2.03	1.06
29:O:75:ALA:CA	40:x:3007:U:OP1	2.04	1.05
40:x:714:G:C2'	48:a:110:GLY:C	2.29	1.05
35:R:158:GLU:O	35:R:162:ARG:N	1.90	1.03
39:T:62:GLY:CA	39:T:75:ILE:H	1.72	1.03
1:A:131:GLY:HA2	40:x:2157:G:H22	1.20	1.02
32:r:648:ALA:O	32:r:651:GLN:N	1.93	1.02
26:o:236:GLU:C	26:o:239:SER:H	1.68	1.01
23:L:2:ALA:CA	48:a:33:GLY:H	1.52	1.01
26:o:29:THR:C	40:x:1302:A:H61	1.68	1.00
40:x:2618:G:N2	40:x:2823:G:C5'	2.24	1.00
1:A:207:VAL:O	40:x:2967:A:O2'	1.79	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:x:440:A:OP1	40:x:441:U:OP2	1.79	1.00
5:C:187:LEU:N	40:x:1388:U:O4	1.95	1.00
40:x:41:G:H5'	48:a:37:GLY:HA2	1.45	0.99
19:J:124:GLY:CA	40:x:2674:A:C2	2.46	0.98
32:r:225:LEU:O	32:r:228:GLU:C	2.06	0.98
40:x:67:A:H4'	40:x:315:C:O2'	1.62	0.98
19:J:126:ASP:CA	40:x:2674:A:C8	2.48	0.96
40:x:714:G:C2'	48:a:111:LYS:N	2.29	0.96
39:T:44:ALA:N	40:x:992:A:OP1	1.98	0.96
39:T:62:GLY:HA3	39:T:75:ILE:N	1.80	0.96
26:o:236:GLU:O	26:o:239:SER:CA	2.14	0.95
29:O:74:ARG:CA	40:x:3008:A:OP1	2.14	0.95
40:x:2618:G:C5'	40:x:2824:G:O6	2.14	0.95
40:x:41:G:O4'	48:a:37:GLY:CA	2.15	0.94
40:x:2617:U:OP1	40:x:2618:G:OP2	1.86	0.94
32:r:440:VAL:O	32:r:443:ALA:N	1.99	0.94
32:r:145:THR:O	32:r:148:GLU:N	2.00	0.94
32:r:691:GLU:O	32:r:694:LEU:N	2.00	0.94
40:x:714:G:N7	48:a:110:GLY:HA3	1.83	0.94
19:J:149:GLY:N	44:z:57:G:H5'	1.81	0.93
39:T:41:ASP:O	39:T:43:LYS:N	2.00	0.93
1:A:207:VAL:C	40:x:916:G:O6	2.11	0.93
1:A:208:ASP:N	40:x:916:G:O6	2.00	0.93
32:r:440:VAL:O	32:r:442:ALA:N	2.01	0.93
39:T:91:LEU:O	40:x:2723:U:O2'	1.87	0.93
19:J:21:ILE:CA	40:x:2674:A:H61	1.79	0.93
32:r:303:GLY:O	32:r:306:LEU:N	2.01	0.93
40:x:2868:U:O2'	40:x:2869:U:O4'	1.85	0.93
40:x:2725:U:H2'	40:x:2726:C:H5'	1.48	0.93
26:o:29:THR:CA	40:x:1302:A:N6	2.33	0.92
40:x:67:A:HO2'	40:x:315:C:H1'	1.33	0.92
1:A:131:GLY:HA2	40:x:2157:G:N2	1.84	0.91
26:o:91:TYR:C	26:o:94:SER:H	1.78	0.91
40:x:41:G:C5'	48:a:37:GLY:HA2	2.01	0.91
40:x:705:A:N3	48:a:111:LYS:N	2.16	0.91
40:x:2256:A:H3'	40:x:2256:A:N3	1.86	0.90
26:o:91:TYR:O	26:o:94:SER:CA	2.19	0.90
40:x:41:G:C4'	48:a:37:GLY:HA2	2.02	0.90
40:x:2817:A:H2'	40:x:2819:A:H5''	1.54	0.90
1:A:207:VAL:N	40:x:2968:G:OP1	2.04	0.89
40:x:41:G:C5'	48:a:37:GLY:H	1.83	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:x:41:G:C5'	48:a:37:GLY:CA	2.50	0.89
1:A:114:SER:CA	1:A:134:VAL:H	1.81	0.89
40:x:315:C:H5''	40:x:315:C:H6	1.35	0.89
1:A:207:VAL:O	40:x:2415:C:O2'	1.90	0.89
19:J:124:GLY:HA3	40:x:2674:A:C2	2.05	0.89
19:J:22:SER:C	40:x:2676:A:H62	1.82	0.88
21:K:101:SER:N	30:q:246:GLY:HA2	1.87	0.88
1:A:206:PRO:O	1:A:208:ASP:N	2.06	0.88
40:x:2617:U:O2'	40:x:2824:G:H8	1.46	0.88
29:O:73:PHE:O	40:x:3008:A:OP1	1.91	0.87
32:r:276:GLU:O	32:r:279:GLU:N	2.07	0.87
19:J:126:ASP:N	40:x:2674:A:C8	2.43	0.87
40:x:2823:G:O2'	40:x:2825:C:OP2	1.93	0.86
35:R:158:GLU:O	35:R:161:ALA:N	2.08	0.86
39:T:43:LYS:CA	40:x:991:G:O2'	2.23	0.86
40:x:705:A:C2	48:a:110:GLY:O	2.29	0.85
19:J:124:GLY:C	40:x:2674:A:N3	2.34	0.85
40:x:302:U:N3	40:x:314:U:O4	2.09	0.85
39:T:46:GLY:CA	40:x:993:G:OP1	2.23	0.85
40:x:2725:U:C2'	40:x:2726:C:H5'	2.07	0.85
38:u:83:LYS:O	38:u:85:ASN:N	2.09	0.84
1:A:129:ALA:CA	40:x:2158:A:C8	2.60	0.84
40:x:2403:G:O2'	40:x:2404:A:H5'	1.78	0.84
1:A:207:VAL:N	40:x:916:G:O6	2.10	0.84
8:f:2:ALA:N	40:x:3214:U:HO2'	1.74	0.84
3:B:19:ARG:O	40:x:3139:A:OP1	1.94	0.84
39:T:16:GLN:CA	40:x:2757:U:H1'	2.07	0.84
39:T:91:LEU:C	40:x:2723:U:O2'	2.21	0.84
26:o:236:GLU:O	26:o:237:MET:C	2.21	0.83
29:O:58:LEU:H	40:x:1307:G:H5'	1.43	0.83
40:x:2618:G:N2	40:x:2823:G:C4'	2.41	0.83
5:C:187:LEU:CA	40:x:1419:A:N1	2.42	0.83
40:x:2410:U:C4	48:a:36:GLY:HA3	2.10	0.83
40:x:2619:G:H2'	40:x:2620:G:H8	1.42	0.83
40:x:2639:G:C8	40:x:2639:G:OP1	2.31	0.83
32:r:537:ILE:O	32:r:540:LEU:N	2.11	0.82
35:R:146:LYS:O	40:x:2092:A:H2	1.52	0.82
40:x:1129:A:N9	40:x:2828:G:C2	2.37	0.82
40:x:41:G:C5'	48:a:37:GLY:N	2.42	0.82
1:A:129:ALA:CA	40:x:2158:A:H2'	2.09	0.82
40:x:1129:A:H1'	40:x:2828:G:H21	1.39	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:LYS:O	1:A:121:GLY:N	2.12	0.82
40:x:39:A:O2'	40:x:94:G:N2	2.12	0.82
21:K:100:HIS:CA	30:q:246:GLY:CA	2.44	0.82
1:A:115:ASN:CA	1:A:133:TYR:CA	2.58	0.81
35:R:146:LYS:CA	40:x:2092:A:N3	2.44	0.81
40:x:2404:A:OP1	40:x:2405:C:C4	2.33	0.81
40:x:2622:C:H2'	40:x:2623:G:C8	2.15	0.81
26:o:87:GLU:O	26:o:89:ASN:N	2.13	0.81
39:T:62:GLY:CA	39:T:75:ILE:N	2.42	0.81
40:x:315:C:C2'	40:x:316:U:H5'	2.11	0.81
40:x:2618:G:H22	40:x:2823:G:H5'	1.41	0.80
40:x:2619:G:H2'	40:x:2620:G:C8	2.17	0.80
40:x:1243:G:C8	40:x:1244:A:H8	2.00	0.80
19:J:8:PRO:CA	44:z:53:U:H5'	2.11	0.80
23:L:99:HIS:O	40:x:76:G:N2	2.13	0.80
40:x:2638:C:OP1	40:x:2639:G:OP1	2.00	0.80
40:x:2826:U:OP1	40:x:2870:C:N4	2.15	0.80
19:J:21:ILE:CA	40:x:2674:A:N6	2.44	0.80
40:x:2639:G:OP1	40:x:2639:G:H8	1.65	0.80
26:o:90:HIS:O	26:o:94:SER:N	2.15	0.80
29:O:59:ARG:N	40:x:1307:G:H2'	1.97	0.80
1:A:115:ASN:N	1:A:133:TYR:CA	2.45	0.80
39:T:16:GLN:N	40:x:1052:U:H5'	1.97	0.80
19:J:140:ARG:O	44:z:43:U:H4'	1.81	0.79
19:J:106:ILE:O	19:J:125:MET:N	2.14	0.79
21:K:60:VAL:O	40:x:1245:A:N6	2.15	0.79
39:T:47:SER:O	40:x:2757:U:H5''	1.82	0.79
1:A:207:VAL:C	40:x:2415:C:HO2'	1.89	0.79
1:A:130:SER:O	40:x:2157:G:N2	2.16	0.79
3:B:19:ARG:C	40:x:3139:A:OP1	2.25	0.79
40:x:2916:U:O2'	43:V:45:ARG:O	1.99	0.79
1:A:113:VAL:N	1:A:134:VAL:C	2.39	0.79
39:T:45:ASN:C	40:x:993:G:OP1	2.26	0.79
19:J:140:ARG:O	44:z:43:U:O2'	2.00	0.78
35:R:157:GLU:O	35:R:161:ALA:N	2.16	0.78
40:x:41:G:H5'	48:a:37:GLY:N	1.98	0.78
19:J:135:GLY:HA2	44:z:28:C:H4'	1.65	0.78
40:x:714:G:C5	48:a:110:GLY:HA3	2.17	0.78
19:J:22:SER:C	40:x:2676:A:N6	2.40	0.78
34:s:736:GLN:O	34:s:738:LYS:N	2.17	0.78
40:x:1003:A:O2'	40:x:1004:U:H5'	1.82	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:x:2618:G:H5'	40:x:2824:G:O6	1.83	0.78
40:x:440:A:H8	40:x:440:A:P	2.06	0.78
40:x:315:C:H5''	40:x:315:C:C6	2.20	0.77
26:o:29:THR:C	40:x:1302:A:N6	2.42	0.77
40:x:2873:U:H2'	40:x:2875:U:P	2.25	0.77
1:A:130:SER:C	40:x:2157:G:N2	2.40	0.77
32:r:126:GLU:C	32:r:129:GLU:H	1.92	0.77
40:x:2410:U:C4	48:a:36:GLY:CA	2.61	0.77
40:x:2823:G:H5''	40:x:2824:G:OP1	1.84	0.77
40:x:2867:C:H2'	40:x:2868:U:OP1	1.85	0.76
40:x:2802:A:H3'	40:x:2802:A:N3	2.00	0.76
39:T:70:SER:N	40:x:2735:U:O2	2.18	0.76
19:J:105:GLY:N	40:x:2673:A:O3'	2.18	0.76
40:x:2799:A:OP1	40:x:2800:G:H5'	1.86	0.76
40:x:2639:G:H8	40:x:2639:G:P	2.08	0.76
40:x:2618:G:H3'	40:x:2824:G:O6	1.86	0.76
3:B:99:LEU:H	40:x:3003:G:H21	1.32	0.76
40:x:2636:A:N3	40:x:2636:A:H3'	2.01	0.76
40:x:228:U:HO2'	46:Y:2:ALA:N	1.85	0.75
40:x:315:C:O2'	40:x:316:U:H5'	1.85	0.75
40:x:1002:A:C8	40:x:1002:A:H3'	2.22	0.75
40:x:1129:A:C8	40:x:2828:G:N1	2.55	0.75
40:x:40:A:H3'	40:x:40:A:N3	2.00	0.75
19:J:124:GLY:N	40:x:2674:A:C2	2.54	0.75
33:Q:2:GLY:N	40:x:1332:A:HO2'	1.85	0.74
40:x:720:A:N6	48:a:115:LYS:O	2.20	0.74
19:J:22:SER:CA	40:x:2676:A:H62	1.97	0.74
40:x:705:A:N3	48:a:111:LYS:CA	2.50	0.74
40:x:2818:U:H3'	40:x:2818:U:H6	1.53	0.74
29:O:59:ARG:H	40:x:1307:G:H2'	1.52	0.74
39:T:15:PHE:H	40:x:1052:U:P	2.11	0.74
40:x:714:G:H2'	48:a:110:GLY:O	1.86	0.73
19:J:22:SER:CA	40:x:2676:A:H61	1.99	0.73
40:x:67:A:C4'	40:x:315:C:O2'	2.36	0.73
1:A:207:VAL:CA	40:x:916:G:O6	2.37	0.73
40:x:2254:U:H5''	40:x:2254:U:H6	1.54	0.73
1:A:129:ALA:CA	40:x:2158:A:C2'	2.67	0.72
29:O:74:ARG:CA	40:x:3007:U:O3'	2.36	0.72
3:B:14:LEU:C	40:x:3011:A:H61	1.96	0.72
40:x:2618:G:H22	40:x:2823:G:C4'	2.02	0.72
40:x:2697:A:H2'	40:x:2698:G:C8	2.24	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:SER:C	1:A:133:TYR:CA	2.63	0.72
26:o:87:GLU:C	26:o:89:ASN:N	2.43	0.72
1:A:207:VAL:C	40:x:2967:A:O2'	2.32	0.72
35:R:142:ILE:O	40:x:2092:A:H1'	1.90	0.72
19:J:8:PRO:C	44:z:53:U:H5'	2.15	0.72
19:J:149:GLY:N	44:z:56:A:O2'	2.23	0.72
3:B:258:ALA:O	40:x:2394:G:N2	2.21	0.72
21:K:100:HIS:CA	30:q:245:PRO:O	2.38	0.72
40:x:2256:A:OP1	40:x:2257:C:OP2	2.08	0.71
40:x:1004:U:H6	40:x:1004:U:O5'	1.74	0.71
40:x:714:G:H2'	48:a:111:LYS:CA	2.20	0.71
40:x:2622:C:O2'	40:x:2623:G:H5'	1.90	0.71
26:o:144:ARG:O	26:o:145:ASP:O	2.09	0.71
40:x:1449:A:H62	40:x:2355:G:H21	1.38	0.71
19:J:94:ARG:O	19:J:96:PHE:N	2.22	0.71
26:o:17:LEU:O	26:o:19:ASP:N	2.24	0.71
26:o:58:VAL:O	26:o:59:GLU:C	2.34	0.71
3:B:19:ARG:O	40:x:3139:A:P	2.48	0.70
40:x:41:G:H5'	48:a:37:GLY:C	2.15	0.70
40:x:2619:G:O2'	40:x:2620:G:H5'	1.91	0.70
19:J:135:GLY:HA2	44:z:28:C:C4'	2.20	0.70
32:r:126:GLU:O	32:r:129:GLU:N	2.24	0.70
13:G:30:THR:O	40:x:2562:A:N6	2.25	0.70
1:A:206:PRO:C	1:A:208:ASP:H	1.98	0.70
21:K:100:HIS:C	30:q:246:GLY:N	2.33	0.70
40:x:2816:G:H4'	40:x:2818:U:OP2	1.91	0.70
40:x:2870:C:O2	40:x:2872:A:N6	2.24	0.70
40:x:314:U:H5''	40:x:314:U:H6	1.56	0.70
19:J:22:SER:CA	40:x:2675:C:H42	2.03	0.69
40:x:2617:U:O2	40:x:2617:U:H5'	1.92	0.69
40:x:2798:C:O2	40:x:2800:G:N2	2.25	0.69
40:x:3024:A:H62	40:x:3031:G:H21	1.40	0.69
19:J:105:GLY:H	40:x:2674:A:P	2.14	0.69
26:o:237:MET:O	26:o:240:ILE:N	2.26	0.69
40:x:715:A:N3	48:a:113:LEU:N	2.37	0.69
26:o:145:ASP:O	26:o:148:ALA:N	2.25	0.69
39:T:74:VAL:O	39:T:89:LEU:N	2.25	0.69
32:r:220:ILE:O	32:r:223:THR:N	2.24	0.69
40:x:41:G:C4'	48:a:37:GLY:CA	2.71	0.69
40:x:2818:U:H3'	40:x:2818:U:C6	2.27	0.69
40:x:2831:G:O2'	40:x:2832:C:H5'	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:o:103:SER:O	26:o:106:GLU:N	2.26	0.68
3:B:19:ARG:O	40:x:3139:A:O5'	2.10	0.68
23:L:2:ALA:CA	48:a:33:GLY:HA3	2.23	0.68
40:x:2618:G:H5''	40:x:2824:G:O6	1.92	0.68
19:J:57:PHE:CA	40:x:2680:A:N1	2.57	0.68
1:A:131:GLY:CA	40:x:2157:G:N2	2.55	0.68
35:R:158:GLU:O	35:R:159:ALA:C	2.36	0.68
35:R:173:ARG:O	35:R:177:VAL:N	2.24	0.68
40:x:2397:A:H8	40:x:2403:G:N2	1.91	0.68
19:J:8:PRO:CA	44:z:53:U:C5'	2.72	0.68
39:T:62:GLY:H	39:T:75:ILE:H	1.42	0.68
40:x:2819:A:H8	40:x:2819:A:OP2	1.77	0.68
32:r:254:LYS:O	32:r:257:MET:N	2.26	0.68
29:O:58:LEU:N	40:x:1307:G:H8	1.92	0.68
19:J:124:GLY:N	40:x:2674:A:H2	1.91	0.67
1:A:131:GLY:CA	40:x:2157:G:H22	2.03	0.67
26:o:144:ARG:O	26:o:145:ASP:C	2.35	0.67
40:x:2821:C:O5'	40:x:2821:C:H6	1.76	0.67
40:x:2826:U:H6	40:x:2826:U:O5'	1.77	0.67
40:x:408:A:H62	42:y:15:G:H21	1.43	0.67
40:x:714:G:C2'	48:a:111:LYS:CA	2.72	0.67
17:I:160:LYS:H	40:x:2464:U:H1'	1.60	0.67
21:K:100:HIS:CA	30:q:245:PRO:C	2.68	0.67
1:A:186:PHE:H	40:x:896:A:H2	1.41	0.67
5:C:187:LEU:CA	40:x:1388:U:O4	2.43	0.67
1:A:113:VAL:N	1:A:134:VAL:O	2.26	0.66
5:C:78:GLY:O	40:x:363:G:N2	2.28	0.66
40:x:1003:A:O5'	40:x:1003:A:H8	1.78	0.66
40:x:2824:G:H2'	40:x:2824:G:N3	2.10	0.66
5:C:43:ASN:O	40:x:338:A:N6	2.28	0.66
31:P:68:GLY:HA3	40:x:2350:C:H5''	1.78	0.66
40:x:714:G:C4	48:a:110:GLY:C	2.72	0.66
32:r:629:PRO:O	32:r:632:ALA:N	2.28	0.66
40:x:1129:A:N7	40:x:2828:G:C2	2.61	0.66
32:r:292:LYS:O	32:r:295:VAL:N	2.28	0.66
35:R:142:ILE:O	40:x:2092:A:C1'	2.44	0.66
40:x:1762:C:O5'	40:x:1762:C:H6	1.78	0.66
19:J:85:LYS:O	19:J:88:GLU:N	2.28	0.66
39:T:16:GLN:N	40:x:1052:U:C5'	2.58	0.66
40:x:715:A:OP2	48:a:110:GLY:O	2.13	0.65
3:B:253:GLY:HA2	40:x:2394:G:H5'	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:x:709:A:H1'	48:a:58:MET:H	1.61	0.65
19:J:147:THR:O	44:z:57:G:H4'	1.97	0.65
40:x:714:G:C8	48:a:110:GLY:CA	2.73	0.65
1:A:2:GLY:N	40:x:2608:G:OP1	2.30	0.65
21:K:101:SER:CA	30:q:246:GLY:HA2	2.27	0.65
40:x:41:G:H5''	48:a:37:GLY:H	1.60	0.65
40:x:705:A:N1	48:a:110:GLY:C	2.49	0.65
39:T:46:GLY:HA2	40:x:993:G:OP1	1.95	0.65
1:A:206:PRO:C	40:x:2968:G:OP1	2.39	0.65
3:B:260:VAL:N	40:x:2987:A:O2'	2.30	0.65
26:o:244:ALA:O	26:o:246:LEU:N	2.30	0.64
40:x:312:C:O2'	40:x:313:A:H5'	1.97	0.64
26:o:87:GLU:C	26:o:89:ASN:H	2.04	0.64
17:I:160:LYS:CA	40:x:2463:G:N2	2.60	0.64
40:x:1500:G:H1	40:x:1516:C:H42	1.44	0.64
5:C:187:LEU:CA	40:x:1419:A:C2	2.81	0.64
5:C:187:LEU:C	40:x:1420:C:N4	2.56	0.64
39:T:15:PHE:N	40:x:1051:U:O3'	2.28	0.64
39:T:69:LYS:CA	40:x:2736:A:O4'	2.46	0.64
19:J:149:GLY:H	44:z:56:A:C2'	2.05	0.64
40:x:33:G:H21	40:x:51:A:H62	1.44	0.64
40:x:2622:C:H2'	40:x:2623:G:H8	1.59	0.64
21:K:101:SER:N	30:q:246:GLY:CA	2.49	0.64
23:L:2:ALA:CA	48:a:32:ARG:C	2.65	0.64
32:r:691:GLU:C	32:r:694:LEU:H	2.03	0.64
40:x:2639:G:C8	40:x:2639:G:P	2.90	0.64
40:x:2825:C:H3'	40:x:2825:C:H6	1.63	0.63
23:L:99:HIS:O	23:L:101:ARG:N	2.28	0.63
35:R:146:LYS:C	40:x:2092:A:N3	2.56	0.63
40:x:491:C:H2'	40:x:492:U:H5'	1.80	0.63
32:r:537:ILE:C	32:r:540:LEU:H	2.07	0.63
39:T:16:GLN:CA	40:x:2757:U:C1'	2.77	0.63
40:x:2279:A:H62	40:x:2286:U:H3	1.44	0.63
19:J:124:GLY:C	40:x:2674:A:C2	2.76	0.63
39:T:47:SER:O	40:x:2757:U:C5'	2.47	0.63
40:x:705:A:C2	48:a:110:GLY:CA	2.82	0.63
5:C:188:ARG:N	40:x:1420:C:H41	1.96	0.63
16:j:12:HIS:O	40:x:1490:A:O2'	2.17	0.63
40:x:2639:G:O2'	40:x:2640:A:H5'	1.99	0.63
19:J:124:GLY:H	40:x:2674:A:H2	1.46	0.62
27:N:88:GLY:HA2	40:x:2423:U:H4'	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:x:2405:C:H5''	40:x:2815:G:H22	1.63	0.62
11:F:101:LYS:CA	40:x:984:G:C2	2.81	0.62
39:T:69:LYS:CA	40:x:2735:U:O2	2.47	0.62
40:x:2618:G:H22	40:x:2823:G:C5'	1.98	0.62
29:O:71:PHE:O	40:x:2382:G:O3'	2.18	0.62
3:B:19:ARG:H	40:x:3138:U:H2'	1.65	0.62
39:T:62:GLY:N	39:T:75:ILE:N	2.36	0.62
19:J:126:ASP:CA	40:x:2674:A:N7	2.61	0.62
32:r:648:ALA:O	32:r:650:LEU:N	2.32	0.62
40:x:2621:G:O5'	40:x:2621:G:H8	1.81	0.62
19:J:140:ARG:O	44:z:43:U:C4'	2.48	0.62
16:j:77:GLY:O	40:x:237:G:O2'	2.17	0.61
39:T:15:PHE:CA	40:x:2757:U:O2'	2.48	0.61
5:C:188:ARG:N	40:x:1419:A:N1	2.48	0.61
1:A:114:SER:C	1:A:134:VAL:H	2.07	0.61
32:r:440:VAL:C	32:r:444:GLY:H	2.09	0.61
40:x:355:A:H62	40:x:364:G:H21	1.48	0.61
40:x:2618:G:C3'	40:x:2824:G:O6	2.49	0.61
3:B:14:LEU:C	40:x:3011:A:N6	2.58	0.61
40:x:39:A:O5'	40:x:39:A:H8	1.82	0.61
40:x:2523:A:N6	40:x:2586:G:OP2	2.34	0.61
40:x:2615:G:H2'	40:x:2616:C:H5'	1.82	0.61
40:x:2819:A:OP2	40:x:2819:A:C8	2.53	0.61
40:x:3062:G:H1	40:x:3081:C:H42	1.49	0.61
40:x:714:G:N3	48:a:111:LYS:CA	2.64	0.61
40:x:2689:A:N7	40:x:2702:A:N6	2.49	0.61
19:J:94:ARG:C	19:J:96:PHE:H	2.09	0.61
32:r:389:PHE:O	32:r:391:LYS:N	2.34	0.61
40:x:440:A:P	40:x:440:A:C8	2.92	0.61
39:T:76:ILE:O	39:T:78:LYS:N	2.34	0.60
35:R:146:LYS:C	40:x:2092:A:C2	2.78	0.60
40:x:714:G:N9	48:a:110:GLY:C	2.59	0.60
40:x:2557:A:OP1	47:Z:135:ARG:N	2.34	0.60
1:A:207:VAL:CA	40:x:2967:A:O3'	2.49	0.60
3:B:19:ARG:O	40:x:3139:A:C5'	2.49	0.60
40:x:40:A:OP1	48:a:33:GLY:O	2.19	0.60
3:B:19:ARG:CA	40:x:3139:A:P	2.90	0.60
40:x:2412:G:H1	40:x:2810:C:H42	1.50	0.60
19:J:125:MET:N	40:x:2674:A:C4	2.70	0.60
23:L:65:TYR:O	40:x:73:C:N4	2.31	0.60
23:L:45:LYS:O	40:x:241:G:N1	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:x:705:A:N1	48:a:110:GLY:N	2.49	0.59
40:x:837:A:H62	40:x:856:G:H21	1.50	0.59
40:x:715:A:N3	48:a:114:GLY:N	2.50	0.59
40:x:2818:U:C6	40:x:2818:U:C3'	2.83	0.59
3:B:14:LEU:O	40:x:3011:A:N6	2.36	0.59
5:C:187:LEU:CA	40:x:1387:G:O6	2.51	0.59
32:r:225:LEU:O	32:r:228:GLU:CA	2.50	0.59
1:A:125:ALA:C	1:A:127:ALA:H	2.10	0.59
3:B:238:LEU:N	3:B:246:LEU:O	2.36	0.59
40:x:2701:U:H1'	40:x:2705:A:N7	2.17	0.59
40:x:15:C:H42	42:y:144:G:H22	1.51	0.59
19:J:126:ASP:N	40:x:2674:A:N7	2.51	0.59
35:R:81:ARG:O	35:R:83:GLY:N	2.35	0.59
1:A:134:VAL:O	1:A:136:ILE:N	2.35	0.59
29:O:62:THR:O	29:O:64:PHE:N	2.29	0.58
35:R:79:GLY:O	35:R:81:ARG:N	2.36	0.58
38:u:380:THR:CA	40:x:1763:U:O2	2.50	0.58
39:T:43:LYS:C	39:T:95:HIS:CA	2.75	0.58
40:x:2873:U:H3'	40:x:2873:U:O2	2.03	0.58
16:j:63:ARG:N	42:y:42:G:OP1	2.37	0.58
3:B:19:ARG:CA	40:x:3138:U:O3'	2.51	0.58
21:K:59:THR:N	40:x:1236:G:H21	2.01	0.58
23:L:2:ALA:N	48:a:33:GLY:N	2.46	0.58
40:x:1243:G:C8	40:x:1244:A:C8	2.89	0.58
40:x:2698:G:O5'	40:x:2698:G:H8	1.86	0.58
29:O:71:PHE:CA	40:x:2382:G:C2'	2.81	0.58
40:x:2557:A:OP1	47:Z:136:PHE:N	2.36	0.58
42:y:50:C:OP2	42:y:51:G:N2	2.37	0.58
13:G:35:GLY:O	13:G:37:GLY:N	2.37	0.58
26:o:87:GLU:O	26:o:88:LYS:C	2.46	0.58
40:x:654:C:H42	40:x:1441:G:H1	1.50	0.58
40:x:1941:C:H42	40:x:2107:A:H61	1.51	0.58
39:T:46:GLY:N	40:x:993:G:P	2.76	0.58
1:A:69:TYR:O	40:x:1649:U:O2'	2.22	0.58
1:A:125:ALA:O	1:A:127:ALA:N	2.37	0.58
29:O:58:LEU:N	40:x:1307:G:H5'	2.16	0.57
32:r:282:ASP:O	32:r:284:PHE:N	2.36	0.57
39:T:61:THR:C	39:T:75:ILE:O	2.46	0.57
40:x:492:U:H6	40:x:492:U:O5'	1.87	0.57
39:T:47:SER:O	40:x:2757:U:H4'	2.03	0.57
40:x:41:G:C4'	48:a:37:GLY:N	2.66	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:x:2585:G:H4'	40:x:2586:G:C5'	2.34	0.57
27:N:108:ARG:O	42:y:140:G:N2	2.36	0.57
38:u:78:GLN:O	40:x:1994:G:N2	2.37	0.57
1:A:207:VAL:CA	40:x:2968:G:OP1	2.52	0.57
5:C:92:ASN:O	40:x:658:G:N2	2.37	0.57
40:x:714:G:C2'	48:a:110:GLY:O	2.50	0.57
40:x:1129:A:C4	40:x:2828:G:C2	2.92	0.57
40:x:2402:A:H4'	40:x:2403:G:OP2	2.05	0.57
3:B:19:ARG:C	40:x:3139:A:P	2.88	0.57
35:R:158:GLU:O	35:R:161:ALA:CA	2.52	0.57
1:A:114:SER:C	1:A:134:VAL:N	2.63	0.57
29:O:58:LEU:N	40:x:1307:G:C8	2.72	0.57
1:A:129:ALA:N	40:x:2158:A:C2'	2.68	0.56
40:x:2692:A:H61	40:x:2701:U:H3	1.51	0.56
1:A:129:ALA:CA	40:x:2158:A:O2'	2.54	0.56
40:x:599:C:H42	40:x:604:G:H1	1.53	0.56
40:x:977:C:H42	40:x:1104:G:H1	1.52	0.56
3:B:19:ARG:N	40:x:3138:U:C2'	2.69	0.56
9:E:61:ASN:O	40:x:3272:C:N4	2.39	0.56
26:o:144:ARG:O	26:o:148:ALA:N	2.39	0.56
29:O:73:PHE:C	40:x:3008:A:OP1	2.48	0.56
3:B:19:ARG:N	40:x:3138:U:O2'	2.38	0.56
40:x:2547:A:H5''	40:x:2548:C:H5	1.71	0.56
39:T:15:PHE:C	40:x:2757:U:O2'	2.49	0.56
40:x:40:A:OP2	48:a:34:MET:C	2.46	0.56
40:x:2831:G:H2'	40:x:2832:C:C6	2.41	0.56
40:x:3269:U:H5''	40:x:3270:U:H2'	1.88	0.56
3:B:19:ARG:H	40:x:3138:U:C2'	2.18	0.55
40:x:2639:G:H8	40:x:2639:G:O5'	1.89	0.55
40:x:1556:C:H5''	40:x:2521:U:O4	2.07	0.55
1:A:125:ALA:C	1:A:127:ALA:N	2.63	0.55
40:x:714:G:C3'	48:a:110:GLY:O	2.55	0.55
31:P:95:LEU:O	31:P:97:ASN:N	2.38	0.55
40:x:1763:U:O2	40:x:1763:U:H2'	2.06	0.55
19:J:125:MET:H	40:x:2674:A:H1'	1.63	0.54
40:x:59:G:O6	42:y:35:C:N4	2.40	0.54
40:x:2213:A:OP2	40:x:2231:C:N4	2.40	0.54
1:A:206:PRO:C	40:x:916:G:O6	2.50	0.54
29:O:59:ARG:CA	40:x:1306:G:N3	2.69	0.54
39:T:61:THR:CA	39:T:75:ILE:O	2.55	0.54
40:x:1446:A:H62	40:x:2357:A:H62	1.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:O:58:LEU:CA	40:x:1307:G:H8	2.21	0.54
40:x:440:A:C8	40:x:440:A:OP2	2.61	0.54
40:x:714:G:C3'	48:a:110:GLY:C	2.80	0.54
40:x:2639:G:C2'	40:x:2640:A:H5'	2.38	0.54
19:J:141:ARG:N	44:z:43:U:H4'	2.20	0.54
21:K:58:VAL:C	40:x:1236:G:H21	2.15	0.54
29:O:110:PRO:O	29:O:112:TYR:N	2.41	0.54
35:R:59:SER:N	40:x:3068:U:OP1	2.39	0.54
40:x:1005:G:H1	40:x:1045:C:H2'	1.73	0.54
1:A:207:VAL:N	40:x:916:G:C6	2.75	0.54
40:x:1218:U:O2'	40:x:1223:A:O2'	2.21	0.54
40:x:2523:A:C6	40:x:2586:G:OP2	2.60	0.54
5:C:188:ARG:N	40:x:1420:C:N4	2.56	0.54
40:x:1496:C:H1'	40:x:1836:C:H1'	1.88	0.54
6:e:2:ALA:N	40:x:439:C:OP1	2.41	0.54
17:I:160:LYS:H	40:x:2464:U:C1'	2.21	0.54
32:r:296:ASN:O	32:r:298:LYS:N	2.40	0.54
40:x:598:A:H61	40:x:605:U:H3	1.54	0.54
40:x:1339:C:H42	40:x:1365:G:H1	1.56	0.54
1:A:213:GLY:N	40:x:2967:A:OP1	2.39	0.54
3:B:19:ARG:N	40:x:3139:A:O5'	2.41	0.54
23:L:2:ALA:O	48:a:33:GLY:HA3	2.07	0.54
32:r:84:THR:O	32:r:87:LEU:N	2.40	0.54
40:x:838:G:N2	40:x:1724:U:OP1	2.40	0.54
40:x:2523:A:H61	40:x:2586:G:P	2.30	0.54
5:C:108:LYS:H	40:x:664:U:H5''	1.73	0.53
23:L:2:ALA:C	48:a:33:GLY:HA3	2.33	0.53
40:x:2289:U:H3	40:x:2303:A:H61	1.54	0.53
40:x:2825:C:C3'	40:x:2825:C:C6	2.91	0.53
39:T:16:GLN:O	40:x:1052:U:H5''	2.07	0.53
23:L:2:ALA:N	48:a:33:GLY:H	2.05	0.53
26:o:1:MET:N	40:x:3029:A:O2'	2.42	0.53
26:o:58:VAL:O	26:o:59:GLU:O	2.27	0.53
43:V:46:LEU:O	43:V:48:ARG:N	2.41	0.53
40:x:688:G:OP2	40:x:690:A:N6	2.41	0.53
40:x:2410:U:O4	48:a:36:GLY:CA	2.57	0.53
40:x:67:A:H1'	40:x:315:C:O2	2.08	0.53
40:x:199:A:O4'	40:x:219:A:N6	2.41	0.53
40:x:714:G:N9	48:a:111:LYS:N	2.57	0.53
48:a:28:HIS:C	48:a:30:GLY:H	2.17	0.53
27:N:107:GLY:O	27:N:111:ALA:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:r:84:THR:O	32:r:86:GLN:N	2.42	0.53
35:R:150:GLN:O	35:R:154:ALA:N	2.40	0.53
40:x:2253:G:H1	40:x:2263:C:H42	1.55	0.53
38:u:78:GLN:CA	40:x:1994:G:N2	2.72	0.53
40:x:763:G:H1	40:x:768:C:H42	1.57	0.53
40:x:1002:A:C8	40:x:1002:A:C3'	2.85	0.53
40:x:1700:G:H1	40:x:1745:C:H42	1.56	0.53
1:A:114:SER:CA	1:A:134:VAL:N	2.64	0.52
1:A:208:ASP:C	40:x:2967:A:H4'	2.34	0.52
26:o:90:HIS:O	26:o:93:ILE:C	2.52	0.52
26:o:232:MET:C	26:o:234:ASN:H	2.17	0.52
40:x:1003:A:C8	40:x:1003:A:H3'	2.45	0.52
19:J:149:GLY:N	44:z:57:G:C5'	2.65	0.52
21:K:100:HIS:CA	30:q:246:GLY:N	2.71	0.52
40:x:166:C:H42	40:x:256:G:H1	1.56	0.52
40:x:720:A:OP1	40:x:784:A:N6	2.42	0.52
5:C:94:CYS:O	5:C:96:GLY:N	2.42	0.52
32:r:440:VAL:N	32:r:443:ALA:CA	2.73	0.52
40:x:542:G:H1	40:x:550:A:H61	1.58	0.52
40:x:1399:A:N6	42:y:8:C:O2'	2.43	0.52
26:o:123:PHE:O	26:o:124:GLN:C	2.51	0.52
27:N:75:VAL:O	27:N:77:LYS:N	2.43	0.52
37:S:132:THR:O	37:S:134:ASP:N	2.43	0.52
40:x:2585:G:H4'	40:x:2586:G:H5''	1.92	0.52
48:a:77:LYS:O	48:a:79:TRP:N	2.42	0.52
8:f:46:GLY:HA3	40:x:584:G:H5''	1.91	0.52
31:P:40:GLU:O	31:P:42:THR:N	2.42	0.52
40:x:1915:A:H61	40:x:1937:U:H3	1.57	0.52
1:A:16:PHE:O	40:x:2172:A:O2'	2.26	0.52
32:r:203:SER:N	32:r:206:ALA:CA	2.73	0.52
32:r:397:GLN:N	32:r:400:VAL:CA	2.73	0.52
40:x:493:G:H3'	40:x:494:G:H8	1.73	0.52
48:a:131:SER:O	48:a:133:LEU:N	2.42	0.52
39:T:69:LYS:C	40:x:2735:U:O2	2.52	0.52
40:x:2252:A:H61	40:x:2264:U:H3	1.58	0.52
40:x:1129:A:C4	40:x:2828:G:N3	2.78	0.52
40:x:1193:A:H62	40:x:1314:C:H42	1.56	0.52
1:A:128:ARG:C	1:A:130:SER:H	2.17	0.52
32:r:402:ARG:C	32:r:404:MET:H	2.18	0.52
40:x:2838:A:N6	40:x:2850:G:O2'	2.43	0.52
38:u:78:GLN:CA	40:x:1994:G:H21	2.23	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:T:74:VAL:O	39:T:88:ARG:CA	2.58	0.51
40:x:283:G:N2	40:x:285:A:OP1	2.44	0.51
40:x:1922:A:H62	40:x:1929:G:H21	1.56	0.51
42:y:91:C:H1'	46:Y:24:SER:H	1.74	0.51
4:d:42:LEU:O	40:x:3386:G:O2'	2.27	0.51
32:r:225:LEU:O	32:r:228:GLU:N	2.43	0.51
40:x:1502:C:N4	40:x:1512:U:OP2	2.43	0.51
32:r:87:LEU:C	32:r:90:LEU:H	2.18	0.51
35:R:81:ARG:C	35:R:83:GLY:H	2.18	0.51
40:x:3319:U:O2'	40:x:3320:A:OP1	2.25	0.51
29:O:87:MET:O	40:x:1175:C:O2'	2.25	0.51
40:x:315:C:C3'	40:x:316:U:H5'	2.40	0.51
40:x:714:G:C4	48:a:110:GLY:HA3	2.45	0.51
40:x:1006:A:O2'	40:x:1007:U:OP1	2.26	0.51
39:T:45:ASN:H	40:x:992:A:H5''	1.75	0.51
40:x:714:G:O2'	48:a:111:LYS:CA	2.59	0.51
40:x:2786:G:H21	48:a:59:ARG:N	2.09	0.51
26:o:236:GLU:O	26:o:237:MET:O	2.29	0.51
40:x:116:A:N6	40:x:153:U:O2	2.44	0.51
1:A:112:ILE:CA	1:A:134:VAL:O	2.59	0.51
35:R:142:ILE:O	40:x:2092:A:O4'	2.28	0.51
40:x:199:A:O2'	40:x:201:A:N6	2.44	0.51
40:x:800:G:N7	40:x:933:A:O2'	2.44	0.51
40:x:2618:G:H21	40:x:2823:G:C4'	2.21	0.51
40:x:1139:G:H22	40:x:1155:C:H5''	1.74	0.51
40:x:2618:G:H21	40:x:2823:G:C5'	2.19	0.51
30:q:71:SER:C	30:q:73:ASP:H	2.16	0.51
40:x:2254:U:H6	40:x:2254:U:C5'	2.23	0.51
17:I:160:LYS:N	40:x:2464:U:H1'	2.26	0.51
35:R:158:GLU:O	35:R:161:ALA:C	2.54	0.51
40:x:1477:A:H61	40:x:1876:U:H3	1.59	0.51
40:x:3045:G:N2	40:x:3097:C:O2	2.44	0.51
1:A:131:GLY:N	40:x:2157:G:N2	2.57	0.50
9:E:45:GLY:H	40:x:3273:A:H4'	1.75	0.50
19:J:22:SER:N	40:x:2675:C:N4	2.16	0.50
40:x:211:A:O2'	40:x:212:G:N2	2.42	0.50
40:x:1493:G:H4'	40:x:1494:U:H5'	1.93	0.50
40:x:2058:G:N7	40:x:2078:C:N4	2.58	0.50
40:x:2634:U:O2'	40:x:2645:G:N2	2.45	0.50
40:x:2637:A:O2'	40:x:2638:C:H5'	2.11	0.50
44:z:52:G:H5''	44:z:53:U:H5	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:x:1187:C:O2'	40:x:1295:G:N2	2.45	0.50
40:x:2636:A:N3	40:x:2636:A:C3'	2.73	0.50
40:x:2786:G:H21	48:a:59:ARG:H	1.59	0.50
17:I:39:LYS:N	17:I:205:VAL:O	2.41	0.50
40:x:2525:G:N2	40:x:2549:G:O6	2.43	0.50
40:x:2639:G:C2'	40:x:2640:A:C5'	2.89	0.50
40:x:714:G:C1'	48:a:111:LYS:N	2.75	0.50
26:o:17:LEU:C	26:o:19:ASP:H	2.19	0.50
27:N:165:THR:O	27:N:169:LYS:N	2.28	0.50
32:r:397:GLN:C	32:r:400:VAL:H	2.19	0.50
40:x:440:A:H8	40:x:440:A:O5'	1.95	0.50
40:x:916:G:O2'	40:x:917:A:O5'	2.26	0.50
40:x:2725:U:C3'	40:x:2726:C:H5'	2.40	0.50
40:x:1553:U:H4'	40:x:1554:U:H5'	1.94	0.50
40:x:2143:A:N3	40:x:2957:G:N2	2.52	0.50
40:x:3303:G:O2'	40:x:3305:A:N6	2.44	0.50
3:B:46:PHE:O	3:B:338:LEU:N	2.45	0.50
28:p:23:ARG:O	28:p:25:GLN:N	2.45	0.50
40:x:1202:A:N6	40:x:1301:A:OP1	2.45	0.50
3:B:346:THR:O	3:B:348:ARG:N	2.45	0.49
7:D:257:GLU:O	7:D:259:LYS:N	2.44	0.49
32:r:111:GLU:C	32:r:115:LEU:CA	2.85	0.49
40:x:681:U:O2	40:x:696:C:N4	2.44	0.49
40:x:2831:G:O2'	40:x:2832:C:C5'	2.59	0.49
42:y:102:U:OP1	42:y:109:A:N6	2.43	0.49
31:P:132:ALA:O	31:P:134:GLY:N	2.45	0.49
19:J:23:VAL:O	19:J:25:GLU:N	2.39	0.49
19:J:73:GLY:O	19:J:75:LYS:N	2.46	0.49
40:x:2867:C:C2'	40:x:2868:U:OP1	2.56	0.49
44:z:85:G:H22	44:z:95:A:H61	1.60	0.49
40:x:638:C:O2	40:x:1434:G:N1	2.45	0.49
40:x:2406:C:O2'	40:x:2407:C:O4'	2.31	0.49
40:x:3216:G:H3'	40:x:3219:G:H21	1.76	0.49
40:x:3304:U:H3'	40:x:3305:A:H8	1.77	0.49
5:C:181:VAL:O	5:C:183:LYS:N	2.43	0.49
35:R:82:LYS:N	40:x:1914:G:H21	2.10	0.49
18:k:2:ALA:N	40:x:1613:A:OP1	2.45	0.49
39:T:47:SER:O	40:x:2757:U:C4'	2.60	0.49
40:x:720:A:HO2'	40:x:783:A:HO2'	1.60	0.49
40:x:1695:U:O2'	40:x:1749:A:N6	2.45	0.49
40:x:1904:C:N4	40:x:2950:G:OP1	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:x:2252:A:C6	40:x:2253:G:C6	3.01	0.49
40:x:2523:A:N1	40:x:2586:G:OP2	2.45	0.49
40:x:1129:A:C5	40:x:2828:G:C2	3.00	0.49
23:L:164:GLU:O	23:L:166:ALA:N	2.45	0.49
40:x:67:A:H4'	40:x:315:C:HO2'	1.70	0.49
40:x:1204:A:H62	40:x:1300:G:H21	1.61	0.49
23:L:2:ALA:CA	48:a:33:GLY:HA2	2.30	0.49
26:o:89:ASN:C	26:o:91:TYR:N	2.71	0.49
40:x:714:G:O2'	48:a:112:ILE:N	2.46	0.49
40:x:1002:A:H3'	40:x:1002:A:H8	1.74	0.49
40:x:3216:G:H21	40:x:3221:C:H41	1.59	0.49
5:C:188:ARG:N	40:x:1419:A:C6	2.75	0.48
19:J:148:VAL:C	44:z:57:G:H5'	2.37	0.48
32:r:402:ARG:C	32:r:404:MET:N	2.69	0.48
40:x:2697:A:H2'	40:x:2698:G:H8	1.75	0.48
40:x:1003:A:C8	40:x:1003:A:C3'	2.95	0.48
42:y:60:U:O2'	42:y:63:G:N2	2.44	0.48
25:M:34:ALA:O	25:M:47:ASP:N	2.46	0.48
31:P:121:GLN:O	42:y:13:A:O2'	2.20	0.48
32:r:92:GLY:O	32:r:94:VAL:N	2.46	0.48
40:x:1529:A:OP2	40:x:1592:G:N2	2.45	0.48
40:x:2620:G:H8	40:x:2620:G:O5'	1.95	0.48
19:J:22:SER:H	40:x:2675:C:H42	0.60	0.48
40:x:13:A:N6	42:y:145:U:O4	2.42	0.48
40:x:371:G:N1	40:x:374:A:OP2	2.43	0.48
40:x:1044:U:O2'	40:x:1045:C:O5'	2.26	0.48
40:x:3014:U:H3	40:x:3040:A:H61	1.61	0.48
42:y:107:G:OP2	42:y:137:C:N4	2.46	0.48
1:A:207:VAL:CA	40:x:2968:G:P	3.01	0.48
5:C:187:LEU:N	40:x:1387:G:O6	2.46	0.48
15:H:80:THR:O	15:H:85:GLY:N	2.47	0.48
29:O:57:PHE:N	40:x:1307:G:H5''	2.28	0.48
32:r:648:ALA:C	32:r:650:LEU:N	2.72	0.48
32:r:679:THR:C	32:r:681:THR:N	2.71	0.48
39:T:45:ASN:N	40:x:992:A:H5''	2.28	0.48
40:x:1901:A:N6	40:x:2336:U:O4	2.46	0.48
40:x:3318:G:O2'	40:x:3320:A:OP2	2.31	0.48
32:r:440:VAL:C	32:r:444:GLY:N	2.71	0.48
11:F:101:LYS:CA	40:x:984:G:N3	2.77	0.48
26:o:123:PHE:O	26:o:126:LYS:N	2.44	0.48
32:r:204:THR:C	32:r:206:ALA:N	2.71	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:T:116:ARG:O	40:x:1092:C:O2'	2.31	0.48
40:x:619:A:H5''	40:x:620:U:H5	1.79	0.48
40:x:1304:A:O2'	40:x:2938:G:N2	2.46	0.48
3:B:49:TYR:O	3:B:80:ASP:N	2.46	0.48
19:J:110:ILE:C	19:J:112:LEU:H	2.21	0.48
37:S:79:VAL:N	37:S:90:MET:O	2.45	0.48
40:x:1293:U:O4	40:x:1294:A:N6	2.47	0.48
40:x:2618:G:H21	40:x:2823:G:H4'	1.79	0.48
26:o:145:ASP:C	26:o:147:LEU:N	2.71	0.48
27:N:95:GLN:O	40:x:288:C:O2	2.32	0.48
40:x:1657:C:H42	40:x:1797:A:H8	1.62	0.48
3:B:19:ARG:N	40:x:3138:U:H2'	2.29	0.47
32:r:133:SER:C	32:r:135:LEU:H	2.22	0.47
35:R:4:LEU:N	40:x:1471:U:O2'	2.46	0.47
40:x:346:C:N4	40:x:349:A:OP2	2.46	0.47
40:x:1175:C:H42	40:x:1311:G:H1	1.61	0.47
40:x:1718:G:N2	40:x:1731:A:O2'	2.47	0.47
16:j:9:GLY:O	16:j:11:ARG:N	2.46	0.47
32:r:292:LYS:C	32:r:294:GLN:N	2.72	0.47
40:x:2618:G:N2	40:x:2823:G:O4'	2.44	0.47
40:x:2770:G:H1	40:x:2788:C:H42	1.62	0.47
1:A:238:ILE:O	40:x:2154:U:O2'	2.23	0.47
32:r:296:ASN:C	32:r:298:LYS:N	2.72	0.47
32:r:389:PHE:C	32:r:391:LYS:N	2.72	0.47
32:r:444:GLY:C	32:r:446:ASN:N	2.72	0.47
40:x:802:C:H41	48:a:26:ARG:H	1.61	0.47
40:x:1492:G:H22	40:x:1836:C:H42	1.62	0.47
32:r:133:SER:C	32:r:135:LEU:N	2.71	0.47
40:x:2397:A:C8	40:x:2403:G:N2	2.77	0.47
40:x:3160:U:H5''	40:x:3396:U:H2'	1.95	0.47
5:C:337:GLU:O	5:C:339:LEU:N	2.48	0.47
32:r:84:THR:C	32:r:86:GLN:N	2.71	0.47
40:x:40:A:N3	40:x:40:A:C3'	2.73	0.47
40:x:441:U:HO2'	40:x:442:G:H8	1.63	0.47
40:x:1383:G:H1	40:x:1423:C:H42	1.62	0.47
40:x:2253:G:C2	40:x:2254:U:C2	3.02	0.47
40:x:2869:U:H2'	40:x:2869:U:O2	2.14	0.47
3:B:330:GLY:H	40:x:3047:U:H5'	1.80	0.47
26:o:94:SER:C	26:o:96:ALA:N	2.72	0.47
32:r:241:VAL:C	32:r:243:ILE:N	2.71	0.47
32:r:282:ASP:C	32:r:284:PHE:N	2.72	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:r:303:GLY:C	32:r:305:LYS:N	2.72	0.47
32:r:384:GLY:C	32:r:386:TYR:N	2.72	0.47
32:r:488:LEU:C	32:r:490:ARG:N	2.72	0.47
32:r:490:ARG:C	32:r:492:VAL:N	2.72	0.47
32:r:554:GLU:O	32:r:557:ASP:N	2.47	0.47
40:x:2086:A:H2'	40:x:2088:A:H62	1.79	0.47
40:x:2256:A:C2	40:x:2258:U:P	3.08	0.47
40:x:2873:U:H2'	40:x:2875:U:OP1	2.15	0.47
40:x:2894:C:H42	40:x:2907:G:H1	1.61	0.47
46:Y:115:ARG:O	46:Y:117:ALA:N	2.48	0.47
26:o:96:ALA:C	26:o:98:ILE:N	2.70	0.47
32:r:406:ALA:C	32:r:408:ALA:H	2.22	0.47
35:R:158:GLU:C	35:R:161:ALA:H	2.22	0.47
44:z:41:G:H21	44:z:44:C:H42	1.63	0.47
19:J:141:ARG:CA	44:z:44:C:P	3.03	0.47
40:x:1464:G:N2	40:x:1467:A:OP2	2.43	0.47
48:a:28:HIS:C	48:a:30:GLY:N	2.73	0.47
21:K:39:PRO:O	21:K:41:LYS:N	2.47	0.47
26:o:236:GLU:O	26:o:240:ILE:N	2.47	0.47
31:P:2:ALA:N	40:x:398:A:OP2	2.47	0.47
32:r:261:MET:C	32:r:263:PHE:N	2.72	0.47
32:r:406:ALA:C	32:r:408:ALA:N	2.71	0.47
33:Q:2:GLY:N	40:x:1159:A:OP1	2.48	0.47
35:R:85:ARG:O	35:R:89:LEU:N	2.47	0.47
40:x:1463:U:H3	40:x:1467:A:H62	1.63	0.47
40:x:2822:U:O5'	40:x:2822:U:H6	1.98	0.47
40:x:2825:C:H6	40:x:2825:C:C3'	2.24	0.47
19:J:22:SER:O	40:x:2675:C:N3	2.47	0.46
26:o:110:ARG:C	26:o:112:TYR:N	2.73	0.46
32:r:92:GLY:C	32:r:94:VAL:N	2.71	0.46
32:r:312:THR:C	32:r:314:LYS:N	2.72	0.46
32:r:431:PHE:C	32:r:433:SER:N	2.72	0.46
32:r:444:GLY:C	32:r:446:ASN:H	2.23	0.46
39:T:47:SER:CA	40:x:2757:U:H4'	2.46	0.46
40:x:714:G:H3'	48:a:110:GLY:O	2.15	0.46
1:A:2:GLY:N	40:x:908:G:H21	2.13	0.46
11:F:108:LEU:O	11:F:110:ARG:N	2.48	0.46
26:o:112:TYR:C	26:o:114:ARG:N	2.73	0.46
35:R:81:ARG:O	40:x:1915:A:H1'	2.15	0.46
40:x:86:G:H22	40:x:98:G:H2'	1.79	0.46
40:x:1648:A:H62	40:x:1807:G:H21	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:x:2256:A:C2	40:x:2258:U:OP1	2.68	0.46
40:x:2923:U:H1'	40:x:2951:G:H21	1.80	0.46
47:Z:16:GLY:O	47:Z:18:TYR:N	2.48	0.46
19:J:125:MET:H	40:x:2674:A:C1'	2.27	0.46
26:o:139:ILE:O	26:o:141:LYS:N	2.49	0.46
32:r:398:ARG:C	32:r:400:VAL:N	2.72	0.46
40:x:950:G:HO2'	40:x:970:A:HO2'	1.62	0.46
19:J:41:SER:C	19:J:43:GLN:H	2.24	0.46
32:r:145:THR:C	32:r:147:GLU:N	2.72	0.46
39:T:69:LYS:N	40:x:2736:A:H1'	2.31	0.46
40:x:705:A:N1	48:a:110:GLY:CA	2.78	0.46
23:L:27:ASP:O	23:L:29:ALA:N	2.49	0.46
32:r:220:ILE:C	32:r:222:ALA:N	2.72	0.46
32:r:629:PRO:C	32:r:631:ALA:N	2.72	0.46
40:x:705:A:C2	48:a:111:LYS:CA	2.96	0.46
32:r:88:ILE:C	32:r:90:LEU:N	2.73	0.46
32:r:206:ALA:C	32:r:208:CYS:N	2.72	0.46
32:r:380:LEU:C	32:r:382:VAL:N	2.73	0.46
40:x:436:A:OP2	40:x:621:A:N6	2.48	0.46
40:x:2831:G:H2'	40:x:2832:C:H6	1.80	0.46
26:o:244:ALA:C	26:o:246:LEU:N	2.73	0.46
40:x:1000:C:O2'	40:x:1045:C:N4	2.45	0.46
40:x:1094:U:O2'	40:x:1095:U:O5'	2.26	0.46
40:x:1234:G:H1	40:x:1254:C:H42	1.63	0.46
40:x:2802:A:N3	40:x:2802:A:C3'	2.73	0.46
40:x:2826:U:H5''	40:x:2870:C:N4	2.30	0.46
40:x:3005:A:N1	40:x:3140:G:O2'	2.48	0.46
42:y:46:G:H1'	42:y:58:G:H22	1.81	0.46
5:C:114:ASN:O	5:C:118:LYS:N	2.42	0.46
32:r:440:VAL:C	32:r:442:ALA:N	2.73	0.46
35:R:82:LYS:CA	40:x:1914:G:H21	2.28	0.46
40:x:42:C:O5'	40:x:42:C:H6	1.99	0.46
40:x:2058:G:O6	40:x:2079:G:N2	2.49	0.46
40:x:2617:U:H4'	40:x:2618:G:OP2	2.16	0.46
3:B:98:GLY:HA2	40:x:3004:C:H1'	1.98	0.46
23:L:165:SER:O	23:L:167:PHE:N	2.47	0.46
32:r:154:PHE:C	32:r:156:LEU:N	2.73	0.46
32:r:555:ASP:C	32:r:557:ASP:N	2.72	0.46
40:x:1346:G:H1	40:x:1358:C:H42	1.63	0.46
40:x:2221:G:N2	40:x:2224:A:OP2	2.49	0.46
32:r:543:TRP:C	32:r:545:LYS:N	2.72	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:x:644:G:O6	40:x:2817:A:OP1	2.32	0.46
40:x:1177:G:H22	40:x:2380:U:H5''	1.81	0.46
32:r:245:THR:C	32:r:247:ALA:N	2.72	0.45
32:r:486:ILE:C	32:r:488:LEU:N	2.72	0.45
39:T:41:ASP:C	39:T:43:LYS:N	2.73	0.45
39:T:130:ARG:O	40:x:1098:A:O2'	2.33	0.45
40:x:515:C:H42	40:x:575:G:H1	1.63	0.45
4:d:5:LYS:O	4:d:7:VAL:N	2.49	0.45
40:x:1985:G:H22	40:x:2036:U:H3	1.64	0.45
40:x:2825:C:H2'	40:x:2826:U:C6	2.51	0.45
32:r:261:MET:O	32:r:263:PHE:N	2.49	0.45
32:r:557:ASP:C	32:r:559:ASN:N	2.73	0.45
35:R:81:ARG:H	40:x:1914:G:H22	1.64	0.45
40:x:441:U:O2'	40:x:442:G:H8	1.98	0.45
40:x:3084:C:O2'	40:x:3332:U:OP1	2.34	0.45
26:o:143:LEU:C	26:o:145:ASP:N	2.74	0.45
26:o:143:LEU:O	26:o:145:ASP:N	2.49	0.45
35:R:66:HIS:O	35:R:70:LYS:N	2.41	0.45
40:x:706:A:H4'	40:x:781:G:H1'	1.99	0.45
40:x:2798:C:H1'	40:x:2800:G:H21	1.81	0.45
32:r:131:ILE:C	32:r:133:SER:N	2.72	0.45
40:x:339:C:OP1	40:x:1380:G:O2'	2.34	0.45
40:x:2317:A:H3'	40:x:2317:A:C8	2.51	0.45
26:o:98:ILE:C	26:o:100:ARG:N	2.72	0.45
32:r:448:ILE:C	32:r:450:GLU:N	2.73	0.45
32:r:652:GLU:C	32:r:654:ARG:N	2.72	0.45
38:u:79:TYR:C	38:u:81:LYS:N	2.73	0.45
40:x:312:C:C2'	40:x:313:A:H5'	2.46	0.45
40:x:943:U:O2'	48:a:12:ARG:O	2.29	0.45
40:x:1965:C:O2'	40:x:1966:U:O5'	2.28	0.45
27:N:172:ARG:N	40:x:288:C:OP1	2.49	0.45
32:r:446:ASN:C	32:r:448:ILE:N	2.71	0.45
3:B:333:LYS:O	40:x:3304:U:N3	2.47	0.45
26:o:103:SER:C	26:o:106:GLU:H	2.25	0.45
32:r:91:VAL:O	32:r:111:GLU:CA	2.65	0.45
32:r:379:LYS:O	32:r:382:VAL:N	2.50	0.45
39:T:69:LYS:CA	40:x:2735:U:C2'	2.95	0.45
40:x:236:G:O2'	42:y:95:G:O6	2.34	0.45
40:x:2253:G:C6	40:x:2254:U:N3	2.84	0.45
2:c:43:ILE:N	2:c:90:VAL:O	2.40	0.45
5:C:206:LEU:O	5:C:249:ILE:N	2.39	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:N:96:ARG:O	40:x:31:C:H5''	2.16	0.45
32:r:243:ILE:C	32:r:245:THR:N	2.72	0.45
39:T:16:GLN:C	40:x:1052:U:H5''	2.42	0.45
40:x:714:G:C5	48:a:110:GLY:CA	2.93	0.45
40:x:2253:G:C2	40:x:2254:U:O2	2.70	0.45
40:x:2294:U:O2'	40:x:2296:A:N7	2.43	0.45
11:F:24:GLU:O	11:F:26:VAL:N	2.50	0.45
32:r:429:ASP:C	32:r:431:PHE:N	2.72	0.45
40:x:361:A:H1'	40:x:813:G:H21	1.82	0.45
40:x:608:A:H2'	40:x:609:G:H21	1.81	0.45
11:F:220:PHE:O	44:z:85:G:O2'	2.32	0.44
32:r:677:ALA:C	32:r:679:THR:N	2.72	0.44
38:u:76:LEU:O	38:u:79:TYR:O	2.35	0.44
40:x:1404:G:N2	40:x:1407:A:OP2	2.47	0.44
19:J:109:HIS:N	19:J:123:PHE:O	2.49	0.44
32:r:656:GLU:C	32:r:658:SER:N	2.72	0.44
40:x:441:U:OP1	40:x:441:U:C5	2.70	0.44
40:x:639:G:N2	40:x:941:G:OP1	2.48	0.44
40:x:1489:A:N7	40:x:1838:G:N2	2.65	0.44
40:x:2618:G:H5'	40:x:2824:G:C6	2.52	0.44
40:x:2991:A:O2'	40:x:3309:G:N7	2.45	0.44
40:x:3055:U:O2'	40:x:3085:G:N2	2.41	0.44
5:C:338:LYS:O	5:C:340:GLY:N	2.50	0.44
17:I:159:LEU:N	40:x:2464:U:H4'	2.32	0.44
32:r:442:ALA:C	32:r:444:GLY:N	2.73	0.44
40:x:2444:C:H42	40:x:2503:G:H22	1.65	0.44
40:x:2701:U:C6	40:x:2701:U:O5'	2.71	0.44
40:x:2829:U:O5'	40:x:2829:U:C6	2.70	0.44
40:x:2873:U:O2	40:x:2873:U:C3'	2.64	0.44
40:x:3204:C:N4	40:x:3205:G:O6	2.50	0.44
32:r:129:GLU:C	32:r:131:ILE:N	2.72	0.44
32:r:308:ASN:C	32:r:310:ILE:N	2.72	0.44
3:B:19:ARG:CA	40:x:3138:U:O2'	2.64	0.44
26:o:152:GLN:C	26:o:154:ARG:N	2.73	0.44
37:S:79:VAL:O	37:S:90:MET:N	2.49	0.44
40:x:38:U:H6	40:x:38:U:O5'	1.99	0.44
40:x:83:U:O2'	40:x:700:C:O2'	2.33	0.44
40:x:2873:U:O2'	40:x:2875:U:OP2	2.29	0.44
5:C:187:LEU:C	40:x:1420:C:H42	2.24	0.44
26:o:139:ILE:C	26:o:141:LYS:N	2.73	0.44
40:x:196:G:N2	40:x:199:A:OP2	2.40	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:X:49:LYS:O	45:X:51:VAL:N	2.51	0.44
3:B:2:SER:N	40:x:2939:G:N7	2.66	0.44
31:P:66:SER:H	40:x:2389:C:C5'	2.31	0.44
32:r:410:ALA:C	32:r:412:HIS:N	2.73	0.44
40:x:423:A:N1	40:x:424:G:N2	2.65	0.44
40:x:835:G:N2	40:x:858:A:N7	2.66	0.44
40:x:2009:C:N4	40:x:2013:C:N3	2.66	0.44
44:z:3:U:O2'	44:z:25:G:N3	2.51	0.44
11:F:222:HIS:O	11:F:227:GLY:N	2.51	0.44
12:h:114:ARG:N	23:L:92:THR:O	2.45	0.44
40:x:714:G:C4	48:a:110:GLY:CA	3.01	0.44
32:r:145:THR:O	32:r:147:GLU:N	2.51	0.44
32:r:408:ALA:C	32:r:410:ALA:N	2.73	0.44
32:r:654:ARG:C	32:r:656:GLU:N	2.72	0.44
40:x:1556:C:C5'	40:x:2521:U:O4	2.66	0.44
40:x:2615:G:H2'	40:x:2616:C:C5'	2.45	0.44
23:L:2:ALA:N	48:a:32:ARG:CA	2.81	0.43
32:r:314:LYS:C	32:r:316:LYS:N	2.73	0.43
40:x:3053:G:H1	40:x:3089:C:H42	1.66	0.43
32:r:310:ILE:C	32:r:312:THR:N	2.72	0.43
33:Q:170:ARG:O	33:Q:172:PHE:N	2.51	0.43
40:x:1996:C:H42	40:x:2025:G:H1	1.66	0.43
40:x:2639:G:C8	40:x:2639:G:O5'	2.68	0.43
40:x:3106:A:H62	40:x:3128:G:H21	1.64	0.43
19:J:104:PHE:CA	40:x:2673:A:H4'	2.48	0.43
32:r:84:THR:C	32:r:86:GLN:H	2.26	0.43
40:x:727:G:O6	40:x:742:G:O2'	2.34	0.43
40:x:2726:C:H3'	40:x:2726:C:O2	2.18	0.43
40:x:2786:G:N2	48:a:59:ARG:H	2.16	0.43
5:C:222:VAL:O	5:C:224:GLY:N	2.52	0.43
15:H:49:ASN:O	15:H:51:GLN:N	2.51	0.43
29:O:59:ARG:CA	40:x:1306:G:C4	3.02	0.43
32:r:691:GLU:C	32:r:693:ARG:N	2.73	0.43
39:T:46:GLY:H	40:x:993:G:P	2.41	0.43
39:T:69:LYS:C	40:x:2735:U:H1'	2.44	0.43
17:I:73:ASP:O	17:I:75:ASP:N	2.51	0.43
27:N:81:TYR:O	40:x:2609:A:O2'	2.34	0.43
32:r:312:THR:C	32:r:314:LYS:H	2.27	0.43
40:x:2041:U:O2'	40:x:2042:G:OP1	2.36	0.43
40:x:2875:U:H4'	40:x:2923:U:H3	1.83	0.43
40:x:911:C:H42	40:x:917:A:H61	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:x:2283:G:H21	40:x:2285:C:H42	1.64	0.43
27:N:172:ARG:H	40:x:288:C:H5''	1.83	0.43
40:x:441:U:O2'	40:x:442:G:C8	2.71	0.43
41:U:97:SER:O	41:U:99:LYS:N	2.52	0.43
44:z:75:G:H2'	44:z:76:A:C8	2.53	0.43
26:o:27:ARG:C	26:o:29:THR:N	2.73	0.43
33:Q:142:GLY:N	40:x:743:C:O2	2.35	0.43
39:T:16:GLN:N	40:x:2757:U:H1'	2.33	0.43
40:x:108:A:H1'	40:x:323:A:H61	1.83	0.43
40:x:1947:G:H22	40:x:2101:C:H42	1.66	0.43
40:x:1996:C:H42	40:x:2025:G:H22	1.67	0.43
26:o:237:MET:C	26:o:239:SER:N	2.71	0.43
32:r:276:GLU:C	32:r:278:SER:N	2.72	0.43
35:R:73:GLY:HA2	40:x:2101:C:H2'	1.99	0.43
40:x:2623:G:H8	40:x:2623:G:O5'	2.02	0.43
40:x:3190:C:H42	40:x:3202:G:H1	1.67	0.43
44:z:75:G:H2'	44:z:76:A:H8	1.83	0.43
26:o:141:LYS:C	26:o:143:LEU:N	2.72	0.43
40:x:1983:G:H1	40:x:2038:C:H42	1.67	0.43
40:x:2872:A:HO2'	40:x:2873:U:H3	1.65	0.43
41:U:43:VAL:O	41:U:45:GLY:N	2.52	0.43
39:T:69:LYS:C	40:x:2735:U:HO2'	2.25	0.42
1:A:207:VAL:C	40:x:2967:A:O3'	2.62	0.42
42:y:49:G:N2	42:y:76:C:O2	2.50	0.42
43:V:23:MET:O	43:V:34:LEU:N	2.43	0.42
3:B:120:LYS:N	40:x:3296:A:OP1	2.52	0.42
32:r:675:VAL:C	32:r:677:ALA:N	2.72	0.42
40:x:2518:C:O2'	40:x:2519:A:OP1	2.36	0.42
19:J:125:MET:N	40:x:2674:A:N3	2.66	0.42
32:r:135:LEU:C	32:r:137:MET:N	2.74	0.42
40:x:1148:G:H22	40:x:1155:C:H42	1.68	0.42
40:x:1260:A:O2'	40:x:1279:C:N4	2.50	0.42
40:x:2873:U:H2'	40:x:2875:U:OP2	2.19	0.42
40:x:1003:A:C2'	40:x:1004:U:H5'	2.50	0.42
40:x:2405:C:O5'	40:x:2405:C:H6	2.02	0.42
40:x:2729:U:H5''	40:x:2729:U:H6	1.84	0.42
15:H:64:HIS:O	15:H:66:ALA:N	2.52	0.42
24:n:26:ILE:O	24:n:28:ASP:N	2.52	0.42
26:o:92:LYS:C	26:o:94:SER:N	2.77	0.42
40:x:2178:A:H5''	40:x:2179:C:H2'	2.01	0.42
40:x:2252:A:H2'	40:x:2253:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:x:3014:U:H2'	40:x:3015:G:C8	2.54	0.42
42:y:57:C:O2	42:y:61:A:O2'	2.35	0.42
19:J:107:ASP:CA	19:J:124:GLY:HA2	2.50	0.42
32:r:404:MET:C	32:r:406:ALA:N	2.73	0.42
32:r:679:THR:O	32:r:681:THR:N	2.52	0.42
40:x:155:G:H5''	40:x:156:G:H2'	2.00	0.42
40:x:2826:U:P	40:x:2870:C:N4	2.91	0.42
5:C:187:LEU:C	40:x:1387:G:O6	2.62	0.42
17:I:159:LEU:H	40:x:2464:U:H4'	1.84	0.42
31:P:113:TYR:O	31:P:151:THR:N	2.48	0.42
35:R:146:LYS:CA	40:x:2092:A:C4	3.02	0.42
35:R:147:ALA:C	35:R:149:ALA:H	2.27	0.42
3:B:99:LEU:H	40:x:3003:G:N2	2.09	0.42
19:J:107:ASP:CA	40:x:2674:A:O2'	2.68	0.42
29:O:130:LYS:O	29:O:132:GLY:N	2.53	0.42
39:T:69:LYS:O	40:x:2735:U:O2'	2.31	0.42
42:y:103:G:N7	42:y:105:A:O2'	2.49	0.42
4:d:74:ARG:O	4:d:94:GLU:N	2.46	0.42
23:L:2:ALA:C	48:a:33:GLY:CA	2.88	0.42
38:u:79:TYR:C	38:u:81:LYS:H	2.26	0.42
40:x:441:U:H6	40:x:441:U:H3'	1.85	0.42
40:x:637:C:H4'	40:x:638:C:OP1	2.20	0.42
40:x:2830:G:N2	40:x:2859:U:C2	2.88	0.42
9:E:97:ASN:O	9:E:99:GLU:N	2.53	0.41
26:o:92:LYS:C	26:o:96:ALA:H	2.17	0.41
32:r:410:ALA:O	32:r:412:HIS:N	2.53	0.41
32:r:441:ALA:C	32:r:444:GLY:H	2.28	0.41
32:r:543:TRP:O	32:r:545:LYS:N	2.53	0.41
35:R:144:GLN:C	35:R:146:LYS:N	2.78	0.41
40:x:2277:C:H42	40:x:2307:G:H1	1.68	0.41
40:x:2759:U:O2'	40:x:2760:C:OP1	2.34	0.41
40:x:705:A:N1	48:a:110:GLY:O	2.52	0.41
16:j:20:ASN:O	42:y:102:U:O2'	2.35	0.41
16:j:81:GLY:N	42:y:95:G:N3	2.59	0.41
23:L:99:HIS:C	23:L:101:ARG:H	2.24	0.41
32:r:240:THR:O	32:r:243:ILE:N	2.53	0.41
32:r:476:LYS:O	32:r:480:MET:CA	2.68	0.41
40:x:441:U:C6	40:x:441:U:O5'	2.73	0.41
40:x:907:G:H4'	40:x:908:G:H5'	2.02	0.41
19:J:150:ASN:N	44:z:57:G:OP1	2.51	0.41
1:A:206:PRO:C	40:x:2968:G:P	3.04	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:f:30:ILE:N	8:f:81:VAL:O	2.53	0.41
26:o:123:PHE:C	26:o:125:CYS:N	2.77	0.41
29:O:38:ALA:H	29:O:107:GLY:HA2	1.85	0.41
39:T:16:GLN:N	40:x:1052:U:H5''	2.35	0.41
40:x:180:C:O2	40:x:237:G:N2	2.53	0.41
40:x:714:G:H3'	48:a:110:GLY:C	2.46	0.41
40:x:2116:G:OP1	40:x:2118:C:N4	2.53	0.41
42:y:56:G:N2	42:y:62:C:O4'	2.54	0.41
19:J:8:PRO:O	44:z:53:U:H5'	2.20	0.41
39:T:69:LYS:CA	40:x:2735:U:O2'	2.68	0.41
40:x:2256:A:N3	40:x:2258:U:OP2	2.53	0.41
19:J:44:THR:O	44:z:39:C:O2'	2.30	0.41
32:r:90:LEU:C	32:r:92:GLY:N	2.74	0.41
32:r:126:GLU:O	32:r:129:GLU:CA	2.69	0.41
40:x:1479:U:O2	40:x:1875:G:N2	2.50	0.41
40:x:3351:U:O2'	40:x:3352:U:OP1	2.35	0.41
40:x:1635:G:N2	40:x:1638:A:OP2	2.45	0.41
40:x:2525:G:O2'	40:x:2526:C:OP2	2.31	0.41
1:A:207:VAL:C	40:x:2415:C:O2'	2.53	0.41
2:c:44:ILE:O	2:c:70:PHE:N	2.53	0.41
25:M:34:ALA:N	25:M:47:ASP:O	2.52	0.41
26:o:139:ILE:C	26:o:141:LYS:H	2.29	0.41
39:T:15:PHE:C	40:x:1052:U:H5'	2.45	0.41
40:x:2256:A:N3	40:x:2256:A:C3'	2.71	0.41
40:x:2835:U:H3	40:x:2853:A:H61	1.69	0.41
32:r:537:ILE:O	32:r:540:LEU:CA	2.69	0.41
40:x:409:A:H2	40:x:1442:U:H1'	1.85	0.41
40:x:1313:G:O2'	40:x:1318:A:N6	2.52	0.41
40:x:2493:U:O2'	40:x:2494:A:O5'	2.27	0.41
40:x:715:A:C4	48:a:113:LEU:N	2.88	0.40
40:x:915:A:N7	40:x:917:A:O2'	2.54	0.40
40:x:2639:G:H2'	40:x:2640:A:C5'	2.51	0.40
19:J:110:ILE:O	19:J:112:LEU:N	2.53	0.40
32:r:404:MET:O	32:r:406:ALA:N	2.54	0.40
40:x:239:G:O2'	40:x:240:U:OP1	2.35	0.40
40:x:1176:C:OP2	40:x:1177:G:O2'	2.36	0.40
40:x:1646:G:H21	40:x:1809:A:H62	1.69	0.40
40:x:2317:A:C8	40:x:2317:A:C3'	3.03	0.40
40:x:2616:C:H6	40:x:2616:C:O5'	2.03	0.40
40:x:2873:U:H3'	40:x:2874:G:H5''	2.03	0.40
19:J:124:GLY:C	40:x:2674:A:C4	2.98	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:n:41:TRP:O	24:n:103:LEU:N	2.55	0.40
29:O:62:THR:N	29:O:69:GLY:HA2	2.36	0.40
29:O:79:ILE:C	29:O:81:TYR:H	2.29	0.40
29:O:79:ILE:C	29:O:81:TYR:N	2.79	0.40
32:r:154:PHE:O	32:r:156:LEU:N	2.55	0.40
32:r:243:ILE:C	32:r:245:THR:H	2.29	0.40
32:r:379:LYS:O	32:r:382:VAL:CA	2.70	0.40
40:x:2500:A:O2'	40:x:2501:U:OP1	2.36	0.40
40:x:714:G:N9	48:a:110:GLY:HA3	2.28	0.40
40:x:880:G:O2'	40:x:881:C:OP1	2.32	0.40
40:x:2462:A:O2'	40:x:2463:G:OP1	2.38	0.40
40:x:2828:G:O5'	40:x:2828:G:H8	2.05	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	250/254 (98%)	156 (62%)	70 (28%)	24 (10%)	0	7
2	c	95/105 (90%)	84 (88%)	10 (10%)	1 (1%)	11	46
3	B	384/387 (99%)	294 (77%)	70 (18%)	20 (5%)	1	15
4	d	107/113 (95%)	88 (82%)	15 (14%)	4 (4%)	2	20
5	C	359/362 (99%)	254 (71%)	80 (22%)	25 (7%)	1	11
6	e	125/130 (96%)	99 (79%)	24 (19%)	2 (2%)	7	38
7	D	294/297 (99%)	229 (78%)	53 (18%)	12 (4%)	2	18
8	f	104/107 (97%)	78 (75%)	19 (18%)	7 (7%)	1	12
9	E	152/176 (86%)	113 (74%)	35 (23%)	4 (3%)	4	25
10	g	110/121 (91%)	78 (71%)	27 (24%)	5 (4%)	2	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	F	220/244 (90%)	181 (82%)	30 (14%)	9 (4%)	2	18
12	h	117/120 (98%)	92 (79%)	21 (18%)	4 (3%)	3	21
13	G	231/256 (90%)	180 (78%)	42 (18%)	9 (4%)	2	19
14	i	97/100 (97%)	78 (80%)	13 (13%)	6 (6%)	1	13
15	H	189/191 (99%)	147 (78%)	37 (20%)	5 (3%)	4	25
16	j	85/88 (97%)	53 (62%)	26 (31%)	6 (7%)	1	11
17	I	215/217 (99%)	159 (74%)	48 (22%)	8 (4%)	2	20
18	k	75/78 (96%)	66 (88%)	8 (11%)	1 (1%)	9	42
19	J	167/174 (96%)	116 (70%)	29 (17%)	22 (13%)	0	4
20	l	48/51 (94%)	33 (69%)	11 (23%)	4 (8%)	0	9
21	K	125/165 (76%)	81 (65%)	27 (22%)	17 (14%)	0	4
22	m	222/245 (91%)	170 (77%)	44 (20%)	8 (4%)	2	20
23	L	191/199 (96%)	141 (74%)	39 (20%)	11 (6%)	1	14
24	n	210/236 (89%)	156 (74%)	48 (23%)	6 (3%)	3	23
25	M	134/138 (97%)	106 (79%)	22 (16%)	6 (4%)	2	17
26	o	345/647 (53%)	223 (65%)	72 (21%)	50 (14%)	0	3
27	N	201/204 (98%)	147 (73%)	44 (22%)	10 (5%)	1	16
28	p	89/92 (97%)	72 (81%)	14 (16%)	3 (3%)	3	21
29	O	195/199 (98%)	143 (73%)	39 (20%)	13 (7%)	1	12
30	q	486/515 (94%)	458 (94%)	22 (4%)	6 (1%)	10	44
31	P	181/184 (98%)	141 (78%)	35 (19%)	5 (3%)	4	24
32	r	277/767 (36%)	155 (56%)	57 (21%)	65 (24%)	0	1
33	Q	183/186 (98%)	143 (78%)	30 (16%)	10 (6%)	1	15
34	s	1991/4910 (40%)	1585 (80%)	229 (12%)	177 (9%)	0	8
35	R	186/189 (98%)	136 (73%)	44 (24%)	6 (3%)	3	21
36	t	61/199 (31%)	52 (85%)	7 (12%)	2 (3%)	3	21
37	S	170/172 (99%)	133 (78%)	31 (18%)	6 (4%)	3	20
38	u	357/593 (60%)	342 (96%)	6 (2%)	9 (2%)	4	26
39	T	157/160 (98%)	90 (57%)	46 (29%)	21 (13%)	0	4
41	U	98/121 (81%)	77 (79%)	17 (17%)	4 (4%)	2	18
43	V	134/137 (98%)	95 (71%)	37 (28%)	2 (2%)	8	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	X	119/142 (84%)	91 (76%)	23 (19%)	5 (4%)	2	17
46	Y	124/127 (98%)	91 (73%)	26 (21%)	7 (6%)	1	14
47	Z	133/136 (98%)	97 (73%)	30 (23%)	6 (4%)	2	17
48	a	146/149 (98%)	89 (61%)	40 (27%)	17 (12%)	0	5
All	All	9939/14383 (69%)	7592 (76%)	1697 (17%)	650 (6%)	2	12

All (650) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	122	ASP
1	A	128	ARG
1	A	133	TYR
1	A	135	ILE
1	A	137	ILE
1	A	196	TRP
1	A	206	PRO
1	A	207	VAL
5	C	95	ARG
5	C	188	ARG
5	C	317	PRO
8	f	103	TYR
8	f	104	PRO
11	F	99	PRO
16	j	5	THR
19	J	8	PRO
19	J	11	ASP
19	J	12	LEU
19	J	74	PRO
19	J	94	ARG
19	J	127	PHE
19	J	165	GLN
20	l	22	PRO
21	K	30	PRO
21	K	58	VAL
23	L	100	ARG
25	M	49	PRO
26	o	13	PRO
26	o	18	LEU
26	o	30	PRO
26	o	31	THR
26	o	32	VAL

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Mol	Chain	Res	Type
26	o	55	GLU
26	o	59	GLU
26	o	61	PHE
26	o	88	LYS
26	o	98	ILE
26	o	100	ARG
26	o	108	VAL
26	o	110	ARG
26	o	112	TYR
26	o	114	ARG
26	o	116	LEU
26	o	139	ILE
26	o	143	LEU
26	o	145	ASP
26	o	157	ILE
26	o	234	ASN
26	o	245	HIS
26	o	246	LEU
26	o	247	ARG
29	O	63	ALA
29	O	75	ALA
29	O	76	PRO
29	O	79	ILE
30	q	249	PRO
31	P	143	PRO
32	r	131	ILE
32	r	137	MET
32	r	154	PHE
32	r	156	LEU
32	r	243	ILE
32	r	382	VAL
32	r	390	LEU
32	r	400	VAL
32	r	402	ARG
32	r	404	MET
32	r	406	ALA
32	r	410	ALA
32	r	441	ALA
32	r	486	ILE
32	r	490	ARG
32	r	559	ASN
32	r	649	LYS

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Mol	Chain	Res	Type
32	r	654	ARG
32	r	679	THR
34	s	368	ARG
34	s	428	VAL
34	s	442	ILE
34	s	443	TYR
34	s	452	ILE
34	s	474	PHE
34	s	475	PRO
34	s	513	SER
34	s	737	TRP
34	s	738	LYS
34	s	754	ILE
34	s	759	ASN
34	s	762	ASN
34	s	773	ARG
34	s	777	HIS
34	s	808	VAL
34	s	809	PHE
34	s	853	SER
34	s	854	ILE
34	s	859	LYS
34	s	866	LYS
34	s	869	PRO
34	s	877	MET
34	s	929	VAL
34	s	1019	VAL
34	s	1076	ARG
34	s	1157	THR
34	s	1285	TYR
34	s	1361	LYS
34	s	1362	GLU
34	s	1409	PRO
34	s	1432	ASN
34	s	1434	GLN
34	s	1467	SER
34	s	1468	LEU
34	s	1500	SER
34	s	1501	VAL
34	s	1517	LEU
34	s	1539	MET
34	s	1613	SER

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Mol	Chain	Res	Type
34	s	1774	SER
34	s	1791	ARG
34	s	1905	PRO
34	s	1933	SER
34	s	2030	LEU
34	s	2047	ASN
34	s	2048	TRP
34	s	2055	PRO
34	s	2060	LYS
34	s	2089	ILE
34	s	2099	THR
34	s	2126	ASN
34	s	2146	THR
34	s	2147	PRO
34	s	2167	HIS
34	s	2184	ILE
34	s	2186	LYS
34	s	2190	VAL
34	s	2192	PHE
34	s	2201	LYS
34	s	2239	GLU
34	s	2244	ASP
34	s	2248	ARG
34	s	2250	LEU
34	s	2303	GLU
34	s	2327	PRO
34	s	2328	LEU
34	s	2356	PRO
34	s	2364	VAL
34	s	2367	ILE
34	s	2375	LYS
34	s	2405	MET
35	R	80	LYS
35	R	144	GLN
38	u	84	VAL
38	u	168	PRO
38	u	235	ASN
38	u	254	GLN
38	u	354	ILE
39	T	17	ARG
39	T	42	ILE
39	T	70	SER

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Mol	Chain	Res	Type
39	T	77	ASN
39	T	87	LYS
39	T	90	ASN
39	T	91	LEU
39	T	92	ARG
39	T	132	PRO
48	a	112	ILE
48	a	119	PRO
1	A	116	VAL
1	A	126	LEU
1	A	185	ALA
1	A	194	ASN
2	c	49	PRO
3	B	4	ARG
3	B	18	PRO
3	B	19	ARG
3	B	20	LYS
3	B	96	PRO
4	d	68	GLU
5	C	76	ARG
5	C	189	ALA
5	C	224	GLY
5	C	270	SER
5	C	282	SER
5	C	338	LYS
7	D	56	THR
7	D	259	LYS
7	D	261	THR
11	F	25	GLN
11	F	109	THR
12	h	112	PRO
13	G	65	LEU
13	G	163	VAL
14	i	22	PRO
14	i	24	PRO
15	H	65	VAL
17	I	98	LYS
19	J	9	MET
19	J	73	GLY
19	J	86	VAL
19	J	115	LYS
19	J	167	TYR

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Mol	Chain	Res	Type
20	l	24	PRO
22	m	30	GLY
22	m	89	PRO
23	L	28	GLN
24	n	27	PHE
25	M	8	LYS
26	o	44	ALA
26	o	57	PHE
26	o	69	PRO
26	o	73	ASP
26	o	89	ASN
26	o	94	SER
26	o	118	PHE
26	o	141	LYS
26	o	144	ARG
26	o	152	GLN
26	o	154	ARG
27	N	18	VAL
27	N	76	PRO
29	O	60	LYS
29	O	61	ALA
29	O	64	PHE
29	O	77	SER
29	O	78	ARG
29	O	111	PRO
29	O	148	LYS
30	q	126	VAL
30	q	127	PHE
32	r	85	SER
32	r	93	PHE
32	r	206	ALA
32	r	208	CYS
32	r	210	ASN
32	r	241	VAL
32	r	245	THR
32	r	261	MET
32	r	262	PHE
32	r	282	ASP
32	r	283	GLY
32	r	296	ASN
32	r	297	LYS
32	r	310	ILE

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Mol	Chain	Res	Type
32	r	312	THR
32	r	386	TYR
32	r	388	PHE
32	r	427	ILE
32	r	429	ASP
32	r	431	PHE
32	r	433	SER
32	r	448	ILE
32	r	477	GLY
32	r	488	LEU
32	r	557	ASP
32	r	633	PHE
32	r	656	GLU
32	r	658	SER
33	Q	19	PRO
33	Q	97	PRO
33	Q	171	LYS
33	Q	173	GLU
34	s	440	ASN
34	s	482	PRO
34	s	483	LYS
34	s	594	THR
34	s	725	HIS
34	s	763	GLU
34	s	768	LYS
34	s	799	GLN
34	s	942	LYS
34	s	960	SER
34	s	992	PHE
34	s	1057	ILE
34	s	1134	GLU
34	s	1139	GLU
34	s	1417	GLN
34	s	1452	ASN
34	s	1465	ARG
34	s	1579	ARG
34	s	1740	HIS
34	s	1950	ASN
34	s	1951	GLN
34	s	2031	GLU
34	s	2056	SER
34	s	2148	GLU

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Mol	Chain	Res	Type
34	s	2185	THR
34	s	2226	ASN
34	s	2246	GLN
34	s	2249	VAL
34	s	2285	LEU
34	s	2305	ILE
34	s	2333	PRO
34	s	2354	GLU
34	s	2359	GLU
34	s	2376	TRP
35	R	82	LYS
36	t	17	HIS
36	t	24	ASN
37	S	22	PRO
37	S	50	LYS
38	u	169	ILE
38	u	390	PHE
39	T	16	GLN
39	T	19	PHE
39	T	21	LYS
39	T	24	ALA
39	T	78	LYS
39	T	124	VAL
41	U	44	GLU
41	U	98	THR
45	X	50	ALA
45	X	87	SER
45	X	102	LEU
46	Y	116	LYS
46	Y	126	LEU
47	Z	17	ARG
48	a	17	ALA
48	a	41	HIS
48	a	104	THR
1	A	120	PRO
1	A	181	LYS
1	A	191	LEU
1	A	193	ARG
1	A	195	SER
3	B	68	HIS
3	B	255	TRP
3	B	257	PRO

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Mol	Chain	Res	Type
3	B	311	PHE
3	B	347	SER
4	d	6	ASP
4	d	61	LYS
5	C	11	LEU
5	C	223	PRO
5	C	268	ALA
5	C	320	ASN
5	C	321	LYS
5	C	339	LEU
6	e	12	LYS
7	D	151	GLN
8	f	20	LYS
8	f	91	ALA
9	E	37	GLY
9	E	98	VAL
10	g	48	GLY
10	g	60	ARG
10	g	78	GLY
11	F	98	LYS
11	F	193	PRO
11	F	226	GLY
14	i	16	LYS
15	H	50	ASN
16	j	10	LYS
16	j	39	TYR
16	j	72	ARG
16	j	77	GLY
17	I	18	LYS
17	I	74	VAL
17	I	136	THR
18	k	18	ALA
19	J	140	ARG
19	J	169	ALA
19	J	173	ASP
20	l	36	ARG
21	K	17	ALA
21	K	39	PRO
21	K	40	LYS
21	K	76	SER
21	K	89	PRO
21	K	98	VAL

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Mol	Chain	Res	Type
21	K	102	GLY
23	L	61	PRO
23	L	62	THR
23	L	165	SER
23	L	166	ALA
24	n	50	THR
26	o	34	ARG
26	o	53	THR
26	o	91	TYR
26	o	96	ALA
26	o	150	LEU
26	o	199	PHE
26	o	244	ALA
27	N	80	THR
27	N	158	HIS
27	N	175	ASN
28	p	23	ARG
28	p	24	ARG
29	O	89	SER
30	q	89	SER
30	q	93	LYS
30	q	129	VAL
31	P	41	LEU
31	P	96	GLN
31	P	133	HIS
32	r	133	SER
32	r	204	THR
32	r	247	ALA
32	r	314	LYS
32	r	316	LYS
32	r	637	ALA
32	r	652	GLU
32	r	698	LEU
33	Q	73	GLN
34	s	308	SER
34	s	362	PRO
34	s	459	GLU
34	s	765	GLU
34	s	787	ALA
34	s	851	SER
34	s	905	GLU
34	s	1063	LYS

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Mol	Chain	Res	Type
34	s	1194	GLN
34	s	1233	GLU
34	s	1469	ASN
34	s	1512	GLU
34	s	1515	LEU
34	s	1523	SER
34	s	1723	ALA
34	s	1752	GLY
34	s	1820	ALA
34	s	1888	THR
34	s	1923	CYS
34	s	2029	PRO
34	s	2098	LEU
34	s	2168	PRO
34	s	2188	ALA
35	R	16	GLY
35	R	136	ARG
35	R	139	VAL
37	S	133	ALA
37	S	154	HIS
38	u	85	ASN
39	T	22	HIS
45	X	41	ALA
46	Y	5	SER
46	Y	89	LYS
47	Z	59	ALA
48	a	32	ARG
48	a	46	ASP
48	a	47	LYS
48	a	52	TYR
48	a	58	MET
48	a	97	GLU
48	a	132	LYS
1	A	69	TYR
1	A	180	LEU
3	B	9	PRO
3	B	15	GLY
3	B	234	GLY
3	B	314	TYR
3	B	353	GLU
3	B	362	ALA
5	C	89	ALA

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Mol	Chain	Res	Type
5	C	288	ARG
5	C	291	ASN
7	D	87	GLY
7	D	256	THR
7	D	258	LYS
8	f	105	SER
9	E	75	PRO
10	g	73	SER
11	F	76	TYR
11	F	172	ASN
12	h	81	ARG
13	G	36	ILE
13	G	196	ALA
15	H	62	ARG
15	H	64	HIS
16	j	15	SER
19	J	95	ASN
19	J	108	GLU
19	J	114	ILE
19	J	117	ASP
21	K	19	GLY
21	K	51	LYS
21	K	52	GLU
21	K	55	GLY
22	m	31	SER
22	m	111	ASN
23	L	152	THR
24	n	133	LEU
24	n	162	GLU
25	M	9	ALA
26	o	87	GLU
26	o	179	GLY
26	o	198	ALA
26	o	212	LYS
26	o	235	ILE
27	N	95	GLN
32	r	92	GLY
32	r	146	ALA
32	r	544	LYS
32	r	677	ALA
33	Q	154	GLY
33	Q	166	LEU

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Mol	Chain	Res	Type
34	s	797	GLU
34	s	1180	GLU
34	s	1389	LEU
34	s	1413	ARG
34	s	1484	ARG
34	s	1564	PRO
34	s	1783	PHE
34	s	1816	GLU
34	s	1949	LEU
34	s	1956	GLU
34	s	2057	ASN
34	s	2097	ASP
37	S	32	SER
38	u	357	PRO
39	T	82	ASN
48	a	78	LEU
1	A	26	ALA
1	A	129	ALA
1	A	209	HIS
1	A	213	GLY
3	B	317	ILE
3	B	349	LYS
5	C	75	PRO
5	C	131	VAL
5	C	221	ASN
6	e	48	GLY
7	D	125	VAL
7	D	260	PHE
8	f	62	SER
11	F	191	VAL
12	h	79	ASP
13	G	50	VAL
13	G	68	ARG
14	i	3	VAL
15	H	59	ASN
17	I	151	VAL
17	I	168	ALA
19	J	24	GLY
19	J	111	ASP
19	J	172	LEU
20	l	5	LYS
21	K	32	ILE

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Mol	Chain	Res	Type
21	K	100	HIS
21	K	109	ILE
22	m	112	ASP
23	L	84	GLY
23	L	94	GLY
23	L	136	GLU
24	n	130	LYS
25	M	6	ILE
25	M	82	SER
25	M	90	VAL
27	N	49	ARG
27	N	55	ALA
27	N	58	GLY
28	p	7	LYS
29	O	131	PRO
32	r	308	ASN
32	r	680	LEU
33	Q	9	GLN
33	Q	38	ARG
34	s	530	ASN
34	s	803	ILE
34	s	1176	PRO
34	s	1238	ALA
34	s	1302	THR
34	s	1447	LYS
34	s	1449	ASP
34	s	1799	ASP
34	s	2080	MET
34	s	2199	LEU
34	s	2213	ASN
34	s	2219	PRO
34	s	2331	TYR
34	s	2347	ASP
34	s	2411	ILE
39	T	28	SER
39	T	127	GLN
41	U	11	ILE
41	U	38	ILE
45	X	23	ALA
46	Y	34	PRO
47	Z	32	GLY
47	Z	38	PHE

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Mol	Chain	Res	Type
47	Z	97	SER
3	B	83	PRO
4	d	7	VAL
7	D	19	PRO
8	f	90	PRO
9	E	36	PRO
13	G	157	VAL
14	i	33	ALA
17	I	104	SER
22	m	44	ASP
23	L	32	LYS
24	n	70	ARG
26	o	121	SER
26	o	140	VAL
32	r	384	GLY
32	r	411	CYS
33	Q	175	ALA
34	s	593	PRO
34	s	602	ILE
34	s	646	THR
34	s	764	ASN
34	s	953	SER
34	s	1170	ASN
34	s	2150	PHE
34	s	2217	CYS
34	s	2330	HIS
37	S	132	THR
43	V	3	GLY
5	C	173	GLY
10	g	104	VAL
12	h	47	VAL
13	G	30	THR
34	s	289	VAL
34	s	604	ILE
34	s	956	LYS
47	Z	103	GLN
21	K	22	VAL
26	o	29	THR
31	P	77	GLY
32	r	462	ILE
34	s	2096	VAL
39	T	23	GLY

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Mol	Chain	Res	Type
39	T	123	GLY
1	A	178	PRO
5	C	204	GLY
5	C	245	GLY
5	C	348	GLY
7	D	181	PRO
34	s	1186	PRO
34	s	1627	VAL
34	s	2338	ARG
46	Y	96	PRO
48	a	57	GLY
13	G	75	ILE
14	i	7	ILE
22	m	105	GLY
22	m	148	VAL
34	s	2365	ILE
46	Y	123	GLY
48	a	72	VAL
3	B	268	GLY
7	D	139	PRO
17	I	125	GLY
27	N	154	PRO
32	r	435	GLY
34	s	693	LYS
34	s	1005	LYS
34	s	2254	PRO
34	s	2355	GLU
43	V	107	GLY
48	a	36	GLY
48	a	110	GLY

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
40	x	3393/3396 (99%)	376 (11%)	0
42	y	157/158 (99%)	20 (12%)	0
44	z	120/121 (99%)	7 (5%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	3670/3675 (99%)	403 (10%)	0

All (403) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
40	x	22	G
40	x	40	A
40	x	41	G
40	x	49	A
40	x	60	A
40	x	66	A
40	x	92	G
40	x	110	G
40	x	113	C
40	x	121	A
40	x	122	A
40	x	123	A
40	x	135	C
40	x	136	G
40	x	156	G
40	x	191	U
40	x	200	C
40	x	210	U
40	x	218	G
40	x	219	A
40	x	240	U
40	x	252	U
40	x	269	G
40	x	295	A
40	x	298	U
40	x	316	U
40	x	323	A
40	x	329	U
40	x	336	A
40	x	337	G
40	x	339	C
40	x	346	C
40	x	376	G
40	x	398	A
40	x	401	U
40	x	402	A
40	x	403	C

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Mol	Chain	Res	Type
40	x	421	G
40	x	422	A
40	x	486	U
40	x	492	U
40	x	521	A
40	x	534	U
40	x	535	G
40	x	546	C
40	x	547	G
40	x	548	G
40	x	552	G
40	x	557	A
40	x	559	A
40	x	579	G
40	x	604	G
40	x	609	G
40	x	611	A
40	x	612	U
40	x	621	A
40	x	638	C
40	x	646	A
40	x	647	A
40	x	649	A
40	x	677	A
40	x	681	U
40	x	705	A
40	x	764	U
40	x	765	C
40	x	767	U
40	x	776	U
40	x	777	U
40	x	780	A
40	x	781	G
40	x	806	A
40	x	817	A
40	x	830	A
40	x	849	C
40	x	874	U
40	x	880	G
40	x	881	C
40	x	907	G
40	x	914	A

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Mol	Chain	Res	Type
40	x	916	G
40	x	917	A
40	x	924	G
40	x	937	G
40	x	944	C
40	x	959	C
40	x	979	U
40	x	980	A
40	x	982	C
40	x	989	A
40	x	995	U
40	x	1001	G
40	x	1006	A
40	x	1007	U
40	x	1028	U
40	x	1045	C
40	x	1046	A
40	x	1049	C
40	x	1063	G
40	x	1065	A
40	x	1072	G
40	x	1081	U
40	x	1095	U
40	x	1098	A
40	x	1103	A
40	x	1104	G
40	x	1116	G
40	x	1117	G
40	x	1139	G
40	x	1159	A
40	x	1160	C
40	x	1180	A
40	x	1181	U
40	x	1192	C
40	x	1200	A
40	x	1201	C
40	x	1202	A
40	x	1222	G
40	x	1236	G
40	x	1240	A
40	x	1241	U
40	x	1242	G

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Mol	Chain	Res	Type
40	x	1243	G
40	x	1244	A
40	x	1245	A
40	x	1246	G
40	x	1254	C
40	x	1263	A
40	x	1264	G
40	x	1274	A
40	x	1278	A
40	x	1279	C
40	x	1287	A
40	x	1289	G
40	x	1295	G
40	x	1302	A
40	x	1305	U
40	x	1308	A
40	x	1309	U
40	x	1330	A
40	x	1351	U
40	x	1352	A
40	x	1354	G
40	x	1355	A
40	x	1357	G
40	x	1367	G
40	x	1386	A
40	x	1390	A
40	x	1399	A
40	x	1400	G
40	x	1419	A
40	x	1437	C
40	x	1446	A
40	x	1481	A
40	x	1508	C
40	x	1511	U
40	x	1563	C
40	x	1568	U
40	x	1570	U
40	x	1571	A
40	x	1572	U
40	x	1583	A
40	x	1589	A
40	x	1607	U

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Mol	Chain	Res	Type
40	x	1629	U
40	x	1643	A
40	x	1645	U
40	x	1657	C
40	x	1717	U
40	x	1728	G
40	x	1750	A
40	x	1751	G
40	x	1760	A
40	x	1765	U
40	x	1780	G
40	x	1797	A
40	x	1816	A
40	x	1819	U
40	x	1821	U
40	x	1841	A
40	x	1842	A
40	x	1880	U
40	x	1893	A
40	x	1906	G
40	x	1953	G
40	x	1966	U
40	x	1973	G
40	x	2010	U
40	x	2011	U
40	x	2013	C
40	x	2032	U
40	x	2042	G
40	x	2056	U
40	x	2061	G
40	x	2067	U
40	x	2071	A
40	x	2076	G
40	x	2080	C
40	x	2087	C
40	x	2089	A
40	x	2094	C
40	x	2102	U
40	x	2113	A
40	x	2121	G
40	x	2122	G
40	x	2131	A

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Mol	Chain	Res	Type
40	x	2158	A
40	x	2170	U
40	x	2179	C
40	x	2188	A
40	x	2205	U
40	x	2228	A
40	x	2244	A
40	x	2249	G
40	x	2255	A
40	x	2260	U
40	x	2273	G
40	x	2275	A
40	x	2279	A
40	x	2281	A
40	x	2298	U
40	x	2307	G
40	x	2363	A
40	x	2374	C
40	x	2388	U
40	x	2397	A
40	x	2411	U
40	x	2418	G
40	x	2440	G
40	x	2446	U
40	x	2451	G
40	x	2453	U
40	x	2463	G
40	x	2469	G
40	x	2472	U
40	x	2477	G
40	x	2478	C
40	x	2479	C
40	x	2484	A
40	x	2490	C
40	x	2493	U
40	x	2494	A
40	x	2495	C
40	x	2496	C
40	x	2501	U
40	x	2502	A
40	x	2505	U
40	x	2508	U

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Mol	Chain	Res	Type
40	x	2510	U
40	x	2514	U
40	x	2519	A
40	x	2523	A
40	x	2524	A
40	x	2526	C
40	x	2531	C
40	x	2538	U
40	x	2540	A
40	x	2541	U
40	x	2542	U
40	x	2547	A
40	x	2548	C
40	x	2549	G
40	x	2552	C
40	x	2569	A
40	x	2570	U
40	x	2571	U
40	x	2572	C
40	x	2573	G
40	x	2590	A
40	x	2593	A
40	x	2601	A
40	x	2606	G
40	x	2614	G
40	x	2619	G
40	x	2621	G
40	x	2622	C
40	x	2627	C
40	x	2630	C
40	x	2636	A
40	x	2652	U
40	x	2656	A
40	x	2674	A
40	x	2677	G
40	x	2689	A
40	x	2691	A
40	x	2694	A
40	x	2696	A
40	x	2700	G
40	x	2701	U
40	x	2714	G

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Mol	Chain	Res	Type
40	x	2726	C
40	x	2728	G
40	x	2729	U
40	x	2730	G
40	x	2753	G
40	x	2760	C
40	x	2762	A
40	x	2772	C
40	x	2777	G
40	x	2778	G
40	x	2785	A
40	x	2797	C
40	x	2798	C
40	x	2800	G
40	x	2801	A
40	x	2802	A
40	x	2803	A
40	x	2805	G
40	x	2806	U
40	x	2828	G
40	x	2830	G
40	x	2831	G
40	x	2845	A
40	x	2873	U
40	x	2887	A
40	x	2896	A
40	x	2899	C
40	x	2935	U
40	x	2936	A
40	x	2957	G
40	x	2983	C
40	x	2996	U
40	x	2997	G
40	x	3012	A
40	x	3056	U
40	x	3078	U
40	x	3086	A
40	x	3092	C
40	x	3093	C
40	x	3101	G
40	x	3122	A
40	x	3130	A

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Mol	Chain	Res	Type
40	x	3131	U
40	x	3142	A
40	x	3143	C
40	x	3144	G
40	x	3155	U
40	x	3165	A
40	x	3173	G
40	x	3174	A
40	x	3176	G
40	x	3179	U
40	x	3181	C
40	x	3187	A
40	x	3198	U
40	x	3207	U
40	x	3217	C
40	x	3219	G
40	x	3229	G
40	x	3243	A
40	x	3245	A
40	x	3247	G
40	x	3259	U
40	x	3260	G
40	x	3270	U
40	x	3272	C
40	x	3273	A
40	x	3276	G
40	x	3279	A
40	x	3281	U
40	x	3294	A
40	x	3304	U
40	x	3313	U
40	x	3316	A
40	x	3318	G
40	x	3319	U
40	x	3320	A
40	x	3351	U
40	x	3352	U
40	x	3353	G
40	x	3355	U
40	x	3369	G
40	x	3370	A
40	x	3375	A

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Mol	Chain	Res	Type
40	x	3376	A
40	x	3378	C
40	x	3390	G
42	y	17	A
42	y	34	U
42	y	35	C
42	y	37	A
42	y	39	G
42	y	52	A
42	y	59	A
42	y	62	C
42	y	63	G
42	y	72	A
42	y	80	A
42	y	86	U
42	y	90	U
42	y	95	G
42	y	104	A
42	y	106	C
42	y	111	A
42	y	113	U
42	y	125	U
42	y	126	A
44	z	13	A
44	z	53	U
44	z	54	U
44	z	65	G
44	z	87	G
44	z	102	A
44	z	112	G

There are no RNA pucker outliers to report.

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

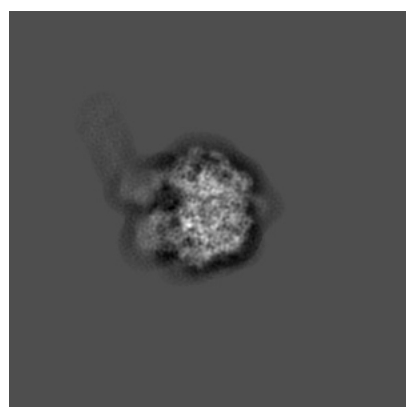
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3199. These allow visual inspection of the internal detail of the map and identification of artifacts.

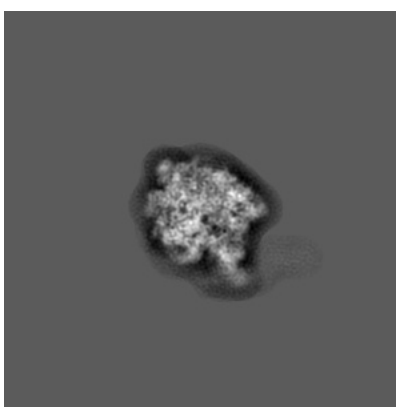
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

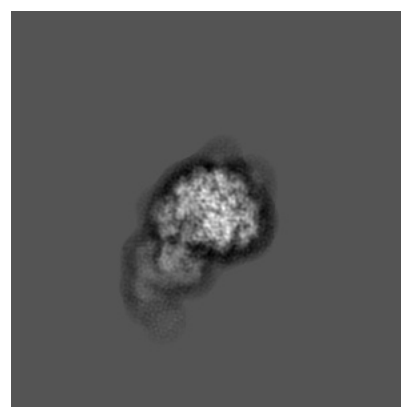
6.1.1 Primary map



X



Y

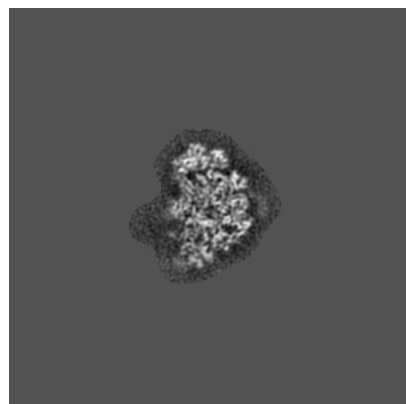


Z

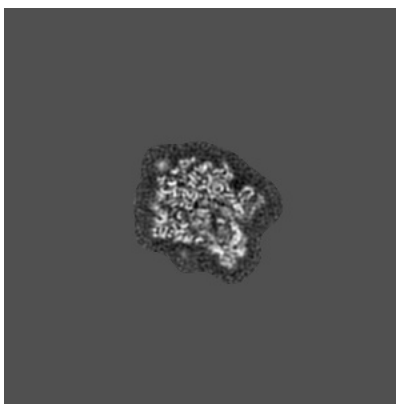
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

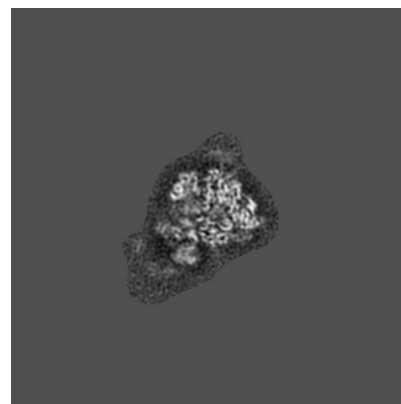
6.2.1 Primary map



X Index: 200



Y Index: 200

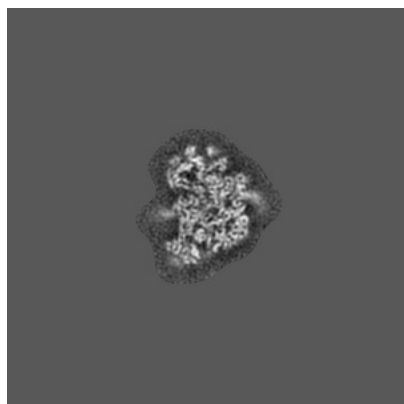


Z Index: 200

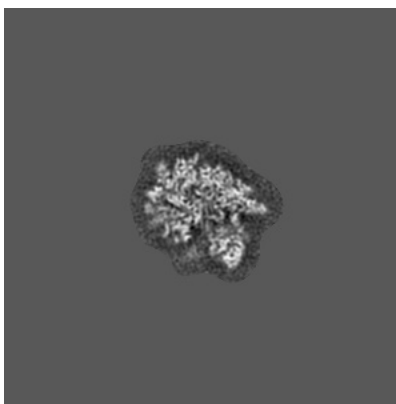
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

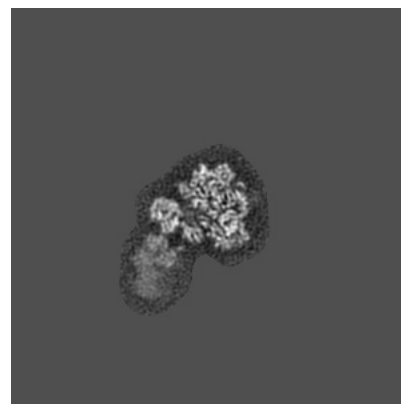
6.3.1 Primary map



X Index: 206



Y Index: 192

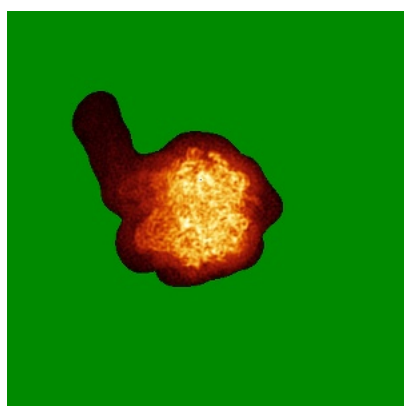


Z Index: 226

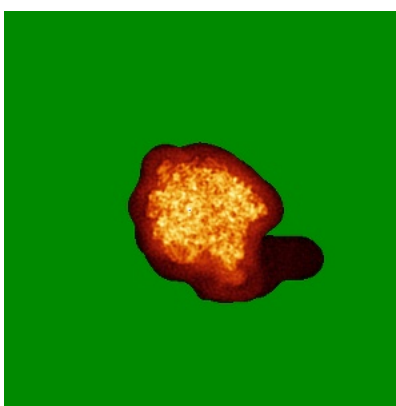
The images above show the largest variance slices of the map in three orthogonal directions.

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

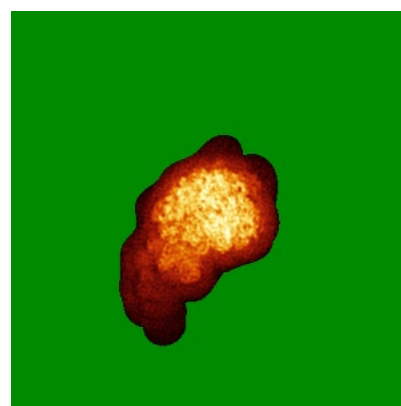
6.4.1 Primary map



X



Y

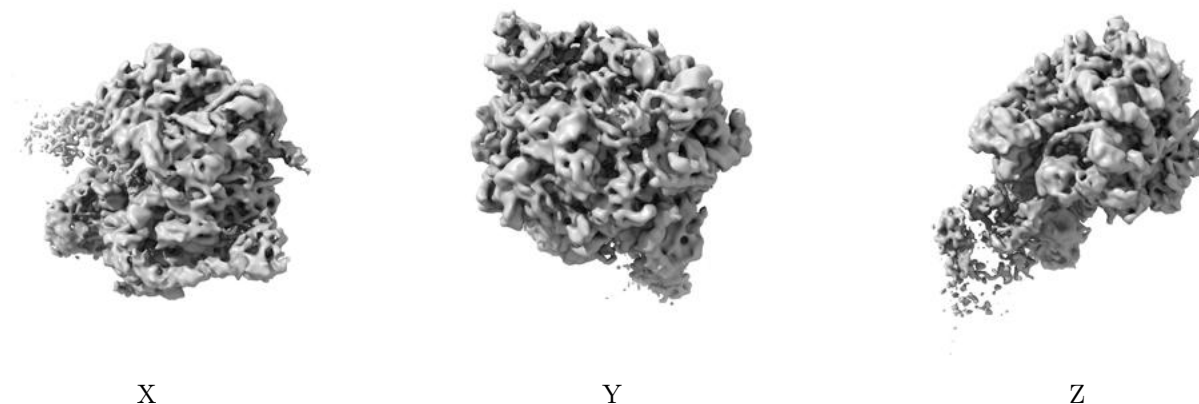


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

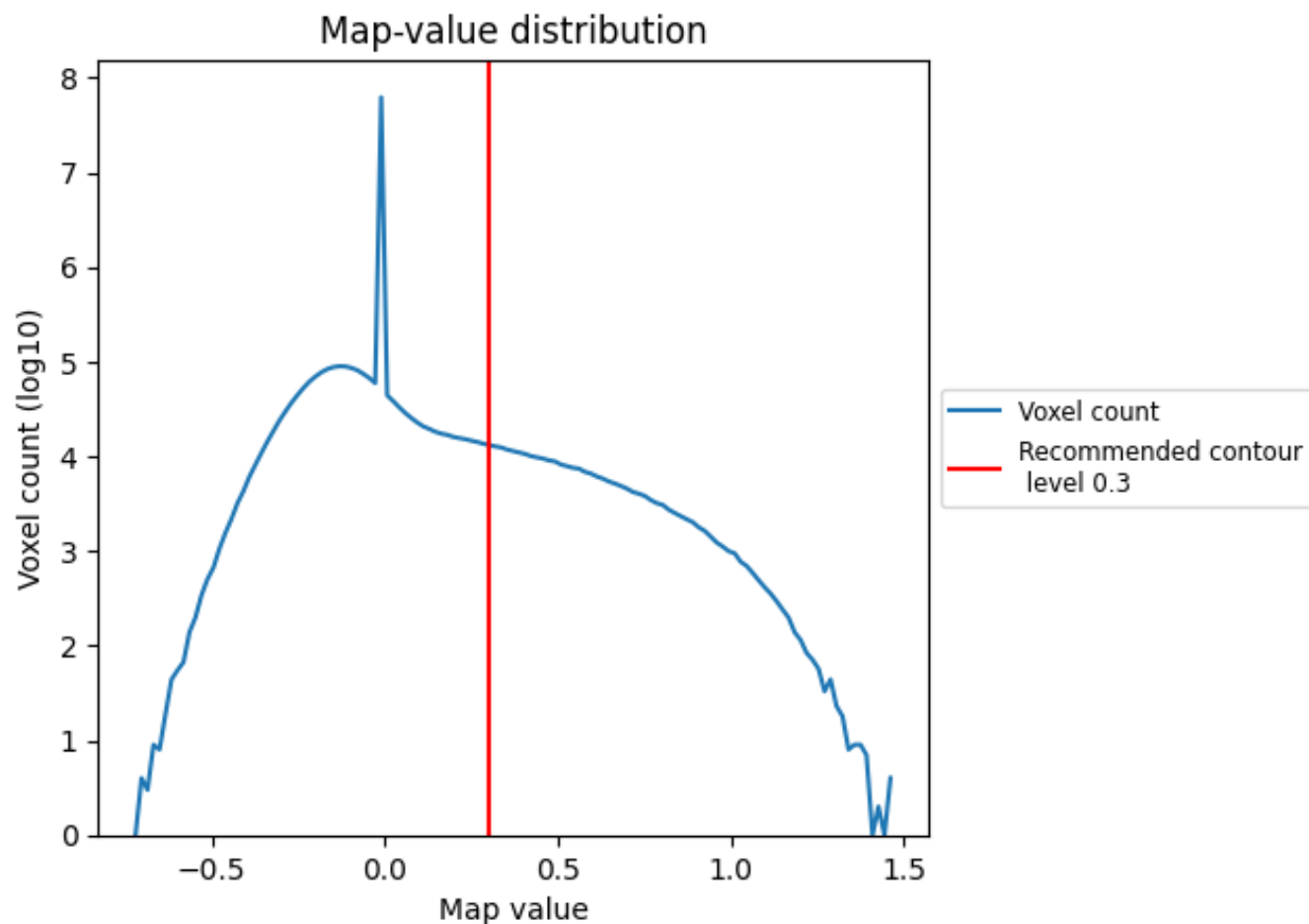
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

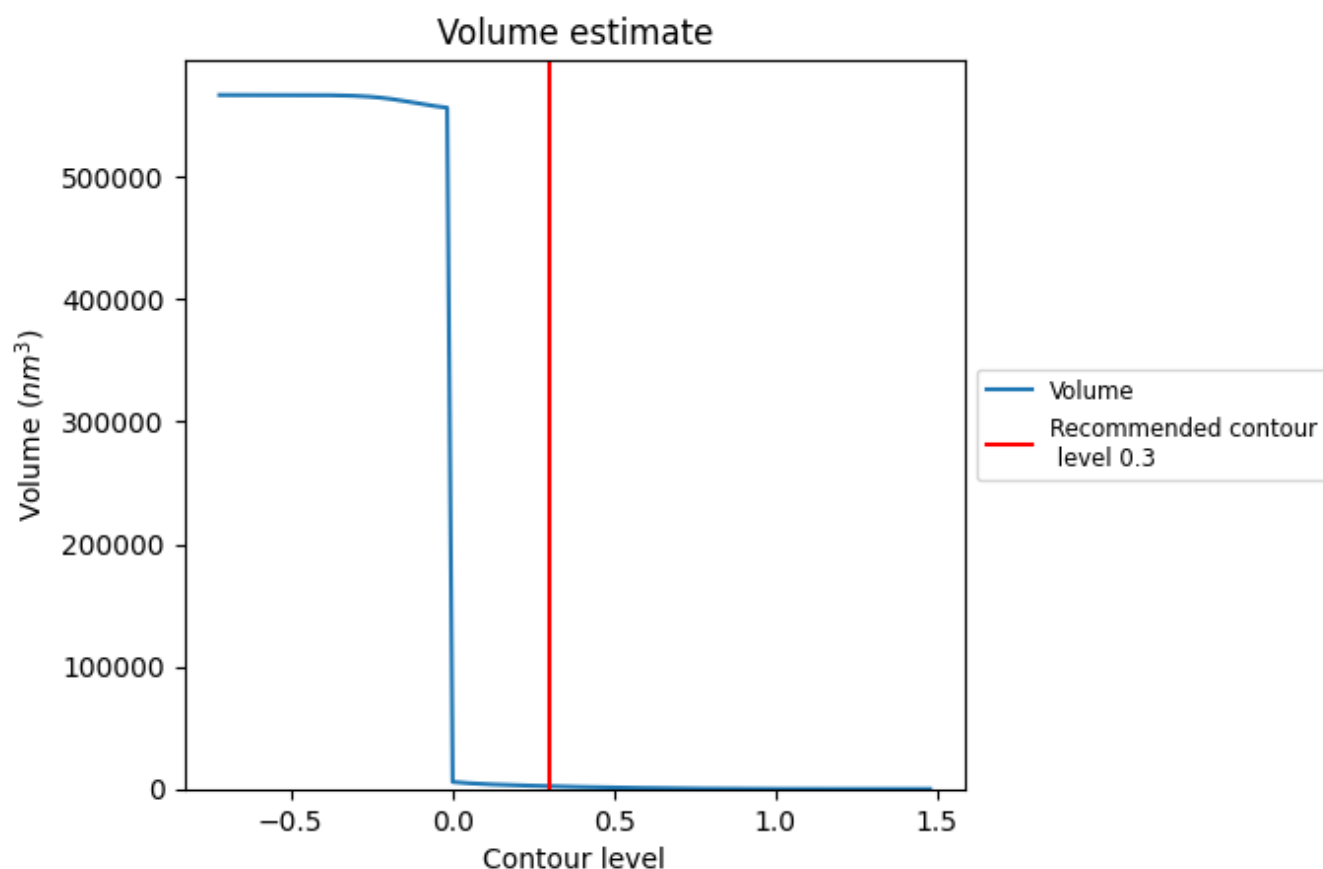
This section contains the results of statistical analysis of the map.

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.

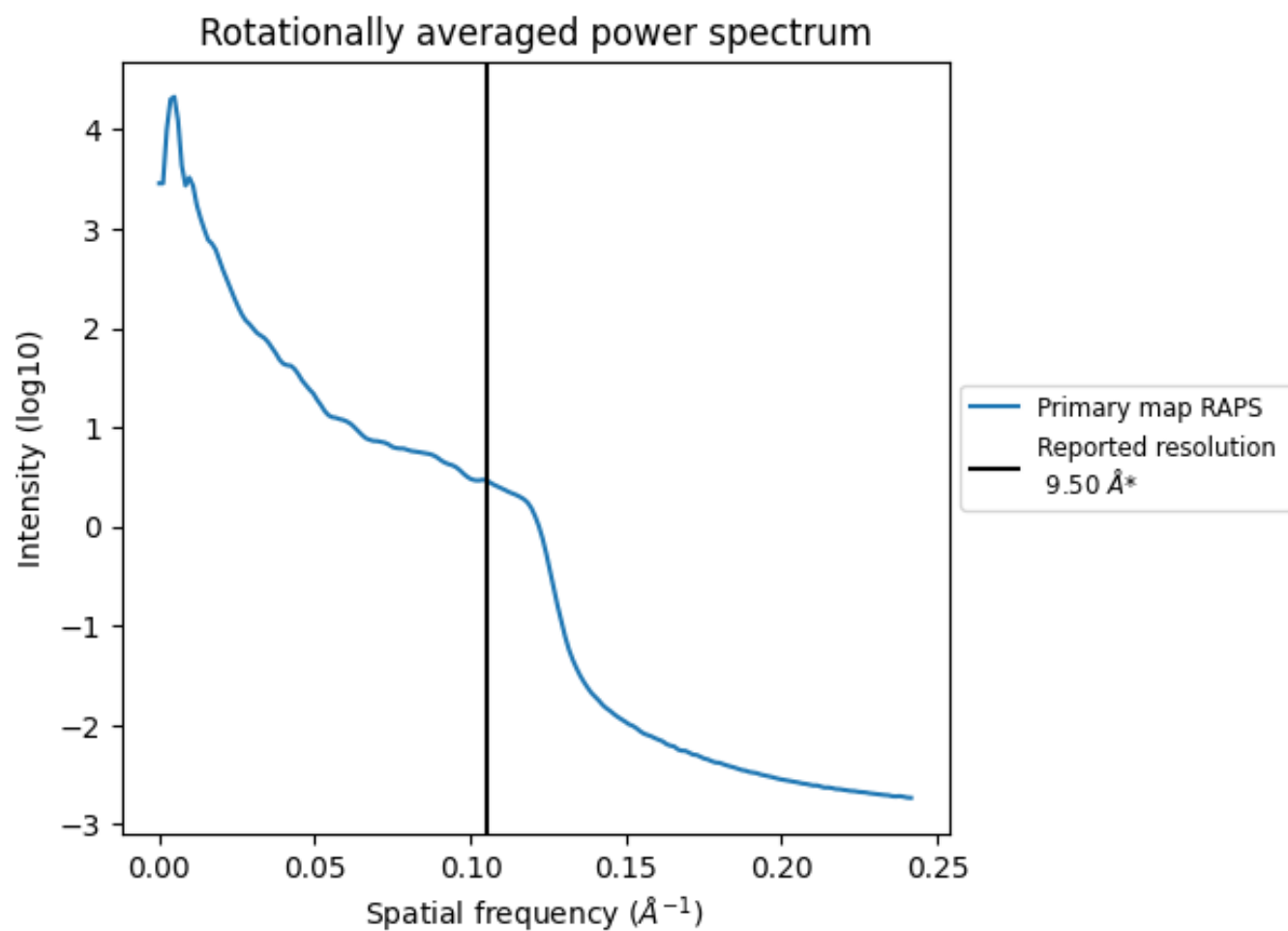
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2263 nm³; this corresponds to an approximate mass of 2044 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 0.105 Å⁻¹

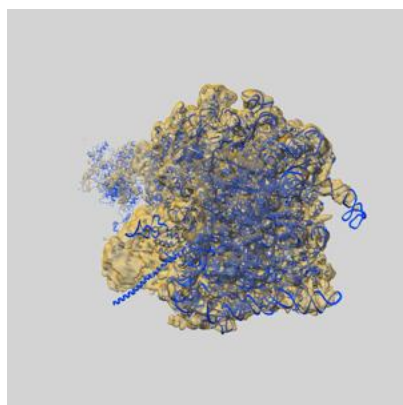
8 Fourier-Shell correlation

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

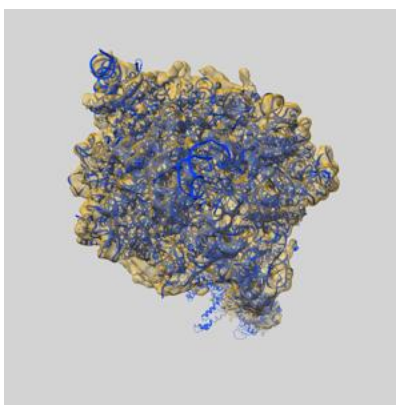
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3199 and PDB model 5JCS. Per-residue inclusion information can be found in section [3](#) on page [12](#).

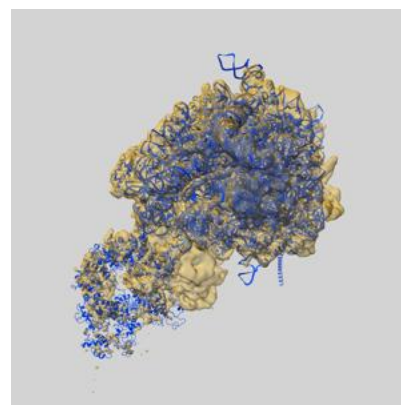
9.1 Map-model overlay [i](#)



X



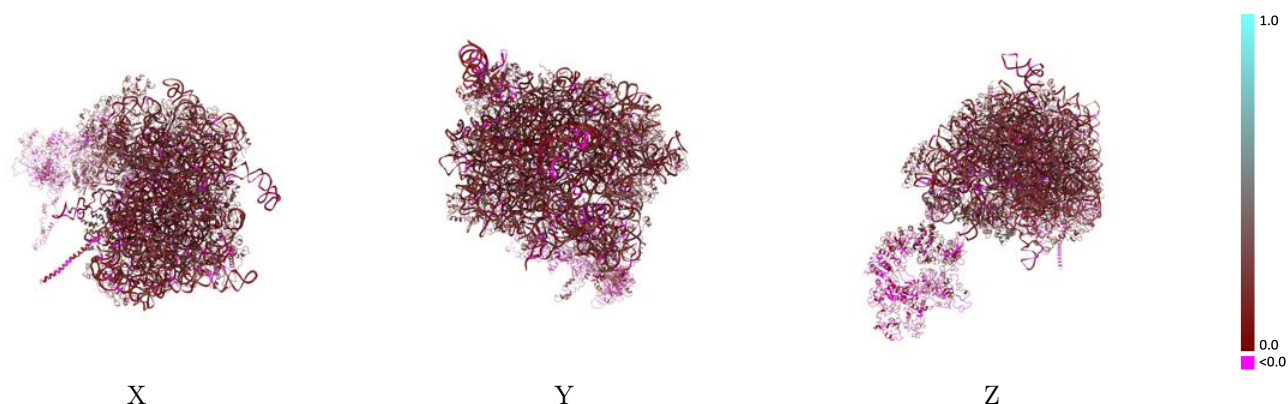
Y



Z

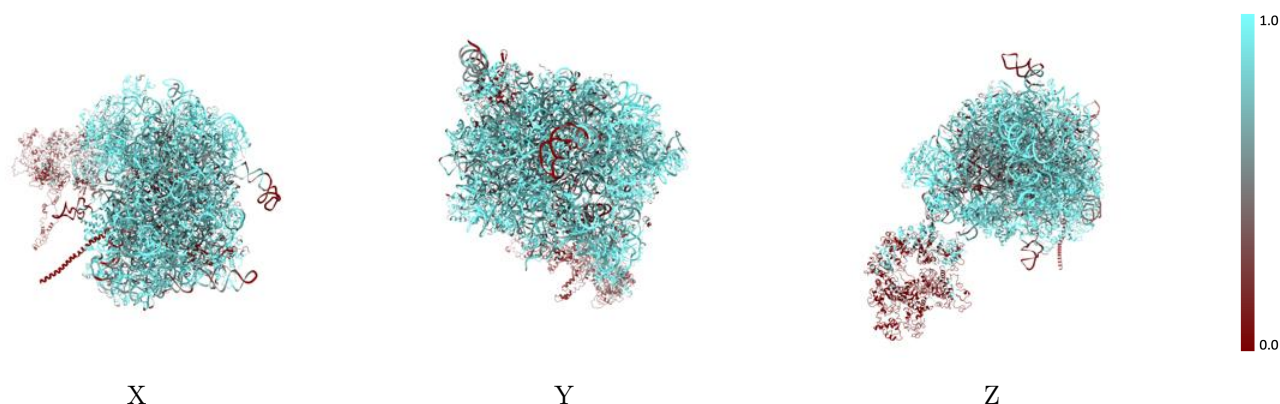
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



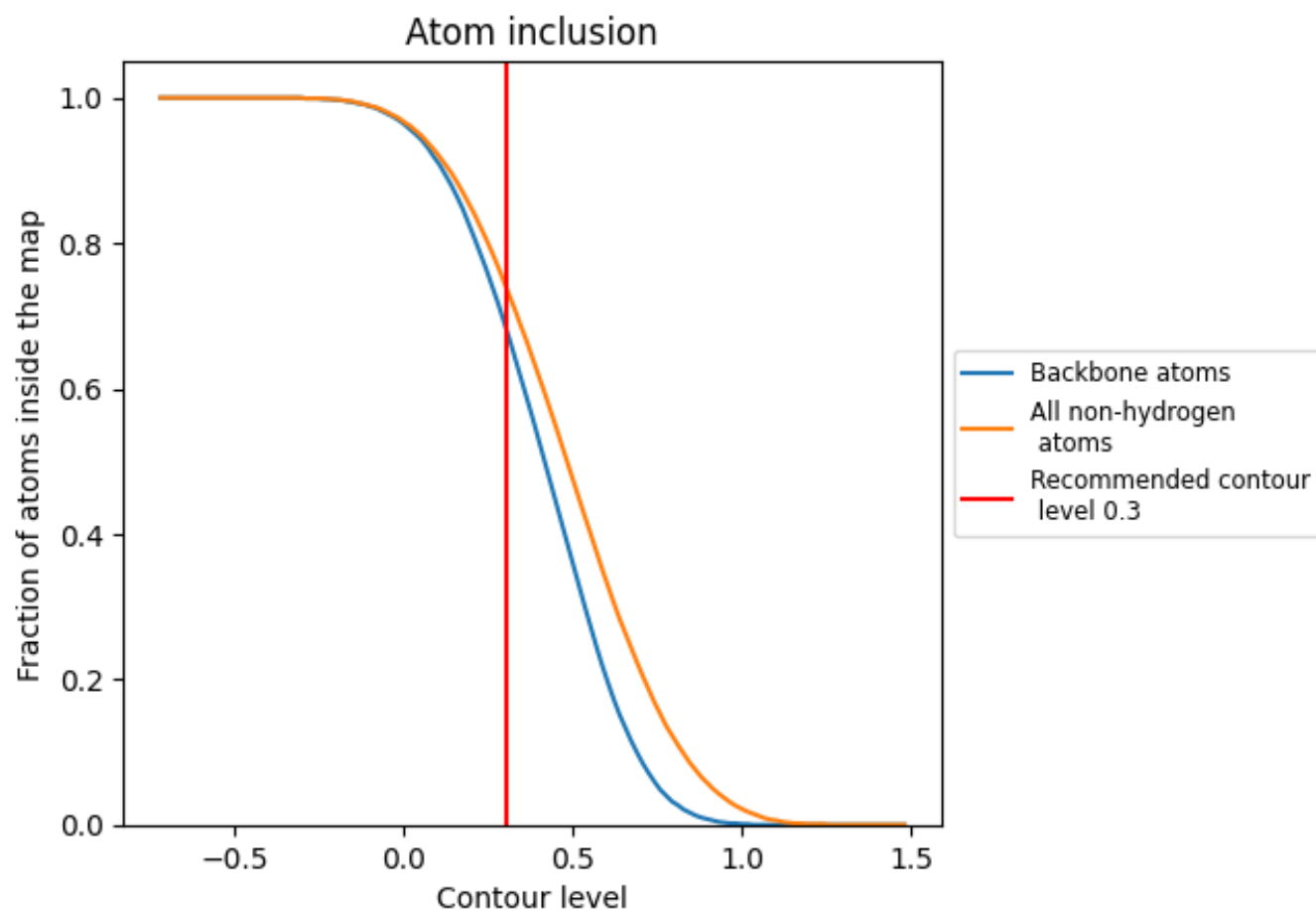
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 74% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7410	 0.1460
A	 0.5510	 0.1300
B	 0.7680	 0.1560
C	 0.6970	 0.1620
D	 0.8290	 0.1880
E	 0.8120	 0.1930
F	 0.8750	 0.2170
G	 0.7940	 0.1700
H	 0.8720	 0.2110
I	 0.1440	 0.0270
J	 0.9730	 0.2200
K	 0.7730	 0.1550
L	 0.8150	 0.2240
M	 0.8550	 0.2100
N	 0.7160	 0.1600
O	 0.7520	 0.1850
P	 0.7000	 0.1780
Q	 0.6290	 0.1620
R	 0.4970	 0.1260
S	 0.8600	 0.2170
T	 0.3450	 0.0350
U	 0.9220	 0.2360
V	 0.7270	 0.1850
X	 0.6830	 0.1650
Y	 0.8090	 0.1760
Z	 0.8530	 0.1750
a	 0.5790	 0.1180
c	 0.8350	 0.2030
d	 0.7770	 0.1850
e	 0.7100	 0.1950
f	 0.7710	 0.1620
g	 0.5350	 0.1170
h	 0.8700	 0.2310
i	 0.7520	 0.1900
j	 0.5590	 0.1000



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Chain	Atom inclusion	Q-score
k	 0.8830	 0.2150
l	 0.6430	 0.1760
m	 0.9350	 0.1940
n	 0.9520	 0.2070
o	 0.8750	 0.2300
p	 0.6420	 0.1540
q	 0.8610	 0.1840
r	 0.9720	 0.3470
s	 0.2120	 0.0620
t	 0.8130	 0.1450
u	 0.5510	 0.1670
x	 0.7880	 0.1400
y	 0.8110	 0.1410
z	 0.8850	 0.1520