



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:01 AM UTC

PDB ID : 6G90 / pdb_00006g90
EMDB ID : EMD-4364
Title : Prespliceosome structure provides insight into spliceosome assembly and regulation (map A2)
Authors : Plaschka, C.; Lin, P.-C.; Charenton, C.; Nagai, K.
Deposited on : 2018-04-10
Resolution : 4.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

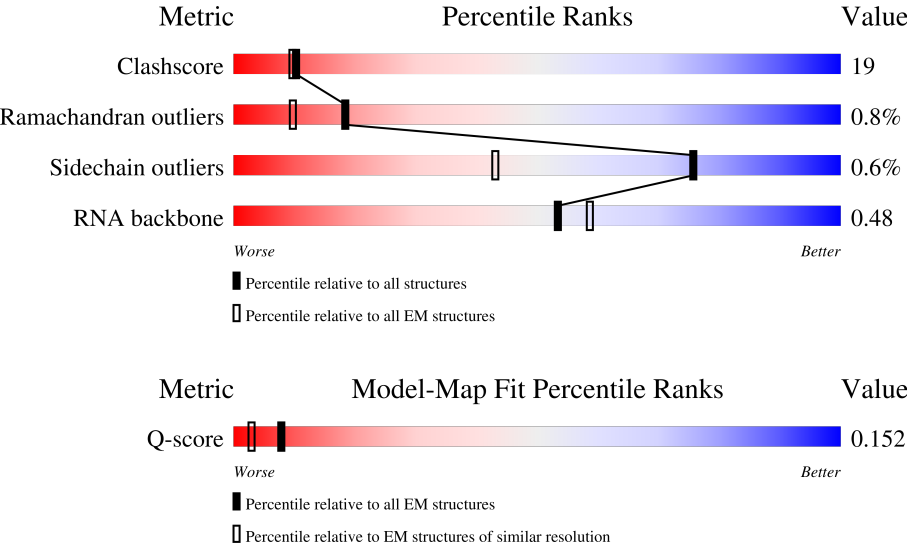
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 4.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7587 (3.50 - 4.50)

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

Mol	Chain	Length	Quality of chain
1	1	407	17% 42% 32% 6% 20%
2	2	143	100% 15% 36% 37% 11%
3	A	298	33% 67%

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Mol	Chain	Length	Quality of chain
4	B	300	
5	C	231	
6	D	629	
7	E	544	
8	F	523	
9	G	492	
10	H	261	
11	I	38	
12	J	620	
13	O	971	
14	P	1361	
15	Q	435	
16	R	213	
17	S	107	
18	T	530	
19	U	266	
20	V	280	
21	W	238	
22	X	51	
23	Y	111	
24	Z	85	
25	b	196	
25	s	196	
26	d	101	
26	v	101	

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Mol	Chain	Length	Quality of chain
27	e	94	
27	w	94	
28	f	86	
28	x	86	
29	g	77	
29	y	77	
30	h	146	
30	t	146	
31	i	110	
31	u	110	

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 65050 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called U1 snRNA,U1 snRNA,U1 snRNA,U1 snRNA,U1 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	327	Total	C	N	O	P	0	0
			6625	2951	1072	2275	327		

- Molecule 2 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	143	Total	C	N	O	P	0	0
			3025	1352	513	1017	143		

- Molecule 3 is a protein called U1 small nuclear ribonucleoprotein A,U1 small nuclear ribonucleoprotein A,U1 small nuclear ribonucleoprotein A,U1 small nuclear ribonucleoprotein A,U1 small nuclear ribonucleoprotein A.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	A	99	Total	C	N	O	0	0
			492	294	99	99		

- Molecule 4 is a protein called U1 small nuclear ribonucleoprotein 70 kDa homolog,U1 small nuclear ribonucleoprotein 70 kDa homolog,U1 small nuclear ribonucleoprotein 70 kDa homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	193	Total	C	N	O	S	0	0
			1450	929	261	258	2		

- Molecule 5 is a protein called U1 small nuclear ribonucleoprotein C.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	177	Total	C	N	O	S	0	0
			1323	832	246	240	5		

- Molecule 6 is a protein called Pre-mRNA-processing factor 39.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	509	Total	C	N	O	S	0	0
			3462	2188	608	659	7		

- Molecule 7 is a protein called U1 small nuclear ribonucleoprotein component PRP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	541	Total	C	N	O	S	0	0
			4574	2996	723	836	19		

- Molecule 8 is a protein called Protein NAM8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	175	Total	C	N	O	S	0	0
			1337	840	232	255	10		

- Molecule 9 is a protein called 56 kDa U1 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	216	Total	C	N	O	S	0	0
			1684	1098	274	301	11		

- Molecule 10 is a protein called Protein LUC7,Protein LUC7,Protein LUC7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	158	Total	C	N	O	S	0	0
			1083	675	198	201	9		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	83	VAL	GLU	conflict	UNP Q07508
H	84	GLU	VAL	conflict	UNP Q07508

- Molecule 11 is a RNA chain called Yeast UBC4 pre-mRNA (mutant).

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	38	Total	C	N	O	P	0	0
			789	355	132	264	38		

- Molecule 12 is a protein called U1 small nuclear ribonucleoprotein component SNU71.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	J	42	Total	C	N	O	0	0
			324	210	55	59		

- Molecule 13 is a protein called U2 snRNP component HSH155.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	833	Total	C	N	O	S	0	0
			6612	4258	1121	1192	41		

- Molecule 14 is a protein called Pre-mRNA-splicing factor RSE1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	1186	Total	C	N	O	S	0	0
			9437	6034	1589	1763	51		

- Molecule 15 is a protein called Cold sensitive U2 snRNA suppressor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	220	Total	C	N	O	S	0	0
			1786	1157	307	313	9		

- Molecule 16 is a protein called Protein HSH49.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	R	173	Total	C	N	O	S	0	0
			1429	930	239	258	2		

- Molecule 17 is a protein called Pre-mRNA-splicing factor RDS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S	103	Total	C	N	O	S	0	0
			814	503	154	143	14		

- Molecule 18 is a protein called Pre-mRNA-splicing factor PRP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	462	Total	C	N	O	S	0	0
			3915	2487	677	735	16		

- Molecule 19 is a protein called Pre-mRNA-splicing factor PRP11,Pre-mRNA-splicing factor PRP11,Pre-mRNA-splicing factor PRP11.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U	196	Total	C	N	O	S	0	0
			1489	934	258	291	6		

- Molecule 20 is a protein called Pre-mRNA-splicing factor PRP21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	127	Total	C	N	O	S	0	0
			1084	689	193	196	6		

- Molecule 21 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	170	Total	C	N	O	S	0	0
			1383	866	253	257	7		

- Molecule 22 is a protein called Unknown.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	X	51	Total	C	N	O		
			255	153	51	51	0	0

- Molecule 23 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	84	Total	C	N	O	S	0	0
			683	439	119	122	3		

- Molecule 24 is a protein called RDS3 complex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	83	Total	C	N	O	S	0	0
			685	424	129	131	1		

- Molecule 25 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	121	Total	C	N	O	S	0	0
			972	613	183	173	3		
25	s	65	Total	C	N	O	S	0	0
			518	331	91	93	3		

- Molecule 26 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	d	93	Total	C	N	O	S	0	0
			714	453	125	133	3		
26	v	82	Total	C	N	O	S	0	0
			632	402	109	119	2		

- Molecule 27 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	e	77	Total	C	N	O	S	0	0
			600	395	96	106	3		
27	w	77	Total	C	N	O	S	0	0
			602	396	95	108	3		

- Molecule 28 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	f	73	Total	C	N	O	S	0	0
			585	376	102	106	1		
28	x	73	Total	C	N	O	S	0	0
			585	376	102	106	1		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	g	72	Total	C	N	O	S	0	0
			556	352	97	105	2		
29	y	75	Total	C	N	O	S	0	0
			577	363	100	112	2		

- Molecule 30 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	h	107	Total	C	N	O	S	0	0
			834	525	149	157	3		
30	t	72	Total	C	N	O	S	0	0
			569	364	99	104	2		

- Molecule 31 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	i	99	Total	C	N	O	S	0	0
			805	514	148	139	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
31	u	92	Total	C	N	O	S	0	0
			752	481	136	131	4		

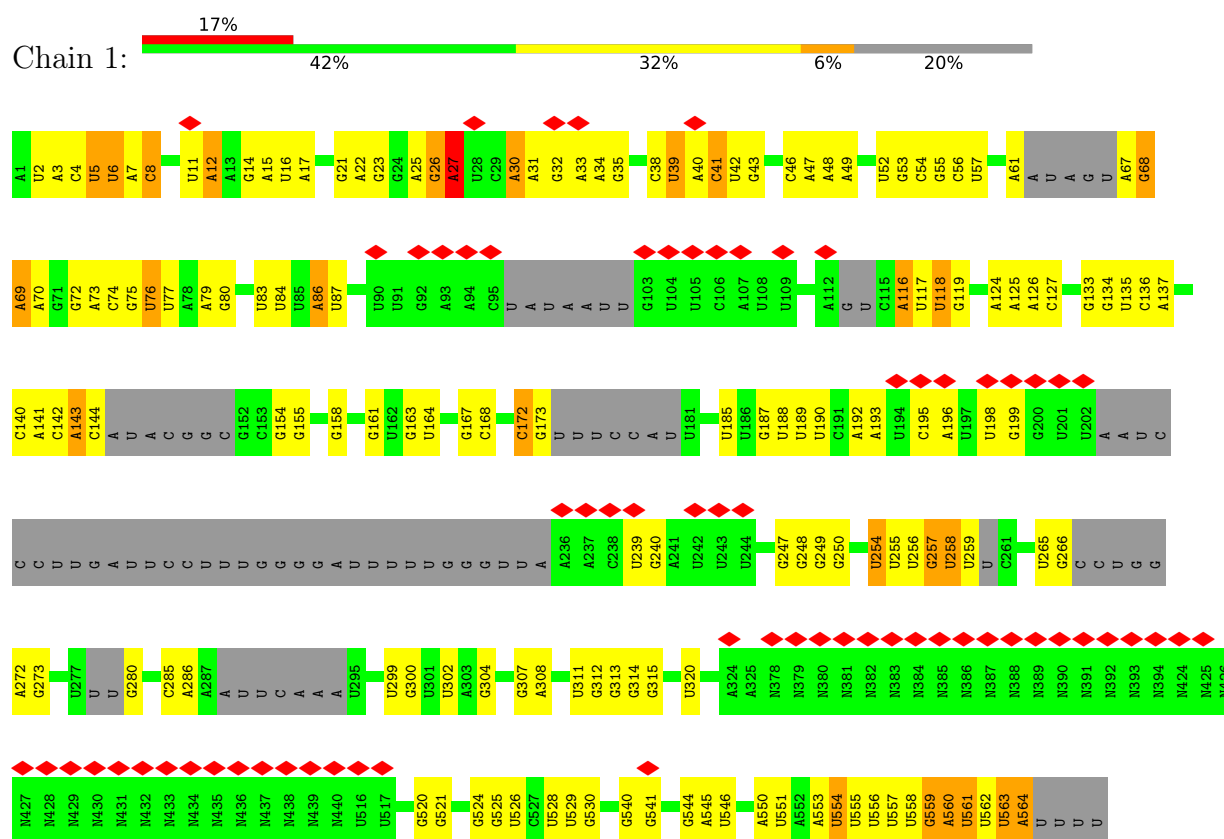
- Molecule 32 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
32	C	1	Total	Zn	0
			1	1	
32	H	2	Total	Zn	0
			2	2	
32	S	3	Total	Zn	0
			3	3	
32	T	2	Total	Zn	0
			2	2	
32	U	1	Total	Zn	0
			1	1	

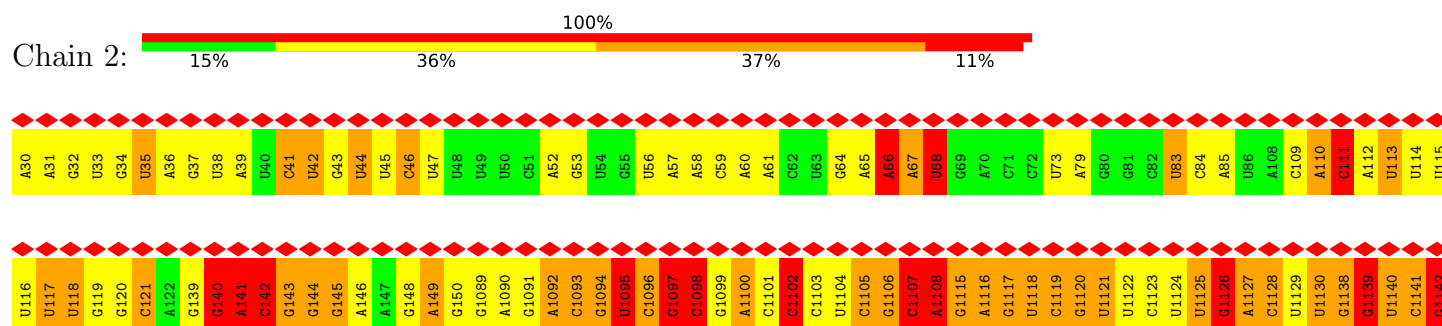
3 Residue-property plots

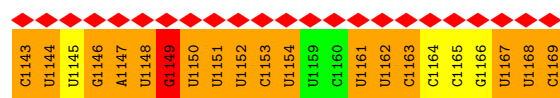
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: U1 snRNA,U1 snRNA,U1 snRNA,U1 snRNA,U1 snRNA

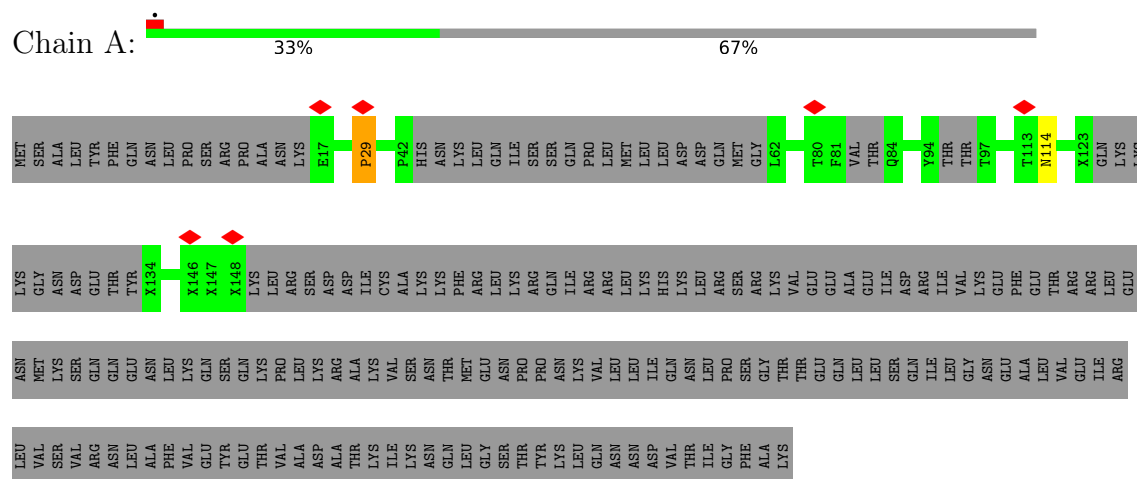


- Molecule 2: U2 snRNA

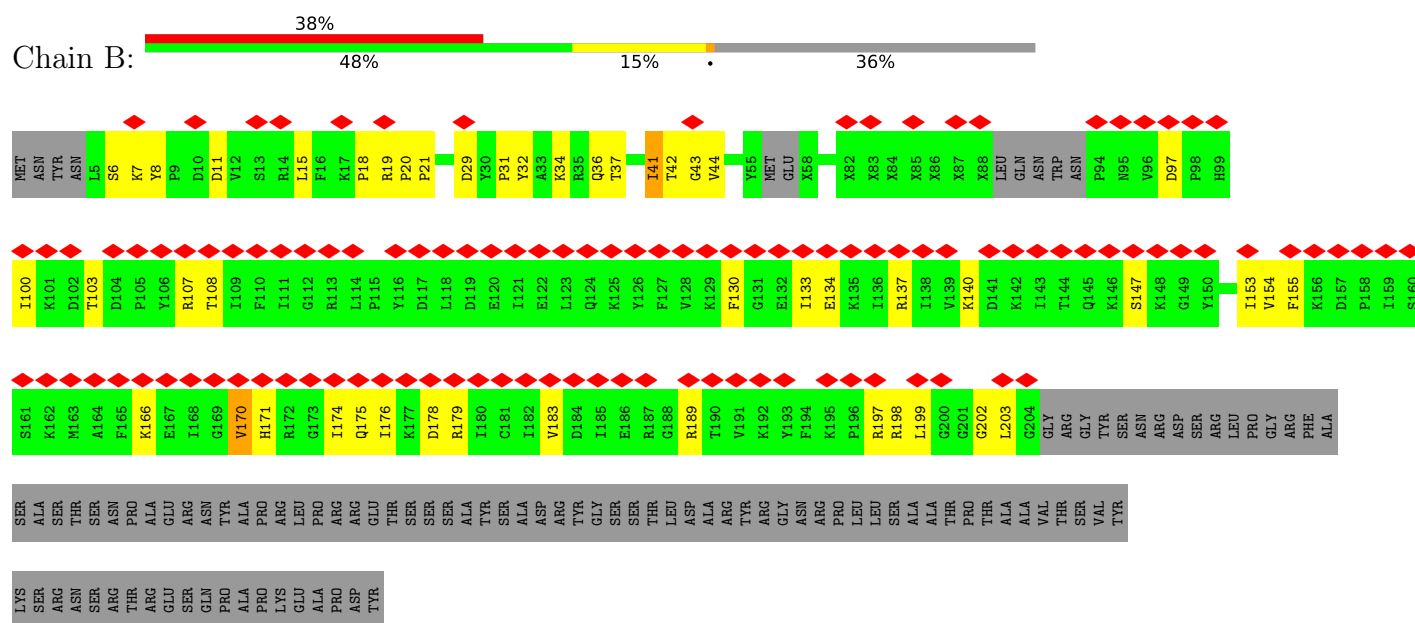




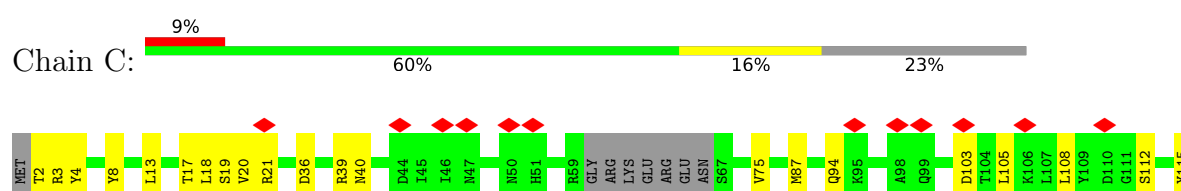
- Molecule 3: U1 small nuclear ribonucleoprotein A,U1 small nuclear ribonucleoprotein A,U1 small nuclear ribonucleoprotein A,U1 small nuclear ribonucleoprotein A,U1 small nuclear ribonucleoprotein A

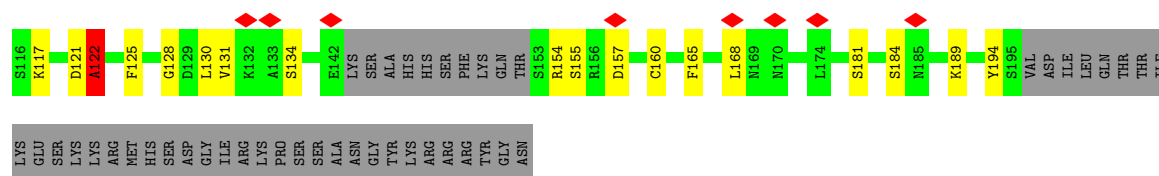


- Molecule 4: U1 small nuclear ribonucleoprotein 70 kDa homolog,U1 small nuclear ribonucleoprotein 70 kDa homolog,U1 small nuclear ribonucleoprotein 70 kDa homolog

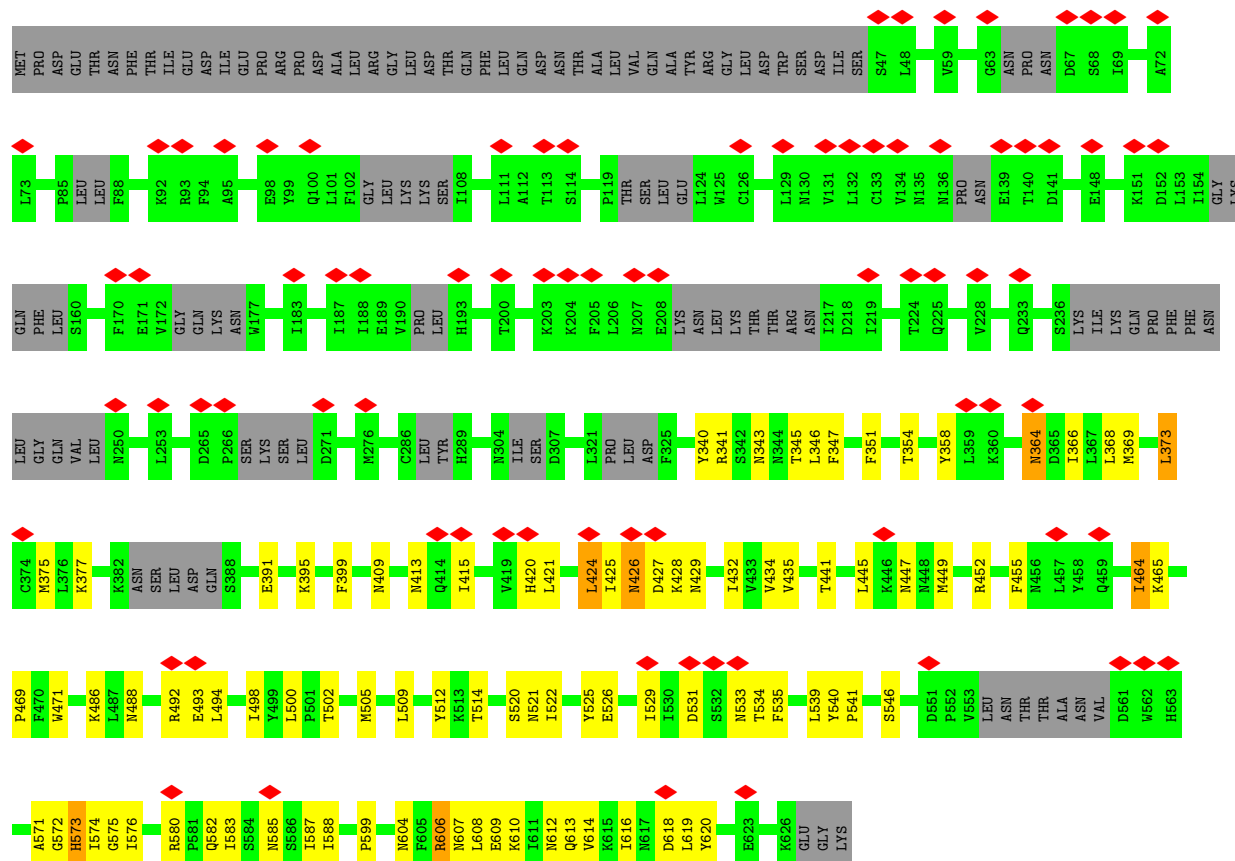


- Molecule 5: U1 small nuclear ribonucleoprotein C

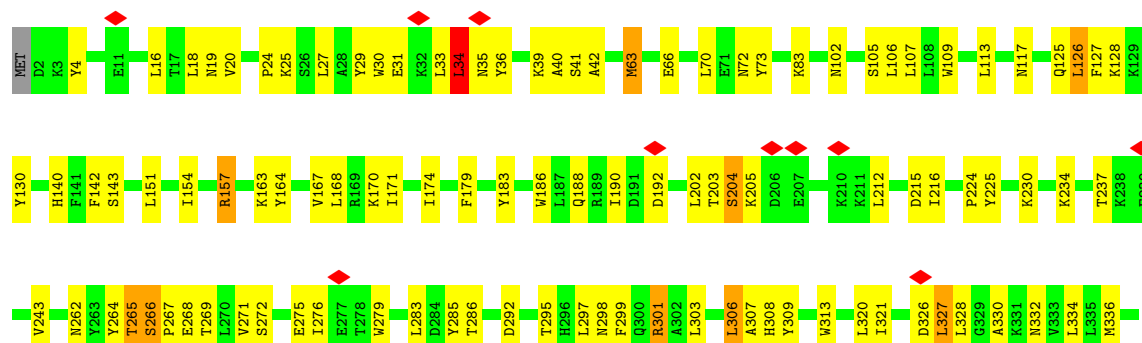


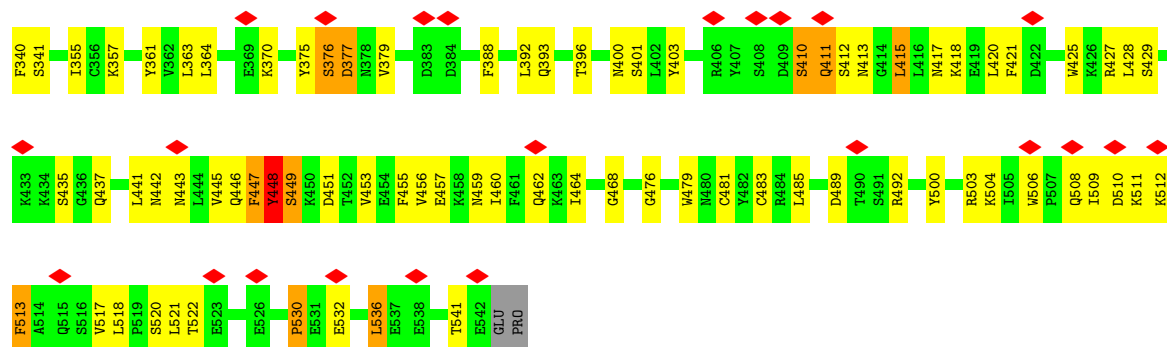


• Molecule 6: Pre-mRNA-processing factor 39



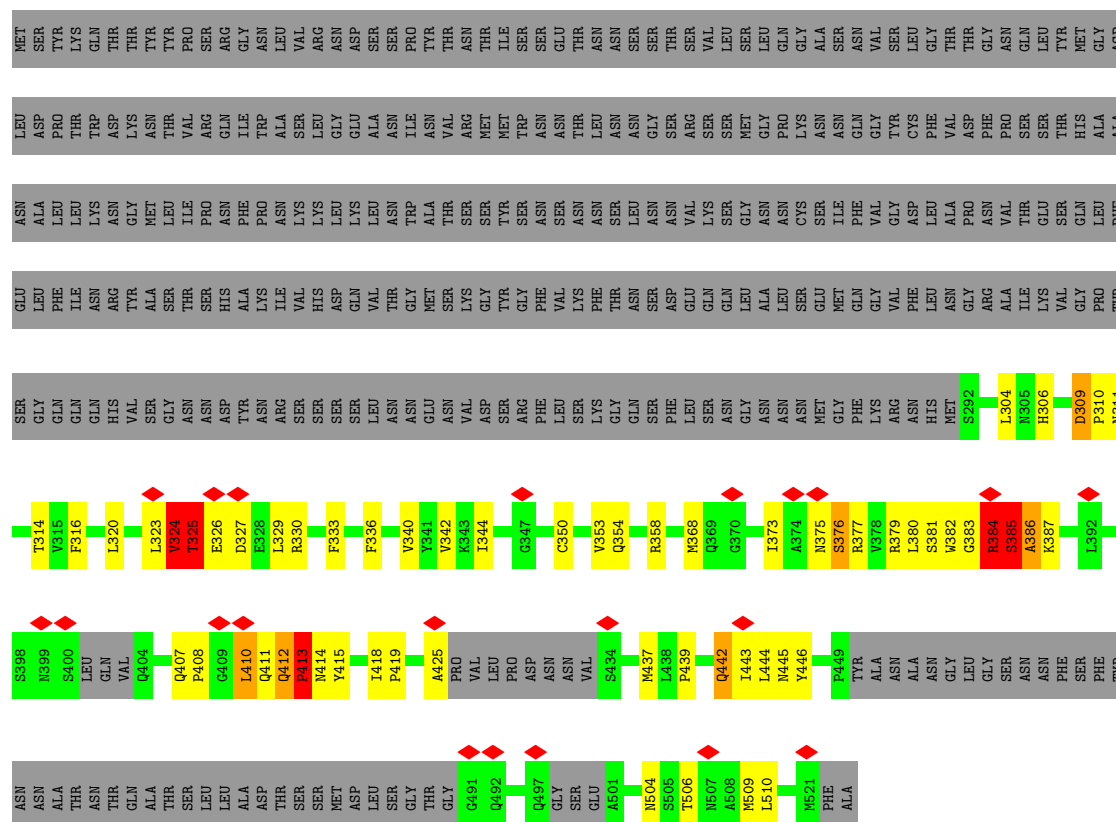
• Molecule 7: U1 small nuclear ribonucleoprotein component PRP42





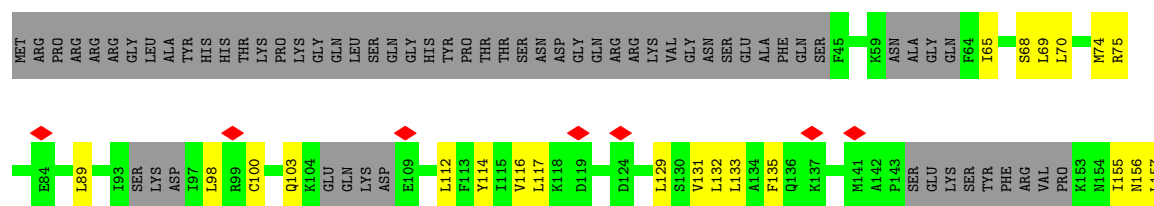
• Molecule 8: Protein NAM8

Chain F: 22% 9% 67%



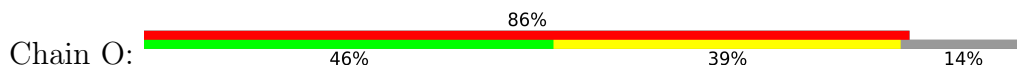
• Molecule 9: 56 kDa U1 small nuclear ribonucleoprotein component

Chain G: 33% 11% 56%



[illegible]

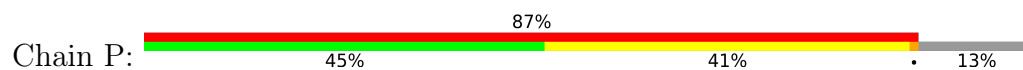
- Molecule 13: U2 snRNP component HSH155



S421	D361	A301	H241	R181	GLU
M422	C362	A302	X242	R182	ASP
I423	L363	V303	I243	T183	SER
P424	M364	V304	L244	S184	TYR
L425	D365	A305	V245	M185	HIS
M426	D366	K306	V246	R186	GLY
D427	H367	A307	A247	I187	ARG
P428	V368	L308	X248	L188	VAL
E429	P369	G309	P249	T189	ASP
Y430	V370	V310	L250	D190	ASN
A431	R371	M311	L251	K191	LEU
G432	I372	Q312	I252	A192	SER
Y433	V373	L313	D253	V193	GLY
Y434	T374	L314	E254	T194	GLN
T435	A375	P315	D255	F195	ASP
T436	H376	F316	P256	G196	THR
E437	T377	I317	M257	P197	GLY
A438	L378	M318	V258	E198	GLN
M439	S379	A319	R259	M199	TYR
R440	T380	A320	S260	T200	SER
I441	L381	C321	T261	F201	ILE
I442	A382	H322	G262	N202	GLU
R443	S383	S323	Q263	R203	ASN
R444	M384	R324	E264	L204	ASP
E445	S385	K325	I265	L205	LEU
F446	Y386	S326	I266	P206	ALA
D447	P387	W327	T267	S149	GLU
S448	Y388	K328	M268	L208	VAL
P449	G389	A329	L269	L209	VAL
D450	I390	R330	S270	R210	PRO
A451	E391	H331	T271	R211	ARG
E452	V392	T332	V272	S212	LYS
M453	F393	G333	A273	L213	ASP
K454	M394	I334	G274	E214	LEU
K455	V395	K335	L275	D215	ASN
I456	V396	L336	K276	Q216	GLY
T457	L397	V337	T277	E217	TYR
L458	E398	Q338	I278	R218	VAL
L459	P399	Q339	L279	H219	PRO
V460	L400	T340	T280	L220	ASP
L461	W401	L341	V281	M221	GLY
Q462	K402	I342	M282	I222	THR
K463	Q403	L343	R283	K223	ALA
C464	I404	L344	P284	T224	ARG
S465	R405	G345	D285	I225	VAL
A466	S406	T346	I286	D226	LYS
					GLN
					ASN
					SER
					ARG

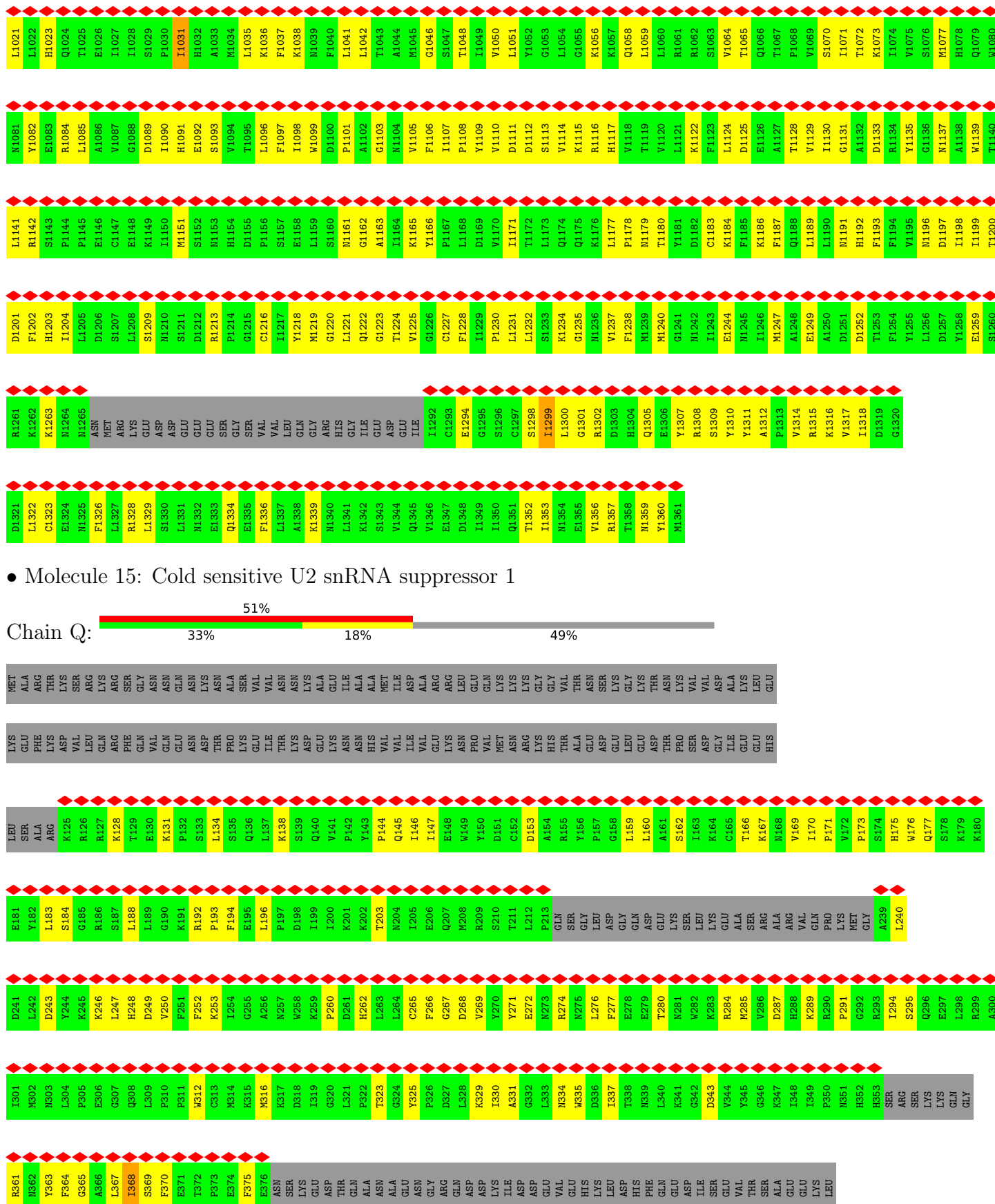
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E482	T541	V602	I662	K722	A782	L842	G902	E962
F483	R543	S603	I663	E723	V783	E843	L903	Y963
F484	T544	T604	N664	W724	A784	D844	E904	I964
Q485	V545	I605	A665	R725	I785	A845	A905	E965
K486	N546	L606	M666	M726	G786	L846	L906	E966
F487	L547	N607	Y667	I727	I787	T847	S907	L967
V488	L548	H608	C668	C728	V788	D848	Q908	D968
V489	G549	L609	I669	E729	A789	R849	A909	L969
R490	T550	K610	T670	F730	K790	D850	L910	V970
R491	A551	H611	S671	L731	V791	L851	G911	L971
V492	D552	K612	V672	L732	C792	V652	P912	
A493	L553	T613	M673	E733	G793	H853	G913	
L494	D554	P614	D674	L734	P794	R854	L914	
D495	E555	L615	L675	L735	Y795	Q855	F915	
R496	R556	V616	D676	K736	N796	T856	N916	
P497	L557	R617	K677	S737	V797	A857	N917	
L498	E558	Q618	L678	T738	L798	S858	Y918	
N499	T559	H619	Q679	N739	P799	N859	I919	
K500	R560	A620	P680	K740	V800	V660	K920	
V501	L561	A621	P681	E741	I801	I661	A921	
V502	I562	D622	L682	I742	M802	T862	G922	
T503	D563	L623	N683	R743	N803	H863	L923	
Y504	A564	C624	Q684	R744	E804	L864	F924	
T505	L565	A625	I685	S745	Y805	A865	H925	
T506	L566	I626	L686	A746	T806	L866	P926	
V507	I567	L627	P687	N747	T807	N867	A927	
T508	A568	I628	T688	A748	P808	C868	K928	
L509	F569	P629	L689	T749	E809	S869	N929	
A510	Q570	V630	T690	F750	T810	T671	V930	
K511	E571	I631	P691	G751	N811	G872	R931	
K512	Q572	K632	I692	F752	V812	H873	K932	
L513	T573	N633	L693	I753	Q813	H874	A934	
G514	N574	C634	R694	A754	N814	D875	F934	
C515	S575	H635	N695	E755	G815	D876	N935	
S516	D576	E636	K696	A756	V816	A876	R936	
Y517	S577	F637	H697	I757	L817	F877	Y937	
T518	I578	E638	K698	G758	K818	L878	Y938	
I519	I579	M639	K699	P759	A819	H879	N939	
D520	F580	L640	V700	H760	M820	L880	N940	
K521	K581	N641	E701	D761	S821	M881	M941	
L522	L582	K642	V702	V762	F822	N882	Y942	
L523	F583	L643	N703	L763	M823	L883	V943	
T524	G584	N644	T704	V764	F824	L884	N944	
P525	A585	I645	I705	A765	E825	T885	Y945	
L526	V586	L646	K706	L766	Y826	P886	Q946	
R527	T587	L647	F707	L767	T827	N887	D947	
D528	V588	E648	V708	N768	G828	L888	A948	
E529	S589	E649	G709	N769	N829	P889	N949	
A530	L590	L650	L710	L770	M830	E890	V950	
E531	D591	L651	I711	K771	S831	T891	P951	
P532	I592	G652	G712	V772	K832	S892	F952	
F533	R593	E653	L713	Q773	D833	P893	Y953	
R534	M594	V654	L714	E774	Y834	H894	N955	
T535	K595	Y655	A715	R775	T835	A895	V956	
M536	P596	P656	P716	Q776	Y836	L896	P957	
A537	F597	E657	T717	L777	F837	N897	D957	
V538	L598	E658	Y718	R778	I838	R898	N958	
H539	A599	L659	A719	V779	T839	L899	N959	
A540	P600	G660	P720	C780	P840	L900	N960	

● Molecule 14: Pre-mRNA-splicing factor RSE1



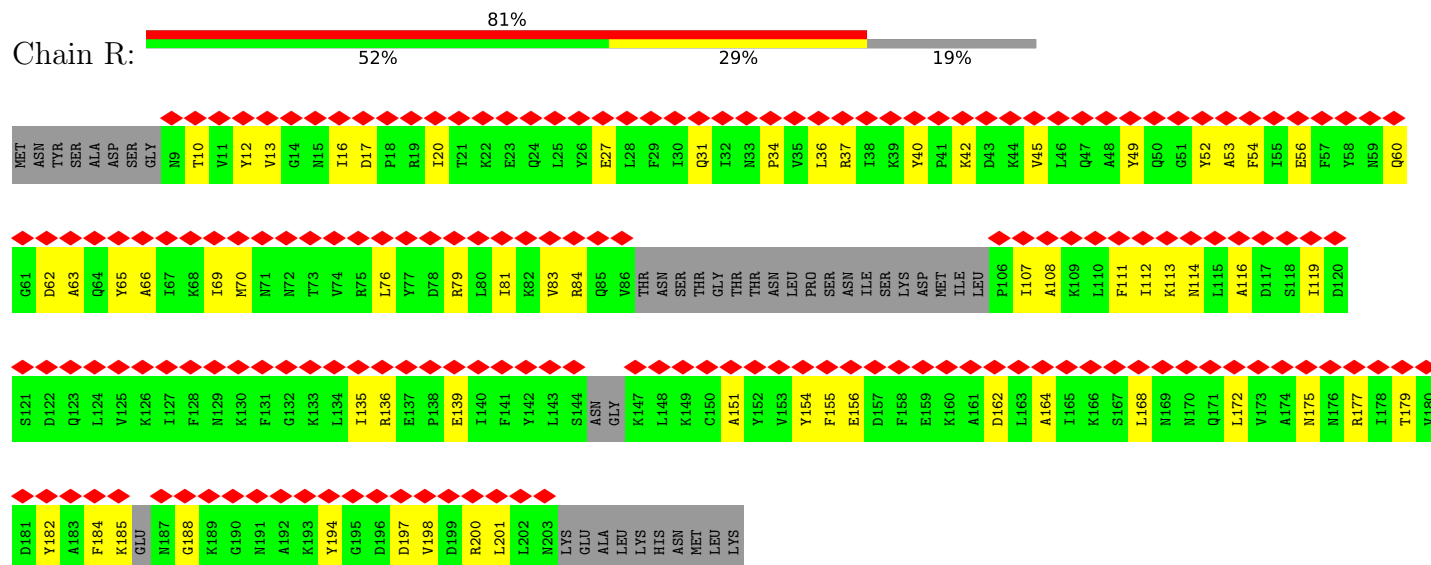
MET	Y61	F121	R181
TRP	H62	A122	T182
GLY	L63	T123	T183
GLY	T64	I124	L184
LYS	L65	T125	R185
MET	K66	S126	R186
ALA	K67	M127	V187
VAL	Q68	K128	S188
SER	T69	L129	P189
LEU	N70	L130	I190
SER	F71	D131	S191
PRO	V72	L132	Y192
HIS	H73	P133	M193
THR	S74	HIS	E194
ALA	C75	MET	I195
LYS	T76	GLY	D196
ARG	G77	SER	P197
LEU	H78	ARG	N198
LEU	F79	ALA	G199
GLN	V80	ALA	R200
ALA	D81	ASN	C201
SER	L82	W144	I202
THR	E83	P145	I203
MET	A84	T146	L204
TYR	G85	F147	S205
ASP	S86	L148	S206
GLY	A87	A149	V207
LEU	R88	L150	V208
LYS	E89	T151	Q209
ARG	Q90	S152	M210
GLU	S91	D153	K211
ALA	Q92	S154	L212
ARG	L93	G155	C213
THR	C94	N156	F214
ARG	Y95	L157	L215
SER	A96	S158	V216
HIS	T97	I159	D217
ASN	E98	V160	Y218
THR	T99	Q161	A219
MET	H100	I162	Q220
VAL	L101	I163	K221
A53	L103	M164	L222
K54	Y104	H165	R223
D55	D105	A166	I224
D56	T106	G167	S225
E57	A107	A168	S226
L58	D108	L169	P227
Y59	G109	R170	L228
L60	L111	L171	E229
	K112	K172	I230
	L113	T173	I231
	L114	L174	R232
	A115	V175	P233
	K116	M176	H234
	F117	Q177	M235
	Q118	P178	V236
	M119	L179	T237
	L120	T180	L238
			D239
			M240



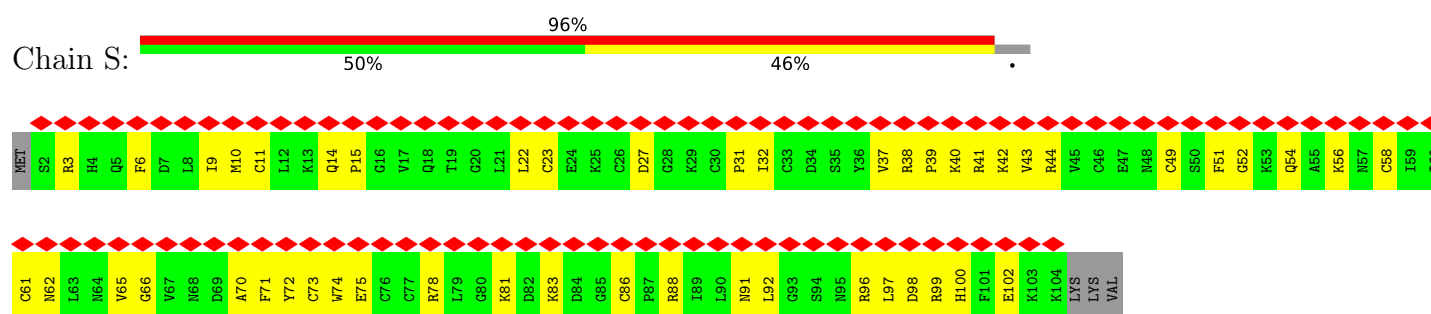


GLU
ARG
ASN
TYR
SER
GLU
ALA
ASP
SER
GLU
LYS
GLN
LEU
TYR
THR
VAL
LEU

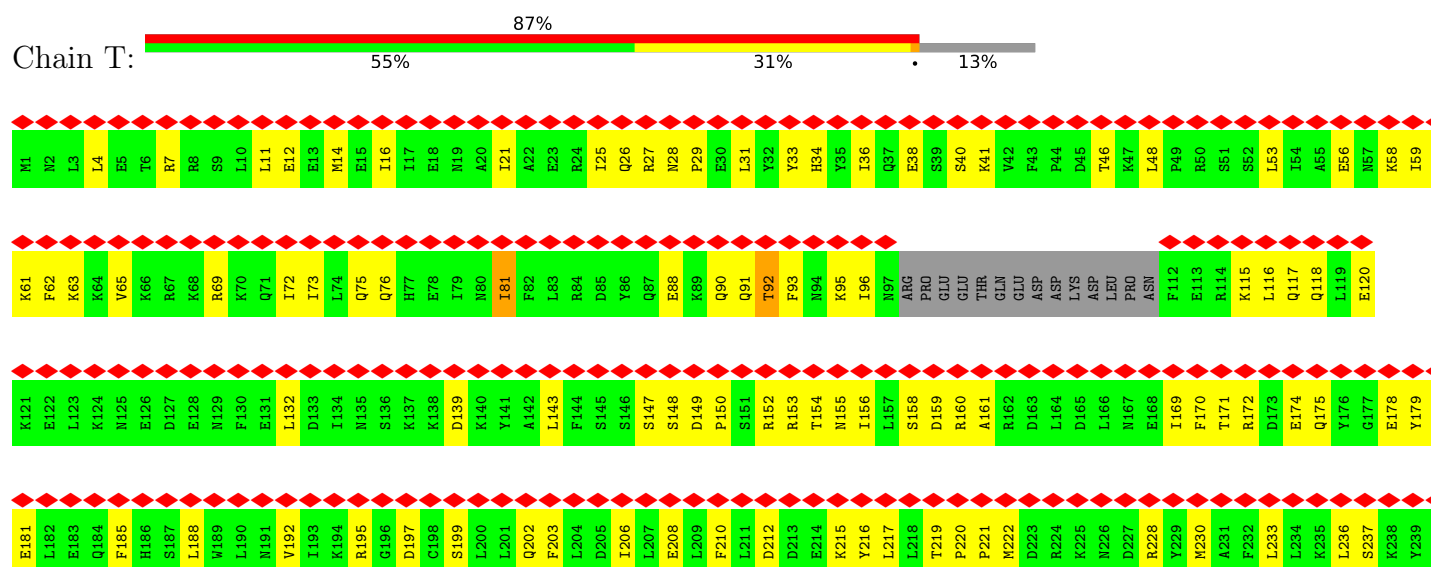
• Molecule 16: Protein HSH49

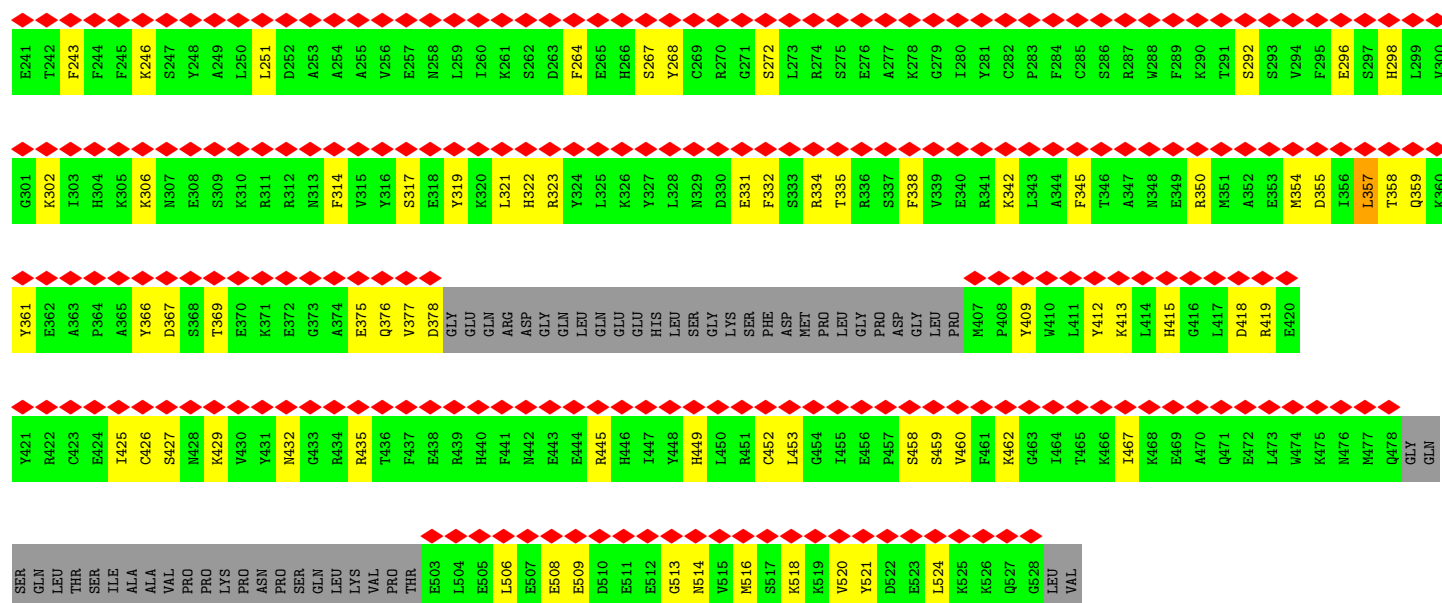


• Molecule 17: Pre-mRNA-splicing factor RDS3

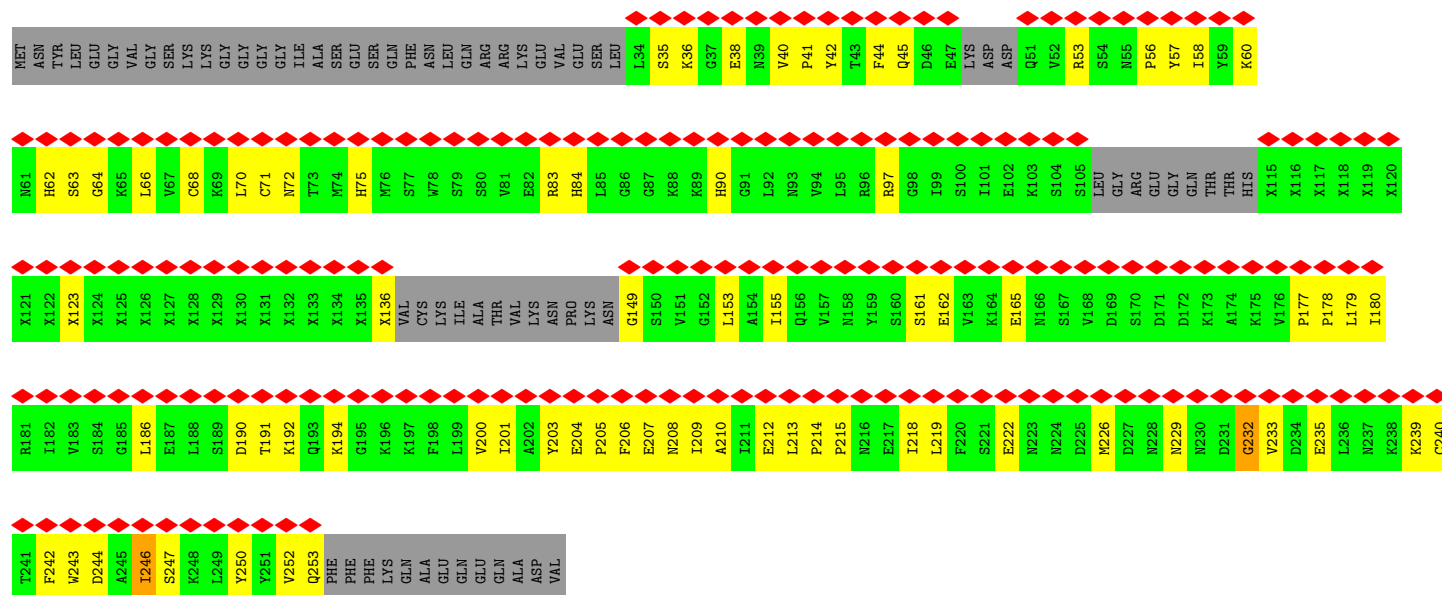
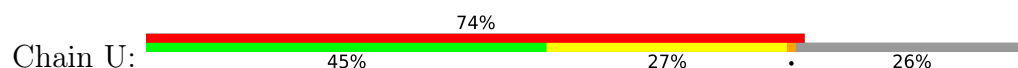


• Molecule 18: Pre-mRNA-splicing factor PRP9

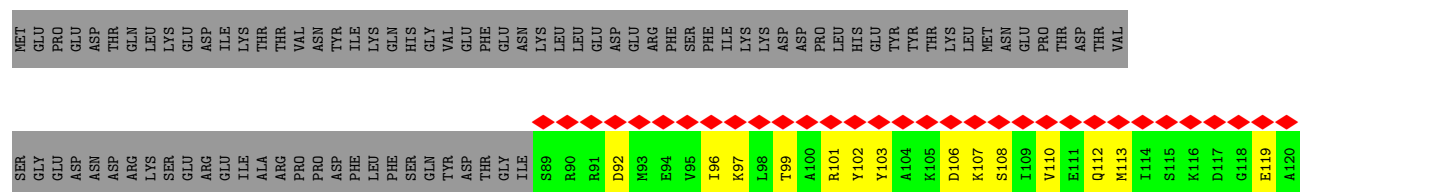
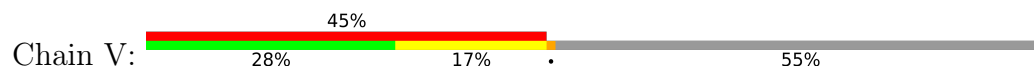


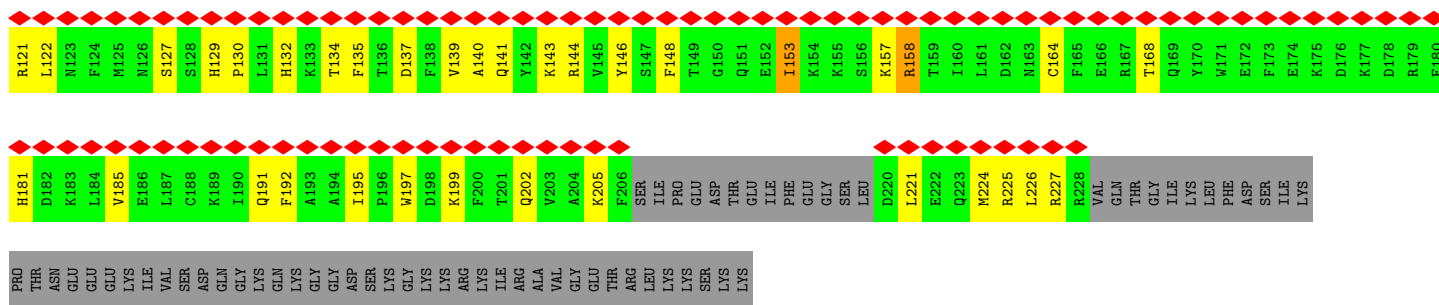


- Molecule 19: Pre-mRNA-splicing factor PRP11,Pre-mRNA-splicing factor PRP11,Pre-mRNA-splicing factor PRP11

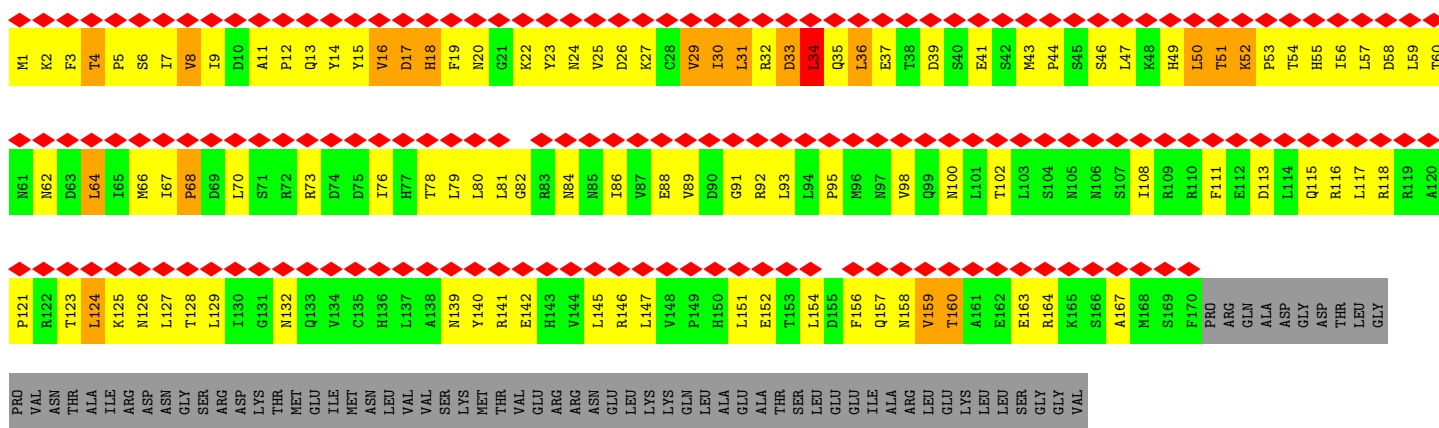
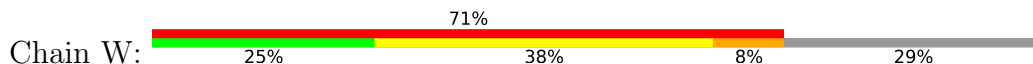


- Molecule 20: Pre-mRNA-splicing factor PRP21

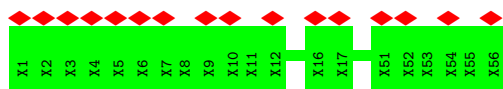




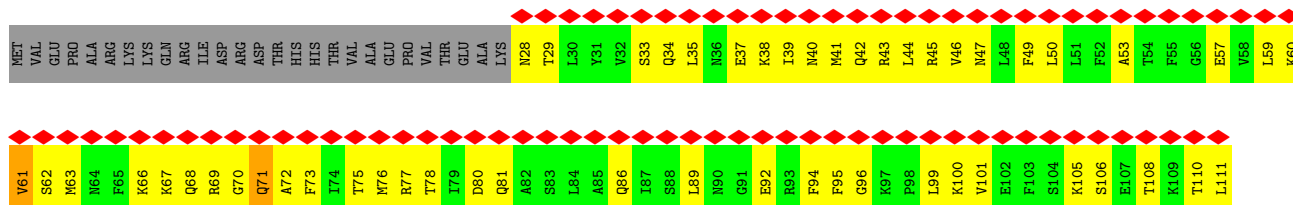
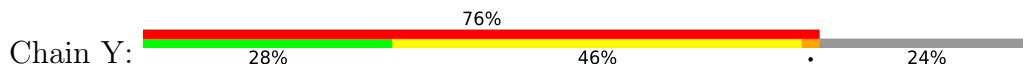
- Molecule 21: U2 small nuclear ribonucleoprotein A'



- Molecule 22: Unknown



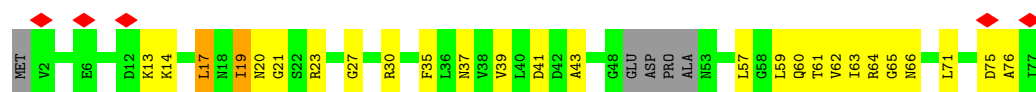
- Molecule 23: U2 small nuclear ribonucleoprotein B''



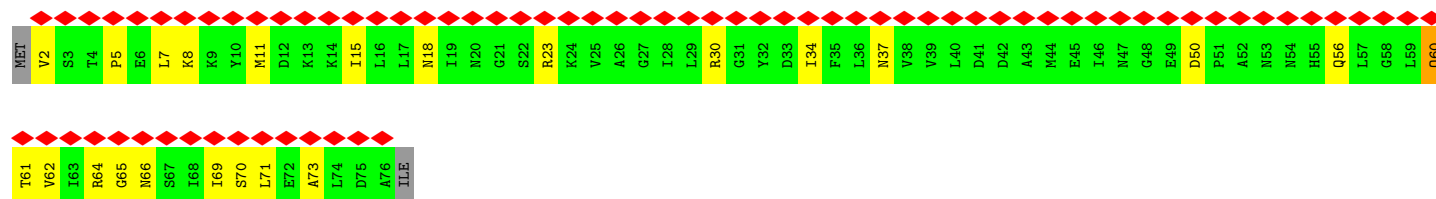
- Molecule 24: RDS3 complex subunit 10



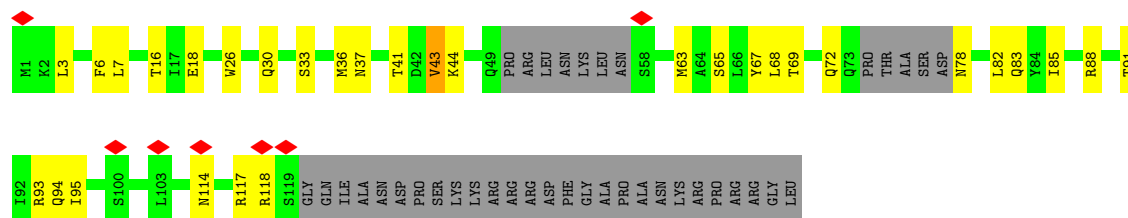




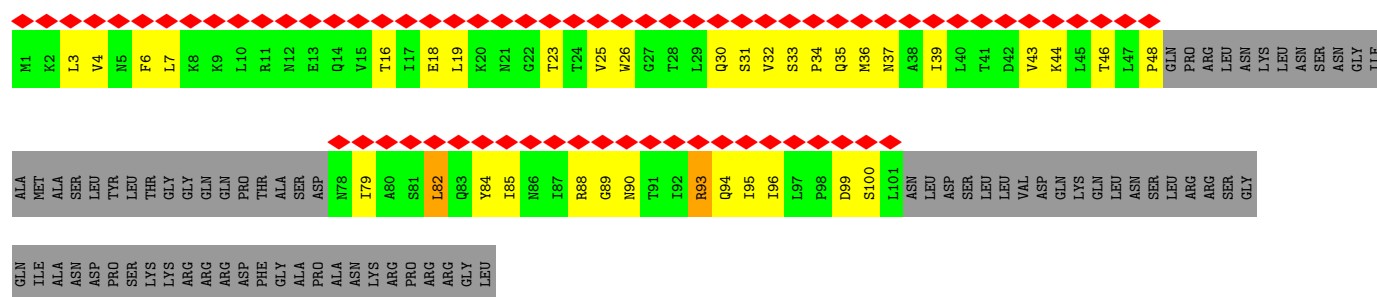
- Molecule 29: Small nuclear ribonucleoprotein G



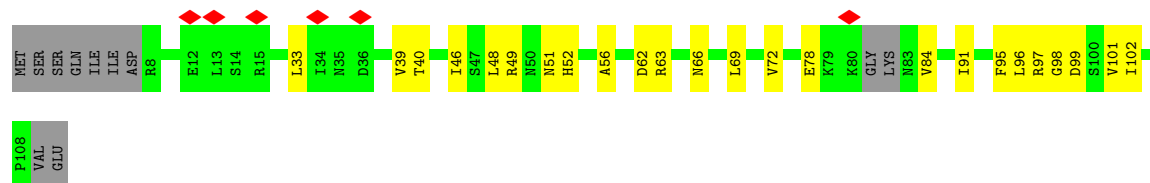
- Molecule 30: Small nuclear ribonucleoprotein Sm D1



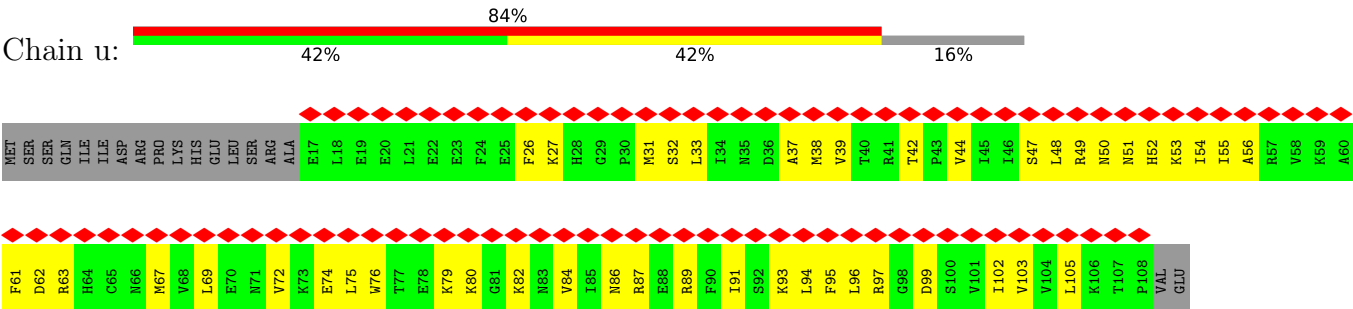
- Molecule 30: Small nuclear ribonucleoprotein Sm D1



- Molecule 31: Small nuclear ribonucleoprotein Sm D2



- Molecule 31: Small nuclear ribonucleoprotein Sm D2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	153556	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.152	Depositor
Minimum map value	-0.083	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0369	Depositor
Map size (Å)	632.8, 632.8, 632.8	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.13, 1.13, 1.13	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.38	0/6890	0.52	4/10700 (0.0%)
2	2	1.22	46/3302 (1.4%)	1.79	138/5123 (2.7%)
3	A	0.28	0/388	0.90	1/535 (0.2%)
4	B	0.45	0/1325	0.93	2/1784 (0.1%)
5	C	0.52	0/1348	0.91	5/1825 (0.3%)
6	D	0.47	0/3499	0.84	6/4772 (0.1%)
7	E	0.68	2/4688 (0.0%)	1.00	16/6331 (0.3%)
8	F	0.61	0/1361	1.02	13/1843 (0.7%)
9	G	0.54	0/1716	0.86	0/2314
10	H	0.41	0/816	0.72	0/1094
11	I	0.24	0/878	0.31	0/1357
12	J	0.48	0/331	0.96	0/448
13	O	0.20	0/6745	0.47	1/9157 (0.0%)
14	P	0.22	0/9623	0.53	1/13041 (0.0%)
15	Q	0.17	0/1835	0.53	0/2480
16	R	0.14	0/1453	0.40	0/1954
17	S	0.21	0/827	0.55	0/1105
18	T	0.28	0/3992	0.66	2/5346 (0.0%)
19	U	0.24	0/1403	0.62	1/1889 (0.1%)
20	V	0.27	0/1105	0.63	0/1475
21	W	0.35	0/1406	0.71	0/1905
23	Y	0.20	0/692	0.47	0/923
24	Z	0.22	0/694	0.46	0/929
25	b	0.64	0/978	0.99	0/1306
25	s	0.32	0/521	0.59	0/701
26	d	0.69	0/726	0.91	0/984
26	v	0.36	0/641	0.58	0/868
27	e	0.58	0/610	0.91	2/826 (0.2%)
27	w	0.39	0/612	0.65	0/830
28	f	0.58	0/597	1.01	0/807
28	x	0.33	0/597	0.63	0/807
29	g	0.62	0/559	0.91	2/751 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
29	y	0.16	0/582	0.41	0/785
30	h	0.55	0/839	0.85	0/1132
30	t	0.38	0/574	0.64	1/777 (0.1%)
31	i	0.54	0/818	0.84	0/1099
31	u	0.33	0/764	0.57	0/1026
All	All	0.47	48/65735 (0.1%)	0.79	195/91029 (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
2	2	0	1
4	B	0	3
5	C	0	3
6	D	0	5
7	E	0	12
8	F	0	8
9	G	0	1
10	H	0	1
14	P	0	2
18	T	0	1
21	W	0	1
27	e	0	1
29	g	0	1
30	h	0	1
All	All	0	41

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1149	G	O3'-P	19.50	1.90	1.61
2	2	143	G	O3'-P	15.07	1.83	1.61
2	2	143	G	C3'-O3'	14.28	1.63	1.42
2	2	1161	U	O3'-P	-12.47	1.42	1.61
2	2	1092	A	O3'-P	-11.84	1.43	1.61
2	2	1090	A	O3'-P	11.56	1.78	1.61
2	2	144	G	O3'-P	-11.46	1.44	1.61
2	2	1163	C	O5'-C5'	11.06	1.59	1.42
2	2	1116	A	O3'-P	-9.29	1.47	1.61
2	2	1149	G	C3'-O3'	9.28	1.56	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1116	A	C3'-O3'	-8.29	1.29	1.42
2	2	1150	U	O5'-C5'	8.13	1.54	1.42
2	2	1166	G	O3'-P	7.98	1.73	1.61
2	2	1165	C	O5'-C5'	7.79	1.54	1.42
2	2	1162	U	O5'-C5'	7.73	1.54	1.42
2	2	1090	A	C3'-O3'	7.27	1.53	1.42
2	2	1154	U	C1'-N1	7.15	1.59	1.48
2	2	1140	U	C1'-N1	7.09	1.59	1.48
2	2	1127	A	O3'-P	-7.00	1.50	1.61
2	2	1167	U	O3'-P	6.90	1.71	1.61
7	E	157	ARG	CZ-NH1	-6.84	1.23	1.32
2	2	1090	A	O5'-C5'	6.79	1.52	1.42
2	2	1169	C	C1'-N1	6.67	1.58	1.48
2	2	1164	C	O3'-P	-6.59	1.51	1.61
2	2	1091	G	O5'-C5'	6.29	1.51	1.42
2	2	1116	A	O5'-C5'	6.13	1.51	1.42
2	2	1096	C	O5'-C5'	6.07	1.51	1.42
2	2	1151	U	O5'-C5'	-6.03	1.33	1.42
2	2	1166	G	O5'-C5'	6.03	1.51	1.42
2	2	68	U	C1'-N1	5.96	1.57	1.48
2	2	118	U	C1'-N1	5.80	1.57	1.48
2	2	121	C	C1'-N1	5.64	1.56	1.48
2	2	111	C	C1'-N1	5.59	1.56	1.48
2	2	1096	C	O3'-P	5.58	1.69	1.61
2	2	1090	A	C4'-O4'	5.57	1.53	1.45
2	2	85	A	C1'-N9	-5.54	1.39	1.48
2	2	146	A	O5'-C5'	5.53	1.50	1.42
2	2	109	C	C1'-N1	5.51	1.56	1.48
2	2	1128	C	C5'-C4'	-5.46	1.43	1.51
2	2	1161	U	C3'-O3'	-5.32	1.34	1.42
2	2	1165	C	O3'-P	5.23	1.69	1.61
2	2	1095	U	O3'-P	5.22	1.69	1.61
2	2	144	G	C3'-O3'	-5.09	1.34	1.42
2	2	1127	A	O5'-C5'	5.09	1.50	1.42
7	E	34	LEU	CG-CD2	-5.06	1.35	1.52
2	2	1117	G	C5'-C4'	5.05	1.58	1.51
2	2	1162	U	P-O5'	5.05	1.67	1.59
2	2	1118	U	O5'-C5'	5.01	1.50	1.42

All (195) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	144	G	C4'-C3'-O3'	-25.53	74.71	113.00
2	2	1151	U	C4'-C3'-O3'	-20.00	83.00	113.00
2	2	143	G	C4'-C3'-O3'	18.16	140.24	113.00
2	2	1092	A	C2'-C3'-O3'	17.91	140.56	113.70
2	2	1097	G	C3'-C2'-O2'	16.46	135.40	110.70
2	2	1093	C	P-O5'-C5'	15.79	144.59	120.90
2	2	144	G	C2'-C3'-O3'	15.16	136.44	113.70
2	2	1147	A	C5'-C4'-C3'	-15.12	93.31	116.00
2	2	1168	U	C4'-C3'-O3'	-14.99	90.51	113.00
2	2	1150	U	C4'-C3'-O3'	-14.97	90.55	113.00
2	2	1148	U	C4'-C3'-O3'	-14.35	91.48	113.00
2	2	1092	A	C4'-C3'-O3'	-13.36	92.95	113.00
2	2	1151	U	P-O5'-C5'	12.48	139.62	120.90
2	2	145	G	C5'-C4'-C3'	-11.97	98.04	116.00
2	2	1096	C	C1'-C2'-O2'	-11.91	90.54	108.40
2	2	1150	U	C5'-C4'-C3'	11.83	133.74	116.00
2	2	1117	G	C5'-C4'-C3'	-11.61	98.59	116.00
2	2	1090	A	C4'-C3'-O3'	11.51	130.27	113.00
2	2	1162	U	C5'-C4'-O4'	11.38	126.87	109.80
2	2	1162	U	C2'-C3'-O3'	-11.22	96.86	113.70
2	2	144	G	C5'-C4'-C3'	11.16	132.74	116.00
2	2	1097	G	C2'-C3'-O3'	-10.96	97.26	113.70
2	2	1091	G	C5'-C4'-C3'	10.56	131.84	116.00
2	2	143	G	C5'-C4'-C3'	-10.54	100.19	116.00
2	2	1163	C	C5'-C4'-C3'	-10.38	100.43	116.00
2	2	1147	A	C4'-C3'-O3'	10.33	128.49	113.00
2	2	1098	C	N1-C1'-C2'	-10.28	96.58	112.00
2	2	1147	A	P-O5'-C5'	10.23	136.24	120.90
2	2	144	G	O3'-P-O5'	-10.16	88.75	104.00
2	2	1149	G	O3'-P-O5'	10.14	119.21	104.00
2	2	1091	G	C4'-C3'-O3'	-10.08	97.88	113.00
2	2	1165	C	C4'-C3'-O3'	10.05	128.08	113.00
2	2	144	G	C5'-C4'-O4'	-9.93	94.91	109.80
2	2	1162	U	C5'-C4'-C3'	-9.81	101.29	116.00
2	2	1089	G	C4'-C3'-O3'	9.66	127.48	113.00
2	2	1149	G	C4'-C3'-O3'	9.62	127.42	113.00
2	2	1115	G	C4'-C3'-O3'	9.39	127.08	113.00
2	2	66	A	C4'-C3'-O3'	9.29	123.33	109.40
2	2	1152	U	P-O5'-C5'	9.25	134.77	120.90
2	2	144	G	C1'-C2'-O2'	-9.19	94.61	108.40
2	2	143	G	P-O3'-C3'	9.18	133.97	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1149	G	P-O3'-C3'	9.18	133.96	120.20
2	2	1150	U	C2'-C3'-O3'	9.11	127.37	113.70
2	2	1092	A	P-O5'-C5'	9.10	134.55	120.90
2	2	145	G	C3'-C2'-O2'	-8.89	97.37	110.70
2	2	145	G	P-O5'-C5'	8.87	134.21	120.90
2	2	148	G	C5'-C4'-C3'	-8.81	102.78	116.00
2	2	1165	C	C5'-C4'-C3'	-8.80	102.79	116.00
2	2	1167	U	C2'-C3'-O3'	8.75	126.83	113.70
2	2	1117	G	C5'-C4'-O4'	8.68	122.82	109.80
2	2	1096	C	C2'-C3'-O3'	-8.55	100.88	113.70
2	2	1150	U	P-O5'-C5'	8.51	133.66	120.90
2	2	1168	U	P-O5'-C5'	-8.43	108.25	120.90
2	2	1108	A	C1'-C2'-O2'	-8.31	95.94	108.40
2	2	1161	U	C5'-C4'-C3'	-8.27	103.60	116.00
2	2	1090	A	C2'-C3'-O3'	-8.22	101.37	113.70
2	2	1093	C	C5'-C4'-C3'	-8.21	103.69	116.00
2	2	1166	G	O5'-C5'-C4'	8.19	123.78	111.50
2	2	1096	C	C4'-C3'-O3'	8.18	125.27	113.00
1	1	27	A	N9-C1'-C2'	8.16	126.24	114.00
2	2	1169	C	P-O5'-C5'	-8.14	108.69	120.90
7	E	157	ARG	NE-CZ-NH1	-8.13	113.37	121.50
2	2	1163	C	C5'-C4'-O4'	8.00	121.81	109.80
2	2	1096	C	C3'-C2'-O2'	7.96	122.65	110.70
2	2	1168	U	C2'-C3'-O3'	7.88	125.51	113.70
7	E	63	MET	CB-CG-SD	-7.87	89.11	112.70
2	2	1162	U	C4'-C3'-O3'	7.85	124.78	113.00
2	2	145	G	O5'-C5'-C4'	-7.76	99.86	111.50
2	2	1168	U	C1'-C2'-O2'	-7.72	96.82	108.40
2	2	141	A	N9-C1'-C2'	-7.70	100.45	112.00
2	2	1105	C	C4'-C3'-O3'	-7.63	97.95	109.40
2	2	1151	U	O3'-P-O5'	-7.62	92.57	104.00
2	2	144	G	C3'-C2'-O2'	7.60	122.09	110.70
2	2	143	G	O3'-P-O5'	7.59	115.38	104.00
2	2	1091	G	O5'-C5'-C4'	7.58	122.88	111.50
2	2	141	A	C4'-C3'-O3'	7.58	124.37	113.00
2	2	1128	C	C4'-C3'-O3'	-7.41	101.88	113.00
2	2	1126	G	N9-C1'-C2'	-7.39	100.92	112.00
2	2	1090	A	P-O3'-C3'	7.30	131.15	120.20
7	E	449	SER	N-CA-CB	-7.29	98.17	110.49
2	2	143	G	C2'-C3'-O3'	-7.22	102.87	113.70
2	2	1090	A	C5'-C4'-C3'	-7.13	105.30	116.00
2	2	1139	G	N9-C1'-C2'	-7.12	101.32	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1165	C	C2'-C3'-O3'	-6.99	103.22	113.70
7	E	376	SER	CA-C-N	6.93	134.78	121.54
7	E	376	SER	C-N-CA	6.93	134.78	121.54
7	E	448	TYR	CA-C-N	6.88	134.69	121.54
7	E	448	TYR	C-N-CA	6.88	134.69	121.54
2	2	1151	U	C1'-C2'-O2'	-6.88	98.08	108.40
2	2	1163	C	C4'-C3'-O3'	6.86	123.29	113.00
2	2	145	G	C4'-C3'-O3'	6.82	123.23	113.00
5	C	168	LEU	N-CA-C	-6.76	104.06	112.72
2	2	1166	G	C5'-C4'-C3'	6.75	126.12	116.00
2	2	1168	U	O3'-P-O5'	-6.75	93.88	104.00
2	2	1092	A	N9-C1'-C2'	6.72	122.08	112.00
5	C	117	LYS	CB-CG-CD	-6.67	95.95	111.30
2	2	1152	U	C5'-C4'-C3'	-6.54	106.18	116.00
2	2	1147	A	O5'-C5'-C4'	6.51	121.26	111.50
2	2	142	C	N1-C1'-C2'	-6.48	102.28	112.00
8	F	384	ARG	CA-C-N	6.47	133.90	121.54
8	F	384	ARG	C-N-CA	6.47	133.90	121.54
2	2	1150	U	C1'-C2'-O2'	-6.41	98.78	108.40
2	2	1150	U	N1-C1'-C2'	6.36	121.54	112.00
2	2	1129	U	C1'-C2'-O2'	6.36	117.94	108.40
2	2	1167	U	C4'-C3'-O3'	-6.33	103.50	113.00
2	2	1152	U	O4'-C4'-C3'	6.28	110.28	104.00
30	t	93	ARG	CG-CD-NE	-6.28	98.18	112.00
2	2	144	G	O5'-C5'-C4'	6.26	120.90	111.50
2	2	1169	C	O5'-C5'-C4'	-6.26	102.11	111.50
2	2	1097	G	C4'-C3'-O3'	6.24	122.35	113.00
2	2	1117	G	C2'-C3'-O3'	-6.16	104.46	113.70
3	A	29	PRO	N-CA-CB	6.12	109.67	103.25
2	2	1153	C	C4'-C3'-O3'	-6.11	103.84	113.00
2	2	1151	U	N1-C1'-C2'	6.07	121.11	112.00
6	D	614	VAL	CB-CA-C	6.06	117.32	110.41
2	2	1093	C	O5'-C5'-C4'	-6.03	102.45	111.50
2	2	1151	U	C5'-C4'-O4'	6.02	118.84	109.80
2	2	1166	G	O3'-P-O5'	5.99	112.98	104.00
2	2	1090	A	C5'-C4'-O4'	5.98	118.77	109.80
8	F	385	SER	CA-C-N	5.97	132.94	121.54
8	F	385	SER	C-N-CA	5.97	132.94	121.54
8	F	442	GLN	CA-CB-CG	5.97	126.03	114.10
2	2	1167	U	C5'-C4'-C3'	5.96	124.94	116.00
5	C	121	ASP	CA-C-N	5.94	132.88	121.54
5	C	121	ASP	C-N-CA	5.94	132.88	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1091	G	C1'-C2'-O2'	-5.91	99.53	108.40
1	1	27	A	O4'-C1'-N9	5.90	117.06	108.20
2	2	1108	A	C4'-C3'-O3'	5.89	121.83	113.00
2	2	1118	U	O5'-C5'-C4'	5.87	120.30	111.50
27	e	32	PHE	CA-C-N	5.81	132.63	121.54
27	e	32	PHE	C-N-CA	5.81	132.63	121.54
2	2	1102	C	C3'-C2'-O2'	5.79	119.39	110.70
6	D	606	ARG	CA-C-N	5.79	132.60	121.54
6	D	606	ARG	C-N-CA	5.79	132.60	121.54
2	2	1151	U	O5'-C5'-C4'	-5.78	102.83	111.50
2	2	1165	C	C5'-C4'-O4'	5.77	118.45	109.80
7	E	301	ARG	CG-CD-NE	-5.75	99.35	112.00
2	2	1117	G	C4'-C3'-O3'	5.73	121.59	113.00
2	2	1107	C	N1-C1'-C2'	-5.69	103.47	112.00
2	2	1107	C	C4'-C3'-O3'	-5.68	104.48	113.00
18	T	28	ASN	CA-C-N	5.58	125.94	119.47
18	T	28	ASN	C-N-CA	5.58	125.94	119.47
13	O	680	PRO	N-CA-C	5.57	117.50	110.70
2	2	1090	A	O3'-P-O5'	5.52	112.29	104.00
6	D	464	ILE	N-CA-CB	-5.48	106.19	112.21
5	C	155	SER	N-CA-C	5.46	116.96	110.19
8	F	325	THR	CA-C-N	5.46	131.97	121.54
8	F	325	THR	C-N-CA	5.46	131.97	121.54
2	2	1148	U	P-O5'-C5'	5.46	129.09	120.90
2	2	1139	G	C4'-C3'-O3'	5.45	121.17	113.00
2	2	1168	U	C4'-C3'-C2'	-5.45	97.15	102.60
7	E	536	LEU	CA-CB-CG	5.44	135.35	116.30
2	2	1162	U	C4'-C3'-C2'	5.44	108.04	102.60
2	2	148	G	C2'-C3'-O3'	-5.42	105.57	113.70
2	2	1092	A	O3'-P-O5'	-5.41	95.89	104.00
8	F	324	VAL	CA-C-N	5.41	131.87	121.54
8	F	324	VAL	C-N-CA	5.41	131.87	121.54
2	2	1126	G	C4'-C3'-O3'	5.40	121.10	113.00
4	B	31	PRO	CA-C-N	5.39	131.84	121.54
4	B	31	PRO	C-N-CA	5.39	131.84	121.54
14	P	961	CYS	CB-CA-C	-5.39	109.37	115.79
2	2	146	A	C5'-C4'-C3'	-5.37	107.95	116.00
2	2	1128	C	C5'-C4'-O4'	5.36	117.84	109.80
2	2	149	A	O5'-C5'-C4'	5.35	119.52	111.50
2	2	1095	U	C3'-C2'-O2'	5.35	118.72	110.70
7	E	204	SER	CA-C-N	5.33	127.74	120.54
7	E	204	SER	C-N-CA	5.33	127.74	120.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	143	G	C3'-C2'-O2'	-5.33	102.71	110.70
7	E	415	LEU	CA-CB-CG	5.32	134.92	116.30
19	U	229	ASN	N-CA-C	5.32	117.30	107.73
7	E	113	LEU	CB-CG-CD2	-5.25	94.94	110.70
29	g	19	ILE	CA-C-N	5.25	131.57	121.54
29	g	19	ILE	C-N-CA	5.25	131.57	121.54
2	2	1089	G	C2'-C3'-O3'	-5.25	105.83	113.70
7	E	264	TYR	CA-C-N	-5.25	115.44	122.42
7	E	264	TYR	C-N-CA	-5.25	115.44	122.42
2	2	140	G	C3'-C2'-O2'	5.24	118.56	110.70
2	2	1129	U	O4'-C4'-C3'	5.24	109.24	104.00
8	F	376	SER	N-CA-C	5.24	117.09	110.33
2	2	1090	A	P-O5'-C5'	5.23	128.74	120.90
6	D	614	VAL	N-CA-CB	-5.22	105.56	112.34
7	E	157	ARG	NH1-CZ-NH2	5.22	126.08	119.30
2	2	1142	G	C1'-C2'-O2'	-5.21	100.58	108.40
1	1	116	A	O3'-P-O5'	5.18	111.78	104.00
2	2	1167	U	C5'-C4'-O4'	-5.18	102.03	109.80
2	2	148	G	C4'-C3'-O3'	5.17	120.75	113.00
2	2	1167	U	P-O3'-C3'	-5.15	112.47	120.20
1	1	76	U	C2'-C3'-O3'	5.13	121.39	113.70
8	F	376	SER	CA-C-N	5.13	128.36	120.82
8	F	376	SER	C-N-CA	5.13	128.36	120.82
2	2	144	G	P-O3'-C3'	-5.12	112.52	120.20
2	2	144	G	N9-C1'-C2'	5.08	119.62	112.00
2	2	1163	C	C2'-C3'-O3'	-5.07	106.09	113.70
6	D	500	LEU	CA-CB-CG	5.05	133.98	116.30
8	F	413	PRO	CA-N-CD	-5.05	104.93	112.00

There are no chirality outliers.

All (41) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	2	141	A	Sidechain
4	B	166	LYS	Peptide
4	B	170	VAL	Peptide
4	B	43	GLY	Peptide
5	C	103	ASP	Peptide
5	C	122	ALA	Peptide
5	C	154	ARG	Peptide
6	D	364	ASN	Peptide
6	D	424	LEU	Peptide

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Mol	Chain	Res	Type	Group
6	D	531	ASP	Peptide
6	D	533	ASN	Peptide
6	D	573	HIS	Peptide
7	E	262	ASN	Peptide
7	E	265	THR	Peptide
7	E	306	LEU	Peptide
7	E	376	SER	Peptide
7	E	377	ASP	Peptide
7	E	403	TYR	Peptide
7	E	410	SER	Peptide
7	E	447	PHE	Peptide
7	E	448	TYR	Peptide
7	E	451	ASP	Peptide
7	E	506	TRP	Peptide
7	E	511	LYS	Peptide
8	F	304	LEU	Peptide
8	F	309	ASP	Peptide
8	F	323	LEU	Peptide
8	F	324	VAL	Peptide
8	F	325	THR	Peptide
8	F	384	ARG	Peptide
8	F	385	SER	Peptide
8	F	413	PRO	Peptide
9	G	227	CYS	Peptide
10	H	69	PRO	Peptide
14	P	1013	ASP	Peptide
14	P	1014	LYS	Peptide
18	T	458	SER	Peptide
21	W	16	VAL	Peptide
27	e	32	PHE	Peptide
29	g	17	LEU	Peptide
30	h	43	VAL	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	6625	0	3415	98	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	2	3025	0	1535	246	0
3	A	492	0	190	1	0
4	B	1450	0	1340	36	0
5	C	1323	0	1217	28	0
6	D	3462	0	2785	64	0
7	E	4574	0	4581	128	0
8	F	1337	0	1304	39	0
9	G	1684	0	1618	40	0
10	H	1083	0	830	19	0
11	I	789	0	403	31	0
12	J	324	0	310	3	0
13	O	6612	0	6823	315	0
14	P	9437	0	9532	493	0
15	Q	1786	0	1778	68	0
16	R	1429	0	1458	44	0
17	S	814	0	809	39	0
18	T	3915	0	3853	147	0
19	U	1489	0	1392	74	0
20	V	1084	0	1081	52	0
21	W	1383	0	1407	225	0
22	X	255	0	55	0	0
23	Y	683	0	715	91	0
24	Z	685	0	693	28	0
25	b	972	0	1048	33	0
25	s	518	0	548	42	0
26	d	714	0	738	18	0
26	v	632	0	653	52	0
27	e	600	0	634	16	0
27	w	602	0	631	46	0
28	f	585	0	587	15	0
28	x	585	0	587	41	0
29	g	556	0	583	22	0
29	y	577	0	595	29	0
30	h	834	0	883	26	0
30	t	569	0	616	54	0
31	i	805	0	834	20	0
31	u	752	0	786	65	0
32	C	1	0	0	0	0
32	H	2	0	0	0	0
32	S	3	0	0	0	0
32	T	2	0	0	0	0
32	U	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	65050	0	58847	2366	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 19.

All (2366) 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)
2:2:143:G:C3'	2:2:143:G:O3'	1.63	1.45
2:2:1098:C:O3'	21:W:158:ASN:ND2	1.69	1.23
2:2:1099:G:O2'	2:2:1100:A:H5'	1.42	1.16
2:2:118:U:C5	31:u:99:ASP:HB3	1.83	1.12
2:2:1099:G:OP1	21:W:158:ASN:CG	1.91	1.12
21:W:22:LYS:HZ2	21:W:34:LEU:HD13	1.14	1.08
2:2:1098:C:OP1	23:Y:43:ARG:NE	1.88	1.06
2:2:118:U:H5	31:u:99:ASP:HB3	1.23	1.04
27:w:83:LYS:NZ	28:x:75:CYS:O	1.95	0.99
21:W:17:ASP:HB3	23:Y:61:VAL:HA	1.42	0.99
13:O:381:LEU:O	13:O:385:SER:HB2	1.64	0.98
21:W:31:LEU:HB2	21:W:36:LEU:HA	1.45	0.98
2:2:1100:A:H2'	23:Y:38:LYS:HE2	1.46	0.98
27:w:59:GLU:HG3	27:w:77:LEU:HD11	1.43	0.96
2:2:1099:G:C2'	2:2:1100:A:H5'	1.97	0.95
2:2:1167:U:OP1	21:W:92:ARG:NH2	1.99	0.94
2:2:1148:U:H4'	25:s:78:GLU:OE2	1.67	0.94
13:O:244:LEU:O	13:O:248:ALA:HB2	1.67	0.94
2:2:116:U:C4	30:t:88:ARG:HD2	2.03	0.93
2:2:1099:G:P	21:W:158:ASN:CG	2.51	0.93
18:T:63:LYS:HB2	18:T:376:GLN:HG3	1.49	0.93
27:w:87:ILE:O	29:y:64:ARG:NE	2.00	0.93
19:U:235:GLU:O	19:U:239:LYS:HB2	1.69	0.92
21:W:17:ASP:HA	23:Y:61:VAL:HG12	1.50	0.91
14:P:827:TRP:HA	14:P:839:ARG:O	1.70	0.91
2:2:44:PSU:HN3	11:I:59:C:H42	1.11	0.91
2:2:1099:G:OP1	21:W:158:ASN:OD1	1.87	0.90
29:y:64:ARG:HH11	29:y:66:ASN:HB3	1.38	0.89
2:2:1138:G:OP2	23:Y:41:MET:HE2	1.72	0.88
1:1:315:G:H1	1:1:526:U:H3	1.20	0.87
18:T:11:LEU:HA	18:T:14:MET:HE3	1.57	0.87
19:U:36:LYS:HD3	19:U:191:THR:HG21	1.55	0.87
13:O:317:ILE:O	13:O:321:CYS:HB3	1.73	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:t:35:GLN:OE1	30:t:37:ASN:ND2	2.07	0.87
27:w:37:ILE:HD11	27:w:59:GLU:HB3	1.55	0.87
14:P:71:PHE:HA	14:P:97:THR:HG22	1.57	0.86
21:W:8:VAL:HA	21:W:25:VAL:HG13	1.57	0.86
14:P:416:SER:HA	14:P:431:SER:HA	1.56	0.86
2:2:1115:G:O6	26:v:77:LEU:HD11	1.75	0.86
2:2:1098:C:O3'	21:W:158:ASN:CG	2.19	0.85
2:2:1098:C:H5'	21:W:152:GLU:CD	2.01	0.85
14:P:379:VAL:O	14:P:390:LYS:HA	1.76	0.85
13:O:198:GLU:O	13:O:202:ASN:HB2	1.76	0.84
21:W:30:ILE:HD12	21:W:41:GLU:HG2	1.57	0.84
2:2:114:U:O4'	26:v:67:SER:HB2	1.78	0.84
18:T:506:LEU:HD23	18:T:521:TYR:HB3	1.57	0.83
25:s:88:ARG:NH2	26:v:66:GLY:O	2.11	0.83
31:u:72:VAL:HB	31:u:91:ILE:O	1.77	0.83
14:P:417:HIS:HB2	14:P:432:GLU:HB3	1.59	0.83
19:U:36:LYS:HD3	19:U:191:THR:CG2	2.08	0.83
21:W:32:ARG:HA	21:W:36:LEU:HD22	1.60	0.83
21:W:157:GLN:HE22	23:Y:96:GLY:H	1.26	0.83
14:P:634:CYS:HG	14:P:645:SER:HG	1.15	0.82
18:T:11:LEU:HD23	18:T:14:MET:CE	2.08	0.82
2:2:1115:G:C6	26:v:77:LEU:HD11	2.14	0.82
2:2:1099:G:P	21:W:158:ASN:ND2	2.53	0.82
21:W:22:LYS:HE3	21:W:34:LEU:HD22	1.62	0.82
2:2:114:U:O2	26:v:39:SER:OG	1.97	0.82
2:2:119:G:OP2	28:x:76:ASN:ND2	2.12	0.82
10:H:201:CYS:SG	10:H:226:HIS:HE1	2.03	0.82
1:1:313:G:H1	1:1:528:U:H3	1.27	0.81
2:2:111:C:H5	31:u:63:ARG:HD3	1.45	0.81
2:2:1099:G:O2'	2:2:1100:A:C5'	2.24	0.81
18:T:331:GLU:O	18:T:335:THR:HG23	1.79	0.81
21:W:25:VAL:HB	21:W:31:LEU:HA	1.61	0.81
28:x:32:LYS:HA	28:x:79:LEU:HD12	1.62	0.81
21:W:22:LYS:NZ	21:W:34:LEU:HD13	1.95	0.80
14:P:609:HIS:O	14:P:620:ASN:HA	1.80	0.80
2:2:141:A:H2'	2:2:142:C:C6	2.15	0.80
2:2:144:G:H3'	2:2:145:G:H8	1.46	0.80
18:T:150:PRO:HG3	18:T:154:THR:H	1.46	0.80
27:w:24:GLN:HB3	27:w:42:LYS:HD2	1.62	0.80
18:T:459:SER:O	18:T:462:LYS:NZ	2.15	0.79
13:O:222:ILE:HG23	13:O:265:ILE:HD11	1.62	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:W:44:PRO:HG3	21:W:64:LEU:HD11	1.64	0.79
27:w:30:TRP:HB3	29:y:23:ARG:HH12	1.48	0.79
21:W:156:PHE:HZ	23:Y:50:LEU:HD22	1.47	0.79
18:T:11:LEU:HD23	18:T:14:MET:HE1	1.65	0.78
1:1:52:U:H3	1:1:161:G:H1	1.31	0.78
2:2:111:C:N4	31:u:63:ARG:CG	2.47	0.78
14:P:363:VAL:HG12	14:P:364:THR:H	1.48	0.78
2:2:1148:U:C4'	25:s:78:GLU:OE2	2.32	0.78
18:T:150:PRO:HB3	18:T:154:THR:HB	1.64	0.78
13:O:686:LEU:HD21	13:O:727:ILE:HD11	1.66	0.77
2:2:111:C:N4	31:u:63:ARG:HG3	2.00	0.77
2:2:116:U:C5	30:t:88:ARG:HD2	2.19	0.77
13:O:835:ILE:HA	13:O:838:ILE:HD12	1.67	0.77
14:P:699:MET:HA	14:P:719:GLN:O	1.85	0.77
2:2:1115:G:N7	26:v:77:LEU:CD1	2.47	0.77
13:O:790:LYS:HD2	13:O:826:TYR:HB3	1.67	0.77
25:s:88:ARG:HH12	26:v:67:SER:C	1.93	0.77
2:2:1115:G:C5	26:v:77:LEU:CD1	2.68	0.76
21:W:36:LEU:HD11	21:W:57:LEU:HG	1.65	0.76
14:P:434:ASN:ND2	14:P:506:THR:OG1	2.19	0.76
19:U:40:VAL:HG23	19:U:53:ARG:HH12	1.49	0.76
19:U:180:ILE:HG22	19:U:201:ILE:HG12	1.68	0.76
2:2:1138:G:OP2	23:Y:41:MET:HB2	1.85	0.76
25:s:86:ILE:HG22	26:v:72:ILE:HG22	1.67	0.76
1:1:312:G:H1	1:1:529:U:H3	1.33	0.76
14:P:104:TYR:HE1	14:P:113:LEU:HD23	1.49	0.76
21:W:50:LEU:HD23	21:W:52:LYS:H	1.51	0.76
1:1:320:U:H3	1:1:521:G:H1	1.35	0.75
31:u:74:GLU:OE2	31:u:89:ARG:NE	2.20	0.75
14:P:526:SER:HA	14:P:870:ARG:HG3	1.67	0.75
13:O:651:LEU:HD21	13:O:692:ILE:HD11	1.65	0.75
14:P:105:ASP:HB2	14:P:114:ILE:HD11	1.69	0.75
2:2:142:C:H2'	2:2:143:G:H8	1.49	0.75
26:v:65:ARG:HE	26:v:67:SER:HB3	1.52	0.75
13:O:317:ILE:O	13:O:321:CYS:CB	2.34	0.75
26:d:21:LEU:O	26:d:28:THR:HA	1.87	0.75
2:2:43:G:N2	11:I:61:U:O2	2.20	0.74
2:2:116:U:C4	30:t:88:ARG:HG3	2.20	0.74
2:2:1138:G:P	2:2:1138:G:O4'	2.45	0.74
30:h:36:MET:SD	31:i:97:ARG:NH2	2.60	0.74
13:O:566:LEU:HD21	13:O:601:ILE:HG12	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Z:54:SER:HA	24:Z:65:THR:HG21	1.69	0.74
27:w:20:PHE:HE1	27:w:92:SER:HB2	1.51	0.74
2:2:116:U:C4	30:t:88:ARG:CD	2.70	0.74
14:P:434:ASN:HD22	14:P:504:HIS:HE1	1.35	0.74
16:R:66:ALA:O	16:R:70:MET:HB3	1.87	0.74
21:W:111:PHE:CE2	21:W:140:TYR:HA	2.22	0.74
21:W:7:ILE:HG22	21:W:25:VAL:HG12	1.69	0.74
1:1:185:U:H3	1:1:304:G:H1	1.35	0.74
13:O:675:LEU:HD11	13:O:714:LEU:HB3	1.69	0.73
18:T:516:MET:HE1	18:T:524:LEU:HD22	1.68	0.73
13:O:310:VAL:O	13:O:314:LEU:HB2	1.88	0.73
17:S:54:GLN:HB3	17:S:88:ARG:HH22	1.52	0.73
18:T:93:PHE:CZ	20:V:148:PHE:HE1	2.06	0.73
13:O:386:TYR:CG	13:O:387:PRO:HD2	2.22	0.73
8:F:316:PHE:HB3	8:F:381:SER:O	1.88	0.73
20:V:158:ARG:HH11	20:V:158:ARG:HB2	1.53	0.73
14:P:250:PRO:HG2	14:P:273:LEU:HB3	1.70	0.73
14:P:1178:PRO:HG3	15:Q:145:GLN:HE21	1.53	0.73
17:S:62:ASN:HD21	17:S:92:LEU:HA	1.53	0.73
13:O:805:TYR:HB2	13:O:816:VAL:HG11	1.69	0.73
21:W:5:PRO:O	21:W:8:VAL:HG12	1.88	0.73
27:e:53:VAL:HA	27:e:80:ILE:O	1.88	0.73
19:U:53:ARG:NH2	19:U:58:ILE:O	2.22	0.73
2:2:142:C:H2'	2:2:143:G:C8	2.23	0.73
1:1:199:G:H1	1:1:239:U:H3	1.33	0.73
2:2:111:C:H41	31:u:63:ARG:HG3	1.50	0.73
14:P:1111:ASP:HB2	14:P:1183:CYS:HB2	1.71	0.73
2:2:111:C:H41	31:u:63:ARG:CG	2.02	0.72
14:P:1294:GLU:HG3	17:S:41:ARG:HG2	1.70	0.72
27:w:59:GLU:OE2	28:x:30:LYS:NZ	2.21	0.72
2:2:116:U:C4	30:t:88:ARG:CG	2.72	0.72
20:V:103:TYR:HD1	20:V:110:VAL:HG21	1.53	0.72
13:O:445:GLU:HG2	13:O:453:MET:HE2	1.70	0.72
2:2:140:G:H1	2:2:1168:U:H3	1.37	0.72
2:2:1093:C:H2'	2:2:1094:G:O4'	1.90	0.72
14:P:638:SER:HB3	14:P:641:GLN:HB3	1.72	0.72
19:U:186:LEU:HA	19:U:194:LYS:HD2	1.71	0.72
2:2:114:U:H5''	2:2:115:U:H5'	1.70	0.72
9:G:98:LEU:HA	9:G:116:VAL:O	1.90	0.72
13:O:594:MET:O	13:O:598:LEU:N	2.22	0.72
13:O:945:TYR:HB3	13:O:948:ALA:HB3	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Y:45:ARG:NH1	23:Y:62:SER:HB3	2.04	0.72
2:2:111:C:C5	31:u:63:ARG:HG2	2.25	0.72
14:P:181:ARG:HD2	14:P:185:ARG:HH22	1.55	0.72
17:S:56:LYS:HB3	17:S:65:VAL:HG23	1.72	0.72
25:s:88:ARG:HG2	25:s:90:GLU:H	1.55	0.72
1:1:198:U:H3	1:1:240:G:H1	1.35	0.72
14:P:410:PHE:HE1	14:P:445:GLY:HA3	1.54	0.72
19:U:179:LEU:HD13	20:V:192:PHE:HB2	1.72	0.72
19:U:246:ILE:H	19:U:246:ILE:HD13	1.54	0.72
14:P:1125:ASP:HB2	14:P:1128:THR:HG22	1.72	0.71
13:O:778:ARG:NH1	13:O:811:ASN:OD1	2.23	0.71
21:W:24:ASN:HA	21:W:32:ARG:O	1.89	0.71
2:2:45:U:O4	11:I:58:U:O4	2.07	0.71
21:W:81:LEU:O	21:W:84:ASN:ND2	2.23	0.71
2:2:1115:G:C5	26:v:77:LEU:HD12	2.25	0.71
20:V:92:ASP:O	20:V:96:ILE:HG12	1.89	0.71
18:T:93:PHE:HZ	20:V:148:PHE:HE1	1.39	0.71
23:Y:35:LEU:HG	23:Y:99:LEU:HD11	1.72	0.71
2:2:111:C:C5	28:x:48:TYR:HE2	2.08	0.71
2:2:1115:G:C6	26:v:77:LEU:CD1	2.73	0.71
16:R:136:ARG:HB2	16:R:154:TYR:HD2	1.55	0.71
19:U:123:UNK:HA	19:U:207:GLU:HB2	1.72	0.71
14:P:825:SER:OG	14:P:827:TRP:NE1	2.24	0.71
14:P:847:LEU:HB3	14:P:865:ILE:HG23	1.73	0.71
2:2:111:C:C4	31:u:63:ARG:HG2	2.25	0.71
14:P:732:ARG:NH2	14:P:737:GLY:O	2.22	0.71
1:1:311:U:H3	1:1:530:G:H1	1.38	0.70
14:P:1122:LYS:NZ	14:P:1202:PHE:O	2.23	0.70
30:t:7:LEU:HB3	30:t:32:VAL:HG11	1.71	0.70
1:1:5:PSU:O4	10:H:216:ARG:NH1	2.25	0.70
1:1:6:PSU:H4'	10:H:220:HIS:HD1	1.57	0.70
2:2:41:C:H42	11:I:63:U:H3	1.40	0.70
13:O:884:LEU:HD12	13:O:906:LEU:HD11	1.74	0.70
14:P:639:LYS:HB3	14:P:686:GLN:HA	1.73	0.70
18:T:377:VAL:O	18:T:378:ASP:HB2	1.91	0.70
30:t:3:LEU:HD23	31:u:95:PHE:HE1	1.56	0.70
2:2:1098:C:H5'	21:W:152:GLU:OE2	1.91	0.70
14:P:130:LEU:HB3	14:P:195:ILE:HD13	1.74	0.70
2:2:44:PSU:HN3	11:I:59:C:N4	1.87	0.70
14:P:75:CYS:HB2	14:P:129:SER:HB3	1.74	0.70
14:P:364:THR:OG1	14:P:384:ASN:ND2	2.21	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:434:ASN:HD22	14:P:504:HIS:CE1	2.10	0.70
18:T:449:HIS:O	18:T:453:LEU:HB2	1.91	0.70
21:W:17:ASP:O	23:Y:61:VAL:HB	1.91	0.70
2:2:43:G:H1	11:I:60:U:H3	1.38	0.70
14:P:983:ALA:O	14:P:995:ILE:HB	1.91	0.70
14:P:857:VAL:O	14:P:875:ARG:NH1	2.25	0.70
21:W:47:LEU:O	21:W:50:LEU:HB3	1.92	0.70
18:T:33:TYR:O	18:T:36:ILE:HG22	1.91	0.69
29:g:19:ILE:O	29:g:23:ARG:HB2	1.91	0.69
25:s:21:ARG:NH1	25:s:51:GLU:OE2	2.25	0.69
14:P:493:VAL:O	14:P:499:SER:OG	2.09	0.69
18:T:148:SER:HB2	18:T:159:ASP:H	1.57	0.69
19:U:53:ARG:HE	19:U:56:PRO:HA	1.54	0.69
30:h:3:LEU:O	30:h:6:PHE:HB3	1.92	0.69
14:P:78:HIS:NE2	14:P:81:ASP:OD1	2.24	0.69
14:P:365:ILE:HD13	14:P:381:LEU:HB3	1.74	0.69
13:O:689:LEU:HD21	13:O:707:PHE:HD2	1.57	0.69
14:P:690:LEU:HB3	14:P:702:ILE:HD11	1.73	0.69
19:U:36:LYS:CD	19:U:191:THR:HG21	2.21	0.69
18:T:150:PRO:HG3	18:T:155:ASN:H	1.55	0.69
2:2:111:C:C5	31:u:63:ARG:HD3	2.28	0.69
21:W:129:LEU:O	21:W:132:ASN:ND2	2.24	0.69
7:E:355:ILE:HG21	7:E:363:LEU:HD12	1.74	0.69
14:P:103:LEU:HG	14:P:114:ILE:HD12	1.72	0.69
14:P:116:LYS:HD2	14:P:883:ASP:HB3	1.73	0.69
19:U:203:TYR:HD1	19:U:205:PRO:HD2	1.57	0.69
1:1:27:A:H61	1:1:34:A:H62	1.39	0.69
2:2:1098:C:C3'	21:W:158:ASN:HD22	2.06	0.69
18:T:11:LEU:HA	18:T:14:MET:CE	2.23	0.69
28:x:19:LEU:HD21	28:x:45:THR:HG21	1.73	0.69
13:O:963:TYR:OH	14:P:1091:HIS:NE2	2.24	0.69
21:W:67:ILE:HD12	21:W:89:VAL:HG12	1.72	0.69
14:P:369:ILE:HD11	14:P:380:LEU:HB2	1.75	0.68
31:u:33:LEU:HD12	28:x:72:PHE:HB2	1.74	0.68
21:W:14:TYR:OH	23:Y:57:GLU:HG3	1.93	0.68
27:w:30:TRP:HB3	29:y:23:ARG:NH1	2.09	0.68
6:D:366:ILE:HG23	6:D:432:ILE:HD11	1.75	0.68
14:P:527:LEU:HD12	14:P:528:PRO:HD2	1.75	0.68
15:Q:184:SER:O	19:U:72:ASN:ND2	2.19	0.68
26:v:68:GLN:HG3	29:y:69:ILE:HA	1.74	0.68
2:2:1092:A:H3'	2:2:1093:C:H6	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:882:ASN:ND2	13:O:918:TYR:OH	2.27	0.68
1:1:188:U:H3	1:1:250:G:H1	1.42	0.68
14:P:496:SER:HB3	14:P:497:PRO:HD3	1.74	0.68
14:P:884:ASN:ND2	14:P:886:PHE:O	2.27	0.68
14:P:1259:GLU:OE2	14:P:1263:LYS:NZ	2.27	0.68
30:t:36:MET:SD	31:u:97:ARG:NH1	2.67	0.68
16:R:36:LEU:HG	16:R:37:ARG:HG3	1.75	0.68
1:1:190:U:H3	1:1:248:G:H1	1.42	0.68
7:E:442:ASN:ND2	7:E:481:CYS:SG	2.67	0.68
14:P:582:LYS:HE2	14:P:610:ILE:HG21	1.76	0.67
14:P:841:LEU:HD23	14:P:843:ASP:H	1.58	0.67
2:2:45:U:H3	11:I:58:U:H3	1.40	0.67
25:s:39:LYS:HE3	30:t:35:GLN:HE21	1.59	0.67
14:P:414:GLN:NE2	14:P:434:ASN:OD1	2.27	0.67
8:F:368:MET:HB2	8:F:380:LEU:HD11	1.77	0.67
13:O:381:LEU:O	13:O:385:SER:CB	2.40	0.67
14:P:104:TYR:OH	14:P:481:GLN:NE2	2.27	0.67
14:P:594:MET:O	14:P:598:SER:OG	2.12	0.67
14:P:927:ARG:HG3	14:P:928:THR:HG23	1.76	0.67
19:U:153:LEU:H	19:U:219:LEU:HD23	1.58	0.67
21:W:8:VAL:HG11	21:W:49:HIS:HB3	1.75	0.67
2:2:141:A:H2'	2:2:142:C:C5	2.28	0.67
13:O:531:GLU:HA	13:O:534:ARG:HE	1.59	0.67
20:V:221:LEU:O	20:V:225:ARG:HG3	1.95	0.67
1:1:280:G:O6	25:b:121:LYS:NZ	2.26	0.67
2:2:1148:U:O2'	25:s:78:GLU:OE2	2.13	0.67
20:V:97:LYS:O	20:V:101:ARG:HG3	1.93	0.67
20:V:132:HIS:O	20:V:135:PHE:HB3	1.94	0.66
27:w:34:GLN:O	29:y:23:ARG:NH2	2.27	0.66
13:O:678:LEU:HD12	13:O:682:ILE:HD11	1.76	0.66
16:R:184:PHE:HA	16:R:188:GLY:HA2	1.77	0.66
18:T:116:LEU:HD13	20:V:102:TYR:CD2	2.30	0.66
2:2:111:C:H5	31:u:63:ARG:CD	2.07	0.66
21:W:7:ILE:HA	21:W:27:LYS:H	1.60	0.66
4:B:19:ARG:HH22	25:b:83:GLY:HA3	1.59	0.66
7:E:400:ASN:HB2	7:E:413:ASN:HB3	1.76	0.66
21:W:8:VAL:CA	21:W:25:VAL:HG13	2.26	0.66
21:W:16:VAL:HG22	21:W:22:LYS:NZ	2.10	0.66
14:P:268:LEU:HD13	14:P:329:ILE:HD11	1.76	0.66
14:P:547:ASN:HA	14:P:563:ILE:O	1.95	0.66
14:P:944:ASN:ND2	14:P:979:CYS:SG	2.65	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:1097:PHE:HB3	14:P:1106:PHE:HB3	1.77	0.66
18:T:415:HIS:HE1	18:T:435:ARG:HH11	1.43	0.66
19:U:212:GLU:HG2	19:U:214:PRO:HD3	1.76	0.66
21:W:141:ARG:HD2	21:W:154:LEU:HD23	1.77	0.66
14:P:704:SER:O	14:P:713:LEU:HA	1.94	0.66
14:P:736:ILE:HG23	14:P:738:GLN:H	1.60	0.66
19:U:36:LYS:HE2	19:U:191:THR:OG1	1.94	0.66
14:P:380:LEU:HA	14:P:389:PHE:O	1.96	0.66
19:U:136:UNK:HA	19:U:149:GLY:HA2	1.77	0.66
21:W:81:LEU:HB3	21:W:102:THR:O	1.96	0.66
29:g:17:LEU:HD23	29:g:71:LEU:HB3	1.77	0.66
2:2:1138:G:O2'	2:2:1139:G:H8	1.79	0.66
14:P:690:LEU:HA	14:P:703:MET:O	1.96	0.66
14:P:1036:LYS:NZ	14:P:1082:TYR:OH	2.28	0.66
7:E:428:LEU:O	7:E:437:GLN:NE2	2.29	0.65
13:O:804:GLU:O	13:O:807:THR:OG1	2.13	0.65
23:Y:69:ARG:HG3	23:Y:71:GLN:HG3	1.78	0.65
2:2:1115:G:C5	26:v:77:LEU:HD11	2.31	0.65
17:S:37:VAL:HG22	17:S:38:ARG:HG2	1.78	0.65
21:W:11:ALA:HB1	21:W:31:LEU:HD23	1.78	0.65
31:i:72:VAL:HB	31:i:91:ILE:O	1.95	0.65
13:O:542:THR:O	13:O:546:ASN:ND2	2.30	0.65
14:P:994:LEU:HB3	14:P:1006:TYR:HB2	1.78	0.65
14:P:1178:PRO:HG2	15:Q:146:ILE:HD11	1.78	0.65
18:T:180:MET:H	18:T:335:THR:HG21	1.61	0.65
4:B:197:ARG:NH2	4:B:203:LEU:O	2.29	0.65
21:W:81:LEU:HD21	21:W:86:ILE:HD13	1.79	0.65
2:2:116:U:O4	30:t:88:ARG:HG3	1.96	0.65
18:T:139:ASP:O	18:T:143:LEU:HB2	1.97	0.65
14:P:268:LEU:HD21	14:P:270:PHE:CE1	2.32	0.65
23:Y:60:LYS:NZ	23:Y:73:PHE:HB2	2.12	0.65
23:Y:94:PHE:HB3	23:Y:99:LEU:HD13	1.78	0.65
31:u:54:ILE:HG23	31:u:72:VAL:HG13	1.78	0.65
27:w:43:ILE:HD12	27:w:52:VAL:HG11	1.79	0.65
2:2:1120:G:H2'	2:2:1121:U:H6	1.62	0.65
17:S:98:ASP:O	17:S:102:GLU:HB2	1.97	0.65
21:W:36:LEU:HB2	21:W:59:LEU:HA	1.78	0.65
26:v:23:LEU:HD21	29:y:69:ILE:HG23	1.78	0.65
23:Y:45:ARG:NH2	23:Y:63:MET:O	2.29	0.65
2:2:1138:G:HO2'	2:2:1139:G:H8	1.44	0.65
13:O:159:ASP:O	13:O:163:GLU:HB2	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:645:ILE:HD11	13:O:679:GLN:HG2	1.79	0.65
13:O:955:VAL:HA	13:O:959:ASN:HD22	1.62	0.65
2:2:1115:G:H1	2:2:1130:U:H3	1.43	0.65
13:O:832:LYS:HB2	13:O:871:THR:HG21	1.78	0.65
21:W:11:ALA:HB3	21:W:24:ASN:HB3	1.77	0.65
1:1:563:U:N3	4:B:34:LYS:O	2.30	0.64
14:P:382:GLN:NE2	14:P:416:SER:O	2.29	0.64
14:P:783:ILE:HG13	14:P:784:SER:H	1.61	0.64
14:P:1165:LYS:HE2	16:R:34:PRO:HG2	1.78	0.64
15:Q:249:ASP:HB3	15:Q:253:LYS:HE3	1.79	0.64
27:w:30:TRP:CE2	27:w:89:LEU:HD22	2.32	0.64
2:2:1098:C:H2'	2:2:1099:G:H8	1.62	0.64
13:O:542:THR:HG22	13:O:582:GLY:HA3	1.79	0.64
13:O:757:ILE:HG22	13:O:758:GLY:H	1.62	0.64
14:P:832:TRP:HB3	14:P:835:VAL:HG23	1.80	0.64
14:P:1336:PHE:O	14:P:1339:LYS:NZ	2.29	0.64
18:T:132:LEU:HD23	18:T:132:LEU:H	1.61	0.64
2:2:1097:G:C5'	23:Y:42:GLN:HE22	2.10	0.64
2:2:1138:G:O2'	2:2:1139:G:C8	2.50	0.64
7:E:16:LEU:HD21	7:E:33:LEU:HA	1.78	0.64
25:s:49:ILE:HG22	25:s:81:VAL:HA	1.79	0.64
2:2:1097:G:C2	2:2:1146:G:C4	2.86	0.64
7:E:320:LEU:HD21	7:E:326:ASP:HB2	1.79	0.64
14:P:738:GLN:NE2	14:P:740:ASN:OD1	2.30	0.64
15:Q:128:LYS:HA	15:Q:131:LYS:HE2	1.79	0.64
15:Q:331:ALA:HB1	15:Q:337:ILE:HA	1.80	0.64
19:U:178:PRO:HD3	19:U:203:TYR:HE2	1.61	0.64
30:t:26:TRP:CE3	30:t:44:LYS:HG2	2.33	0.64
30:t:3:LEU:HD13	31:u:62:ASP:HB2	1.79	0.64
5:C:36:ASP:O	5:C:40:ASN:HB2	1.98	0.64
14:P:1009:LEU:HB2	14:P:1018:ASP:HB3	1.80	0.64
23:Y:67:LYS:HB3	23:Y:69:ARG:HH11	1.62	0.64
13:O:872:GLY:HA2	14:P:1315:ARG:HG3	1.79	0.64
21:W:3:PHE:CZ	21:W:25:VAL:HG11	2.33	0.64
7:E:106:LEU:H	7:E:109:TRP:HD1	1.46	0.64
9:G:250:LEU:HA	9:G:253:LEU:HD13	1.79	0.64
13:O:484:PHE:HA	13:O:488:TRP:HD1	1.63	0.64
13:O:700:VAL:O	13:O:704:THR:OG1	2.09	0.64
15:Q:176:TRP:O	15:Q:177:GLN:HG2	1.98	0.64
18:T:445:ARG:O	18:T:449:HIS:ND1	2.28	0.64
2:2:1097:G:C3'	23:Y:40:ASN:HD22	2.11	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:359:ILE:HG21	13:O:378:LEU:HD21	1.79	0.64
18:T:81:ILE:HD11	18:T:160:ARG:HG3	1.78	0.64
7:E:286:THR:HG21	7:E:298:ASN:HD22	1.62	0.63
14:P:195:ILE:HG12	14:P:202:ILE:HG12	1.81	0.63
14:P:540:PRO:HB2	14:P:612:PRO:HG3	1.81	0.63
14:P:822:HIS:ND1	14:P:846:MET:O	2.31	0.63
29:y:56:GLN:HG3	29:y:61:THR:HB	1.79	0.63
13:O:966:GLU:HA	13:O:969:LEU:HD13	1.78	0.63
21:W:25:VAL:HG21	21:W:32:ARG:HB3	1.81	0.63
13:O:606:LEU:HD23	13:O:609:LEU:HD12	1.79	0.63
13:O:963:TYR:O	24:Z:36:ARG:NH2	2.30	0.63
14:P:776:SER:HB2	14:P:822:HIS:HB2	1.79	0.63
23:Y:45:ARG:NE	23:Y:63:MET:H	1.97	0.63
28:x:28:GLY:HA2	28:x:38:TYR:O	1.97	0.63
2:2:113:U:H1'	29:y:66:ASN:HB2	1.81	0.63
7:E:479:TRP:HH2	7:E:508:GLN:HB3	1.64	0.63
9:G:188:VAL:HB	9:G:202:GLN:HE21	1.63	0.63
14:P:1124:LEU:HG	14:P:1130:ILE:HD11	1.81	0.63
23:Y:44:LEU:HD22	23:Y:68:GLN:OE1	1.99	0.63
2:2:143:G:O3'	2:2:143:G:H3'	1.91	0.63
6:D:426:ASN:HB2	6:D:429:ASN:HD22	1.64	0.63
13:O:914:LEU:HD13	15:Q:266:PHE:CE1	2.33	0.63
14:P:236:VAL:HB	14:P:257:ILE:HG23	1.79	0.63
14:P:548:THR:O	14:P:563:ILE:HB	1.99	0.63
14:P:1056:LYS:O	18:T:514:ASN:ND2	2.31	0.63
14:P:1096:LEU:HD13	14:P:1187:PHE:HZ	1.63	0.63
21:W:5:PRO:HB3	21:W:49:HIS:CG	2.34	0.63
28:f:77:ASN:OD1	31:i:49:ARG:NH1	2.31	0.63
1:1:302:U:O4	25:b:121:LYS:NZ	2.32	0.63
13:O:810:THR:HG23	19:U:64:GLY:H	1.63	0.63
21:W:7:ILE:HG23	21:W:26:ASP:HA	1.80	0.63
13:O:252:ILE:HD11	13:O:296:VAL:HA	1.80	0.63
21:W:16:VAL:HG12	21:W:18:HIS:H	1.64	0.63
11:I:68:A:OP2	13:O:778:ARG:NH2	2.32	0.63
14:P:270:PHE:HE2	14:P:340:MET:HA	1.64	0.63
21:W:25:VAL:O	21:W:31:LEU:HA	1.99	0.63
27:w:40:LYS:O	27:w:57:ALA:HA	1.99	0.63
7:E:330:ALA:O	7:E:334:LEU:HB2	1.99	0.62
24:Z:22:GLY:HA2	24:Z:26:THR:HG21	1.80	0.62
25:s:88:ARG:NH1	26:v:67:SER:O	2.32	0.62
2:2:1098:C:O3'	21:W:158:ASN:CB	2.46	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:642:LEU:HD21	14:P:644:ILE:HG23	1.80	0.62
21:W:59:LEU:HD21	21:W:64:LEU:HD13	1.80	0.62
2:2:1098:C:O5'	2:2:1098:C:H6	1.82	0.62
7:E:308:HIS:HB2	7:E:341:SER:HA	1.82	0.62
13:O:943:VAL:O	14:P:185:ARG:NH1	2.32	0.62
2:2:116:U:O4'	30:t:90:ASN:HB2	1.99	0.62
14:P:1003:LEU:HD23	14:P:1059:LEU:HD11	1.81	0.62
14:P:1179:ASN:OD1	14:P:1180:THR:N	2.31	0.62
2:2:1099:G:H2'	2:2:1100:A:H5'	1.80	0.62
19:U:36:LYS:HD3	19:U:191:THR:CB	2.29	0.62
21:W:11:ALA:HB3	21:W:25:VAL:N	2.15	0.62
5:C:112:SER:OG	7:E:72:ASN:ND2	2.32	0.62
6:D:607:ASN:O	6:D:609:GLU:N	2.31	0.62
13:O:435:THR:HG21	13:O:467:VAL:HG21	1.82	0.62
14:P:211:LYS:HD2	14:P:230:ILE:HD11	1.81	0.62
1:1:550:A:OP1	31:i:63:ARG:NH1	2.33	0.62
14:P:994:LEU:HB2	14:P:1008:ILE:HD11	1.82	0.62
16:R:40:TYR:HD1	16:R:53:ALA:HB2	1.64	0.62
28:f:30:LYS:HA	28:f:37:GLU:HG2	1.82	0.62
7:E:70:LEU:HD13	7:E:73:TYR:HD2	1.65	0.62
9:G:65:ILE:HB	9:G:68:SER:HB2	1.80	0.62
14:P:1116:ARG:HH12	14:P:1189:LEU:HD13	1.64	0.62
19:U:178:PRO:HD3	19:U:203:TYR:CE2	2.35	0.62
21:W:8:VAL:HA	21:W:25:VAL:CG1	2.29	0.62
14:P:365:ILE:HG21	14:P:381:LEU:HB3	1.82	0.61
14:P:943:ASP:HB2	14:P:952:ARG:HG2	1.82	0.61
6:D:465:LYS:O	6:D:471:TRP:NE1	2.25	0.61
13:O:357:SER:HA	13:O:360:LYS:HE2	1.81	0.61
13:O:416:LEU:HD12	13:O:453:MET:HE1	1.82	0.61
19:U:242:PHE:HD1	20:V:225:ARG:HG2	1.65	0.61
21:W:35:GLN:HE22	23:Y:77:ARG:HH22	1.46	0.61
2:2:114:U:C2	26:v:39:SER:OG	2.50	0.61
8:F:311:ASN:O	8:F:407:GLN:NE2	2.32	0.61
13:O:767:LEU:HD22	13:O:804:GLU:HG2	1.81	0.61
14:P:156:ASN:HA	14:P:177:GLN:O	2.00	0.61
14:P:270:PHE:CE2	14:P:340:MET:HA	2.34	0.61
14:P:820:VAL:HG21	14:P:849:CYS:HB3	1.82	0.61
25:s:39:LYS:HE3	30:t:35:GLN:NE2	2.14	0.61
13:O:810:THR:HG22	19:U:63:SER:HB3	1.82	0.61
14:P:1235:GLY:HA2	14:P:1238:PHE:HB3	1.83	0.61
16:R:200:ARG:HB3	18:T:453:LEU:HA	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:f:72:PHE:HB2	31:i:33:LEU:HD12	1.83	0.61
30:t:44:LYS:HB2	30:t:79:ILE:HG21	1.81	0.61
14:P:62:HIS:HE2	14:P:1218:TYR:HH	1.46	0.61
23:Y:67:LYS:HB3	23:Y:69:ARG:NH1	2.15	0.61
7:E:445:VAL:HG21	7:E:481:CYS:HB3	1.81	0.61
17:S:31:PRO:HG2	17:S:43:VAL:HG11	1.83	0.61
2:2:1107:C:H2'	23:Y:105:LYS:HD2	1.82	0.61
4:B:171:HIS:HB3	4:B:183:VAL:HG21	1.81	0.61
15:Q:323:THR:OG1	16:R:62:ASP:OD1	2.17	0.61
18:T:508:GLU:HG2	18:T:509:GLU:H	1.66	0.61
14:P:426:TYR:HB3	14:P:438:LEU:HD21	1.83	0.61
14:P:816:MET:HE2	14:P:830:TYR:HB2	1.83	0.61
14:P:836:TRP:HZ3	14:P:838:ILE:HG23	1.66	0.61
21:W:111:PHE:HE2	21:W:140:TYR:HA	1.63	0.61
7:E:168:LEU:HD13	7:E:186:TRP:HD1	1.66	0.61
7:E:427:ARG:NH1	7:E:435:SER:O	2.34	0.61
13:O:850:ASP:HB2	13:O:853:HIS:HD2	1.65	0.61
13:O:855:GLN:O	13:O:858:SER:OG	2.18	0.61
14:P:426:TYR:HA	14:P:439:PHE:O	2.00	0.61
2:2:1167:U:OP1	21:W:92:ARG:CZ	2.49	0.61
13:O:226:ASP:OD1	13:O:268:ASN:ND2	2.34	0.61
14:P:768:ARG:NH1	14:P:1209:SER:O	2.34	0.61
14:P:957:ILE:HG22	14:P:962:LEU:HD11	1.81	0.61
9:G:70:LEU:O	9:G:116:VAL:HA	2.01	0.60
18:T:342:LYS:HE3	30:t:100:SER:HA	1.82	0.60
21:W:17:ASP:C	21:W:19:PHE:H	2.09	0.60
19:U:218:ILE:O	19:U:219:LEU:HG	2.00	0.60
21:W:13:GLN:HB2	21:W:23:TYR:HA	1.83	0.60
21:W:36:LEU:HG	21:W:58:ASP:C	2.25	0.60
18:T:179:TYR:HA	18:T:335:THR:HG22	1.83	0.60
19:U:41:PRO:HD2	19:U:53:ARG:HH11	1.65	0.60
21:W:32:ARG:CA	21:W:36:LEU:HD22	2.29	0.60
18:T:243:PHE:HA	18:T:246:LYS:HE2	1.83	0.60
2:2:1108:A:C2	23:Y:73:PHE:CZ	2.90	0.60
14:P:61:TYR:HB2	14:P:1231:LEU:HD11	1.83	0.60
14:P:643:ILE:HD11	14:P:653:TYR:HD1	1.66	0.60
18:T:415:HIS:CE1	18:T:435:ARG:HH11	2.18	0.60
1:1:189:U:H3	1:1:249:G:H1	1.49	0.60
2:2:67:A:HO2'	2:2:68:U:H6	1.46	0.60
14:P:154:SER:HB3	14:P:1302:ARG:HD2	1.83	0.60
18:T:26:GLN:HB2	20:V:168:THR:HG23	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:63:LYS:HE3	18:T:378:ASP:HB2	1.82	0.60
21:W:78:THR:HG23	21:W:100:ASN:HD22	1.65	0.60
13:O:240:VAL:HG13	13:O:269:LEU:HD21	1.82	0.60
13:O:605:ILE:HD11	13:O:627:LEU:HD12	1.83	0.60
14:P:493:VAL:HG23	14:P:937:LYS:HG2	1.84	0.60
19:U:232:GLY:HA2	20:V:185:VAL:HG13	1.84	0.60
21:W:57:LEU:HD22	21:W:79:LEU:HD22	1.84	0.60
26:v:65:ARG:HH12	29:y:66:ASN:C	2.09	0.60
2:2:65:A:O2'	2:2:66:A:H5'	2.02	0.60
2:2:1161:U:O2'	2:2:1162:U:H5'	2.01	0.60
25:s:21:ARG:HH11	25:s:29:VAL:HG11	1.66	0.60
31:u:72:VAL:HG21	31:u:94:LEU:HB3	1.83	0.60
14:P:379:VAL:HG22	14:P:391:LEU:HB2	1.83	0.60
2:2:1108:A:C2	23:Y:73:PHE:CE1	2.90	0.60
14:P:638:SER:HA	14:P:683:GLN:HA	1.84	0.60
30:t:43:VAL:HG11	30:t:85:ILE:HD12	1.84	0.60
27:w:40:LYS:NZ	27:w:93:ALA:HB3	2.17	0.60
2:2:115:U:H3	25:s:42:ASN:HD21	1.50	0.59
2:2:1141:C:H2'	2:2:1142:G:H8	1.67	0.59
13:O:223:LYS:NZ	17:S:98:ASP:OD2	2.34	0.59
21:W:29:VAL:HA	21:W:39:ASP:OD2	2.02	0.59
5:C:112:SER:HB3	5:C:115:TYR:HB2	1.83	0.59
13:O:324:ARG:HD2	13:O:330:ARG:HH21	1.67	0.59
14:P:1177:LEU:HD22	15:Q:171:PRO:HD2	1.83	0.59
21:W:139:ASN:HB2	21:W:142:GLU:HG2	1.84	0.59
2:2:111:C:C5	31:u:63:ARG:CD	2.85	0.59
2:2:1139:G:H2'	2:2:1140:U:C6	2.36	0.59
14:P:380:LEU:HD23	14:P:388:LEU:HD21	1.82	0.59
2:2:1152:U:H2'	2:2:1153:C:C6	2.38	0.59
13:O:361:ASP:OD1	13:O:362:CYS:N	2.35	0.59
14:P:363:VAL:O	14:P:364:THR:HG23	2.03	0.59
14:P:630:ILE:HG21	14:P:646:LEU:HB2	1.83	0.59
18:T:516:MET:HE2	18:T:521:TYR:HA	1.84	0.59
23:Y:33:SER:HB3	23:Y:100:LYS:HE3	1.84	0.59
14:P:128:LYS:NZ	14:P:194:GLU:OE1	2.32	0.59
14:P:629:GLY:O	14:P:630:ILE:HG13	2.02	0.59
14:P:1218:TYR:O	14:P:1225:VAL:HA	2.03	0.59
1:1:39:U:O2'	1:1:41:C:OP2	2.19	0.59
1:1:561:U:H5	4:B:29:ASP:HB2	1.67	0.59
2:2:1099:G:OP1	21:W:158:ASN:CB	2.50	0.59
2:2:1140:U:C2	2:2:1141:C:C5	2.91	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:117:ASN:OD1	7:E:130:TYR:OH	2.19	0.59
7:E:489:ASP:OD2	7:E:492:ARG:NH2	2.36	0.59
13:O:532:PRO:O	13:O:535:THR:OG1	2.14	0.59
14:P:369:ILE:HD13	14:P:421:ILE:HD11	1.85	0.59
14:P:924:PHE:CD2	14:P:952:ARG:HD2	2.38	0.59
21:W:16:VAL:HG22	21:W:22:LYS:HZ3	1.67	0.59
21:W:156:PHE:HB3	23:Y:95:PHE:CE1	2.38	0.59
27:w:87:ILE:O	29:y:64:ARG:NH2	2.35	0.59
14:P:1112:ASP:OD1	14:P:1113:SER:N	2.35	0.59
21:W:31:LEU:CB	21:W:36:LEU:HA	2.29	0.59
2:2:1115:G:N7	26:v:77:LEU:HG	2.18	0.59
13:O:632:LYS:HD2	13:O:672:VAL:HG13	1.83	0.59
19:U:60:LYS:HE2	19:U:66:LEU:HD11	1.83	0.59
18:T:516:MET:HE3	18:T:520:VAL:HG12	1.84	0.59
21:W:160:THR:HG22	21:W:163:GLU:HG2	1.85	0.59
13:O:294:ARG:HB3	13:O:332:THR:HG21	1.83	0.59
14:P:106:THR:C	14:P:108:ASP:H	2.11	0.59
18:T:31:LEU:HD11	18:T:75:GLN:OE1	2.02	0.59
18:T:148:SER:HB2	18:T:159:ASP:N	2.17	0.59
21:W:18:HIS:CE1	23:Y:46:VAL:HA	2.38	0.59
21:W:23:TYR:O	21:W:33:ASP:HB2	2.03	0.59
25:s:96:VAL:HG12	30:t:85:ILE:HG12	1.84	0.59
27:w:35:ILE:HA	29:y:23:ARG:HH21	1.65	0.59
13:O:599:ALA:HA	13:O:639:MET:HE1	1.85	0.58
13:O:602:VAL:HA	13:O:605:ILE:HD12	1.84	0.58
13:O:927:ALA:C	13:O:929:ASN:H	2.11	0.58
15:Q:265:CYS:SG	15:Q:266:PHE:N	2.76	0.58
21:W:157:GLN:HE22	23:Y:96:GLY:N	1.97	0.58
27:e:24:GLN:HB3	27:e:42:LYS:HD2	1.84	0.58
13:O:903:LEU:HB3	13:O:915:PHE:CZ	2.39	0.58
2:2:43:G:O6	11:I:60:U:O4	2.20	0.58
2:2:115:U:O2	25:s:88:ARG:HG3	2.02	0.58
2:2:1097:G:H5'	23:Y:42:GLN:HE22	1.68	0.58
6:D:583:ILE:HG13	7:E:243:VAL:HG11	1.85	0.58
13:O:639:MET:HG3	13:O:642:LYS:HE2	1.84	0.58
14:P:337:VAL:HG22	14:P:346:LEU:HB2	1.83	0.58
14:P:412:THR:O	14:P:413:ILE:HG23	2.03	0.58
14:P:1302:ARG:NH2	14:P:1307:TYR:HA	2.18	0.58
19:U:242:PHE:CD1	20:V:225:ARG:HG2	2.38	0.58
14:P:104:TYR:CE1	14:P:113:LEU:HD23	2.36	0.58
14:P:703:MET:HE3	14:P:713:LEU:HB2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:1070:SER:HB3	15:Q:167:LYS:HD3	1.86	0.58
21:W:8:VAL:HG11	21:W:49:HIS:CB	2.32	0.58
29:g:64:ARG:HG3	29:g:66:ASN:H	1.68	0.58
31:i:48:LEU:HD12	31:i:52:HIS:HB2	1.85	0.58
13:O:278:ILE:HG21	13:O:304:VAL:HG11	1.85	0.58
18:T:170:PHE:CZ	18:T:246:LYS:HG2	2.39	0.58
21:W:57:LEU:CD1	21:W:73:ARG:HH12	2.16	0.58
28:x:46:ASP:OD1	28:x:50:ASN:N	2.36	0.58
10:H:73:LEU:HB2	10:H:76:HIS:HD2	1.69	0.58
13:O:859:ASN:O	13:O:862:THR:OG1	2.19	0.58
13:O:869:SER:OG	17:S:78:ARG:NH1	2.37	0.58
14:P:60:LEU:HB2	14:P:1317:VAL:HG22	1.85	0.58
19:U:214:PRO:N	19:U:215:PRO:HD2	2.19	0.58
23:Y:43:ARG:O	23:Y:47:ASN:ND2	2.33	0.58
27:w:87:ILE:O	29:y:64:ARG:CZ	2.51	0.58
1:l:118:U:O2'	7:E:128:LYS:NZ	2.34	0.58
13:O:288:ASN:OD1	13:O:289:GLU:N	2.37	0.58
13:O:346:ILE:HG13	17:S:51:PHE:HB3	1.86	0.58
14:P:638:SER:OG	14:P:685:THR:O	2.21	0.58
14:P:704:SER:O	14:P:712:PHE:O	2.22	0.58
18:T:377:VAL:HG12	18:T:378:ASP:N	2.19	0.58
18:T:377:VAL:HG12	18:T:378:ASP:H	1.69	0.58
20:V:134:THR:O	20:V:137:ASP:HB2	2.04	0.58
21:W:11:ALA:HB2	21:W:25:VAL:C	2.29	0.58
30:t:7:LEU:HD11	31:u:95:PHE:CZ	2.39	0.58
6:D:377:LYS:HB3	7:E:530:PRO:HG2	1.85	0.58
6:D:502:THR:HA	6:D:505:MET:HB3	1.86	0.58
13:O:921:ALA:HB2	15:Q:169:VAL:HB	1.86	0.58
14:P:369:ILE:HG21	14:P:419:LEU:HB2	1.85	0.58
14:P:719:GLN:HG2	14:P:762:PHE:HD2	1.69	0.58
14:P:1037:PHE:HB2	14:P:1042:LEU:HB2	1.85	0.58
21:W:36:LEU:O	21:W:62:ASN:ND2	2.33	0.58
4:B:19:ARG:O	26:d:30:ARG:NH1	2.37	0.58
7:E:532:GLU:O	7:E:536:LEU:HB2	2.04	0.58
11:I:67:C:OP2	13:O:773:GLN:NE2	2.33	0.58
18:T:29:PRO:HG3	18:T:59:ILE:HG13	1.84	0.58
21:W:35:GLN:NE2	23:Y:77:ARG:HH22	2.02	0.58
11:I:72:A:N3	17:S:99:ARG:NH2	2.52	0.57
13:O:516:SER:O	13:O:520:ASP:HB2	2.04	0.57
14:P:600:ILE:HD13	14:P:642:LEU:HD13	1.85	0.57
14:P:1193:PHE:HA	14:P:1314:VAL:HG12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:W:8:VAL:HA	21:W:25:VAL:HG22	1.86	0.57
2:2:141:A:C2'	2:2:142:C:C6	2.87	0.57
4:B:21:PRO:HD2	7:E:157:ARG:HH21	1.68	0.57
13:O:881:MET:O	13:O:884:LEU:N	2.36	0.57
14:P:643:ILE:HG23	14:P:651:LEU:HD21	1.86	0.57
16:R:162:ASP:OD1	16:R:182:TYR:OH	2.22	0.57
28:x:74:ARG:HB3	28:x:77:ASN:HD22	1.69	0.57
2:2:1097:G:H1'	2:2:1146:G:N2	2.20	0.57
2:2:1098:C:C3'	21:W:158:ASN:ND2	2.66	0.57
14:P:65:LEU:HB3	14:P:886:PHE:HE2	1.69	0.57
14:P:380:LEU:HB3	14:P:388:LEU:HD11	1.85	0.57
14:P:622:LEU:HD21	14:P:663:LEU:HB2	1.86	0.57
14:P:1142:ARG:HH12	15:Q:363:TYR:HB3	1.70	0.57
20:V:140:ALA:HA	20:V:143:LYS:HD2	1.86	0.57
21:W:17:ASP:O	21:W:19:PHE:N	2.38	0.57
2:2:111:C:C4	28:x:48:TYR:CD2	2.93	0.57
14:P:538:PRO:HA	14:P:548:THR:HG23	1.85	0.57
15:Q:329:LYS:HB3	15:Q:335:TRP:HB2	1.85	0.57
25:b:86:ILE:HG23	26:d:72:ILE:HG23	1.86	0.57
14:P:1035:LEU:HD11	14:P:1042:LEU:HD23	1.85	0.57
14:P:1096:LEU:HD13	14:P:1187:PHE:CZ	2.39	0.57
21:W:3:PHE:CE2	21:W:25:VAL:HG11	2.40	0.57
31:u:67:MET:HE2	31:u:69:LEU:HD21	1.87	0.57
2:2:1126:G:HO2'	2:2:1127:A:H8	1.52	0.57
8:F:385:SER:OG	8:F:386:ALA:N	2.38	0.57
15:Q:194:PHE:HE2	15:Q:196:LEU:HD23	1.69	0.57
17:S:23:CYS:HA	17:S:66:GLY:HA2	1.87	0.57
18:T:199:SER:H	18:T:202:GLN:HE21	1.53	0.57
25:s:40:HIS:O	25:s:89:GLY:HA3	2.05	0.57
27:w:90:ILE:HB	29:y:62:VAL:HG13	1.86	0.57
14:P:854:ASN:OD1	14:P:855:ALA:N	2.38	0.57
15:Q:203:THR:HG22	15:Q:250:VAL:HG21	1.87	0.57
6:D:366:ILE:HG13	6:D:428:LYS:HE2	1.87	0.57
14:P:965:GLY:N	14:P:1016:SER:OG	2.38	0.57
27:e:27:VAL:HG21	27:e:43:ILE:HG12	1.87	0.57
1:1:12:A:OP1	5:C:2:THR:OG1	2.23	0.57
2:2:66:A:OP2	2:2:66:A:H8	1.87	0.57
13:O:359:ILE:O	13:O:363:LEU:HB2	2.05	0.57
14:P:232:ARG:HE	14:P:235:MET:HG3	1.70	0.57
14:P:339:ASP:OD1	14:P:340:MET:N	2.38	0.57
14:P:1009:LEU:O	14:P:1017:PHE:HA	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:U:42:TYR:HD1	19:U:60:LYS:HB2	1.70	0.57
28:f:74:ARG:NH1	31:i:98:GLY:O	2.38	0.57
13:O:689:LEU:HA	13:O:692:ILE:HD12	1.86	0.57
14:P:1023:HIS:HB3	14:P:1058:GLN:HA	1.87	0.57
18:T:148:SER:HB2	18:T:158:SER:HA	1.87	0.57
21:W:17:ASP:CB	23:Y:61:VAL:HA	2.26	0.57
21:W:89:VAL:HG23	21:W:116:ARG:HB2	1.86	0.57
23:Y:60:LYS:HE3	23:Y:75:THR:HG23	1.86	0.57
1:l:143:A:N6	3:A:114:ASN:O	2.37	0.56
14:P:205:SER:HB2	14:P:211:LYS:HG2	1.86	0.56
16:R:107:ILE:HD13	16:R:154:TYR:HB3	1.86	0.56
9:G:288:MET:O	9:G:292:ASN:HB2	2.05	0.56
13:O:916:MET:HB3	13:O:920:TRP:HE1	1.69	0.56
14:P:378:PHE:HA	14:P:391:LEU:O	2.05	0.56
14:P:644:ILE:HG13	14:P:652:VAL:HB	1.86	0.56
18:T:11:LEU:HD23	18:T:14:MET:HE3	1.87	0.56
21:W:3:PHE:CZ	21:W:32:ARG:HB2	2.40	0.56
30:t:95:ILE:HG23	31:u:95:PHE:HB3	1.87	0.56
31:u:102:ILE:HG22	31:u:103:VAL:HG23	1.87	0.56
26:v:68:GLN:CD	29:y:69:ILE:HD13	2.30	0.56
13:O:324:ARG:O	13:O:330:ARG:NH2	2.38	0.56
13:O:408:ARG:HA	13:O:412:LEU:HB2	1.87	0.56
19:U:233:VAL:HG11	20:V:192:PHE:CD2	2.39	0.56
21:W:1:MET:H2	21:W:29:VAL:HG11	1.69	0.56
21:W:2:LYS:NZ	21:W:43:MET:HE2	2.21	0.56
21:W:17:ASP:OD2	23:Y:59:LEU:C	2.48	0.56
4:B:134:GLU:HB3	4:B:154:VAL:HG23	1.87	0.56
13:O:205:LEU:HD21	13:O:243:ILE:HG12	1.86	0.56
15:Q:262:HIS:HB3	15:Q:280:THR:HG22	1.86	0.56
6:D:409:ASN:HD22	6:D:421:LEU:HD11	1.71	0.56
13:O:689:LEU:HD21	13:O:707:PHE:CD2	2.38	0.56
14:P:782:GLU:O	14:P:816:MET:N	2.39	0.56
14:P:820:VAL:HG12	14:P:828:VAL:HG12	1.87	0.56
21:W:156:PHE:CZ	23:Y:50:LEU:HD22	2.35	0.56
23:Y:45:ARG:HD3	23:Y:62:SER:HA	1.88	0.56
25:b:28:ARG:HG2	25:b:52:ARG:HG2	1.87	0.56
26:d:65:ARG:HD3	26:d:67:SER:H	1.69	0.56
4:B:97:ASP:HB3	4:B:100:ILE:HG22	1.86	0.56
14:P:200:ARG:HH12	14:P:245:VAL:HG11	1.70	0.56
11:I:77:C:O2'	11:I:79:A:N7	2.36	0.56
14:P:153:ASP:OD1	14:P:154:SER:N	2.33	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:293:ASN:HD22	14:P:364:THR:HB	1.70	0.56
18:T:508:GLU:H	18:T:513:GLY:HA3	1.69	0.56
25:b:19:LYS:HD3	25:b:99:ASP:HB2	1.88	0.56
5:C:130:LEU:O	5:C:134:SER:N	2.34	0.56
7:E:188:GLN:NE2	7:E:192:ASP:OD2	2.39	0.56
14:P:105:ASP:OD1	14:P:106:THR:N	2.39	0.56
16:R:139:GLU:O	16:R:151:ALA:HA	2.06	0.56
26:d:65:ARG:NH1	29:g:65:GLY:O	2.39	0.56
2:2:1126:G:O2'	2:2:1127:A:C5'	2.54	0.56
7:E:307:ALA:O	7:E:313:TRP:NE1	2.37	0.56
13:O:948:ALA:HA	14:P:1311:TYR:HD1	1.70	0.56
14:P:1244:GLU:HG3	14:P:1322:LEU:HD23	1.86	0.56
21:W:11:ALA:HB2	21:W:26:ASP:N	2.21	0.56
30:t:30:GLN:HE22	30:t:84:TYR:HE1	1.54	0.56
6:D:619:LEU:HD21	8:F:379:ARG:HB3	1.86	0.56
14:P:1223:GLY:O	14:P:1224:THR:OG1	2.22	0.56
21:W:35:GLN:HE22	23:Y:77:ARG:HH12	1.54	0.56
21:W:58:ASP:HA	21:W:80:LEU:HB2	1.88	0.56
21:W:156:PHE:HB3	23:Y:95:PHE:CD1	2.41	0.56
31:u:37:ALA:HA	31:u:42:THR:HG22	1.87	0.56
1:1:5:PSU:H4'	10:H:207:TYR:HB2	1.88	0.55
2:2:111:C:C5	31:u:63:ARG:CG	2.89	0.55
9:G:100:CYS:HA	9:G:114:TYR:O	2.06	0.55
14:P:382:GLN:HA	14:P:387:ASP:O	2.06	0.55
14:P:1084:ARG:HG2	14:P:1098:ILE:HG12	1.87	0.55
21:W:32:ARG:HA	21:W:36:LEU:CD2	2.35	0.55
21:W:64:LEU:HB3	21:W:86:ILE:HD11	1.88	0.55
2:2:1139:G:C4	2:2:1140:U:C5	2.94	0.55
7:E:388:PHE:O	7:E:392:LEU:HB2	2.06	0.55
7:E:457:GLU:OE2	7:E:462:GLN:NE2	2.40	0.55
13:O:442:ILE:HG23	13:O:457:ILE:HG23	1.88	0.55
14:P:494:SER:OG	14:P:497:PRO:HD2	2.06	0.55
14:P:773:LYS:HD2	14:P:823:SER:HA	1.88	0.55
14:P:1191:ASN:ND2	14:P:1316:LYS:HB2	2.21	0.55
28:f:31:LEU:HA	28:f:78:VAL:HA	1.88	0.55
28:x:16:LYS:HB2	28:x:17:PRO:HD3	1.87	0.55
1:1:254:U:OP2	1:1:258:U:N3	2.26	0.55
7:E:517:VAL:O	7:E:521:LEU:HB3	2.07	0.55
13:O:851:LEU:HD21	13:O:895:ALA:HB2	1.89	0.55
14:P:384:ASN:O	14:P:415:ASN:ND2	2.39	0.55
2:2:111:C:C4	31:u:63:ARG:CG	2.90	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:420:HIS:CE1	6:D:424:LEU:HD21	2.42	0.55
14:P:486:PRO:HG2	14:P:505:PHE:CG	2.40	0.55
14:P:1117:HIS:O	14:P:1133:ASP:HA	2.06	0.55
2:2:67:A:O2'	2:2:68:U:H6	1.89	0.55
2:2:116:U:N3	30:t:88:ARG:HG3	2.22	0.55
7:E:205:LYS:HG3	7:E:216:ILE:HD12	1.88	0.55
10:H:197:LYS:HA	10:H:210:ARG:H	1.71	0.55
14:P:157:LEU:O	14:P:176:ASN:HA	2.07	0.55
16:R:13:VAL:HG12	16:R:16:ILE:HD11	1.89	0.55
21:W:7:ILE:O	21:W:26:ASP:N	2.40	0.55
31:u:76:TRP:NE1	31:u:87:ARG:HB2	2.22	0.55
2:2:1139:G:C5	2:2:1140:U:C5	2.94	0.55
9:G:187:ILE:HG22	9:G:203:VAL:HG12	1.88	0.55
14:P:691:LEU:HB3	14:P:703:MET:HB2	1.86	0.55
14:P:1301:GLY:O	17:S:41:ARG:NH2	2.37	0.55
18:T:21:ILE:HD11	20:V:164:CYS:SG	2.47	0.55
25:b:21:ARG:NH2	25:b:51:GLU:OE2	2.38	0.55
31:i:78:GLU:O	31:i:84:VAL:HA	2.06	0.55
2:2:143:G:O3'	2:2:143:G:C2'	2.47	0.55
2:2:1098:C:H2'	2:2:1099:G:C8	2.40	0.55
4:B:103:THR:HG21	4:B:154:VAL:HG21	1.89	0.55
7:E:443:ASN:OD1	7:E:446:GLN:NE2	2.39	0.55
14:P:209:GLN:HE22	14:P:233:PRO:HA	1.71	0.55
14:P:493:VAL:HB	14:P:939:ILE:HD11	1.89	0.55
16:R:114:ASN:ND2	16:R:177:ARG:O	2.40	0.55
18:T:150:PRO:CB	18:T:154:THR:HB	2.36	0.55
21:W:22:LYS:HG3	21:W:34:LEU:HB2	1.88	0.55
2:2:111:C:C5	28:x:48:TYR:CE2	2.92	0.55
8:F:410:LEU:HD23	8:F:411:GLN:H	1.71	0.55
14:P:446:VAL:HG21	14:P:453:ASN:HD21	1.71	0.55
21:W:56:ILE:HG13	21:W:78:THR:HB	1.89	0.55
2:2:1097:G:H5'	23:Y:40:ASN:CB	2.37	0.55
2:2:1102:C:H5	23:Y:38:LYS:HE3	1.71	0.55
13:O:680:PRO:HG2	13:O:685:ILE:HD11	1.88	0.55
14:P:770:LEU:HB2	14:P:827:TRP:NE1	2.22	0.55
16:R:201:LEU:HA	18:T:452:CYS:HB3	1.89	0.55
18:T:426:CYS:O	18:T:429:LYS:N	2.37	0.55
21:W:20:ASN:HB3	21:W:55:HIS:HB3	1.89	0.55
21:W:25:VAL:HB	21:W:31:LEU:CA	2.35	0.55
2:2:142:C:C2'	2:2:143:G:H8	2.20	0.54
2:2:1148:U:H2'	2:2:1149:G:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:390:ILE:HD12	13:O:426:MET:HA	1.90	0.54
13:O:916:MET:HB3	13:O:920:TRP:NE1	2.22	0.54
18:T:62:PHE:HB3	18:T:375:GLU:HB2	1.89	0.54
1:1:32:G:N3	4:B:198:ARG:NH2	2.54	0.54
5:C:4:TYR:HB3	5:C:13:LEU:HB2	1.89	0.54
7:E:283:LEU:HD22	7:E:299:PHE:HD1	1.72	0.54
14:P:641:GLN:HE21	14:P:653:TYR:HE1	1.54	0.54
14:P:1216:CYS:SG	14:P:1228:PHE:HB2	2.47	0.54
23:Y:28:ASN:HD21	23:Y:111:LEU:HB2	1.72	0.54
23:Y:39:ILE:HG13	23:Y:95:PHE:CD2	2.42	0.54
30:h:69:THR:HB	30:h:82:LEU:HD21	1.89	0.54
1:1:311:U:H2'	1:1:312:G:H8	1.72	0.54
13:O:244:LEU:O	13:O:248:ALA:CB	2.50	0.54
14:P:292:ALA:HA	14:P:331:PHE:CD1	2.42	0.54
14:P:382:GLN:NE2	14:P:416:SER:OG	2.39	0.54
2:2:67:A:C4	2:2:68:U:C5	2.96	0.54
2:2:1126:G:O2'	2:2:1127:A:O5'	2.24	0.54
9:G:75:ARG:NH2	9:G:239:TYR:OH	2.41	0.54
20:V:129:HIS:ND1	20:V:130:PRO:HD2	2.23	0.54
23:Y:43:ARG:HG2	23:Y:47:ASN:ND2	2.22	0.54
23:Y:89:LEU:HD22	23:Y:92:GLU:HG3	1.89	0.54
28:f:46:ASP:OD1	28:f:50:ASN:N	2.39	0.54
4:B:140:LYS:HG3	4:B:147:SER:HA	1.90	0.54
13:O:696:LYS:HG2	13:O:697:HIS:H	1.72	0.54
14:P:209:GLN:HE21	14:P:231:ILE:HG23	1.71	0.54
16:R:116:ALA:HB3	16:R:119:ILE:HG12	1.88	0.54
18:T:147:SER:HA	18:T:155:ASN:O	2.08	0.54
30:h:33:SER:HB3	30:h:37:ASN:H	1.72	0.54
31:i:56:ALA:HB2	31:i:72:VAL:HA	1.90	0.54
27:w:85:ASP:OD2	28:x:32:LYS:NZ	2.39	0.54
6:D:522:ILE:HG12	7:E:401:SER:HB2	1.90	0.54
7:E:279:TRP:CD1	7:E:306:LEU:HD21	2.42	0.54
13:O:519:ILE:HA	13:O:522:LEU:HB2	1.89	0.54
14:P:207:VAL:O	14:P:237:THR:N	2.39	0.54
14:P:768:ARG:NH2	14:P:1359:ASN:O	2.41	0.54
14:P:981:SER:OG	14:P:1031:ILE:O	2.20	0.54
14:P:1130:ILE:HD13	14:P:1204:ILE:HD11	1.90	0.54
14:P:1193:PHE:CZ	14:P:1308:ARG:HD2	2.42	0.54
21:W:11:ALA:CB	21:W:31:LEU:HD23	2.37	0.54
23:Y:43:ARG:HA	23:Y:46:VAL:HG12	1.90	0.54
28:f:74:ARG:HG3	28:f:76:ASN:H	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1097:G:C5	2:2:1146:G:C6	2.96	0.54
13:O:971:LEU:HD23	24:Z:56:SER:HB3	1.89	0.54
30:t:34:PRO:C	30:t:36:MET:H	2.15	0.54
27:w:59:GLU:O	27:w:74:GLY:CA	2.56	0.54
8:F:410:LEU:HD21	8:F:414:ASN:OD1	2.07	0.54
14:P:885:TRP:CH2	14:P:1357:ARG:HB3	2.42	0.54
18:T:409:TYR:HA	18:T:412:TYR:CE2	2.43	0.54
21:W:47:LEU:HD12	21:W:70:LEU:HA	1.89	0.54
28:x:33:PHE:C	28:x:35:SER:H	2.15	0.54
2:2:110:A:H5''	2:2:111:C:OP2	2.07	0.54
13:O:539:HIS:CE1	13:O:578:ILE:HG12	2.43	0.54
14:P:1305:GLN:O	14:P:1309:SER:CB	2.56	0.54
19:U:36:LYS:HD3	19:U:191:THR:HB	1.90	0.54
21:W:32:ARG:HG2	21:W:50:LEU:HD12	1.90	0.54
25:s:50:GLU:O	25:s:79:LYS:HA	2.08	0.54
1:1:8:C:O2'	5:C:19:SER:OG	2.25	0.54
7:E:151:LEU:HD21	7:E:171:ILE:HD11	1.90	0.54
9:G:186:SER:HA	9:G:204:LYS:HB2	1.89	0.54
10:H:204:CYS:HA	10:H:229:TYR:HD2	1.73	0.54
14:P:390:LYS:HD2	14:P:410:PHE:CZ	2.43	0.54
30:t:7:LEU:HD11	31:u:95:PHE:CE2	2.43	0.54
13:O:188:LEU:O	13:O:192:ALA:HB2	2.08	0.53
14:P:396:ASP:HB2	14:P:404:LEU:HD11	1.90	0.53
14:P:1163:ALA:HB1	14:P:1165:LYS:NZ	2.23	0.53
14:P:1326:PHE:O	14:P:1334:GLN:NE2	2.38	0.53
19:U:41:PRO:HD2	19:U:53:ARG:NH1	2.23	0.53
31:u:38:MET:SD	31:u:61:PHE:HE2	2.31	0.53
29:y:5:PRO:HB2	29:y:7:LEU:HG	1.90	0.53
5:C:122:ALA:HB2	5:C:131:VAL:HB	1.89	0.53
7:E:417:ASN:O	7:E:421:PHE:N	2.38	0.53
7:E:500:TYR:HD1	7:E:503:ARG:HD3	1.73	0.53
13:O:531:GLU:HB3	13:O:534:ARG:HH21	1.73	0.53
14:P:208:GLU:HA	14:P:236:VAL:HA	1.89	0.53
18:T:116:LEU:HG	20:V:113:MET:HE3	1.89	0.53
19:U:57:TYR:HD1	19:U:70:LEU:HD13	1.73	0.53
21:W:2:LYS:C	21:W:30:ILE:HD11	2.34	0.53
1:1:559:G:O6	30:h:93:ARG:NH1	2.40	0.53
5:C:194:TYR:N	8:F:309:ASP:OD1	2.40	0.53
6:D:343:ASN:ND2	6:D:345:THR:OG1	2.42	0.53
7:E:24:PRO:HB2	7:E:25:LYS:HD2	1.91	0.53
13:O:159:ASP:O	13:O:163:GLU:CB	2.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:827:ILE:HD12	13:O:830:MET:HB2	1.90	0.53
16:R:66:ALA:O	16:R:70:MET:CB	2.57	0.53
8:F:408:PRO:O	9:G:284:HIS:NE2	2.37	0.53
13:O:820:MET:HA	13:O:823:MET:HG2	1.90	0.53
13:O:863:HIS:HD1	17:S:75:GLU:CD	2.16	0.53
14:P:179:LEU:HD11	14:P:214:PHE:HZ	1.74	0.53
14:P:607:LEU:HB2	14:P:624:TRP:HB3	1.90	0.53
14:P:643:ILE:HD13	14:P:653:TYR:HA	1.89	0.53
14:P:692:ALA:HB2	14:P:730:MET:HE3	1.91	0.53
14:P:1323:CYS:HB3	14:P:1353:ILE:HD12	1.90	0.53
20:V:103:TYR:CD1	20:V:110:VAL:HG21	2.40	0.53
2:2:1125:U:O2'	2:2:1126:G:C8	2.57	0.53
7:E:190:ILE:O	7:E:230:LYS:NZ	2.41	0.53
7:E:202:LEU:HD23	7:E:203:THR:HG23	1.89	0.53
13:O:219:HIS:NE2	17:S:97:LEU:HD23	2.23	0.53
13:O:230:TYR:HE2	24:Z:5:GLN:HB3	1.74	0.53
13:O:435:THR:O	13:O:439:MET:HG2	2.09	0.53
13:O:881:MET:HG2	13:O:885:ILE:HD11	1.89	0.53
14:P:102:GLU:OE1	14:P:104:TYR:OH	2.18	0.53
14:P:328:VAL:HG22	14:P:337:VAL:HG12	1.90	0.53
14:P:704:SER:OG	14:P:712:PHE:O	2.24	0.53
18:T:117:GLN:HB3	20:V:113:MET:HE1	1.90	0.53
18:T:319:TYR:O	18:T:322:HIS:HB3	2.08	0.53
21:W:81:LEU:O	21:W:81:LEU:HD23	2.09	0.53
2:2:42:PSU:H1'	19:U:83:ARG:HH21	1.73	0.53
2:2:139:G:H2'	2:2:140:G:O5'	2.09	0.53
2:2:1127:A:O2'	2:2:1128:C:H5'	2.08	0.53
13:O:256:PRO:HA	13:O:259:ARG:HB2	1.91	0.53
13:O:695:ASN:HD22	13:O:700:VAL:HG11	1.74	0.53
14:P:332:GLU:HG2	14:P:333:ASN:N	2.24	0.53
14:P:1042:LEU:HD21	14:P:1085:LEU:HD11	1.91	0.53
18:T:251:LEU:HD12	18:T:251:LEU:O	2.08	0.53
21:W:36:LEU:HG	21:W:59:LEU:N	2.23	0.53
2:2:58:A:H2'	2:2:59:C:O4'	2.09	0.53
2:2:1099:G:P	21:W:158:ASN:CB	2.95	0.53
13:O:327:TRP:HA	13:O:330:ARG:HH11	1.73	0.53
14:P:1110:VAL:HG12	14:P:1111:ASP:O	2.09	0.53
14:P:1298:SER:C	14:P:1300:LEU:H	2.16	0.53
19:U:210:ALA:HB3	20:V:202:GLN:HB3	1.90	0.53
21:W:11:ALA:HB3	21:W:24:ASN:CB	2.39	0.53
21:W:35:GLN:HE22	23:Y:77:ARG:NH2	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:b:28:ARG:NH1	26:d:22:GLU:OE2	2.41	0.53
27:w:59:GLU:O	27:w:74:GLY:HA2	2.09	0.53
1:l:554:U:H3	29:g:37:ASN:HD21	1.57	0.53
2:2:1115:G:N7	26:v:77:LEU:HD11	2.23	0.53
8:F:310:PRO:O	8:F:358:ARG:NH1	2.42	0.53
9:G:156:ASN:ND2	9:G:205:ALA:O	2.41	0.53
13:O:813:GLN:HB2	13:O:853:HIS:HE1	1.74	0.53
14:P:370:VAL:HA	14:P:379:VAL:HG12	1.91	0.53
15:Q:363:TYR:C	15:Q:365:GLY:H	2.16	0.53
23:Y:43:ARG:HG2	23:Y:47:ASN:HD21	1.72	0.53
25:s:76:LYS:HD3	25:s:79:LYS:HD3	1.91	0.53
6:D:582:GLN:HE21	6:D:606:ARG:HD2	1.74	0.53
7:E:234:LYS:HA	7:E:237:THR:HG22	1.90	0.53
13:O:198:GLU:O	13:O:202:ASN:CB	2.51	0.53
13:O:903:LEU:HB3	13:O:915:PHE:HZ	1.73	0.53
14:P:1006:TYR:HD1	14:P:1021:LEU:HA	1.74	0.53
19:U:204:GLU:HB3	19:U:205:PRO:HD3	1.91	0.53
19:U:212:GLU:HB3	20:V:205:LYS:HB3	1.90	0.53
7:E:154:ILE:HD11	7:E:163:LYS:HG2	1.90	0.53
13:O:599:ALA:HB3	13:O:600:PRO:HD3	1.91	0.53
14:P:59:TYR:HE1	14:P:1316:LYS:HD2	1.73	0.53
14:P:239:ASP:OD2	14:P:295:VAL:N	2.36	0.53
16:R:164:ALA:O	16:R:168:LEU:HB2	2.09	0.53
19:U:42:TYR:HB2	19:U:45:GLN:HG3	1.90	0.53
6:D:585:ASN:OD1	6:D:604:ASN:ND2	2.43	0.52
13:O:257:MET:HG3	17:S:100:HIS:CG	2.43	0.52
15:Q:131:LYS:NZ	15:Q:153:ASP:OD1	2.39	0.52
23:Y:86:GLN:NE2	23:Y:101:VAL:HG23	2.23	0.52
30:t:3:LEU:HD23	31:u:95:PHE:CE1	2.40	0.52
26:v:49:ALA:O	26:v:56:VAL:HA	2.08	0.52
2:2:1100:A:H2'	23:Y:38:LYS:CE	2.32	0.52
6:D:441:THR:O	6:D:447:ASN:ND2	2.42	0.52
7:E:415:LEU:HD12	7:E:420:LEU:HD11	1.91	0.52
13:O:667:TYR:HA	13:O:707:PHE:HD1	1.74	0.52
14:P:154:SER:HA	14:P:182:THR:HA	1.90	0.52
24:Z:57:ARG:HH12	24:Z:68:HIS:CG	2.28	0.52
25:b:54:PRO:HD2	25:b:57:GLN:HB3	1.90	0.52
1:l:23:G:H1	1:l:38:C:H42	1.56	0.52
2:2:1115:G:N7	26:v:77:LEU:CG	2.72	0.52
5:C:122:ALA:HA	5:C:128:GLY:HA2	1.92	0.52
7:E:105:SER:O	7:E:105:SER:OG	2.26	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:U:123:UNK:C	19:U:207:GLU:HB2	2.39	0.52
25:b:46:ASN:HD21	26:d:79:LYS:HE3	1.75	0.52
27:e:31:LEU:HD12	27:e:37:ILE:H	1.73	0.52
27:w:35:ILE:HG22	29:y:23:ARG:HE	1.73	0.52
2:2:1146:G:O2'	2:2:1147:A:O5'	2.15	0.52
4:B:103:THR:HB	4:B:107:ARG:HE	1.73	0.52
8:F:320:LEU:HD11	8:F:324:VAL:HG11	1.91	0.52
9:G:74:MET:HE3	9:G:132:LEU:HB3	1.90	0.52
13:O:484:PHE:HA	13:O:488:TRP:CD1	2.42	0.52
13:O:636:GLU:O	13:O:639:MET:N	2.35	0.52
14:P:182:THR:O	14:P:183:THR:HG23	2.08	0.52
14:P:493:VAL:HG13	14:P:499:SER:OG	2.09	0.52
17:S:40:LYS:HE2	17:S:74:TRP:HD1	1.73	0.52
18:T:148:SER:CB	18:T:159:ASP:H	2.20	0.52
26:v:10:LEU:HB2	26:v:83:LEU:HD11	1.91	0.52
9:G:69:LEU:HA	9:G:117:LEU:O	2.10	0.52
13:O:682:ILE:HA	13:O:685:ILE:HD12	1.90	0.52
14:P:154:SER:HA	14:P:182:THR:HG22	1.91	0.52
15:Q:193:PRO:HA	19:U:62:HIS:HB2	1.91	0.52
17:S:51:PHE:HD2	17:S:52:GLY:H	1.56	0.52
26:v:10:LEU:HD12	26:v:83:LEU:HD12	1.90	0.52
14:P:1109:TYR:CD2	14:P:1110:VAL:HG23	2.44	0.52
28:x:60:VAL:HG12	28:x:65:HIS:HB2	1.92	0.52
7:E:307:ALA:HB1	7:E:340:PHE:HE2	1.75	0.52
13:O:470:ILE:HD12	13:O:475:LEU:HD21	1.90	0.52
14:P:130:LEU:HD23	14:P:149:ALA:HB2	1.91	0.52
14:P:186:ARG:O	14:P:206:SER:HB3	2.10	0.52
14:P:930:LEU:HD13	14:P:984:ILE:HG23	1.91	0.52
18:T:90:GLN:HG3	20:V:153:ILE:HG13	1.91	0.52
31:i:39:VAL:HG13	31:i:40:THR:HG23	1.92	0.52
14:P:1133:ASP:HB2	14:P:1137:ASN:H	1.75	0.52
21:W:8:VAL:HG23	21:W:25:VAL:HG22	1.92	0.52
13:O:956:THR:H	13:O:959:ASN:HB3	1.75	0.52
14:P:609:HIS:HD2	14:P:621:LYS:HB2	1.75	0.52
14:P:1006:TYR:HB3	14:P:1019:ILE:HD11	1.92	0.52
14:P:1048:THR:OG1	14:P:1065:THR:O	2.22	0.52
28:x:14:ASN:HB2	28:x:17:PRO:HD2	1.91	0.52
5:C:189:LYS:H	6:D:612:ASN:HD22	1.57	0.52
17:S:22:LEU:HD13	17:S:27:ASP:HA	1.92	0.52
18:T:425:ILE:HG13	18:T:467:ILE:HG22	1.91	0.52
21:W:5:PRO:HD3	21:W:46:SER:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:6:PSU:H2'	1:1:7:A:H8	1.74	0.51
4:B:197:ARG:HD3	4:B:202:GLY:HA3	1.90	0.51
6:D:354:THR:HB	6:D:358:TYR:HE2	1.75	0.51
6:D:492:ARG:HG3	6:D:493:GLU:HG3	1.92	0.51
6:D:572:GLY:HA3	7:E:285:TYR:HD1	1.74	0.51
13:O:848:ASP:OD1	13:O:849:ARG:N	2.44	0.51
14:P:75:CYS:SG	14:P:94:CYS:HB3	2.50	0.51
14:P:766:LYS:HD3	14:P:836:TRP:CE2	2.45	0.51
14:P:836:TRP:CZ3	14:P:838:ILE:HG23	2.45	0.51
14:P:1107:ILE:HD12	14:P:1108:PRO:HD2	1.91	0.51
14:P:1201:ASP:O	14:P:1218:TYR:HA	2.10	0.51
27:w:13:PRO:HG3	29:y:37:ASN:HB2	1.92	0.51
2:2:1097:G:C2	2:2:1146:G:C5	2.98	0.51
5:C:8:TYR:OH	26:d:13:GLU:OE2	2.26	0.51
7:E:140:HIS:HB2	7:E:297:LEU:HD11	1.92	0.51
9:G:131:VAL:O	9:G:135:PHE:N	2.43	0.51
10:H:11:GLN:HB2	29:g:35:PHE:HE2	1.75	0.51
13:O:146:ASP:OD2	13:O:167:SER:OG	2.25	0.51
13:O:306:LYS:HD3	13:O:343:LEU:HB3	1.92	0.51
14:P:539:ASP:OD1	14:P:618:TYR:OH	2.27	0.51
15:Q:367:LEU:O	15:Q:368:ILE:HG22	2.10	0.51
26:v:65:ARG:NH1	29:y:65:GLY:O	2.43	0.51
28:x:51:LEU:HB2	28:x:73:ILE:HB	1.91	0.51
2:2:52:A:N6	2:2:64:G:O6	2.42	0.51
2:2:1140:U:H2'	2:2:1141:C:H6	1.75	0.51
6:D:452:ARG:HH12	6:D:486:LYS:HZ3	1.58	0.51
15:Q:183:LEU:HD23	15:Q:272:GLU:HG3	1.91	0.51
16:R:112:ILE:HA	16:R:179:THR:O	2.10	0.51
30:h:88:ARG:O	30:h:91:THR:OG1	2.27	0.51
30:t:19:LEU:HA	30:t:93:ARG:H	1.76	0.51
29:y:8:LYS:HA	29:y:11:MET:HG2	1.92	0.51
11:I:78:A:C2	13:O:499:ASN:HB3	2.46	0.51
13:O:215:ASP:OD1	13:O:216:GLN:N	2.43	0.51
14:P:643:ILE:HD12	14:P:651:LEU:HD21	1.92	0.51
14:P:678:LYS:NZ	14:P:726:SER:O	2.36	0.51
14:P:783:ILE:HG13	14:P:784:SER:N	2.24	0.51
14:P:924:PHE:HA	14:P:944:ASN:O	2.10	0.51
14:P:1305:GLN:O	14:P:1309:SER:HB2	2.10	0.51
23:Y:75:THR:HG21	23:Y:108:THR:HG21	1.91	0.51
30:h:95:ILE:HG23	31:i:95:PHE:HB3	1.93	0.51
2:2:117:U:O3'	31:u:99:ASP:OD2	2.27	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:142:C:O2'	2:2:143:G:O4'	2.27	0.51
6:D:573:HIS:NE2	6:D:576:ILE:O	2.43	0.51
13:O:386:TYR:CD2	13:O:387:PRO:HD2	2.46	0.51
13:O:535:THR:HG21	13:O:574:ASN:HD21	1.76	0.51
13:O:925:HIS:ND1	13:O:926:PRO:HD2	2.25	0.51
14:P:71:PHE:O	14:P:430:LEU:HD21	2.11	0.51
14:P:433:MET:O	14:P:485:ASN:HB2	2.10	0.51
14:P:701:LYS:HG2	14:P:718:LEU:HD23	1.93	0.51
18:T:292:SER:O	18:T:296:GLU:HG2	2.10	0.51
31:u:80:LYS:HE3	31:u:82:LYS:HG3	1.91	0.51
6:D:341:ARG:HH11	7:E:541:THR:HG21	1.75	0.51
13:O:169:LEU:O	13:O:173:ILE:HD12	2.11	0.51
13:O:835:ILE:HG21	13:O:873:HIS:CG	2.45	0.51
21:W:60:THR:HA	21:W:82:GLY:O	2.10	0.51
4:B:19:ARG:HG2	4:B:20:PRO:O	2.10	0.51
14:P:1219:MET:HA	14:P:1224:THR:O	2.10	0.51
15:Q:183:LEU:HD22	15:Q:188:LEU:HD11	1.93	0.51
21:W:7:ILE:HG12	21:W:29:VAL:HG23	1.93	0.51
6:D:409:ASN:O	6:D:413:ASN:N	2.44	0.51
7:E:127:PHE:HA	7:E:130:TYR:HD2	1.75	0.51
8:F:306:HIS:HB3	8:F:384:ARG:HD3	1.92	0.51
13:O:624:CYS:O	13:O:628:ILE:HG12	2.11	0.51
13:O:950:VAL:HG21	24:Z:42:THR:HG21	1.93	0.51
14:P:699:MET:HB3	14:P:720:LEU:HD23	1.93	0.51
14:P:1114:VAL:HG12	14:P:1115:LYS:N	2.25	0.51
15:Q:289:LYS:HD3	16:R:27:GLU:HB2	1.93	0.51
25:s:28:ARG:HD3	25:s:50:GLU:OE2	2.11	0.51
7:E:375:TYR:HD1	9:G:254:PRO:HG3	1.76	0.51
14:P:103:LEU:HD22	14:P:162:ILE:HD13	1.93	0.51
14:P:301:LEU:HD12	14:P:326:PHE:CD2	2.45	0.51
14:P:1089:ASP:HB2	14:P:1092:GLU:O	2.11	0.51
14:P:1161:ASN:OD1	14:P:1162:GLY:N	2.44	0.51
16:R:60:GLN:HA	16:R:63:ALA:HB3	1.93	0.51
20:V:195:ILE:HD11	20:V:197:TRP:CZ2	2.45	0.51
27:e:47:ASP:OD1	27:e:51:ASN:N	2.44	0.51
29:y:15:ILE:HG22	29:y:73:ALA:HA	1.93	0.51
2:2:121:C:O2'	31:u:51:ASN:ND2	2.39	0.51
13:O:462:GLN:HG3	13:O:508:THR:HG21	1.93	0.51
13:O:908:GLN:HG2	17:S:78:ARG:HD3	1.93	0.51
15:Q:312:TRP:O	15:Q:316:MET:HB2	2.11	0.51
27:w:89:LEU:HD23	27:w:91:THR:HG23	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:111:C:C4	28:x:48:TYR:HD2	2.29	0.50
2:2:1151:U:H2'	2:2:1152:U:C6	2.46	0.50
4:B:8:TYR:HE2	4:B:11:ASP:HB2	1.75	0.50
7:E:456:VAL:HG13	7:E:460:ILE:HD12	1.92	0.50
13:O:901:GLU:OE1	17:S:3:ARG:NH2	2.43	0.50
14:P:1124:LEU:HD23	14:P:1204:ILE:HG12	1.93	0.50
18:T:81:ILE:HD13	18:T:161:ALA:HB2	1.92	0.50
18:T:171:THR:HG21	18:T:181:GLU:OE2	2.11	0.50
25:b:104:SER:OG	25:b:105:LYS:N	2.44	0.50
30:t:23:THR:HA	30:t:48:PRO:HD3	1.93	0.50
27:w:20:PHE:CE1	27:w:92:SER:HB2	2.40	0.50
6:D:588:ILE:HG23	7:E:174:ILE:HG12	1.92	0.50
10:H:19:MET:HE2	28:f:14:ASN:HD21	1.76	0.50
13:O:292:TYR:O	13:O:296:VAL:HG23	2.11	0.50
13:O:963:TYR:HH	14:P:1091:HIS:CE1	2.29	0.50
14:P:155:GLY:O	14:P:179:LEU:HB2	2.10	0.50
14:P:1221:LEU:HD22	24:Z:52:TYR:HD1	1.77	0.50
18:T:56:GLU:OE1	18:T:63:LYS:HE2	2.11	0.50
2:2:52:A:H2'	2:2:53:G:H8	1.76	0.50
6:D:546:SER:HB3	8:F:336:PHE:HE1	1.77	0.50
7:E:29:TYR:OH	9:G:262:ASP:OD2	2.22	0.50
10:H:201:CYS:HB3	10:H:204:CYS:SG	2.52	0.50
14:P:183:THR:OG1	14:P:185:ARG:NE	2.45	0.50
14:P:190:ILE:O	14:P:191:SER:OG	2.23	0.50
18:T:237:SER:HA	18:T:321:LEU:HD13	1.94	0.50
21:W:25:VAL:HG12	21:W:30:ILE:O	2.11	0.50
30:t:31:SER:HB2	30:t:39:ILE:HD11	1.93	0.50
13:O:618:GLN:HB3	13:O:658:VAL:HG22	1.93	0.50
13:O:796:ASN:HA	15:Q:247:LEU:HD13	1.92	0.50
13:O:950:VAL:HG13	24:Z:39:THR:HG22	1.94	0.50
14:P:1131:GLY:HA3	14:P:1139:TRP:CZ2	2.47	0.50
14:P:1234:LYS:O	14:P:1237:VAL:N	2.44	0.50
15:Q:144:PRO:HG2	18:T:460:VAL:HG23	1.92	0.50
16:R:13:VAL:HG22	16:R:83:VAL:HG22	1.93	0.50
16:R:20:ILE:O	16:R:40:TYR:OH	2.25	0.50
18:T:75:GLN:HE21	18:T:156:ILE:HG21	1.76	0.50
20:V:139:VAL:O	20:V:143:LYS:HG3	2.12	0.50
21:W:59:LEU:HD11	21:W:64:LEU:HD13	1.94	0.50
28:f:19:LEU:HD21	28:f:45:THR:HG21	1.92	0.50
30:t:96:ILE:HG13	31:u:94:LEU:HD13	1.93	0.50
2:2:44:PSU:C4	2:2:45:U:C5	2.99	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:610:LYS:HB3	6:D:613:GLN:HE21	1.76	0.50
11:I:68:A:H2'	11:I:69:A:C8	2.46	0.50
14:P:78:HIS:N	14:P:146:THR:OG1	2.44	0.50
14:P:504:HIS:HD2	14:P:511:ILE:HD11	1.76	0.50
14:P:551:PHE:HD2	14:P:591:THR:HG21	1.76	0.50
14:P:1114:VAL:HG12	14:P:1115:LYS:H	1.76	0.50
18:T:185:PHE:CE2	18:T:236:LEU:HA	2.46	0.50
18:T:302:LYS:O	18:T:306:LYS:HG2	2.11	0.50
21:W:25:VAL:HB	21:W:32:ARG:N	2.27	0.50
21:W:31:LEU:HD22	21:W:35:GLN:O	2.12	0.50
24:Z:18:TYR:HB2	24:Z:21:LEU:HD11	1.93	0.50
30:t:43:VAL:CG1	30:t:85:ILE:HD12	2.42	0.50
2:2:111:C:N4	31:u:63:ARG:HG2	2.24	0.50
2:2:111:C:C4	28:x:48:TYR:CE2	2.99	0.50
6:D:520:SER:OG	6:D:521:ASN:N	2.45	0.50
13:O:168:MET:O	13:O:172:LYS:HG2	2.12	0.50
13:O:827:ILE:HB	13:O:830:MET:HB2	1.94	0.50
18:T:91:GLN:HG2	18:T:95:LYS:HE2	1.93	0.50
21:W:3:PHE:CE2	21:W:32:ARG:HB2	2.46	0.50
21:W:16:VAL:HG12	21:W:18:HIS:N	2.27	0.50
13:O:739:ASN:HB3	13:O:742:ILE:HB	1.94	0.50
14:P:1096:LEU:HD11	14:P:1129:VAL:HG21	1.92	0.50
16:R:16:ILE:HD12	16:R:52:TYR:HA	1.94	0.50
18:T:342:LYS:HA	18:T:345:PHE:CD2	2.47	0.50
18:T:506:LEU:HB2	18:T:518:LYS:HD2	1.93	0.50
31:u:79:LYS:HD3	31:u:84:VAL:HG22	1.93	0.50
13:O:720:PRO:HG2	13:O:723:GLU:HB2	1.94	0.50
13:O:855:GLN:HG3	13:O:898:ARG:HG3	1.93	0.50
14:P:324:ASN:OD1	14:P:341:ASN:ND2	2.44	0.50
18:T:220:PRO:HB2	18:T:222:MET:O	2.10	0.50
21:W:35:GLN:OE1	23:Y:57:GLU:HB2	2.12	0.50
21:W:89:VAL:CG2	21:W:116:ARG:HB2	2.41	0.50
2:2:73:U:N3	2:2:79:A:N1	2.53	0.50
6:D:514:THR:HG22	7:E:393:GLN:HE22	1.77	0.50
13:O:229:LEU:HD21	13:O:243:ILE:HD13	1.94	0.50
14:P:65:LEU:HB3	14:P:886:PHE:CE2	2.47	0.50
14:P:439:PHE:CE1	14:P:477:ILE:HG13	2.47	0.50
14:P:1353:ILE:O	14:P:1356:VAL:HG22	2.12	0.50
16:R:172:LEU:HD21	16:R:175:ASN:HA	1.92	0.50
19:U:190:ASP:HB2	19:U:192:LYS:HE3	1.94	0.50
1:1:6:PSU:H2'	1:1:7:A:C8	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:116:A:H4'	7:E:125:GLN:HE22	1.77	0.49
2:2:67:A:O2'	2:2:68:U:P	2.70	0.49
13:O:229:LEU:HD11	13:O:243:ILE:HG21	1.93	0.49
13:O:685:ILE:O	13:O:688:THR:OG1	2.27	0.49
14:P:1065:THR:HG21	14:P:1106:PHE:H	1.77	0.49
17:S:10:MET:HA	17:S:88:ARG:O	2.12	0.49
18:T:26:GLN:CB	20:V:168:THR:HG23	2.42	0.49
18:T:377:VAL:O	18:T:378:ASP:CB	2.60	0.49
19:U:123:UNK:CA	19:U:207:GLU:HB2	2.40	0.49
21:W:8:VAL:N	21:W:25:VAL:HG13	2.27	0.49
21:W:91:GLY:HA2	21:W:116:ARG:HB3	1.95	0.49
29:g:59:LEU:HD23	29:g:60:GLN:HG3	1.93	0.49
26:v:28:THR:O	26:v:49:ALA:HA	2.11	0.49
1:1:8:C:HO2'	5:C:19:SER:HG	1.60	0.49
15:Q:173:PRO:O	15:Q:176:TRP:HD1	1.95	0.49
18:T:93:PHE:HZ	20:V:148:PHE:CE1	2.24	0.49
23:Y:76:MET:HB3	23:Y:81:GLN:HG3	1.95	0.49
25:b:88:ARG:NH1	25:b:91:GLN:OE1	2.45	0.49
1:1:285:C:H2'	1:1:286:A:H8	1.78	0.49
2:2:141:A:HO2'	2:2:142:C:H6	1.56	0.49
2:2:1097:G:C2	2:2:1098:C:C4	3.00	0.49
5:C:160:CYS:HB2	7:E:27:LEU:HD23	1.94	0.49
13:O:881:MET:HB2	13:O:906:LEU:HD13	1.94	0.49
14:P:514:THR:OG1	14:P:887:HIS:NE2	2.45	0.49
14:P:1097:PHE:CE1	14:P:1108:PRO:HB3	2.47	0.49
18:T:11:LEU:HD11	20:V:148:PHE:HZ	1.77	0.49
20:V:191:GLN:O	20:V:195:ILE:HG23	2.12	0.49
28:f:32:LYS:N	28:f:77:ASN:O	2.42	0.49
31:u:27:LYS:O	31:u:32:SER:OG	2.20	0.49
7:E:265:THR:O	7:E:269:THR:OG1	2.30	0.49
7:E:309:TYR:CE1	8:F:439:PRO:HB3	2.47	0.49
13:O:916:MET:O	13:O:919:ILE:N	2.46	0.49
14:P:228:LEU:HD12	14:P:273:LEU:HD11	1.94	0.49
14:P:514:THR:O	14:P:886:PHE:HA	2.12	0.49
17:S:11:CYS:HB3	17:S:86:CYS:O	2.12	0.49
23:Y:59:LEU:HD23	23:Y:59:LEU:O	2.12	0.49
31:u:53:LYS:O	31:u:74:GLU:HA	2.11	0.49
2:2:1115:G:O6	26:v:77:LEU:CD1	2.53	0.49
5:C:18:LEU:HA	5:C:21:ARG:HE	1.76	0.49
13:O:601:ILE:O	13:O:604:THR:OG1	2.28	0.49
13:O:874:GLU:O	13:O:878:ILE:N	2.36	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:Q:361:ARG:HH21	15:Q:363:TYR:HE2	1.60	0.49
20:V:141:GLN:O	20:V:144:ARG:HB2	2.13	0.49
21:W:57:LEU:HD12	21:W:73:ARG:HH12	1.77	0.49
21:W:81:LEU:HD21	21:W:86:ILE:CD1	2.42	0.49
21:W:157:GLN:NE2	23:Y:96:GLY:H	2.03	0.49
25:b:29:VAL:HG21	30:h:68:LEU:HB3	1.94	0.49
2:2:116:U:O4	30:t:88:ARG:CD	2.59	0.49
13:O:507:VAL:HG21	13:O:543:ARG:HB2	1.95	0.49
14:P:159:ILE:HD12	14:P:224:ILE:HD11	1.94	0.49
14:P:719:GLN:HG2	14:P:762:PHE:CD2	2.47	0.49
14:P:1222:GLN:HG2	24:Z:48:ALA:HA	1.95	0.49
21:W:31:LEU:O	21:W:36:LEU:HB3	2.12	0.49
13:O:519:ILE:HD12	13:O:553:LEU:HD11	1.95	0.49
14:P:130:LEU:HD22	14:P:202:ILE:HD11	1.95	0.49
14:P:832:TRP:CG	14:P:833:LYS:H	2.30	0.49
14:P:1201:ASP:HB3	14:P:1203:HIS:CE1	2.47	0.49
21:W:3:PHE:N	21:W:30:ILE:HD11	2.27	0.49
21:W:5:PRO:HB3	21:W:49:HIS:CD2	2.48	0.49
21:W:17:ASP:HA	23:Y:61:VAL:CG1	2.35	0.49
2:2:43:G:C4	2:2:44:PSU:C6	3.00	0.49
14:P:58:LEU:HD11	14:P:1230:PRO:HB3	1.95	0.49
14:P:1240:MET:HB3	14:P:1318:ILE:HD13	1.95	0.49
14:P:1356:VAL:HA	14:P:1360:TYR:CD2	2.47	0.49
18:T:115:LYS:HA	18:T:118:GLN:HB3	1.93	0.49
21:W:22:LYS:HB2	21:W:33:ASP:C	2.37	0.49
21:W:123:THR:O	21:W:125:LYS:N	2.45	0.49
25:s:39:LYS:HA	25:s:39:LYS:HD2	1.50	0.49
1:1:68:G:H2'	1:1:69:A:H8	1.78	0.49
6:D:369:MET:HE3	6:D:429:ASN:HD21	1.78	0.49
18:T:506:LEU:HD13	18:T:518:LYS:NZ	2.28	0.49
21:W:118:ARG:HB3	21:W:147:LEU:HD13	1.93	0.49
6:D:573:HIS:O	6:D:575:GLY:N	2.46	0.49
13:O:439:MET:HA	13:O:442:ILE:HD12	1.94	0.49
14:P:671:GLU:C	14:P:673:ASP:H	2.21	0.49
14:P:1071:ILE:HG12	14:P:1089:ASP:OD2	2.12	0.49
18:T:178:GLU:HA	18:T:334:ARG:HH11	1.78	0.49
21:W:17:ASP:OD2	23:Y:60:LYS:O	2.30	0.49
21:W:30:ILE:HD12	21:W:41:GLU:CG	2.36	0.49
21:W:88:GLU:HA	21:W:113:ASP:OD1	2.13	0.49
25:s:38:ASP:OD1	25:s:42:ASN:N	2.45	0.49
1:1:125:A:H2'	1:1:126:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:314:G:H2'	1:1:315:G:H8	1.78	0.48
2:2:42:PSU:C4	2:2:43:G:C8	3.01	0.48
13:O:252:ILE:HD13	13:O:296:VAL:HG22	1.95	0.48
13:O:374:THR:O	13:O:377:THR:OG1	2.22	0.48
14:P:106:THR:O	14:P:108:ASP:N	2.44	0.48
14:P:975:ASP:O	14:P:977:ILE:HD12	2.12	0.48
21:W:36:LEU:HD12	21:W:59:LEU:HD13	1.95	0.48
30:h:114:ASN:OD1	30:h:117:ARG:NH2	2.45	0.48
31:i:48:LEU:HD21	31:i:96:LEU:HD21	1.94	0.48
2:2:1097:G:H2'	2:2:1098:C:H5	1.78	0.48
7:E:154:ILE:HG23	7:E:164:TYR:HD1	1.78	0.48
13:O:801:ILE:HG23	13:O:816:VAL:HG13	1.95	0.48
13:O:888:ILE:HG12	13:O:903:LEU:HD11	1.94	0.48
14:P:739:LEU:O	14:P:755:ILE:HB	2.13	0.48
14:P:852:PHE:CE2	14:P:854:ASN:HB2	2.47	0.48
18:T:195:ARG:HD3	18:T:197:ASP:OD2	2.14	0.48
18:T:206:ILE:HG23	18:T:221:PRO:HG3	1.94	0.48
21:W:57:LEU:HD13	21:W:73:ARG:HH22	1.76	0.48
2:2:64:G:H2'	2:2:65:A:C8	2.47	0.48
6:D:599:PRO:HB2	7:E:204:SER:HB3	1.94	0.48
11:I:61:U:N3	11:I:62:A:N7	2.61	0.48
14:P:272:VAL:HG23	14:P:283:LYS:HG3	1.94	0.48
14:P:431:SER:H	14:P:436:ASN:HD22	1.60	0.48
20:V:119:GLU:C	20:V:121:ARG:H	2.21	0.48
21:W:8:VAL:CG2	21:W:25:VAL:HG22	2.43	0.48
27:e:84:GLY:O	29:g:64:ARG:NH1	2.47	0.48
27:w:80:ILE:HG23	28:x:80:TYR:HB2	1.96	0.48
27:w:85:ASP:OD1	27:w:86:ASN:N	2.47	0.48
1:1:69:A:H2'	1:1:70:A:H8	1.78	0.48
1:1:299:U:H2'	1:1:300:G:H8	1.77	0.48
2:2:45:U:C4	11:I:58:U:O4	2.66	0.48
2:2:1139:G:H2'	2:2:1140:U:H6	1.76	0.48
6:D:539:LEU:HD11	7:E:321:ILE:HG21	1.95	0.48
13:O:172:LYS:HE3	13:O:180:SER:HB3	1.95	0.48
13:O:178:THR:HA	13:O:181:ARG:HG2	1.94	0.48
13:O:955:VAL:HG21	24:Z:35:VAL:HG11	1.94	0.48
26:v:34:VAL:HG22	26:v:45:ARG:HD2	1.95	0.48
6:D:364:ASN:HB3	6:D:428:LYS:HG2	1.95	0.48
6:D:434:VAL:HG21	6:D:464:ILE:HD11	1.95	0.48
7:E:441:LEU:O	7:E:445:VAL:HB	2.13	0.48
9:G:103:GLN:HG3	9:G:240:ASN:HD21	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:503:LYS:HD3	14:P:941:PHE:CD1	2.49	0.48
14:P:594:MET:HB3	14:P:656:ILE:HG21	1.95	0.48
14:P:1099:TRP:HB2	14:P:1106:PHE:CE1	2.48	0.48
14:P:1299:ILE:C	14:P:1300:LEU:HD12	2.39	0.48
21:W:14:TYR:CE2	21:W:34:LEU:HD21	2.48	0.48
2:2:1108:A:N7	23:Y:106:SER:OG	2.47	0.48
2:2:1116:A:O2'	2:2:1117:G:H5'	2.13	0.48
2:2:1148:U:HO2'	25:s:78:GLU:CD	2.21	0.48
2:2:1162:U:O2'	2:2:1163:C:H5'	2.14	0.48
6:D:425:ILE:O	6:D:427:ASP:N	2.47	0.48
7:E:4:TYR:OH	12:J:2:ARG:NE	2.46	0.48
9:G:129:LEU:HD12	9:G:215:LEU:HD11	1.96	0.48
13:O:410:LYS:O	13:O:413:SER:OG	2.16	0.48
13:O:681:PRO:HG2	13:O:683:ASN:OD1	2.14	0.48
14:P:600:ILE:HD11	14:P:607:LEU:HD23	1.96	0.48
21:W:11:ALA:HB3	21:W:24:ASN:C	2.37	0.48
21:W:73:ARG:NH2	21:W:76:ILE:HG12	2.29	0.48
31:u:47:SER:OG	31:u:103:VAL:HB	2.14	0.48
2:2:1120:G:H2'	2:2:1121:U:C6	2.45	0.48
13:O:232:LEU:HD12	13:O:233:GLY:N	2.29	0.48
13:O:270:SER:HA	13:O:278:ILE:HD11	1.94	0.48
13:O:823:MET:O	13:O:827:ILE:HG12	2.14	0.48
14:P:545:ASP:OD1	14:P:546:ASN:N	2.44	0.48
14:P:565:ASN:C	14:P:567:SER:H	2.22	0.48
18:T:267:SER:C	18:T:272:SER:HB2	2.39	0.48
28:x:50:ASN:HB3	28:x:72:PHE:CE1	2.49	0.48
1:1:73:A:H2'	1:1:75:G:C8	2.49	0.48
14:P:212:LEU:HD21	17:S:14:GLN:HG3	1.94	0.48
18:T:208:GLU:HG3	18:T:332:PHE:CE2	2.49	0.48
18:T:267:SER:O	18:T:272:SER:HB2	2.13	0.48
25:b:75:ILE:HD13	30:h:67:TYR:CZ	2.48	0.48
26:v:64:VAL:HG23	29:y:70:SER:HB2	1.94	0.48
1:1:26:G:H5'	1:1:27:A:H5'	1.95	0.48
6:D:358:TYR:OH	6:D:368:LEU:O	2.32	0.48
7:E:303:LEU:HD11	7:E:313:TRP:CE2	2.48	0.48
7:E:443:ASN:HA	7:E:446:GLN:HG2	1.96	0.48
14:P:847:LEU:N	14:P:865:ILE:O	2.40	0.48
14:P:1197:ASP:OD2	14:P:1224:THR:OG1	2.30	0.48
21:W:141:ARG:CD	21:W:154:LEU:HD23	2.42	0.48
25:b:24:THR:HG22	25:b:92:ILE:HG22	1.96	0.48
6:D:488:ASN:ND2	6:D:512:TYR:OH	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:325:THR:O	8:F:327:ASP:N	2.47	0.48
11:I:70:A:OP1	13:O:898:ARG:NH1	2.47	0.48
13:O:387:PRO:HA	13:O:425:LEU:HB3	1.96	0.48
13:O:538:VAL:O	13:O:542:THR:HG23	2.13	0.48
13:O:943:VAL:HG13	24:Z:18:TYR:CE2	2.49	0.48
14:P:80:VAL:HG11	14:P:169:LEU:HD22	1.96	0.48
14:P:245:VAL:HG21	14:P:249:ASN:H	1.79	0.48
14:P:630:ILE:HD13	14:P:646:LEU:HD13	1.95	0.48
14:P:831:THR:HA	14:P:836:TRP:HA	1.96	0.48
21:W:17:ASP:OD2	23:Y:60:LYS:N	2.47	0.48
21:W:31:LEU:O	21:W:36:LEU:HD13	2.14	0.48
27:e:13:PRO:HB3	29:g:62:VAL:HG21	1.96	0.48
1:l:560:A:O4'	4:B:37:THR:OG1	2.32	0.47
7:E:102:ASN:HD22	9:G:192:PHE:HE1	1.60	0.47
13:O:528:ASP:OD1	13:O:529:GLU:N	2.46	0.47
14:P:406:GLN:HA	14:P:455:LEU:O	2.13	0.47
14:P:1193:PHE:CE1	14:P:1308:ARG:HD2	2.49	0.47
15:Q:184:SER:N	15:Q:272:GLU:OE2	2.46	0.47
21:W:127:LEU:HD23	21:W:151:LEU:HD11	1.95	0.47
23:Y:70:GLY:O	23:Y:72:ALA:N	2.45	0.47
25:s:88:ARG:NH1	26:v:67:SER:C	2.69	0.47
31:u:56:ALA:HB2	31:u:72:VAL:HA	1.96	0.47
27:w:27:VAL:O	27:w:40:LYS:HA	2.13	0.47
27:w:43:ILE:HG23	27:w:52:VAL:HG13	1.95	0.47
2:2:1097:G:O3'	23:Y:40:ASN:ND2	2.47	0.47
4:B:32:TYR:CZ	29:g:20:ASN:HB3	2.49	0.47
6:D:373:LEU:HD11	6:D:399:PHE:HZ	1.79	0.47
13:O:698:ARG:HG3	13:O:699:LYS:H	1.79	0.47
13:O:733:GLU:O	13:O:736:LYS:NZ	2.40	0.47
14:P:632:ILE:HA	14:P:646:LEU:HA	1.95	0.47
14:P:702:ILE:O	14:P:715:VAL:HA	2.15	0.47
23:Y:41:MET:HE3	23:Y:66:LYS:HA	1.96	0.47
1:l:560:A:OP2	28:f:32:LYS:NZ	2.46	0.47
2:2:1094:G:C6	2:2:1149:G:C6	3.03	0.47
2:2:1097:G:C6	2:2:1146:G:C6	3.03	0.47
4:B:103:THR:O	4:B:189:ARG:NH1	2.47	0.47
6:D:452:ARG:HA	6:D:455:PHE:HD2	1.79	0.47
13:O:935:TRP:CZ3	24:Z:22:GLY:HA3	2.50	0.47
14:P:186:ARG:N	24:Z:41:ASN:HD21	2.12	0.47
14:P:766:LYS:HD3	14:P:836:TRP:NE1	2.29	0.47
14:P:1011:ASN:CG	14:P:1014:LYS:HB2	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:1050:VAL:HG22	14:P:1064:VAL:HG12	1.97	0.47
18:T:62:PHE:HA	18:T:376:GLN:O	2.14	0.47
19:U:155:ILE:HD12	19:U:155:ILE:N	2.29	0.47
19:U:155:ILE:HB	19:U:252:VAL:CG2	2.44	0.47
20:V:158:ARG:HB2	20:V:158:ARG:NH1	2.25	0.47
24:Z:50:LEU:HD11	24:Z:66:ARG:HB2	1.97	0.47
25:b:38:ASP:OD1	25:b:42:ASN:N	2.40	0.47
1:1:524:G:H2'	1:1:525:G:H8	1.79	0.47
2:2:116:U:N3	30:t:88:ARG:CG	2.78	0.47
4:B:174:ILE:HG23	4:B:176:ILE:HG13	1.95	0.47
9:G:133:LEU:HB3	9:G:157:LEU:HB2	1.95	0.47
13:O:422:MET:O	13:O:426:MET:HG2	2.14	0.47
13:O:557:LEU:HD23	13:O:560:ARG:HD3	1.96	0.47
14:P:881:THR:HG23	14:P:883:ASP:H	1.79	0.47
16:R:197:ASP:OD1	16:R:198:VAL:N	2.46	0.47
19:U:71:CYS:SG	19:U:90:HIS:HA	2.54	0.47
23:Y:60:LYS:HD2	23:Y:73:PHE:O	2.14	0.47
25:b:6:VAL:H	30:h:83:GLN:HG2	1.79	0.47
25:s:89:GLY:O	25:s:92:ILE:HG22	2.15	0.47
30:t:18:GLU:O	30:t:93:ARG:HB3	2.15	0.47
27:w:24:GLN:CB	27:w:42:LYS:HD2	2.38	0.47
2:2:1099:G:H5'	21:W:158:ASN:HB2	1.95	0.47
2:2:1126:G:O2'	2:2:1127:A:H8	1.97	0.47
14:P:634:CYS:SG	14:P:645:SER:OG	2.38	0.47
14:P:1133:ASP:OD2	14:P:1137:ASN:HB2	2.14	0.47
15:Q:330:ILE:N	15:Q:334:ASN:OD1	2.42	0.47
21:W:1:MET:H2	21:W:29:VAL:HG21	1.79	0.47
2:2:139:G:C2'	2:2:140:G:O5'	2.62	0.47
2:2:1140:U:H2'	2:2:1141:C:C6	2.50	0.47
13:O:221:MET:O	13:O:224:THR:OG1	2.28	0.47
13:O:841:LEU:HA	15:Q:194:PHE:HE1	1.79	0.47
14:P:127:MET:HG3	14:P:148:LEU:HD13	1.96	0.47
14:P:843:ASP:OD1	14:P:844:GLN:N	2.48	0.47
14:P:945:HIS:CE1	14:P:947:GLY:HA3	2.50	0.47
15:Q:176:TRP:CE3	15:Q:177:GLN:HB3	2.49	0.47
19:U:161:SER:C	19:U:162:GLU:HG3	2.39	0.47
21:W:51:THR:C	21:W:53:PRO:HD2	2.40	0.47
26:v:20:SER:OG	26:v:73:VAL:HB	2.14	0.47
1:1:158:G:O2'	25:b:5:GLN:NE2	2.40	0.47
1:1:195:C:H2'	1:1:196:A:H8	1.79	0.47
1:1:257:G:C2	5:C:87:MET:HG3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:529:U:H2'	1:1:530:G:H8	1.80	0.47
2:2:1093:C:C2	2:2:1094:G:C8	3.02	0.47
2:2:1146:G:HO2'	2:2:1147:A:P	2.38	0.47
13:O:161:LYS:HA	13:O:164:ARG:HG2	1.96	0.47
13:O:613:THR:O	13:O:617:ARG:HG2	2.15	0.47
13:O:922:GLY:O	13:O:934:PHE:HD2	1.98	0.47
14:P:149:ALA:HB3	14:P:195:ILE:HD11	1.95	0.47
14:P:374:LYS:C	14:P:376:ASP:H	2.23	0.47
14:P:484:LEU:HD11	14:P:511:ILE:HD13	1.95	0.47
17:S:49:CYS:O	17:S:88:ARG:NH1	2.48	0.47
18:T:156:ILE:HG12	18:T:366:TYR:HB2	1.97	0.47
18:T:210:PHE:CE1	18:T:216:TYR:HB2	2.49	0.47
18:T:350:ARG:O	18:T:354:MET:HG2	2.15	0.47
25:s:29:VAL:HB	25:s:51:GLU:HG3	1.97	0.47
1:1:524:G:H2'	1:1:525:G:C8	2.50	0.47
1:1:559:G:H8	31:i:99:ASP:HB3	1.80	0.47
2:2:38:U:H2'	2:2:39:A:C8	2.50	0.47
2:2:45:U:O2'	2:2:46:C:H5'	2.15	0.47
2:2:144:G:H3'	2:2:145:G:C8	2.38	0.47
13:O:526:LEU:HD23	13:O:537:ALA:HB1	1.96	0.47
14:P:124:ILE:HD13	14:P:150:LEU:HD11	1.97	0.47
14:P:387:ASP:HA	14:P:412:THR:HG22	1.95	0.47
14:P:634:CYS:SG	14:P:678:LYS:HA	2.54	0.47
18:T:12:GLU:O	18:T:16:ILE:HG13	2.15	0.47
21:W:35:GLN:HE22	23:Y:77:ARG:NH1	2.13	0.47
2:2:1150:U:H5'	2:2:1151:U:OP2	2.15	0.47
4:B:42:THR:HG23	31:i:51:ASN:HD22	1.80	0.47
6:D:435:VAL:HG21	6:D:469:PRO:HB2	1.97	0.47
7:E:445:VAL:HG22	7:E:485:LEU:HB2	1.97	0.47
13:O:584:GLY:HA3	13:O:626:ILE:HG21	1.97	0.47
13:O:822:PHE:HA	13:O:825:GLU:HG2	1.96	0.47
13:O:925:HIS:CG	13:O:926:PRO:HD2	2.50	0.47
13:O:935:TRP:CE3	24:Z:22:GLY:HA3	2.49	0.47
14:P:1166:TYR:HB2	14:P:1171:ILE:HD11	1.97	0.47
15:Q:265:CYS:N	15:Q:268:ASP:OD2	2.45	0.47
16:R:108:ALA:O	16:R:154:TYR:HA	2.15	0.47
18:T:171:THR:HG22	18:T:174:GLU:CD	2.40	0.47
21:W:3:PHE:HE2	21:W:31:LEU:O	1.98	0.47
21:W:30:ILE:HA	21:W:31:LEU:HD12	1.97	0.47
21:W:145:LEU:CD2	21:W:159:VAL:HG13	2.45	0.47
25:b:49:ILE:HD12	25:b:79:LYS:HD3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:s:86:ILE:O	26:v:71:PHE:HB2	2.15	0.47
1:1:554:U:O4'	29:g:64:ARG:NH2	2.44	0.47
2:2:1099:G:C5'	21:W:158:ASN:HB2	2.45	0.47
4:B:32:TYR:CE2	29:g:20:ASN:HB3	2.50	0.47
10:H:73:LEU:HB2	10:H:76:HIS:CD2	2.50	0.47
13:O:836:TYR:HB3	15:Q:260:PRO:HD3	1.97	0.47
14:P:63:LEU:HB2	14:P:1227:CYS:SG	2.55	0.47
14:P:561:LEU:HD21	14:P:568:MET:HG3	1.97	0.47
15:Q:170:ILE:HD13	15:Q:267:GLY:HA2	1.95	0.47
15:Q:248:HIS:CE1	15:Q:252:PHE:HD2	2.33	0.47
21:W:129:LEU:HD22	21:W:140:TYR:HE1	1.79	0.47
21:W:145:LEU:HD21	21:W:159:VAL:HG13	1.97	0.47
23:Y:78:THR:HG22	23:Y:81:GLN:OE1	2.15	0.47
25:s:15:LEU:HB3	25:s:20:LEU:HD11	1.97	0.47
30:t:4:VAL:HG11	30:t:34:PRO:HA	1.97	0.47
27:w:17:ILE:HA	27:w:20:PHE:HD2	1.79	0.47
1:1:31:A:H3'	1:1:32:G:H21	1.80	0.46
2:2:1139:G:O2'	2:2:1140:U:O5'	2.33	0.46
10:H:39:LEU:N	10:H:41:ASP:OD2	2.47	0.46
10:H:208:LEU:HD11	10:H:217:LEU:HD12	1.97	0.46
13:O:467:VAL:HG12	13:O:469:SER:H	1.80	0.46
13:O:472:PRO:HB2	13:O:476:ARG:HH22	1.80	0.46
13:O:865:ALA:HB3	13:O:905:ALA:HB1	1.97	0.46
14:P:117:PHE:HA	14:P:1328:ARG:HH22	1.80	0.46
14:P:490:SER:N	14:P:1201:ASP:OD2	2.36	0.46
14:P:961:CYS:O	14:P:962:LEU:HD12	2.14	0.46
15:Q:291:PRO:HA	16:R:31:GLN:OE1	2.15	0.46
18:T:169:ILE:O	18:T:246:LYS:HD2	2.15	0.46
18:T:219:THR:N	18:T:220:PRO:HD3	2.30	0.46
30:t:44:LYS:HB2	30:t:79:ILE:CG2	2.44	0.46
26:v:23:LEU:HD23	26:v:24:THR:N	2.30	0.46
1:1:46:C:H2'	1:1:47:A:H8	1.80	0.46
7:E:272:SER:O	7:E:276:ILE:HG12	2.15	0.46
9:G:116:VAL:HG21	9:G:232:ILE:HD11	1.98	0.46
17:S:42:LYS:HA	17:S:71:PHE:HD1	1.79	0.46
19:U:244:ASP:OD2	19:U:247:SER:HB3	2.14	0.46
20:V:99:THR:HG21	20:V:122:LEU:HD22	1.97	0.46
20:V:139:VAL:HG23	20:V:140:ALA:H	1.80	0.46
26:d:65:ARG:HD2	26:d:68:GLN:HE22	1.80	0.46
26:v:23:LEU:HD23	26:v:24:THR:H	1.80	0.46
2:2:1143:C:H4'	2:2:1144:U:H2'	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:25:LYS:NZ	7:E:66:GLU:OE2	2.34	0.46
10:H:203:VAL:HG13	10:H:233:ARG:HD3	1.97	0.46
13:O:378:LEU:HB3	13:O:422:MET:HE2	1.98	0.46
14:P:125:THR:HG22	14:P:191:SER:HA	1.98	0.46
14:P:257:ILE:HD11	14:P:264:LEU:HD11	1.97	0.46
14:P:353:ARG:HE	14:P:385:HIS:HB3	1.80	0.46
14:P:428:PHE:CE2	14:P:430:LEU:HB2	2.50	0.46
14:P:1310:TYR:HE2	14:P:1311:TYR:CZ	2.33	0.46
18:T:31:LEU:HD23	18:T:72:ILE:HG23	1.96	0.46
18:T:60:TYR:CE2	18:T:61:LYS:HG2	2.51	0.46
20:V:127:SER:HA	20:V:132:HIS:CG	2.50	0.46
21:W:17:ASP:C	21:W:19:PHE:N	2.74	0.46
21:W:139:ASN:HB2	21:W:142:GLU:OE2	2.15	0.46
31:u:52:HIS:C	31:u:53:LYS:HD2	2.40	0.46
26:v:34:VAL:CG2	26:v:45:ARG:HG3	2.46	0.46
14:P:487:SER:O	14:P:1200:THR:HG21	2.16	0.46
21:W:14:TYR:CZ	21:W:34:LEU:HD21	2.50	0.46
29:g:14:LYS:HA	29:g:27:GLY:O	2.16	0.46
25:s:21:ARG:NH1	25:s:29:VAL:HG11	2.29	0.46
1:1:520:G:H2'	1:1:521:G:H8	1.79	0.46
2:2:116:U:H5'	30:t:90:ASN:ND2	2.31	0.46
6:D:535:PHE:HB2	6:D:540:TYR:HB2	1.98	0.46
7:E:20:VAL:HG11	7:E:30:TRP:HE3	1.81	0.46
8:F:443:ILE:HG21	9:G:274:ILE:HD13	1.96	0.46
13:O:275:LEU:HD22	13:O:312:GLN:HB3	1.97	0.46
14:P:485:ASN:HB2	14:P:486:PRO:HD3	1.98	0.46
14:P:1199:ILE:HA	14:P:1220:GLY:HA2	1.96	0.46
17:S:22:LEU:HD23	17:S:70:ALA:HB2	1.98	0.46
18:T:150:PRO:CG	18:T:154:THR:H	2.24	0.46
21:W:93:LEU:C	21:W:95:PRO:HD3	2.40	0.46
25:s:28:ARG:NH1	26:v:22:GLU:OE2	2.45	0.46
30:t:88:ARG:NH1	30:t:90:ASN:HB3	2.31	0.46
7:E:479:TRP:CH2	7:E:508:GLN:HB3	2.46	0.46
11:I:72:A:H2'	11:I:73:A:C8	2.51	0.46
13:O:675:LEU:HD13	13:O:715:ALA:HB2	1.96	0.46
14:P:98:GLU:OE1	14:P:1196:ASN:ND2	2.49	0.46
14:P:331:PHE:HB2	14:P:334:HIS:O	2.14	0.46
14:P:337:VAL:CG2	14:P:346:LEU:HB2	2.45	0.46
14:P:643:ILE:HG13	14:P:691:LEU:HD12	1.97	0.46
14:P:1098:ILE:O	14:P:1106:PHE:HA	2.15	0.46
15:Q:138:LYS:NZ	15:Q:147:ILE:O	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:R:108:ALA:HB3	16:R:155:PHE:HB2	1.97	0.46
21:W:7:ILE:HG22	21:W:25:VAL:CG1	2.43	0.46
21:W:95:PRO:HG2	21:W:98:VAL:HG21	1.97	0.46
25:b:23:LEU:HD21	30:h:65:SER:HB3	1.98	0.46
30:h:26:TRP:HE3	30:h:44:LYS:HG2	1.81	0.46
1:1:299:U:H2'	1:1:300:G:C8	2.51	0.46
6:D:340:TYR:HA	6:D:346:LEU:HD22	1.98	0.46
6:D:358:TYR:CE1	6:D:368:LEU:HG	2.51	0.46
13:O:915:PHE:CE2	13:O:919:ILE:HD11	2.50	0.46
14:P:286:TYR:OH	14:P:340:MET:O	2.31	0.46
14:P:586:ASP:OD1	14:P:587:THR:N	2.49	0.46
14:P:732:ARG:CZ	14:P:739:LEU:HB2	2.46	0.46
14:P:849:CYS:SG	14:P:862:VAL:HG21	2.56	0.46
18:T:7:ARG:HD2	18:T:96:ILE:HG22	1.97	0.46
13:O:747:ASN:HD21	13:O:780:CYS:HB3	1.81	0.46
14:P:827:TRP:CH2	14:P:1209:SER:HB3	2.51	0.46
14:P:1065:THR:HG21	14:P:1106:PHE:HD2	1.80	0.46
15:Q:291:PRO:HG3	15:Q:325:TYR:CE1	2.51	0.46
18:T:188:LEU:O	18:T:192:VAL:HG23	2.16	0.46
18:T:264:PHE:CE1	18:T:268:TYR:CD2	3.04	0.46
21:W:30:ILE:HG21	21:W:41:GLU:CA	2.45	0.46
21:W:139:ASN:HB2	21:W:142:GLU:CG	2.46	0.46
23:Y:34:GLN:HB2	23:Y:100:LYS:HE2	1.98	0.46
27:w:90:ILE:HB	29:y:62:VAL:CG1	2.46	0.46
7:E:476:GLY:HA3	7:E:520:SER:HB3	1.97	0.46
8:F:425:ALA:O	8:F:504:ASN:ND2	2.49	0.46
13:O:191:LYS:O	13:O:194:THR:OG1	2.33	0.46
13:O:443:ARG:HH11	13:O:479:ILE:HD11	1.80	0.46
14:P:301:LEU:HD21	14:P:393:VAL:HG21	1.98	0.46
14:P:651:LEU:HB3	14:P:670:PRO:HG2	1.96	0.46
19:U:212:GLU:HB3	20:V:205:LYS:CB	2.46	0.46
21:W:80:LEU:HD13	23:Y:53:ALA:CB	2.46	0.46
21:W:159:VAL:HG11	21:W:164:ARG:NE	2.31	0.46
26:d:65:ARG:HH12	29:g:66:ASN:HA	1.81	0.46
1:1:68:G:H2'	1:1:69:A:C8	2.50	0.46
2:2:37:G:H4'	13:O:893:PRO:HG3	1.98	0.46
2:2:118:U:O4	31:u:49:ARG:HD3	2.16	0.46
2:2:141:A:C2'	2:2:142:C:H6	2.29	0.46
10:H:82:ARG:NH2	27:e:19:ASN:OD1	2.42	0.46
14:P:242:VAL:HG22	14:P:252:PHE:HB3	1.98	0.46
14:P:500:ILE:HD13	14:P:1225:VAL:HG11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:654:PHE:HE1	14:P:665:GLU:HB3	1.81	0.46
14:P:1101:PRO:C	14:P:1103:GLY:H	2.23	0.46
15:Q:162:SER:O	15:Q:166:THR:OG1	2.28	0.46
16:R:185:LYS:HD2	18:T:427:SER:HB2	1.98	0.46
19:U:165:GLU:O	19:U:165:GLU:HG2	2.16	0.46
21:W:11:ALA:CB	21:W:25:VAL:N	2.79	0.46
21:W:25:VAL:O	21:W:31:LEU:HG	2.15	0.46
25:b:19:LYS:HB2	25:b:99:ASP:HB2	1.98	0.46
25:b:24:THR:HA	25:b:92:ILE:HA	1.97	0.46
26:d:47:VAL:HB	26:d:59:MET:HB2	1.98	0.46
1:1:2:U:H2'	1:1:3:A:C8	2.51	0.45
2:2:52:A:H2'	2:2:53:G:C8	2.51	0.45
13:O:213:LEU:HD13	13:O:218:ARG:HB3	1.98	0.45
13:O:555:GLU:HG2	13:O:593:ARG:NH1	2.31	0.45
13:O:698:ARG:HG3	13:O:699:LYS:N	2.31	0.45
13:O:865:ALA:HA	13:O:877:PHE:HE1	1.79	0.45
13:O:912:PRO:O	13:O:916:MET:N	2.23	0.45
14:P:73:HIS:CE1	14:P:126:SER:HA	2.51	0.45
19:U:68:CYS:O	19:U:72:ASN:N	2.43	0.45
27:w:27:VAL:HG13	27:w:91:THR:O	2.17	0.45
1:1:48:A:H2'	1:1:49:A:C8	2.51	0.45
1:1:125:A:H2'	1:1:126:A:H8	1.80	0.45
1:1:285:C:H2'	1:1:286:A:C8	2.51	0.45
2:2:1139:G:H2'	2:2:1140:U:C5	2.51	0.45
7:E:332:ASN:HB3	9:G:194:VAL:HG23	1.97	0.45
13:O:450:ASP:OD1	13:O:451:ASP:N	2.49	0.45
13:O:928:LYS:HD2	24:Z:24:GLU:OE2	2.16	0.45
14:P:59:TYR:O	14:P:1230:PRO:HA	2.16	0.45
14:P:60:LEU:HB3	14:P:1228:PHE:HB3	1.99	0.45
21:W:51:THR:HG23	21:W:53:PRO:HD2	1.98	0.45
23:Y:108:THR:HG22	23:Y:110:THR:H	1.82	0.45
25:b:61:LEU:HD22	30:h:63:MET:HB3	1.97	0.45
28:x:27:VAL:O	28:x:39:ARG:HA	2.16	0.45
2:2:38:U:OP2	13:O:186:ARG:NH2	2.50	0.45
5:C:125:PHE:HB3	7:E:83:LYS:HD2	1.98	0.45
5:C:157:ASP:OD1	7:E:39:LYS:NZ	2.34	0.45
11:I:62:A:H2'	11:I:63:U:C6	2.51	0.45
13:O:197:PRO:HA	13:O:200:ILE:HB	1.97	0.45
13:O:531:GLU:O	13:O:535:THR:HG23	2.17	0.45
13:O:602:VAL:HG21	13:O:639:MET:HE2	1.98	0.45
13:O:889:PHE:CE1	13:O:930:VAL:HG22	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:363:VAL:HG12	14:P:364:THR:N	2.25	0.45
17:S:61:CYS:HB2	17:S:96:ARG:NH2	2.31	0.45
23:Y:76:MET:SD	23:Y:81:GLN:HG3	2.55	0.45
30:t:26:TRP:O	30:t:43:VAL:HA	2.17	0.45
26:v:77:LEU:HD23	26:v:77:LEU:O	2.16	0.45
27:w:27:VAL:HG21	27:w:43:ILE:HG12	1.99	0.45
1:1:42:U:H2'	1:1:43:G:H8	1.82	0.45
2:2:65:A:H2'	2:2:66:A:O4'	2.16	0.45
4:B:15:LEU:HD11	5:C:39:ARG:HA	1.98	0.45
5:C:165:PHE:HB3	8:F:415:TYR:HE2	1.82	0.45
7:E:16:LEU:HA	7:E:19:ASN:HD22	1.81	0.45
7:E:168:LEU:HD13	7:E:186:TRP:CD1	2.48	0.45
13:O:866:LEU:O	17:S:78:ARG:NH1	2.50	0.45
14:P:269:ILE:HD11	14:P:282:LYS:HG3	1.99	0.45
14:P:494:SER:HB3	14:P:499:SER:OG	2.16	0.45
14:P:924:PHE:HD2	14:P:952:ARG:HD2	1.79	0.45
18:T:4:LEU:HD21	20:V:146:TYR:OH	2.16	0.45
18:T:175:GLN:HB2	18:T:178:GLU:HB3	1.99	0.45
18:T:419:ARG:N	18:T:432:ASN:O	2.44	0.45
19:U:240:CYS:HB2	19:U:253:GLN:C	2.42	0.45
20:V:108:SER:O	20:V:112:GLN:HG3	2.15	0.45
21:W:15:TYR:CD1	21:W:15:TYR:N	2.84	0.45
21:W:37:GLU:HG2	21:W:60:THR:HG22	1.98	0.45
21:W:66:MET:HG3	21:W:88:GLU:O	2.16	0.45
30:t:37:ASN:OD1	30:t:89:GLY:N	2.42	0.45
27:w:40:LYS:HZ3	27:w:93:ALA:HB3	1.78	0.45
2:2:116:U:O4	25:s:41:MET:HG3	2.17	0.45
2:2:142:C:HO2'	2:2:143:G:H8	1.63	0.45
2:2:1152:U:H2'	2:2:1153:C:H6	1.79	0.45
6:D:620:TYR:HB3	8:F:306:HIS:CE1	2.52	0.45
13:O:230:TYR:CE2	24:Z:5:GLN:HB3	2.51	0.45
13:O:839:THR:HG22	13:O:880:LEU:HD21	1.98	0.45
15:Q:134:LEU:O	15:Q:138:LYS:HG2	2.16	0.45
15:Q:173:PRO:HB3	15:Q:269:VAL:HG11	1.99	0.45
18:T:169:ILE:HG22	18:T:246:LYS:CD	2.47	0.45
31:i:62:ASP:OD2	31:i:66:ASN:ND2	2.48	0.45
25:s:33:GLN:O	25:s:45:LEU:HA	2.16	0.45
2:2:119:G:C8	27:w:32:PHE:HD2	2.34	0.45
2:2:120:G:H2'	2:2:121:C:C6	2.51	0.45
7:E:167:VAL:O	7:E:171:ILE:HG12	2.17	0.45
11:I:69:A:H4'	13:O:898:ARG:HH11	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:334:ILE:HD11	13:O:362:CYS:SG	2.56	0.45
13:O:719:ALA:HB3	13:O:724:TRP:CE2	2.52	0.45
13:O:760:HIS:HB3	15:Q:240:LEU:HD12	1.99	0.45
13:O:820:MET:HE1	13:O:841:LEU:HD13	1.98	0.45
13:O:964:ILE:HG22	13:O:966:GLU:H	1.82	0.45
14:P:61:TYR:HD1	14:P:1318:ILE:HD11	1.81	0.45
14:P:76:ILE:HD11	14:P:422:PHE:CD1	2.51	0.45
14:P:178:PRO:C	14:P:179:LEU:HD12	2.42	0.45
14:P:865:ILE:HD11	14:P:869:GLY:HA2	1.98	0.45
14:P:936:PRO:O	14:P:937:LYS:HD2	2.16	0.45
14:P:1065:THR:HG22	14:P:1105:VAL:HG23	1.98	0.45
2:2:34:G:C6	11:I:72:A:C6	3.04	0.45
2:2:1098:C:O3'	21:W:158:ASN:HB3	2.16	0.45
13:O:244:LEU:HD23	13:O:281:VAL:HG11	1.98	0.45
13:O:732:LEU:HD11	13:O:769:ASN:HB2	1.98	0.45
13:O:855:GLN:NE2	13:O:894:HIS:HB3	2.32	0.45
21:W:129:LEU:HD22	21:W:140:TYR:CE1	2.52	0.45
2:2:1150:U:H3'	2:2:1151:U:O4'	2.17	0.45
7:E:297:LEU:O	7:E:301:ARG:HB2	2.17	0.45
8:F:376:SER:OG	8:F:377:ARG:N	2.49	0.45
13:O:904:GLU:O	13:O:907:SER:OG	2.25	0.45
14:P:153:ASP:OD2	14:P:1302:ARG:NH1	2.50	0.45
14:P:1035:LEU:HD23	14:P:1077:MET:HG3	1.98	0.45
15:Q:243:ASP:HB3	15:Q:246:LYS:HG3	1.98	0.45
16:R:65:TYR:O	16:R:69:ILE:HG22	2.17	0.45
18:T:418:ASP:N	18:T:432:ASN:O	2.49	0.45
21:W:6:SER:O	21:W:9:ILE:HG22	2.16	0.45
13:O:376:HIS:O	13:O:379:SER:OG	2.23	0.45
13:O:562:ILE:HD11	13:O:590:LEU:HD11	1.99	0.45
13:O:827:ILE:O	13:O:827:ILE:HG13	2.17	0.45
14:P:694:ALA:HB2	14:P:728:MET:SD	2.57	0.45
14:P:754:HIS:HB3	14:P:764:ASP:HB3	1.99	0.45
14:P:770:LEU:HD22	14:P:827:TRP:CG	2.52	0.45
14:P:1037:PHE:CE2	14:P:1038:LYS:HG2	2.52	0.45
15:Q:276:LEU:O	15:Q:280:THR:HG23	2.17	0.45
21:W:67:ILE:O	21:W:93:LEU:HD21	2.17	0.45
2:2:35:PSU:O2	2:2:36:A:N6	2.49	0.45
2:2:56:U:H1'	2:2:59:C:H5	1.82	0.45
2:2:115:U:O2	25:s:88:ARG:CG	2.64	0.45
6:D:494:LEU:HA	6:D:498:ILE:HD12	1.98	0.45
8:F:373:ILE:C	8:F:375:ASN:H	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:163:GLU:HG3	13:O:199:MET:HE2	1.99	0.45
13:O:393:PHE:CD1	13:O:422:MET:HE1	2.52	0.45
13:O:472:PRO:HB2	13:O:476:ARG:NH2	2.32	0.45
14:P:181:ARG:HD2	14:P:185:ARG:NH2	2.28	0.45
14:P:294:PHE:HE1	14:P:365:ILE:HB	1.81	0.45
14:P:1192:HIS:CE1	14:P:1312:ALA:HB3	2.52	0.45
15:Q:183:LEU:HB3	15:Q:188:LEU:HD11	1.97	0.45
16:R:42:LYS:HD3	16:R:49:TYR:CE1	2.51	0.45
21:W:8:VAL:HG23	21:W:25:VAL:CG2	2.47	0.45
31:u:38:MET:HG3	31:u:39:VAL:N	2.32	0.45
31:u:50:ASN:ND2	31:u:52:HIS:HD2	2.15	0.45
2:2:1139:G:C6	2:2:1140:U:C4	3.04	0.44
6:D:445:LEU:HD12	6:D:447:ASN:HD21	1.82	0.44
8:F:314:THR:OG1	8:F:383:GLY:O	2.35	0.44
11:I:78:A:N7	13:O:539:HIS:NE2	2.66	0.44
13:O:399:PRO:HA	13:O:402:LYS:HG2	1.99	0.44
14:P:519:TYR:CZ	14:P:874:GLY:HA3	2.51	0.44
14:P:582:LYS:CE	14:P:610:ILE:HG21	2.47	0.44
21:W:151:LEU:O	21:W:159:VAL:HG21	2.17	0.44
23:Y:94:PHE:HB3	23:Y:99:LEU:CD1	2.44	0.44
30:h:16:THR:HG22	30:h:26:TRP:HD1	1.81	0.44
31:u:62:ASP:OD1	31:u:63:ARG:N	2.48	0.44
1:1:192:A:H2'	1:1:193:A:H8	1.82	0.44
7:E:355:ILE:HB	7:E:364:LEU:HD21	1.99	0.44
13:O:510:ALA:HA	13:O:518:THR:HG21	1.98	0.44
13:O:757:ILE:HG22	13:O:758:GLY:N	2.30	0.44
14:P:1249:GLU:O	14:P:1252:ASP:N	2.50	0.44
15:Q:248:HIS:CD2	15:Q:375:PHE:HB2	2.52	0.44
19:U:177:PRO:HB3	19:U:243:TRP:CD1	2.53	0.44
20:V:139:VAL:HG23	20:V:140:ALA:N	2.32	0.44
23:Y:78:THR:HG23	23:Y:81:GLN:HG2	1.98	0.44
25:s:53:VAL:HB	25:s:54:PRO:HD3	1.98	0.44
9:G:195:VAL:HG11	9:G:235:PHE:HE1	1.83	0.44
13:O:387:PRO:HA	13:O:425:LEU:CB	2.47	0.44
13:O:881:MET:O	13:O:885:ILE:HD12	2.18	0.44
14:P:443:LYS:C	14:P:445:GLY:H	2.24	0.44
14:P:552:ILE:HG22	14:P:553:THR:H	1.81	0.44
14:P:951:CYS:SG	14:P:952:ARG:N	2.90	0.44
14:P:1183:CYS:O	14:P:1184:LYS:HG2	2.18	0.44
17:S:32:ILE:HG21	17:S:81:LYS:HD3	1.98	0.44
18:T:180:MET:H	18:T:335:THR:CG2	2.28	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:V:99:THR:O	20:V:103:TYR:HB2	2.17	0.44
20:V:106:ASP:O	20:V:107:LYS:HB2	2.16	0.44
21:W:6:SER:O	21:W:27:LYS:HB2	2.17	0.44
21:W:35:GLN:NE2	23:Y:77:ARG:NH2	2.64	0.44
29:y:2:VAL:HG11	29:y:34:ILE:HD13	1.98	0.44
1:1:69:A:H2'	1:1:70:A:C8	2.52	0.44
1:1:307:G:H2'	1:1:308:A:C8	2.52	0.44
7:E:35:ASN:O	7:E:39:LYS:HB2	2.17	0.44
13:O:244:LEU:HD21	13:O:282:MET:HE2	2.00	0.44
14:P:292:ALA:HA	14:P:331:PHE:HD1	1.80	0.44
18:T:178:GLU:O	18:T:334:ARG:HD2	2.17	0.44
19:U:40:VAL:HG23	19:U:53:ARG:NH1	2.26	0.44
19:U:200:VAL:HA	19:U:209:ILE:O	2.18	0.44
21:W:14:TYR:O	21:W:22:LYS:HG2	2.17	0.44
24:Z:40:LEU:HD22	24:Z:69:LEU:HD22	1.99	0.44
25:b:20:LEU:HD11	25:b:34:LEU:HD23	1.98	0.44
26:v:44:LEU:HB3	26:v:62:ILE:CG2	2.48	0.44
7:E:140:HIS:CD2	7:E:297:LEU:HD21	2.51	0.44
13:O:297:THR:HA	13:O:300:ALA:HB3	2.00	0.44
13:O:797:VAL:HG12	13:O:801:ILE:HD11	1.99	0.44
14:P:827:TRP:HH2	14:P:1209:SER:HB3	1.82	0.44
14:P:1222:GLN:H	14:P:1222:GLN:CD	2.26	0.44
14:P:1356:VAL:HG12	14:P:1360:TYR:CE2	2.53	0.44
17:S:42:LYS:HA	17:S:71:PHE:CD1	2.52	0.44
21:W:80:LEU:HA	21:W:102:THR:HB	2.00	0.44
25:s:96:VAL:HG11	30:t:82:LEU:HD23	1.99	0.44
31:u:33:LEU:HD11	28:x:52:GLN:HG3	1.98	0.44
2:2:59:C:H3'	2:2:60:A:H8	1.82	0.44
13:O:886:PRO:HA	15:Q:175:HIS:CE1	2.52	0.44
14:P:653:TYR:HE2	14:P:655:LYS:NZ	2.15	0.44
14:P:839:ARG:HG3	14:P:840:GLN:O	2.17	0.44
14:P:952:ARG:HA	14:P:972:LYS:O	2.17	0.44
14:P:1111:ASP:OD1	14:P:1112:ASP:N	2.48	0.44
15:Q:295:SER:N	16:R:27:GLU:OE2	2.38	0.44
18:T:219:THR:HG22	18:T:219:THR:O	2.17	0.44
21:W:141:ARG:HE	21:W:145:LEU:HD11	1.82	0.44
24:Z:23:ASP:CG	24:Z:24:GLU:H	2.25	0.44
27:e:47:ASP:HB3	28:f:15:PRO:HD2	1.99	0.44
26:v:49:ALA:HB3	26:v:57:THR:HG22	1.99	0.44
28:x:58:GLU:C	28:x:59:PHE:HD1	2.25	0.44
2:2:149:A:H2'	2:2:150:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:94:GLN:HE22	7:E:188:GLN:HE21	1.65	0.44
6:D:347:PHE:HE1	6:D:375:MET:HG2	1.83	0.44
7:E:308:HIS:HB3	7:E:340:PHE:HD2	1.82	0.44
13:O:257:MET:HG3	17:S:100:HIS:CD2	2.53	0.44
13:O:667:TYR:HA	13:O:707:PHE:CD1	2.52	0.44
14:P:498:LEU:HD23	14:P:498:LEU:O	2.18	0.44
18:T:355:ASP:O	18:T:359:GLN:HG2	2.17	0.44
18:T:409:TYR:OH	18:T:413:LYS:NZ	2.31	0.44
24:Z:54:SER:HB2	24:Z:62:ILE:HG23	2.00	0.44
2:2:116:U:O4	30:t:88:ARG:CG	2.63	0.44
5:C:165:PHE:HZ	9:G:270:THR:HG22	1.82	0.44
7:E:393:GLN:O	7:E:396:THR:OG1	2.31	0.44
8:F:418:ILE:HD12	8:F:442:GLN:HB3	1.99	0.44
10:H:54:PRO:HB3	10:H:57:LEU:HD12	2.00	0.44
11:I:69:A:H3'	13:O:775:ARG:NH2	2.33	0.44
11:I:77:C:O3'	13:O:496:ARG:NH1	2.50	0.44
13:O:363:LEU:HA	13:O:374:THR:HG21	2.00	0.44
13:O:386:TYR:CD1	13:O:387:PRO:HD2	2.51	0.44
13:O:594:MET:SD	13:O:630:VAL:HG11	2.58	0.44
13:O:913:GLY:HA3	14:P:1114:VAL:HG11	1.99	0.44
14:P:640:THR:OG1	14:P:686:GLN:O	2.34	0.44
14:P:826:THR:O	14:P:840:GLN:HA	2.18	0.44
16:R:45:VAL:HG13	19:U:97:ARG:HD2	1.99	0.44
18:T:34:HIS:CD2	18:T:76:GLN:HE22	2.35	0.44
18:T:172:ARG:HG3	18:T:361:TYR:HB2	1.99	0.44
31:i:56:ALA:HB3	31:i:69:LEU:HD12	1.98	0.44
31:u:44:VAL:O	31:u:55:ILE:HD12	2.17	0.44
27:w:81:LEU:HB3	28:x:81:ILE:HG22	2.00	0.44
28:x:60:VAL:O	28:x:63:VAL:HG12	2.18	0.44
1:1:247:G:H2'	1:1:248:G:H8	1.83	0.44
1:1:265:U:H2'	1:1:266:G:H8	1.82	0.44
2:2:64:G:C2	2:2:65:A:C5	3.06	0.44
4:B:199:LEU:HD13	4:B:199:LEU:HA	1.66	0.44
7:E:417:ASN:HD22	7:E:418:LYS:N	2.16	0.44
13:O:313:LEU:HD23	13:O:317:ILE:HG13	2.00	0.44
14:P:62:HIS:HA	14:P:1227:CYS:O	2.18	0.44
14:P:110:GLU:HG2	14:P:479:SER:OG	2.17	0.44
14:P:527:LEU:HD21	14:P:552:ILE:HG21	1.99	0.44
14:P:1198:ILE:O	14:P:1221:LEU:N	2.42	0.44
19:U:178:PRO:HG2	19:U:250:TYR:CD1	2.52	0.44
20:V:181:HIS:O	20:V:185:VAL:HG23	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:W:124:LEU:O	21:W:151:LEU:HD23	2.17	0.44
27:w:29:ILE:HD11	27:w:87:ILE:HA	2.00	0.44
27:w:83:LYS:NZ	28:x:75:CYS:C	2.73	0.44
1:1:32:G:O5'	4:B:198:ARG:NH2	2.51	0.43
1:1:83:U:H2'	1:1:84:U:C6	2.53	0.43
2:2:1099:G:H2'	2:2:1100:A:H8	1.83	0.43
7:E:215:ASP:N	7:E:225:TYR:OH	2.49	0.43
7:E:410:SER:O	7:E:410:SER:OG	2.32	0.43
10:H:12:ARG:NH2	27:e:48:GLU:OE2	2.43	0.43
13:O:335:LYS:O	13:O:338:GLN:HB2	2.18	0.43
14:P:348:VAL:HG21	14:P:405:VAL:HB	2.00	0.43
14:P:387:ASP:HA	14:P:412:THR:CG2	2.48	0.43
15:Q:367:LEU:C	15:Q:369:SER:H	2.26	0.43
18:T:212:ASP:HB3	18:T:215:LYS:HB2	2.00	0.43
18:T:508:GLU:HG2	18:T:509:GLU:N	2.31	0.43
19:U:35:SER:O	19:U:38:GLU:HG2	2.18	0.43
19:U:155:ILE:HD13	19:U:252:VAL:HG23	2.00	0.43
19:U:226:MET:HG3	19:U:226:MET:O	2.18	0.43
25:b:8:HIS:O	30:h:30:GLN:NE2	2.50	0.43
28:x:36:THR:HG23	28:x:58:GLU:HG3	2.00	0.43
1:1:307:G:H2'	1:1:308:A:H8	1.83	0.43
1:1:311:U:H2'	1:1:312:G:C8	2.52	0.43
2:2:66:A:OP2	2:2:66:A:C8	2.70	0.43
2:2:1098:C:OP1	23:Y:43:ARG:CD	2.63	0.43
7:E:292:ASP:HA	7:E:295:THR:HG22	2.00	0.43
13:O:164:ARG:HG3	13:O:165:THR:N	2.32	0.43
14:P:155:GLY:HA3	14:P:179:LEU:O	2.19	0.43
14:P:361:LYS:C	14:P:363:VAL:H	2.25	0.43
14:P:564:ASP:HB3	14:P:567:SER:HB3	1.99	0.43
21:W:22:LYS:HZ2	21:W:34:LEU:CD1	2.06	0.43
30:h:43:VAL:HG11	30:h:85:ILE:HD12	1.99	0.43
31:u:50:ASN:ND2	31:u:52:HIS:CD2	2.85	0.43
31:u:75:LEU:HD11	31:u:86:ASN:HB3	1.99	0.43
26:v:45:ARG:HH11	26:v:45:ARG:HD3	1.65	0.43
27:w:45:GLY:HA3	28:x:13:VAL:O	2.18	0.43
28:x:54:ASN:OD1	28:x:55:GLU:N	2.46	0.43
2:2:118:U:O2'	2:2:120:G:OP1	2.25	0.43
7:E:513:PHE:HB3	7:E:517:VAL:HG22	2.00	0.43
7:E:518:LEU:O	7:E:522:THR:OG1	2.25	0.43
13:O:916:MET:HE2	13:O:919:ILE:HD12	2.00	0.43
13:O:928:LYS:HA	13:O:931:ARG:NH1	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:561:LEU:HG	14:P:569:GLU:O	2.19	0.43
14:P:782:GLU:HB3	14:P:860:ASN:OD1	2.18	0.43
18:T:38:GLU:O	18:T:41:LYS:HG2	2.19	0.43
1:1:192:A:H2'	1:1:193:A:C8	2.53	0.43
7:E:370:LYS:HD3	9:G:247:SER:HA	2.00	0.43
13:O:910:LEU:HD23	13:O:914:LEU:HD23	2.00	0.43
14:P:130:LEU:HD11	14:P:147:PHE:CE1	2.54	0.43
14:P:704:SER:O	14:P:712:PHE:C	2.62	0.43
14:P:770:LEU:HD12	14:P:770:LEU:O	2.18	0.43
14:P:1308:ARG:HG3	14:P:1314:VAL:HG11	1.99	0.43
18:T:152:ARG:C	18:T:153:ARG:HG3	2.44	0.43
31:u:103:VAL:HG11	28:x:71:ILE:HD11	1.99	0.43
1:1:42:U:H2'	1:1:43:G:C8	2.53	0.43
2:2:1094:G:H2'	2:2:1095:U:C6	2.54	0.43
13:O:683:ASN:HB3	13:O:718:TYR:HB3	1.99	0.43
13:O:916:MET:HB3	13:O:920:TRP:CD1	2.53	0.43
14:P:180:THR:O	17:S:83:LYS:HB3	2.19	0.43
15:Q:248:HIS:CG	15:Q:375:PHE:HB2	2.54	0.43
17:S:15:PRO:HB3	17:S:44:ARG:O	2.19	0.43
19:U:57:TYR:CD1	19:U:70:LEU:HD13	2.54	0.43
21:W:25:VAL:HB	21:W:31:LEU:C	2.43	0.43
31:u:80:LYS:HE3	31:u:82:LYS:CG	2.48	0.43
1:1:26:G:H5''	4:B:179:ARG:HH22	1.83	0.43
7:E:271:VAL:HB	7:E:309:TYR:HE2	1.83	0.43
7:E:363:LEU:HD23	9:G:75:ARG:NH1	2.33	0.43
13:O:865:ALA:HA	13:O:877:PHE:CE1	2.53	0.43
14:P:353:ARG:HH21	14:P:385:HIS:HB3	1.83	0.43
14:P:379:VAL:CG2	14:P:391:LEU:HB2	2.48	0.43
14:P:393:VAL:HA	14:P:404:LEU:O	2.18	0.43
15:Q:246:LYS:O	15:Q:250:VAL:HG23	2.18	0.43
18:T:264:PHE:CE1	18:T:268:TYR:HD2	2.37	0.43
18:T:354:MET:SD	30:t:100:SER:HB3	2.59	0.43
19:U:222:GLU:HG3	19:U:222:GLU:O	2.18	0.43
21:W:17:ASP:OD2	23:Y:60:LYS:C	2.62	0.43
21:W:129:LEU:HD13	21:W:154:LEU:HD11	1.99	0.43
23:Y:28:ASN:OD1	23:Y:29:THR:N	2.52	0.43
25:b:51:GLU:HA	25:b:78:GLU:O	2.18	0.43
30:h:18:GLU:OE1	30:h:94:GLN:NE2	2.45	0.43
2:2:1146:G:H2'	2:2:1147:A:H8	1.84	0.43
6:D:449:MET:O	6:D:452:ARG:N	2.52	0.43
7:E:41:SER:OG	7:E:42:ALA:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:328:LEU:HD22	9:G:190:VAL:HG21	2.01	0.43
7:E:336:MET:HG3	9:G:192:PHE:HZ	1.82	0.43
9:G:89:LEU:HD22	9:G:98:LEU:HD11	2.01	0.43
13:O:591:ASP:OD1	13:O:592:ILE:HD12	2.19	0.43
14:P:885:TRP:CZ3	14:P:1357:ARG:HD3	2.54	0.43
14:P:1041:LEU:O	14:P:1051:LEU:HD12	2.19	0.43
14:P:1124:LEU:HB2	14:P:1128:THR:HG23	2.00	0.43
17:S:43:VAL:HG12	17:S:72:TYR:CE1	2.54	0.43
21:W:8:VAL:HA	21:W:25:VAL:CB	2.49	0.43
21:W:11:ALA:HB2	21:W:26:ASP:CB	2.48	0.43
21:W:23:TYR:H	21:W:33:ASP:CB	2.32	0.43
21:W:115:GLN:O	21:W:118:ARG:HG2	2.18	0.43
23:Y:28:ASN:HD22	23:Y:111:LEU:HD13	1.83	0.43
2:2:1115:G:N7	26:v:77:LEU:HD12	2.26	0.43
2:2:1138:G:C6	2:2:1139:G:O6	2.71	0.43
6:D:354:THR:HB	6:D:358:TYR:CE2	2.54	0.43
8:F:443:ILE:HG23	8:F:444:LEU:HG	2.01	0.43
13:O:775:ARG:HA	13:O:778:ARG:HE	1.84	0.43
15:Q:277:PHE:O	15:Q:280:THR:OG1	2.18	0.43
18:T:21:ILE:O	18:T:25:ILE:HG13	2.18	0.43
20:V:195:ILE:HD11	20:V:197:TRP:CH2	2.54	0.43
21:W:8:VAL:HA	21:W:25:VAL:CG2	2.48	0.43
21:W:11:ALA:HA	21:W:26:ASP:HB3	2.01	0.43
21:W:125:LYS:HG3	21:W:126:ASN:N	2.34	0.43
30:t:99:ASP:HA	31:u:93:LYS:HG3	2.00	0.43
26:v:65:ARG:NH1	29:y:66:ASN:C	2.77	0.43
28:x:29:VAL:HG22	28:x:81:ILE:HG13	2.00	0.43
1:1:46:C:H2'	1:1:47:A:C8	2.54	0.43
1:1:272:A:H2'	1:1:273:G:H8	1.83	0.43
2:2:57:A:C6	15:Q:177:GLN:HB2	2.53	0.43
2:2:140:G:H2'	2:2:141:A:H8	1.83	0.43
2:2:1094:G:H2'	2:2:1095:U:H6	1.83	0.43
13:O:253:ASP:OD1	13:O:254:GLU:N	2.49	0.43
21:W:66:MET:HG3	21:W:88:GLU:C	2.44	0.43
1:1:72:G:H2'	1:1:73:A:C8	2.54	0.43
1:1:564:A:H62	4:B:36:GLN:HB2	1.84	0.43
2:2:119:G:C8	27:w:32:PHE:CD2	3.07	0.43
4:B:18:PRO:HG2	26:d:18:ILE:HB	2.01	0.43
7:E:483:CYS:SG	7:E:504:LYS:NZ	2.92	0.43
7:E:517:VAL:O	7:E:521:LEU:CB	2.67	0.43
13:O:349:LEU:HD21	13:O:385:SER:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:197:PRO:HG2	14:P:244:ASP:HB3	2.01	0.43
14:P:547:ASN:ND2	14:P:564:ASP:HB2	2.34	0.43
14:P:1124:LEU:HD13	15:Q:364:PHE:CD2	2.53	0.43
21:W:4:THR:HG22	21:W:7:ILE:HD13	2.00	0.43
21:W:5:PRO:O	21:W:8:VAL:N	2.52	0.43
21:W:16:VAL:HG13	23:Y:49:PHE:CZ	2.54	0.43
23:Y:80:ASP:OD1	23:Y:81:GLN:N	2.52	0.43
29:g:13:LYS:HB3	29:g:75:ASP:HB3	2.01	0.43
29:g:19:ILE:HD11	29:g:63:ILE:HD13	2.01	0.43
30:h:7:LEU:HD21	30:h:36:MET:HE3	2.00	0.43
25:s:86:ILE:CG2	26:v:72:ILE:HG22	2.45	0.43
27:w:46:PHE:O	28:x:14:ASN:ND2	2.51	0.43
1:1:163:G:H2'	1:1:164:U:C6	2.54	0.42
2:2:1143:C:H4'	2:2:1144:U:H3'	2.01	0.42
6:D:502:THR:HG21	8:F:368:MET:HE1	2.01	0.42
14:P:453:ASN:HA	14:P:464:LEU:HD11	2.01	0.42
14:P:597:HIS:ND1	14:P:597:HIS:O	2.52	0.42
15:Q:294:ILE:O	15:Q:343:ASP:HB2	2.19	0.42
21:W:23:TYR:H	21:W:33:ASP:HB3	1.84	0.42
23:Y:78:THR:O	23:Y:81:GLN:HG2	2.19	0.42
27:e:30:TRP:CE3	27:e:89:LEU:HD22	2.54	0.42
29:g:30:ARG:HE	29:g:41:ASP:HB2	1.84	0.42
26:v:40:MET:O	26:v:42:VAL:HG13	2.18	0.42
2:2:1108:A:C2	23:Y:73:PHE:CD1	3.08	0.42
8:F:329:LEU:HD12	8:F:344:ILE:HD11	2.01	0.42
13:O:674:ASP:O	13:O:678:LEU:HG	2.20	0.42
13:O:842:LEU:HA	13:O:845:ALA:HB3	2.01	0.42
13:O:950:VAL:HA	13:O:953:TYR:CE2	2.54	0.42
14:P:776:SER:O	14:P:821:CYS:HA	2.18	0.42
14:P:1056:LYS:C	14:P:1058:GLN:H	2.28	0.42
18:T:33:TYR:O	18:T:34:HIS:C	2.62	0.42
21:W:52:LYS:O	21:W:54:THR:N	2.52	0.42
21:W:59:LEU:HD21	21:W:64:LEU:HD22	2.00	0.42
21:W:66:MET:C	21:W:68:PRO:HD3	2.45	0.42
21:W:146:ARG:HB2	21:W:167:ALA:HB1	2.01	0.42
30:t:30:GLN:NE2	30:t:84:TYR:HE1	2.17	0.42
30:t:33:SER:HB3	30:t:37:ASN:HB2	2.00	0.42
31:u:105:LEU:HD12	28:x:70:GLU:O	2.18	0.42
2:2:1148:U:H2'	2:2:1149:G:H8	1.83	0.42
7:E:20:VAL:HG22	7:E:29:TYR:HB3	2.02	0.42
7:E:179:PHE:HB2	7:E:183:TYR:HE2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:306:HIS:ND1	8:F:382:TRP:O	2.52	0.42
8:F:412:GLN:HG2	8:F:413:PRO:HD2	2.01	0.42
13:O:305:ALA:HB2	13:O:313:LEU:HD22	2.00	0.42
13:O:338:GLN:HG3	13:O:377:THR:HG22	2.00	0.42
13:O:849:ARG:O	13:O:854:ARG:NH1	2.52	0.42
14:P:178:PRO:O	14:P:179:LEU:HD12	2.19	0.42
14:P:770:LEU:HD13	14:P:827:TRP:CD1	2.54	0.42
21:W:4:THR:HG22	21:W:7:ILE:CD1	2.50	0.42
23:Y:61:VAL:HG23	23:Y:62:SER:OG	2.18	0.42
26:v:65:ARG:NE	26:v:67:SER:HB3	2.28	0.42
27:w:16:CYS:SG	29:y:60:GLN:NE2	2.75	0.42
8:F:445:ASN:HD22	8:F:446:TYR:N	2.18	0.42
13:O:327:TRP:HE1	13:O:367:HIS:HB3	1.84	0.42
14:P:522:LEU:C	14:P:523:ILE:HG13	2.44	0.42
14:P:528:PRO:HG2	14:P:554:PHE:HZ	1.85	0.42
18:T:319:TYR:CZ	18:T:323:ARG:HD2	2.54	0.42
21:W:117:LEU:HD13	21:W:127:LEU:HD21	2.00	0.42
27:e:83:LYS:HA	27:e:83:LYS:HD3	1.75	0.42
30:t:46:THR:OG1	30:t:79:ILE:HG12	2.19	0.42
31:u:26:PHE:CE1	31:u:31:MET:HB3	2.54	0.42
4:B:6:SER:OG	4:B:7:LYS:N	2.42	0.42
4:B:175:GLN:HE21	4:B:178:ASP:HA	1.85	0.42
5:C:105:LEU:HA	5:C:108:LEU:HB2	2.02	0.42
5:C:181:SER:HA	5:C:184:SER:HB2	2.02	0.42
6:D:616:ILE:HG22	6:D:618:ASP:H	1.84	0.42
7:E:31:GLU:O	7:E:34:LEU:HB3	2.20	0.42
7:E:411:GLN:O	7:E:413:ASN:N	2.52	0.42
13:O:177:ASN:OD1	13:O:178:THR:N	2.52	0.42
13:O:386:TYR:O	13:O:388:TYR:N	2.52	0.42
13:O:927:ALA:C	13:O:929:ASN:N	2.77	0.42
14:P:1135:TYR:HB3	14:P:1311:TYR:CE2	2.54	0.42
15:Q:285:MET:HE3	15:Q:285:MET:HB2	1.90	0.42
16:R:76:LEU:HB2	16:R:81:ILE:HD11	1.99	0.42
16:R:108:ALA:HA	16:R:194:TYR:OH	2.18	0.42
16:R:113:LYS:HB3	16:R:179:THR:OG1	2.18	0.42
18:T:132:LEU:H	18:T:132:LEU:CD2	2.31	0.42
18:T:203:PHE:O	18:T:206:ILE:HB	2.18	0.42
21:W:24:ASN:CG	21:W:34:LEU:HB3	2.45	0.42
28:x:82:ARG:HG3	28:x:84:LEU:CD1	2.50	0.42
1:1:172:C:H2'	1:1:173:G:H8	1.85	0.42
6:D:525:TYR:O	6:D:529:ILE:N	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:363:LEU:HD23	9:G:75:ARG:HH11	1.84	0.42
9:G:69:LEU:H	9:G:224:PHE:HE2	1.67	0.42
13:O:294:ARG:HB3	13:O:332:THR:CG2	2.49	0.42
13:O:294:ARG:NE	13:O:328:LYS:HD3	2.34	0.42
13:O:331:HIS:CE1	13:O:335:LYS:HD2	2.54	0.42
13:O:724:TRP:HA	13:O:727:ILE:HD12	2.01	0.42
13:O:963:TYR:CG	13:O:964:ILE:N	2.87	0.42
14:P:291:SER:HB3	14:P:332:GLU:OE1	2.19	0.42
14:P:1098:ILE:CD1	14:P:1151:MET:HE2	2.49	0.42
14:P:1201:ASP:HB3	14:P:1203:HIS:HE1	1.84	0.42
14:P:1240:MET:HE2	14:P:1352:THR:HG22	2.01	0.42
15:Q:271:TYR:CZ	15:Q:274:ARG:HB2	2.54	0.42
21:W:7:ILE:HA	21:W:27:LYS:N	2.30	0.42
26:d:10:LEU:HD21	26:d:74:VAL:HG21	2.02	0.42
25:s:21:ARG:HB3	25:s:96:VAL:CG2	2.49	0.42
29:y:18:ASN:O	29:y:69:ILE:HB	2.20	0.42
1:1:14:G:H2'	1:1:15:A:H8	1.85	0.42
1:1:86:A:N6	9:G:227:CYS:HA	2.35	0.42
1:1:544:G:H2'	1:1:545:A:H8	1.85	0.42
2:2:60:A:H3'	2:2:61:A:H8	1.84	0.42
2:2:141:A:H2'	2:2:142:C:H6	1.78	0.42
2:2:1097:G:C4	2:2:1146:G:C2	3.07	0.42
2:2:1153:C:H2'	2:2:1154:U:H6	1.84	0.42
4:B:41:ILE:HD12	28:f:33:PHE:HD2	1.85	0.42
7:E:36:TYR:O	7:E:40:ALA:HB3	2.20	0.42
7:E:455:PHE:O	7:E:459:ASN:N	2.44	0.42
8:F:437:MET:SD	9:G:267:ILE:HG12	2.59	0.42
13:O:319:ALA:O	13:O:323:SER:HB2	2.19	0.42
14:P:97:THR:O	14:P:97:THR:OG1	2.28	0.42
14:P:1234:LYS:O	14:P:1237:VAL:HG12	2.20	0.42
19:U:213:LEU:C	19:U:215:PRO:HD2	2.45	0.42
23:Y:41:MET:SD	23:Y:68:GLN:NE2	2.93	0.42
31:i:49:ARG:HA	31:i:102:ILE:HD11	2.01	0.42
31:i:62:ASP:OD1	31:i:63:ARG:N	2.53	0.42
1:1:255:U:O2'	1:1:258:U:O2	2.34	0.42
5:C:17:THR:HG22	5:C:20:VAL:HG22	2.02	0.42
13:O:173:ILE:HG12	13:O:185:MET:SD	2.60	0.42
13:O:419:VAL:O	13:O:423:ILE:HG12	2.19	0.42
13:O:493:ALA:HA	13:O:499:ASN:OD1	2.20	0.42
13:O:519:ILE:HG21	13:O:561:LEU:HD12	2.00	0.42
14:P:333:ASN:O	14:P:350:ILE:HG22	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:385:HIS:CE1	24:Z:60:LEU:HD13	2.55	0.42
14:P:542:THR:HG22	14:P:615:LYS:NZ	2.35	0.42
14:P:590:HIS:CD2	14:P:591:THR:H	2.38	0.42
14:P:693:ILE:HG23	14:P:701:LYS:HB2	2.02	0.42
16:R:12:TYR:HB3	16:R:84:ARG:O	2.20	0.42
16:R:136:ARG:HB2	16:R:154:TYR:CD2	2.45	0.42
18:T:359:GLN:OE1	18:T:359:GLN:HA	2.20	0.42
25:b:96:VAL:HG11	30:h:82:LEU:HD23	2.02	0.42
30:h:78:ASN:N	30:h:78:ASN:OD1	2.51	0.42
31:i:46:ILE:HG23	31:i:101:VAL:HG13	2.01	0.42
30:t:4:VAL:HG11	30:t:34:PRO:O	2.20	0.42
1:1:5:PSU:O2'	10:H:207:TYR:O	2.37	0.42
1:1:559:G:N7	31:i:49:ARG:HD3	2.34	0.42
13:O:842:LEU:HB3	13:O:846:LEU:HD13	2.02	0.42
14:P:153:ASP:OD1	14:P:183:THR:N	2.52	0.42
14:P:667:THR:O	14:P:668:THR:OG1	2.34	0.42
14:P:1002:ARG:NH2	14:P:1004:LEU:HD11	2.35	0.42
16:R:135:ILE:HB	16:R:156:GLU:HG2	2.02	0.42
18:T:88:GLU:O	18:T:92:THR:HG23	2.20	0.42
20:V:221:LEU:HA	20:V:224:MET:HB3	2.02	0.42
20:V:226:LEU:O	20:V:227:ARG:HD3	2.20	0.42
21:W:16:VAL:CG2	21:W:20:ASN:HB2	2.49	0.42
21:W:81:LEU:HD11	21:W:86:ILE:HG12	2.01	0.42
24:Z:57:ARG:HH12	24:Z:68:HIS:CD2	2.38	0.42
25:b:21:ARG:NH2	30:h:68:LEU:O	2.50	0.42
30:h:67:TYR:HD1	30:h:72:GLN:HG2	1.85	0.42
31:u:76:TRP:CZ3	31:u:89:ARG:HG2	2.54	0.42
31:u:76:TRP:HZ3	31:u:89:ARG:HG2	1.85	0.42
26:v:63:PHE:O	29:y:71:LEU:HG	2.20	0.42
2:2:44:PSU:H2'	2:2:45:U:H6	1.84	0.42
5:C:3:ARG:HD3	26:d:94:PRO:HD2	2.01	0.42
11:I:59:C:H2'	11:I:60:U:C6	2.55	0.42
11:I:75:A:H2'	11:I:76:U:C6	2.55	0.42
13:O:875:ASP:OD1	13:O:876:ALA:N	2.53	0.42
14:P:211:LYS:HB2	14:P:230:ILE:HG13	2.01	0.42
14:P:369:ILE:HD13	14:P:421:ILE:CD1	2.50	0.42
14:P:832:TRP:CD1	14:P:833:LYS:H	2.38	0.42
14:P:1213:ARG:HD2	14:P:1360:TYR:CD1	2.54	0.42
14:P:1213:ARG:HH21	14:P:1232:LEU:HB2	1.84	0.42
18:T:58:LYS:HB3	18:T:63:LYS:HA	2.02	0.42
18:T:192:VAL:HG13	18:T:228:ARG:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:U:205:PRO:HG2	19:U:206:PHE:CD1	2.55	0.42
24:Z:23:ASP:OD1	24:Z:24:GLU:N	2.50	0.42
26:d:44:LEU:HB2	26:d:62:ILE:HG22	2.02	0.42
29:g:30:ARG:HB2	29:g:39:VAL:HG12	2.02	0.42
31:u:74:GLU:HG3	31:u:76:TRP:HZ3	1.84	0.42
27:w:30:TRP:N	27:w:30:TRP:CD1	2.87	0.42
29:y:56:GLN:NE2	29:y:60:GLN:O	2.53	0.42
2:2:1097:G:N1	2:2:1146:G:C5	2.88	0.41
2:2:1098:C:O5'	2:2:1098:C:C6	2.69	0.41
2:2:1106:G:N2	23:Y:69:ARG:HD3	2.35	0.41
6:D:409:ASN:HD21	6:D:415:ILE:HA	1.85	0.41
7:E:361:TYR:HA	7:E:364:LEU:HD12	2.02	0.41
8:F:316:PHE:CE1	8:F:350:CYS:HB2	2.55	0.41
8:F:340:VAL:N	8:F:354:GLN:O	2.42	0.41
13:O:299:ARG:HG2	13:O:339:GLN:HG2	2.02	0.41
13:O:433:TYR:O	13:O:437:GLU:HG2	2.20	0.41
16:R:200:ARG:CB	18:T:453:LEU:HA	2.49	0.41
23:Y:37:GLU:HB3	23:Y:69:ARG:HA	2.00	0.41
30:t:3:LEU:O	30:t:6:PHE:HB3	2.20	0.41
2:2:46:C:N4	11:I:58:U:O4	2.53	0.41
2:2:1098:C:C4'	21:W:158:ASN:HD22	2.32	0.41
7:E:279:TRP:O	7:E:283:LEU:HG	2.20	0.41
8:F:330:ARG:HB2	8:F:342:VAL:HG11	2.02	0.41
10:H:12:ARG:HH12	28:f:16:LYS:NZ	2.18	0.41
11:I:52:U:H2'	11:I:53:U:C6	2.55	0.41
11:I:73:A:C5	13:O:738:THR:HB	2.55	0.41
13:O:748:ALA:HA	13:O:787:ILE:HD13	2.01	0.41
14:P:504:HIS:CD2	14:P:511:ILE:HD11	2.55	0.41
14:P:1093:SER:OG	14:P:1116:ARG:N	2.53	0.41
14:P:1247:MET:HE1	14:P:1329:LEU:HD11	2.02	0.41
15:Q:193:PRO:HD3	19:U:44:PHE:CG	2.55	0.41
19:U:178:PRO:O	19:U:179:LEU:HD23	2.19	0.41
21:W:14:TYR:CD2	21:W:34:LEU:HD21	2.55	0.41
21:W:31:LEU:HD12	21:W:31:LEU:N	2.35	0.41
30:h:82:LEU:HD22	30:h:85:ILE:HD11	2.02	0.41
1:1:30:A:H2	4:B:137:ARG:HD2	1.85	0.41
2:2:117:U:O2'	31:u:99:ASP:OD1	2.28	0.41
2:2:1108:A:N1	23:Y:73:PHE:CD2	2.88	0.41
7:E:126:LEU:HD13	7:E:130:TYR:HE2	1.84	0.41
13:O:451:ASP:OD1	13:O:498:LEU:HD12	2.21	0.41
13:O:701:GLU:OE1	13:O:701:GLU:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:767:LEU:HD11	13:O:800:VAL:HG12	2.01	0.41
13:O:964:ILE:HB	13:O:967:LEU:HD13	2.01	0.41
17:S:9:ILE:HG22	17:S:91:ASN:OD1	2.19	0.41
18:T:40:SER:HA	18:T:46:THR:OG1	2.20	0.41
18:T:81:ILE:CD1	18:T:161:ALA:HB2	2.50	0.41
18:T:233:LEU:HD12	18:T:233:LEU:HA	1.82	0.41
18:T:418:ASP:HA	18:T:432:ASN:HB2	2.03	0.41
19:U:214:PRO:N	19:U:215:PRO:CD	2.83	0.41
21:W:128:THR:HG21	23:Y:50:LEU:HD21	2.02	0.41
31:u:44:VAL:C	31:u:55:ILE:HD12	2.45	0.41
27:w:86:ASN:HD21	28:x:79:LEU:HA	1.85	0.41
2:2:83:U:H2'	2:2:84:C:C6	2.56	0.41
2:2:1108:A:C2	23:Y:73:PHE:CE2	3.08	0.41
2:2:1125:U:O2'	2:2:1126:G:H8	2.00	0.41
7:E:18:LEU:HD22	12:J:38:ARG:HB2	2.01	0.41
9:G:189:GLU:HG2	9:G:201:PHE:CE1	2.55	0.41
13:O:382:ALA:HB3	13:O:421:SER:HB2	2.02	0.41
13:O:515:CYS:HB2	13:O:548:LEU:HD13	2.03	0.41
13:O:674:ASP:OD1	13:O:675:LEU:N	2.54	0.41
13:O:793:GLY:HA2	13:O:794:PRO:HD3	1.88	0.41
13:O:927:ALA:O	13:O:929:ASN:N	2.52	0.41
14:P:76:ILE:HD11	14:P:422:PHE:HD1	1.84	0.41
14:P:332:GLU:OE1	14:P:332:GLU:N	2.34	0.41
21:W:13:GLN:CB	21:W:24:ASN:H	2.32	0.41
26:d:23:LEU:N	26:d:27:ALA:O	2.46	0.41
26:v:30:ARG:O	26:v:47:VAL:HA	2.21	0.41
1:1:48:A:H2'	1:1:49:A:H8	1.85	0.41
1:1:545:A:H2'	1:1:546:U:C6	2.56	0.41
6:D:526:GLU:HB3	9:G:155:ILE:HG21	2.03	0.41
7:E:107:LEU:HA	7:E:107:LEU:HD12	1.72	0.41
7:E:453:VAL:O	7:E:457:GLU:HB2	2.20	0.41
8:F:333:PHE:HD2	8:F:353:VAL:HG11	1.86	0.41
11:I:60:U:H2'	11:I:61:U:C6	2.56	0.41
13:O:916:MET:O	13:O:917:ASN:C	2.63	0.41
14:P:69:THR:OG1	14:P:484:LEU:O	2.39	0.41
14:P:89:GLU:HG3	14:P:91:SER:H	1.85	0.41
14:P:1112:ASP:O	14:P:1186:LYS:NZ	2.32	0.41
18:T:69:ARG:O	18:T:73:ILE:HG12	2.20	0.41
19:U:219:LEU:HD12	19:U:219:LEU:O	2.20	0.41
21:W:73:ARG:HE	21:W:76:ILE:HG21	1.85	0.41
23:Y:50:LEU:C	23:Y:50:LEU:HD23	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Y:76:MET:HB3	23:Y:81:GLN:NE2	2.35	0.41
25:b:51:GLU:HB3	25:b:79:LYS:HG2	2.01	0.41
25:s:35:MET:HB2	25:s:44:VAL:HG23	2.02	0.41
26:v:44:LEU:HB3	26:v:62:ILE:HG23	2.01	0.41
2:2:30:A:H2'	2:2:31:A:C8	2.56	0.41
7:E:142:PHE:HD2	7:E:301:ARG:HH12	1.68	0.41
7:E:275:GLU:HG3	7:E:279:TRP:HE1	1.86	0.41
12:J:31:ILE:HD13	12:J:31:ILE:HG21	1.79	0.41
13:O:330:ARG:O	13:O:334:ILE:HG13	2.21	0.41
13:O:600:PRO:O	13:O:603:SER:OG	2.21	0.41
14:P:76:ILE:HD13	14:P:420:HIS:HB3	2.01	0.41
14:P:642:LEU:HB3	14:P:654:PHE:HB2	2.02	0.41
14:P:643:ILE:HG21	14:P:691:LEU:HD11	2.02	0.41
14:P:748:GLY:HA2	14:P:775:VAL:HG13	2.02	0.41
14:P:1006:TYR:CD1	14:P:1021:LEU:HA	2.53	0.41
18:T:53:LEU:HD23	18:T:58:LYS:HE3	2.03	0.41
19:U:178:PRO:HB3	19:U:203:TYR:HD2	1.84	0.41
25:b:8:HIS:CD2	30:h:41:THR:HG21	2.56	0.41
25:b:86:ILE:HD13	25:b:86:ILE:HG21	1.82	0.41
29:g:43:ALA:HB3	29:g:57:LEU:HB2	2.02	0.41
25:s:16:ILE:HD11	25:s:35:MET:O	2.21	0.41
5:C:4:TYR:HD2	5:C:13:LEU:HD13	1.86	0.41
6:D:534:THR:HB	6:D:535:PHE:H	1.58	0.41
7:E:327:LEU:HD21	7:E:357:LYS:HD3	2.02	0.41
14:P:832:TRP:CG	14:P:833:LYS:N	2.88	0.41
18:T:48:LEU:HD12	18:T:48:LEU:O	2.21	0.41
18:T:202:GLN:O	18:T:206:ILE:HG13	2.20	0.41
19:U:208:ASN:HB2	20:V:199:LYS:O	2.20	0.41
21:W:33:ASP:OD1	21:W:33:ASP:N	2.52	0.41
27:e:90:ILE:O	29:g:61:THR:OG1	2.30	0.41
29:g:30:ARG:N	29:g:39:VAL:O	2.48	0.41
30:t:16:THR:OG1	30:t:96:ILE:HB	2.21	0.41
28:x:33:PHE:N	28:x:33:PHE:CD1	2.88	0.41
6:D:514:THR:HG22	7:E:393:GLN:NE2	2.35	0.41
9:G:75:ARG:HH22	9:G:243:TYR:HD2	1.68	0.41
13:O:695:ASN:HD22	13:O:700:VAL:HG21	1.85	0.41
13:O:797:VAL:HG12	13:O:801:ILE:CD1	2.51	0.41
14:P:60:LEU:HD22	14:P:1228:PHE:HB3	2.03	0.41
14:P:365:ILE:HG23	14:P:382:GLN:O	2.21	0.41
14:P:472:LEU:HD13	14:P:919:LEU:H	1.85	0.41
14:P:929:ILE:HG12	14:P:941:PHE:HD1	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:Q:159:LEU:O	15:Q:162:SER:OG	2.38	0.41
16:R:17:ASP:N	16:R:79:ARG:HD2	2.36	0.41
18:T:36:ILE:HD12	18:T:36:ILE:HA	1.86	0.41
18:T:149:ASP:N	18:T:150:PRO:HD2	2.35	0.41
18:T:230:MET:HA	18:T:314:PHE:CE1	2.55	0.41
25:b:46:ASN:OD1	25:b:47:GLU:N	2.53	0.41
26:d:75:PRO:HG2	26:d:78:LEU:HD13	2.01	0.41
30:t:19:LEU:C	30:t:93:ARG:HB2	2.46	0.41
1:1:75:G:H1	1:1:127:C:H42	1.69	0.41
1:1:247:G:H2'	1:1:248:G:C8	2.55	0.41
2:2:45:U:C2'	2:2:46:C:H5'	2.50	0.41
2:2:1139:G:C2'	2:2:1140:U:H6	2.34	0.41
4:B:130:PHE:HZ	4:B:170:VAL:HG11	1.85	0.41
4:B:133:ILE:HA	4:B:155:PHE:HA	2.03	0.41
6:D:351:PHE:O	6:D:354:THR:OG1	2.32	0.41
6:D:509:LEU:HB3	6:D:541:PRO:HB3	2.03	0.41
7:E:36:TYR:O	7:E:40:ALA:CB	2.69	0.41
7:E:283:LEU:HD22	7:E:299:PHE:CD1	2.54	0.41
7:E:375:TYR:HD2	7:E:379:VAL:HG12	1.86	0.41
7:E:427:ARG:HD2	7:E:427:ARG:HA	1.88	0.41
8:F:506:THR:HG23	8:F:509:MET:HE2	2.03	0.41
9:G:112:LEU:HD23	9:G:112:LEU:HA	1.83	0.41
13:O:314:LEU:N	13:O:315:PRO:HD2	2.36	0.41
13:O:371:ARG:O	13:O:374:THR:OG1	2.38	0.41
13:O:693:LEU:HD12	13:O:730:GLU:OE1	2.21	0.41
13:O:700:VAL:O	13:O:704:THR:CB	2.69	0.41
13:O:947:ASP:OD2	14:P:1310:TYR:OH	2.29	0.41
14:P:414:GLN:NE2	14:P:437:PHE:HE2	2.18	0.41
14:P:528:PRO:HG2	14:P:554:PHE:CZ	2.56	0.41
14:P:582:LYS:O	14:P:608:ARG:NH2	2.53	0.41
14:P:950:GLN:HE21	14:P:973:ILE:CG2	2.34	0.41
14:P:1046:GLY:O	14:P:1073:LYS:HA	2.21	0.41
14:P:1073:LYS:HD2	14:P:1090:ILE:HD12	2.03	0.41
14:P:1307:TYR:O	14:P:1310:TYR:HB2	2.21	0.41
17:S:6:PHE:O	24:Z:6:ARG:NH2	2.54	0.41
17:S:39:PRO:HA	17:S:73:CYS:HA	2.03	0.41
20:V:140:ALA:O	20:V:143:LYS:HB2	2.21	0.41
21:W:16:VAL:HG22	21:W:22:LYS:HZ1	1.86	0.41
24:Z:20:GLY:HA3	24:Z:34:ASN:ND2	2.35	0.41
27:e:27:VAL:O	27:e:40:LYS:HA	2.21	0.41
25:s:26:ASP:OD2	26:v:70:LYS:HE2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:t:26:TRP:HB3	30:t:44:LYS:HG2	2.02	0.41
31:u:76:TRP:CE2	31:u:87:ARG:HB2	2.56	0.41
26:v:41:ASN:HB3	26:v:63:PHE:CZ	2.56	0.41
27:w:30:TRP:CD2	27:w:89:LEU:HD22	2.55	0.41
1:1:4:C:H2'	1:1:5:PSU:H6	1.86	0.41
2:2:67:A:O2'	2:2:68:U:C6	2.65	0.41
6:D:391:GLU:O	6:D:395:LYS:HB2	2.21	0.41
6:D:571:ALA:HB3	6:D:580:ARG:HH22	1.86	0.41
6:D:587:ILE:H	6:D:587:ILE:HG13	1.74	0.41
7:E:30:TRP:CZ2	7:E:63:MET:HB2	2.55	0.41
7:E:70:LEU:HD13	7:E:73:TYR:CD2	2.51	0.41
7:E:464:ILE:O	7:E:468:GLY:N	2.54	0.41
13:O:385:SER:O	13:O:386:TYR:HB3	2.21	0.41
13:O:524:THR:N	13:O:525:PRO:HD2	2.36	0.41
13:O:925:HIS:HA	15:Q:160:LEU:HD11	2.03	0.41
14:P:593:LEU:HG	14:P:598:SER:O	2.21	0.41
14:P:816:MET:HE3	14:P:831:THR:O	2.21	0.41
14:P:859:ILE:O	14:P:860:ASN:HB2	2.21	0.41
15:Q:284:ARG:O	15:Q:287:ASP:HB2	2.20	0.41
15:Q:363:TYR:O	15:Q:365:GLY:N	2.53	0.41
17:S:58:CYS:HB3	17:S:61:CYS:SG	2.61	0.41
20:V:135:PHE:O	20:V:139:VAL:HG22	2.21	0.41
20:V:157:LYS:O	20:V:158:ARG:C	2.65	0.41
26:d:22:GLU:HB3	26:d:70:LYS:HB3	2.03	0.41
30:t:94:GLN:HB3	31:u:96:LEU:HD12	2.03	0.41
31:u:38:MET:SD	31:u:61:PHE:CE2	3.13	0.41
1:1:248:G:H2'	1:1:249:G:H8	1.86	0.40
2:2:41:C:H4'	19:U:75:HIS:CE1	2.56	0.40
2:2:1118:U:H2'	2:2:1119:C:H6	1.86	0.40
2:2:1168:U:H2'	2:2:1169:C:C6	2.56	0.40
4:B:41:ILE:HG22	28:f:35:SER:HB2	2.04	0.40
8:F:311:ASN:HB3	8:F:407:GLN:HE21	1.86	0.40
14:P:353:ARG:HE	14:P:385:HIS:CB	2.35	0.40
14:P:504:HIS:HB3	14:P:509:LYS:H	1.86	0.40
14:P:672:LEU:C	14:P:674:THR:H	2.29	0.40
14:P:673:ASP:OD1	14:P:674:THR:HG23	2.20	0.40
14:P:764:ASP:OD2	14:P:766:LYS:HE2	2.22	0.40
14:P:766:LYS:HD3	14:P:836:TRP:CZ2	2.56	0.40
14:P:881:THR:HG23	14:P:884:ASN:H	1.86	0.40
14:P:978:ASP:O	14:P:998:ALA:HA	2.20	0.40
14:P:1113:SER:HA	14:P:1186:LYS:HE3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:R:10:THR:HA	16:R:56:GLU:HA	2.02	0.40
16:R:111:PHE:HE2	16:R:113:LYS:HE3	1.86	0.40
18:T:171:THR:HG21	18:T:181:GLU:CD	2.46	0.40
18:T:181:GLU:O	18:T:181:GLU:HG3	2.21	0.40
30:t:16:THR:HA	30:t:25:VAL:O	2.20	0.40
26:v:24:THR:HA	26:v:70:LYS:HE3	2.02	0.40
28:x:33:PHE:C	28:x:35:SER:N	2.79	0.40
5:C:75:VAL:HA	7:E:224:PRO:HB3	2.03	0.40
7:E:140:HIS:HB3	7:E:143:SER:HB2	2.02	0.40
8:F:418:ILE:HA	8:F:419:PRO:HD3	1.95	0.40
8:F:444:LEU:HD23	8:F:444:LEU:HA	1.92	0.40
13:O:493:ALA:HB2	13:O:533:PHE:HD1	1.86	0.40
13:O:945:TYR:O	13:O:949:MET:HE2	2.21	0.40
14:P:54:LYS:HG2	15:Q:370:PHE:CE2	2.56	0.40
14:P:535:TRP:O	14:P:550:LEU:HD12	2.20	0.40
14:P:702:ILE:HB	14:P:762:PHE:CZ	2.57	0.40
14:P:783:ILE:HG22	14:P:815:TRP:HA	2.03	0.40
16:R:12:TYR:HD1	16:R:54:PHE:CE1	2.40	0.40
31:u:69:LEU:HD23	31:u:69:LEU:HA	1.95	0.40
28:x:36:THR:HG21	28:x:38:TYR:CZ	2.57	0.40
1:1:116:A:O2'	7:E:125:GLN:NE2	2.55	0.40
2:2:1092:A:H3'	2:2:1093:C:C6	2.47	0.40
6:D:587:ILE:HD11	7:E:170:LYS:HA	2.02	0.40
7:E:266:SER:O	7:E:268:GLU:N	2.55	0.40
11:I:76:U:O4	11:I:77:C:N4	2.54	0.40
13:O:222:ILE:HA	13:O:225:ILE:HD12	2.04	0.40
13:O:682:ILE:O	13:O:685:ILE:N	2.54	0.40
13:O:686:LEU:N	13:O:687:PRO:HD2	2.37	0.40
14:P:106:THR:C	14:P:108:ASP:N	2.78	0.40
14:P:594:MET:CE	14:P:642:LEU:HB2	2.51	0.40
18:T:116:LEU:HD11	18:T:120:GLU:OE2	2.20	0.40
18:T:367:ASP:C	18:T:369:THR:H	2.29	0.40
21:W:25:VAL:CB	21:W:31:LEU:HA	2.41	0.40
21:W:33:ASP:OD2	21:W:50:LEU:HG	2.20	0.40
25:b:18:TYR:CD1	25:b:101:PRO:HD3	2.57	0.40
27:e:21:LEU:HD13	27:e:43:ILE:HG22	2.02	0.40
27:e:57:ALA:HB3	27:e:77:LEU:HB2	2.02	0.40
30:h:114:ASN:O	30:h:118:ARG:N	2.52	0.40
25:s:89:GLY:HA2	25:s:92:ILE:HG22	2.02	0.40
1:1:545:A:H2'	1:1:546:U:H6	1.87	0.40
2:2:1161:U:H2'	2:2:1162:U:H6	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:108:THR:HA	4:B:153:ILE:O	2.20	0.40
6:D:420:HIS:O	6:D:424:LEU:HG	2.21	0.40
7:E:425:TRP:O	7:E:429:SER:N	2.48	0.40
8:F:510:LEU:HD23	8:F:510:LEU:HA	1.95	0.40
14:P:187:VAL:HG11	24:Z:18:TYR:HD1	1.87	0.40
14:P:515:ASN:OD1	14:P:839:ARG:NH2	2.55	0.40
14:P:633:VAL:HG23	14:P:647:SER:HA	2.03	0.40
14:P:670:PRO:O	14:P:672:LEU:HG	2.21	0.40
14:P:1058:GLN:HG2	18:T:514:ASN:HD22	1.87	0.40
14:P:1072:THR:HG22	14:P:1073:LYS:HG3	2.04	0.40
14:P:1139:TRP:CE3	14:P:1141:LEU:HG	2.56	0.40
18:T:152:ARG:HG3	18:T:153:ARG:HG3	2.02	0.40
19:U:84:HIS:CE1	19:U:90:HIS:HB2	2.56	0.40
21:W:108:ILE:HG22	21:W:132:ASN:OD1	2.22	0.40
23:Y:59:LEU:HD21	23:Y:110:THR:HG21	2.03	0.40
1:1:195:C:H2'	1:1:196:A:C8	2.55	0.40
2:2:116:U:OP1	25:s:90:GLU:HG3	2.21	0.40
2:2:1099:G:OP1	21:W:158:ASN:HB2	2.19	0.40
2:2:1150:U:O2	2:2:1150:U:H2'	2.22	0.40
9:G:69:LEU:HD22	9:G:164:PRO:HG3	2.02	0.40
13:O:264:GLU:HA	13:O:267:THR:HG22	2.03	0.40
13:O:373:VAL:O	13:O:377:THR:HG23	2.22	0.40
13:O:820:MET:HG2	13:O:824:PHE:CE2	2.56	0.40
14:P:185:ARG:O	14:P:188:SER:OG	2.37	0.40
14:P:421:ILE:HG22	14:P:422:PHE:O	2.21	0.40
14:P:823:SER:OG	14:P:824:SER:N	2.53	0.40
14:P:942:ILE:HG12	14:P:953:ILE:HG12	2.03	0.40
14:P:1007:LYS:O	14:P:1019:ILE:HA	2.21	0.40
15:Q:192:ARG:HH11	19:U:44:PHE:HB2	1.86	0.40
15:Q:367:LEU:HD12	15:Q:370:PHE:HE1	1.85	0.40
18:T:11:LEU:HD11	20:V:148:PHE:CZ	2.55	0.40
18:T:338:PHE:CZ	18:T:357:LEU:HD11	2.57	0.40
21:W:24:ASN:ND2	21:W:35:GLN:H	2.18	0.40
21:W:159:VAL:HG11	21:W:164:ARG:CZ	2.51	0.40
29:g:75:ASP:OD1	29:g:76:ALA:N	2.55	0.40
31:u:48:LEU:HD11	31:u:54:ILE:HD12	2.02	0.40
28:x:41:THR:HG23	28:x:55:GLU:OE2	2.22	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	
3	A	72/298 (24%)	59 (82%)	12 (17%)	1 (1%)	9	39
4	B	158/300 (53%)	135 (85%)	22 (14%)	1 (1%)	21	57
5	C	171/231 (74%)	152 (89%)	18 (10%)	1 (1%)	21	57
6	D	475/629 (76%)	435 (92%)	37 (8%)	3 (1%)	21	57
7	E	539/544 (99%)	482 (89%)	44 (8%)	13 (2%)	4	30
8	F	165/523 (32%)	142 (86%)	17 (10%)	6 (4%)	2	23
9	G	204/492 (42%)	186 (91%)	18 (9%)	0	100	100
10	H	94/261 (36%)	89 (95%)	5 (5%)	0	100	100
12	J	40/620 (6%)	34 (85%)	6 (15%)	0	100	100
13	O	829/971 (85%)	788 (95%)	41 (5%)	0	100	100
14	P	1170/1361 (86%)	1059 (90%)	104 (9%)	7 (1%)	21	57
15	Q	214/435 (49%)	202 (94%)	11 (5%)	1 (0%)	24	60
16	R	165/213 (78%)	162 (98%)	3 (2%)	0	100	100
17	S	101/107 (94%)	88 (87%)	13 (13%)	0	100	100
18	T	454/530 (86%)	416 (92%)	38 (8%)	0	100	100
19	U	168/266 (63%)	143 (85%)	24 (14%)	1 (1%)	21	57
20	V	123/280 (44%)	112 (91%)	11 (9%)	0	100	100
21	W	168/238 (71%)	129 (77%)	28 (17%)	11 (6%)	1	15
23	Y	82/111 (74%)	76 (93%)	5 (6%)	1 (1%)	10	42
24	Z	81/85 (95%)	76 (94%)	4 (5%)	1 (1%)	10	42
25	b	117/196 (60%)	108 (92%)	9 (8%)	0	100	100
25	s	61/196 (31%)	58 (95%)	3 (5%)	0	100	100
26	d	91/101 (90%)	87 (96%)	4 (4%)	0	100	100
26	v	80/101 (79%)	77 (96%)	3 (4%)	0	100	100
27	e	73/94 (78%)	68 (93%)	4 (6%)	1 (1%)	9	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	w	73/94 (78%)	72 (99%)	1 (1%)	0	100	100
28	f	71/86 (83%)	66 (93%)	5 (7%)	0	100	100
28	x	71/86 (83%)	69 (97%)	2 (3%)	0	100	100
29	g	68/77 (88%)	61 (90%)	6 (9%)	1 (2%)	8	38
29	y	73/77 (95%)	64 (88%)	6 (8%)	3 (4%)	2	21
30	h	101/146 (69%)	97 (96%)	4 (4%)	0	100	100
30	t	68/146 (47%)	67 (98%)	1 (2%)	0	100	100
31	i	95/110 (86%)	90 (95%)	5 (5%)	0	100	100
31	u	90/110 (82%)	89 (99%)	1 (1%)	0	100	100
All	All	6605/10115 (65%)	6038 (91%)	515 (8%)	52 (1%)	18	52

All (52) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	D	426	ASN
6	D	608	LEU
7	E	448	TYR
8	F	325	THR
8	F	385	SER
8	F	386	ALA
8	F	387	LYS
14	P	1299	ILE
15	Q	368	ILE
21	W	34	LEU
21	W	52	LYS
27	e	33	GLU
29	y	50	ASP
3	A	29	PRO
6	D	574	ILE
7	E	411	GLN
7	E	412	SER
7	E	449	SER
7	E	510	ASP
8	F	326	GLU
8	F	412	GLN
14	P	363	VAL
14	P	413	ILE
21	W	17	ASP
21	W	18	HIS

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Mol	Chain	Res	Type
21	W	51	THR
21	W	68	PRO
21	W	121	PRO
21	W	124	LEU
23	Y	71	GLN
4	B	44	VAL
5	C	122	ALA
7	E	377	ASP
7	E	512	LYS
7	E	513	PHE
7	E	530	PRO
21	W	29	VAL
29	g	21	GLY
7	E	447	PHE
14	P	107	ALA
21	W	12	PRO
24	Z	19	ILE
7	E	267	PRO
19	U	232	GLY
29	y	30	ARG
29	y	60	GLN
7	E	266	SER
14	P	364	THR
14	P	486	PRO
21	W	159	VAL
7	E	509	ILE
14	P	1031	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	B	136/236 (58%)	135 (99%)	1 (1%)	76	79
5	C	127/214 (59%)	127 (100%)	0	100	100
6	D	266/603 (44%)	265 (100%)	1 (0%)	84	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	E	515/519 (99%)	511 (99%)	4 (1%)	73	77
8	F	148/451 (33%)	146 (99%)	2 (1%)	59	71
9	G	175/448 (39%)	175 (100%)	0	100	100
10	H	84/183 (46%)	83 (99%)	1 (1%)	63	73
12	J	34/568 (6%)	34 (100%)	0	100	100
13	O	739/867 (85%)	739 (100%)	0	100	100
14	P	1093/1244 (88%)	1093 (100%)	0	100	100
15	Q	192/391 (49%)	192 (100%)	0	100	100
16	R	154/189 (82%)	154 (100%)	0	100	100
17	S	93/97 (96%)	93 (100%)	0	100	100
18	T	429/492 (87%)	420 (98%)	9 (2%)	47	65
19	U	158/216 (73%)	157 (99%)	1 (1%)	78	81
20	V	118/259 (46%)	116 (98%)	2 (2%)	53	68
21	W	161/219 (74%)	151 (94%)	10 (6%)	16	41
23	Y	76/100 (76%)	75 (99%)	1 (1%)	61	72
24	Z	75/77 (97%)	75 (100%)	0	100	100
25	b	108/176 (61%)	108 (100%)	0	100	100
25	s	58/176 (33%)	58 (100%)	0	100	100
26	d	81/89 (91%)	81 (100%)	0	100	100
26	v	71/89 (80%)	71 (100%)	0	100	100
27	e	68/83 (82%)	68 (100%)	0	100	100
27	w	69/83 (83%)	69 (100%)	0	100	100
28	f	65/77 (84%)	65 (100%)	0	100	100
28	x	65/77 (84%)	65 (100%)	0	100	100
29	g	62/66 (94%)	62 (100%)	0	100	100
29	y	64/66 (97%)	64 (100%)	0	100	100
30	h	96/129 (74%)	96 (100%)	0	100	100
30	t	67/129 (52%)	66 (98%)	1 (2%)	57	70
31	i	90/103 (87%)	90 (100%)	0	100	100
31	u	85/103 (82%)	85 (100%)	0	100	100
All	All	5822/8819 (66%)	5789 (99%)	33 (1%)	76	81

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	B	41	ILE
6	D	373	LEU
7	E	34	LEU
7	E	126	LEU
7	E	212	LEU
7	E	327	LEU
8	F	325	THR
8	F	410	LEU
10	H	39	LEU
18	T	27	ARG
18	T	65	VAL
18	T	81	ILE
18	T	92	THR
18	T	217	LEU
18	T	298	HIS
18	T	317	SER
18	T	357	LEU
18	T	358	THR
19	U	246	ILE
20	V	153	ILE
20	V	158	ARG
21	W	4	THR
21	W	8	VAL
21	W	30	ILE
21	W	31	LEU
21	W	33	ASP
21	W	34	LEU
21	W	36	LEU
21	W	50	LEU
21	W	64	LEU
21	W	160	THR
23	Y	61	VAL
30	t	82	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (137) such sidechains are listed below:

Mol	Chain	Res	Type
4	B	175	GLN
5	C	40	ASN
5	C	47	ASN
5	C	170	ASN

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Mol	Chain	Res	Type
6	D	343	ASN
6	D	413	ASN
6	D	447	ASN
6	D	488	ASN
6	D	519	HIS
6	D	582	GLN
6	D	612	ASN
7	E	19	ASN
7	E	51	GLN
7	E	72	ASN
7	E	122	HIS
7	E	125	GLN
7	E	177	HIS
7	E	188	GLN
7	E	245	GLN
7	E	262	ASN
7	E	296	HIS
7	E	298	ASN
7	E	300	GLN
7	E	378	ASN
7	E	381	ASN
7	E	393	GLN
7	E	417	ASN
7	E	442	ASN
7	E	480	ASN
8	F	407	GLN
8	F	411	GLN
8	F	412	GLN
8	F	445	ASN
9	G	202	GLN
9	G	217	ASN
9	G	240	ASN
10	H	72	HIS
10	H	76	HIS
13	O	141	HIS
13	O	318	ASN
13	O	376	HIS
13	O	539	HIS
13	O	695	ASN
13	O	703	ASN
13	O	769	ASN
13	O	853	HIS

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Mol	Chain	Res	Type
13	O	882	ASN
13	O	887	ASN
13	O	894	HIS
13	O	908	GLN
14	P	209	GLN
14	P	249	ASN
14	P	289	ASN
14	P	362	ASN
14	P	375	ASN
14	P	382	GLN
14	P	385	HIS
14	P	414	GLN
14	P	434	ASN
14	P	436	ASN
14	P	474	ASN
14	P	481	GLN
14	P	546	ASN
14	P	585	GLN
14	P	590	HIS
14	P	609	HIS
14	P	641	GLN
14	P	738	GLN
14	P	740	ASN
14	P	878	ASN
14	P	920	GLN
14	P	944	ASN
14	P	945	HIS
14	P	950	GLN
14	P	1023	HIS
14	P	1024	GLN
14	P	1032	HIS
14	P	1117	HIS
14	P	1203	HIS
14	P	1210	ASN
14	P	1332	ASN
14	P	1359	ASN
15	Q	136	GLN
15	Q	145	GLN
15	Q	288	HIS
15	Q	296	GLN
15	Q	352	HIS
16	R	31	GLN

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Mol	Chain	Res	Type
16	R	47	GLN
16	R	170	ASN
17	S	14	GLN
18	T	34	HIS
18	T	91	GLN
18	T	167	ASN
18	T	175	GLN
18	T	202	GLN
18	T	307	ASN
18	T	415	HIS
18	T	440	HIS
18	T	514	ASN
19	U	39	ASN
21	W	20	ASN
21	W	55	HIS
21	W	61	ASN
21	W	99	GLN
21	W	133	GLN
21	W	143	HIS
21	W	157	GLN
21	W	158	ASN
23	Y	28	ASN
23	Y	34	GLN
23	Y	47	ASN
24	Z	7	GLN
24	Z	37	ASN
24	Z	41	ASN
25	b	5	GLN
26	d	61	GLN
26	d	68	GLN
26	d	87	ASN
28	f	14	ASN
29	g	47	ASN
30	h	12	ASN
30	h	30	GLN
30	h	78	ASN
31	i	35	ASN
31	i	51	ASN
31	i	64	HIS
25	s	33	GLN
30	t	30	GLN
30	t	90	ASN

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Mol	Chain	Res	Type
30	t	94	GLN
31	u	51	ASN
31	u	52	HIS
27	w	15	ASN
28	x	77	ASN
29	y	20	ASN
29	y	54	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	281/407 (69%)	67 (23%)	12 (4%)
11	I	35/38 (92%)	8 (22%)	2 (5%)
2	2	136/143 (95%)	46 (33%)	25 (18%)
All	All	452/588 (76%)	121 (26%)	39 (8%)

All (121) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	8	C
1	1	11	U
1	1	12	A
1	1	17	A
1	1	21	G
1	1	22	A
1	1	25	A
1	1	26	G
1	1	27	A
1	1	30	A
1	1	33	A
1	1	35	G
1	1	39	U
1	1	40	A
1	1	41	C
1	1	53	G
1	1	55	G
1	1	56	C
1	1	57	U
1	1	61	A
1	1	68	G
1	1	69	A

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Mol	Chain	Res	Type
1	1	74	C
1	1	77	U
1	1	79	A
1	1	80	G
1	1	86	A
1	1	87	U
1	1	117	U
1	1	118	U
1	1	119	G
1	1	124	A
1	1	133	G
1	1	134	G
1	1	135	U
1	1	136	C
1	1	137	A
1	1	140	C
1	1	141	A
1	1	142	C
1	1	143	A
1	1	144	C
1	1	154	G
1	1	155	G
1	1	167	G
1	1	168	C
1	1	172	C
1	1	187	G
1	1	254	U
1	1	256	U
1	1	257	G
1	1	258	U
1	1	259	U
1	1	540	G
1	1	541	G
1	1	551	U
1	1	554	U
1	1	555	U
1	1	556	U
1	1	557	U
1	1	558	U
1	1	559	G
1	1	560	A
1	1	561	U

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Mol	Chain	Res	Type
1	1	562	U
1	1	563	U
1	1	564	A
2	2	33	U
2	2	41	C
2	2	46	C
2	2	47	U
2	2	66	A
2	2	67	A
2	2	68	U
2	2	83	U
2	2	111	C
2	2	112	A
2	2	113	U
2	2	117	U
2	2	140	G
2	2	141	A
2	2	142	C
2	2	1094	G
2	2	1095	U
2	2	1096	C
2	2	1097	G
2	2	1098	C
2	2	1100	A
2	2	1101	C
2	2	1102	C
2	2	1103	C
2	2	1104	U
2	2	1105	C
2	2	1106	G
2	2	1107	C
2	2	1108	A
2	2	1119	C
2	2	1120	G
2	2	1121	U
2	2	1122	U
2	2	1123	C
2	2	1124	U
2	2	1125	U
2	2	1126	G
2	2	1130	U
2	2	1139	G

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Mol	Chain	Res	Type
2	2	1141	C
2	2	1142	G
2	2	1143	C
2	2	1144	U
2	2	1145	U
2	2	1146	G
2	2	1149	G
11	I	58	U
11	I	62	A
11	I	70	A
11	I	71	C
11	I	72	A
11	I	74	A
11	I	78	A
11	I	79	A

All (39) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	16	U
1	1	21	G
1	1	39	U
1	1	54	C
1	1	67	A
1	1	76	U
1	1	86	A
1	1	134	G
1	1	135	U
1	1	136	C
1	1	553	A
1	1	560	A
2	2	32	G
2	2	46	C
2	2	66	A
2	2	67	A
2	2	110	A
2	2	1095	U
2	2	1096	C
2	2	1097	G
2	2	1100	A
2	2	1101	C
2	2	1102	C

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Mol	Chain	Res	Type
2	2	1105	C
2	2	1107	C
2	2	1119	C
2	2	1120	G
2	2	1121	U
2	2	1122	U
2	2	1123	C
2	2	1124	U
2	2	1125	U
2	2	1138	G
2	2	1141	C
2	2	1142	G
2	2	1144	U
2	2	1145	U
11	I	77	C
11	I	78	A

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

5 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PSU	2	42	2,11	18,21,22	1.13	1 (5%)	21,30,33	1.85	4 (19%)
1	PSU	1	6	11,1	18,21,22	1.40	2 (11%)	21,30,33	1.31	2 (9%)
1	PSU	1	5	1	18,21,22	1.51	2 (11%)	21,30,33	1.37	2 (9%)
2	PSU	2	44	2,11	18,21,22	1.07	1 (5%)	21,30,33	1.80	4 (19%)
2	PSU	2	35	2,11	18,21,22	1.10	1 (5%)	21,30,33	1.86	5 (23%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PSU	2	42	2,11	-	0/7/25/26	0/2/2/2
1	PSU	1	6	11,1	-	0/7/25/26	0/2/2/2
1	PSU	1	5	1	-	0/7/25/26	0/2/2/2
2	PSU	2	44	2,11	-	0/7/25/26	0/2/2/2
2	PSU	2	35	2,11	-	0/7/25/26	0/2/2/2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	5	PSU	C2-N1	4.54	1.42	1.36
1	1	6	PSU	C2-N1	4.11	1.42	1.36
2	2	42	PSU	C6-C5	3.71	1.39	1.35
2	2	35	PSU	C6-C5	3.53	1.39	1.35
2	2	44	PSU	C6-C5	3.44	1.39	1.35
1	1	5	PSU	C4-C5	-2.14	1.38	1.44
1	1	6	PSU	C4-C5	-2.00	1.38	1.44

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	42	PSU	C4-N3-C2	-4.82	119.74	126.37
2	2	35	PSU	C4-N3-C2	-4.70	119.90	126.37
2	2	42	PSU	N1-C2-N3	4.67	120.09	115.17
2	2	35	PSU	N1-C2-N3	4.65	120.07	115.17
2	2	44	PSU	N1-C2-N3	4.60	120.02	115.17
2	2	44	PSU	C4-N3-C2	-4.30	120.45	126.37
1	1	6	PSU	C6-N1-C2	-4.00	118.98	122.69
1	1	5	PSU	O2-C2-N1	3.77	126.68	122.79
1	1	5	PSU	C6-N1-C2	-3.30	119.62	122.69
2	2	44	PSU	C6-N1-C2	-3.05	119.86	122.69
2	2	44	PSU	O2-C2-N1	-2.62	120.09	122.79
2	2	35	PSU	O2-C2-N1	-2.51	120.20	122.79
2	2	35	PSU	C6-N1-C2	-2.45	120.42	122.69
2	2	42	PSU	O2-C2-N1	-2.32	120.40	122.79
2	2	42	PSU	C6-N1-C2	-2.26	120.59	122.69
1	1	6	PSU	C5-C6-N1	2.19	125.19	122.14
2	2	35	PSU	O4'-C1'-C2'	2.04	107.97	105.15

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	42	PSU	2	0
1	1	6	PSU	3	0
1	1	5	PSU	4	0
2	2	44	PSU	5	0
2	2	35	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	2	10
1	1	4
11	I	2
10	H	2
22	X	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	10:A	O3'	51:C	P	64.91
1	1	440:N	O3'	516:U	P	49.12
1	1	325:A	O3'	378:N	P	48.87
1	2	122:A	O3'	139:G	P	46.36
1	1	532:U	O3'	538:C	P	25.27
1	2	86:U	O3'	108:A	P	24.04
1	2	1130:U	O3'	1138:G	P	22.40
1	2	150:G	O3'	1089:G	P	18.75
1	2	73:U	O3'	79:A	P	17.45
1	1	394:N	O3'	424:N	P	17.14
1	I	53:U	O3'	57:C	P	15.85
1	2	1154:U	O3'	1159:U	P	14.23
1	X	44:UNK	C	50:UNK	N	11.40
1	2	1108:A	O3'	1115:G	P	10.88
1	H	138:UNK	C	175:UNK	N	9.48
1	H	120:UNK	C	126:UNK	N	8.29
1	2	1149:G	O3'	1150:U	P	1.90
1	2	143:G	O3'	144:G	P	1.83
1	2	1090:A	O3'	1091:G	P	1.78

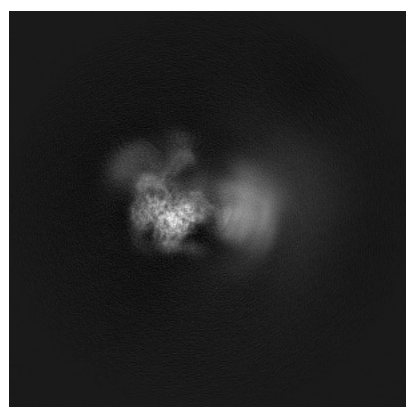
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4364. These allow visual inspection of the internal detail of the map and identification of artifacts.

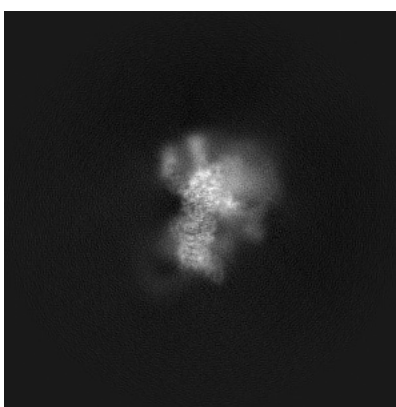
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

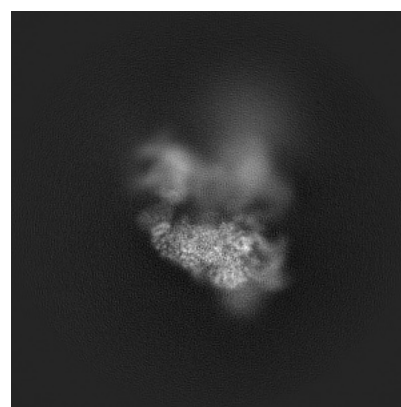
6.1.1 Primary map



X



Y

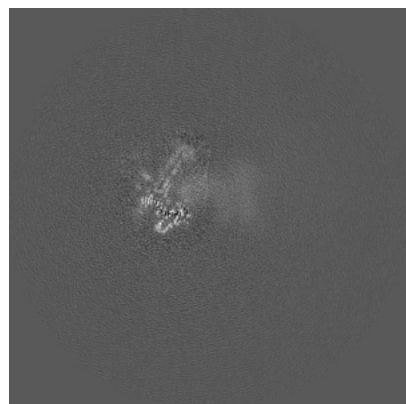


Z

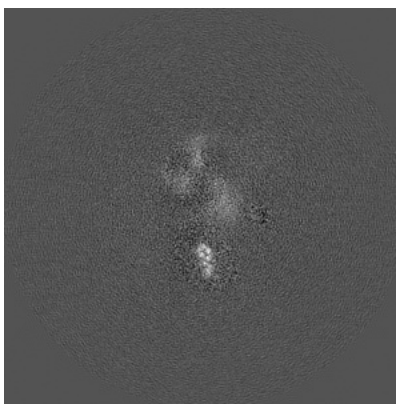
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

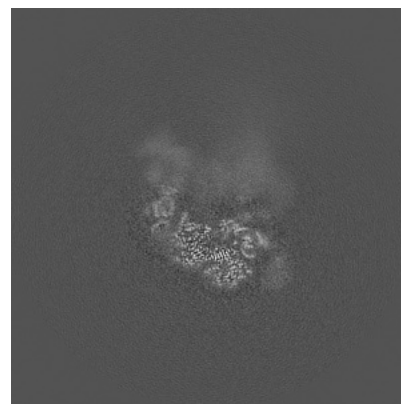
6.2.1 Primary map



X Index: 280



Y Index: 280

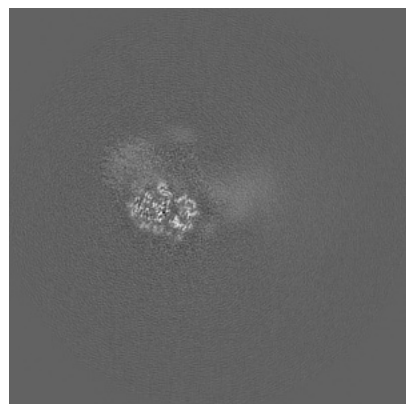


Z Index: 280

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

6.3 Largest variance slices [i](#)

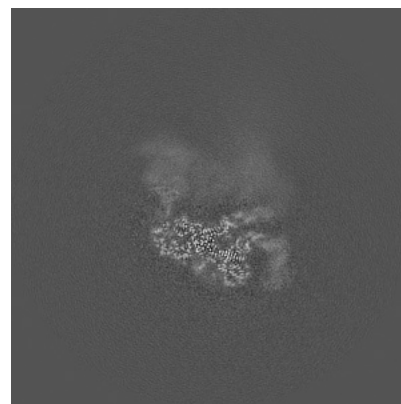
6.3.1 Primary map



X Index: 303



Y Index: 225

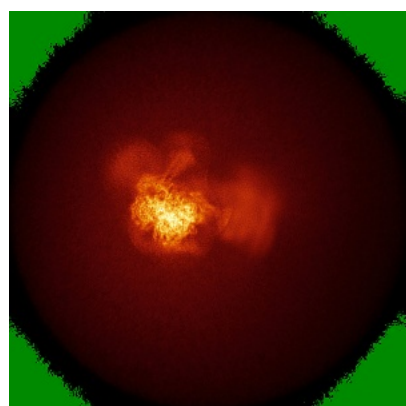


Z Index: 271

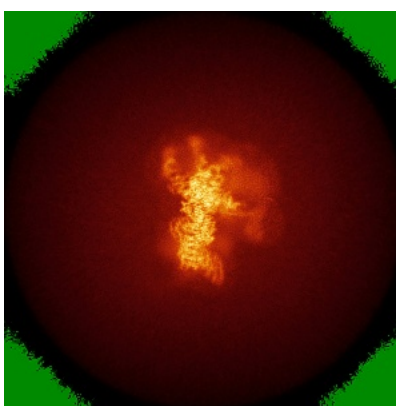
The images above show the largest variance slices of the map in three orthogonal directions.

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

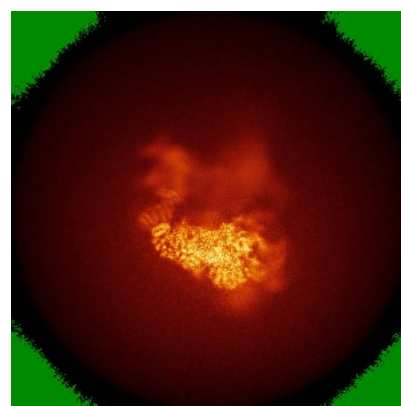
6.4.1 Primary map



X



Y

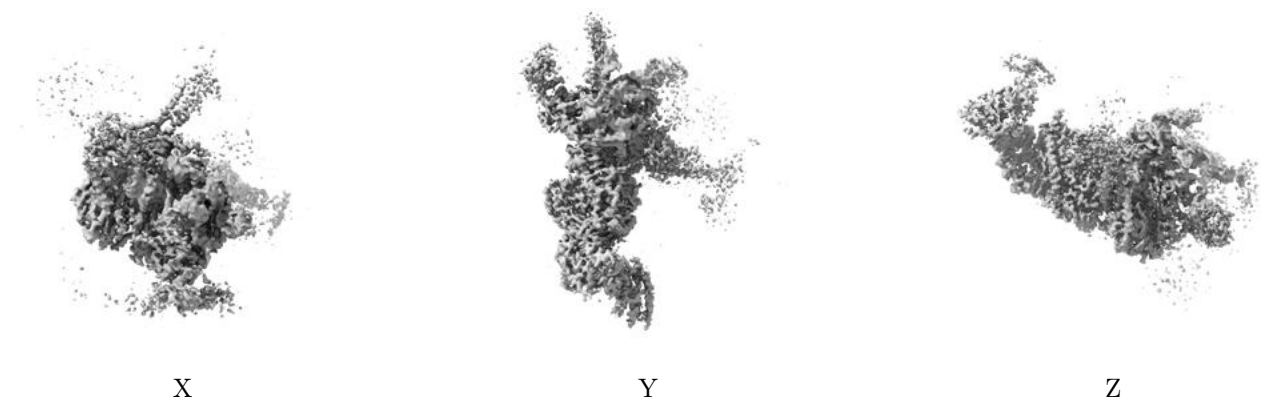


Z

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 0.0369. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

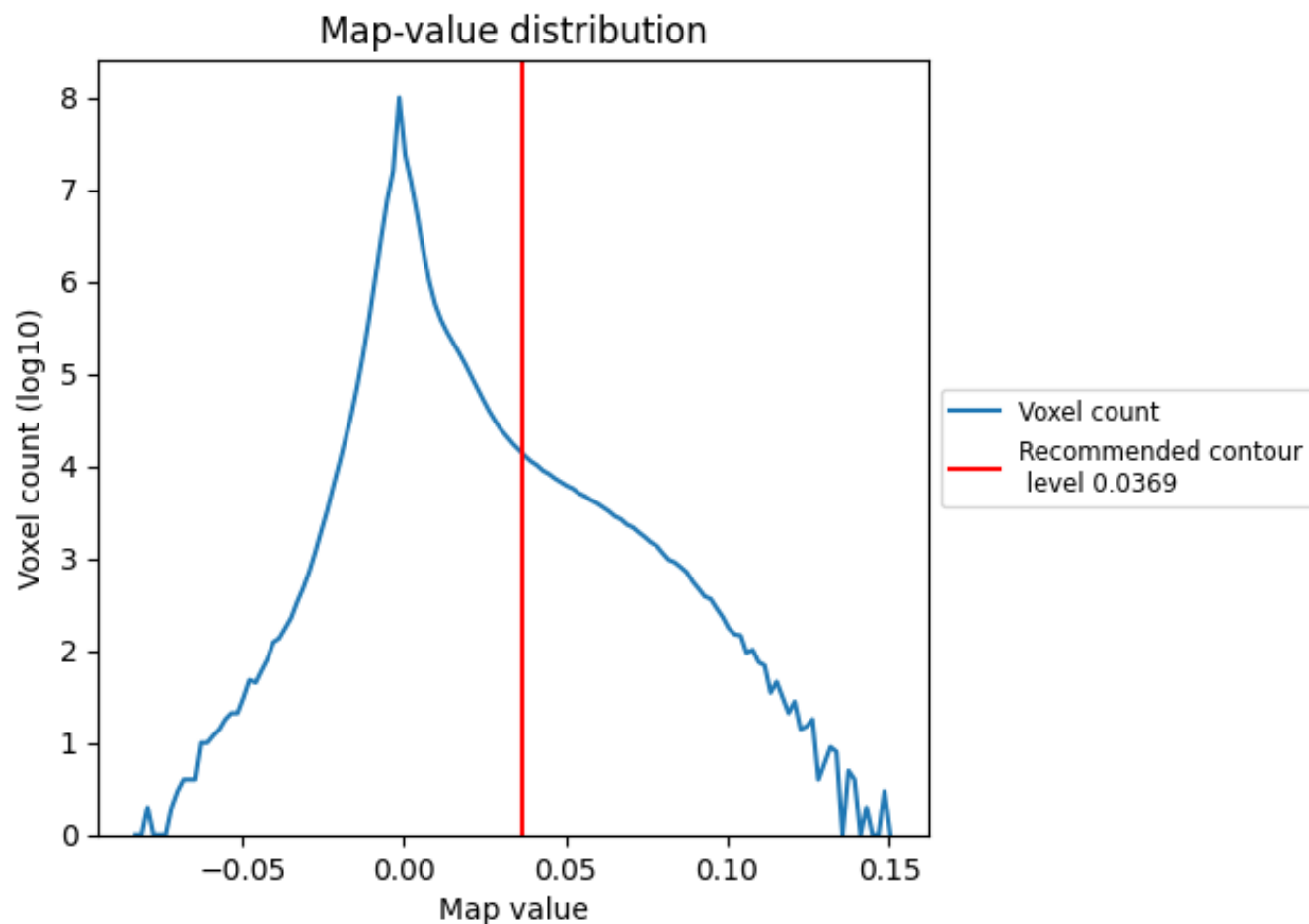
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

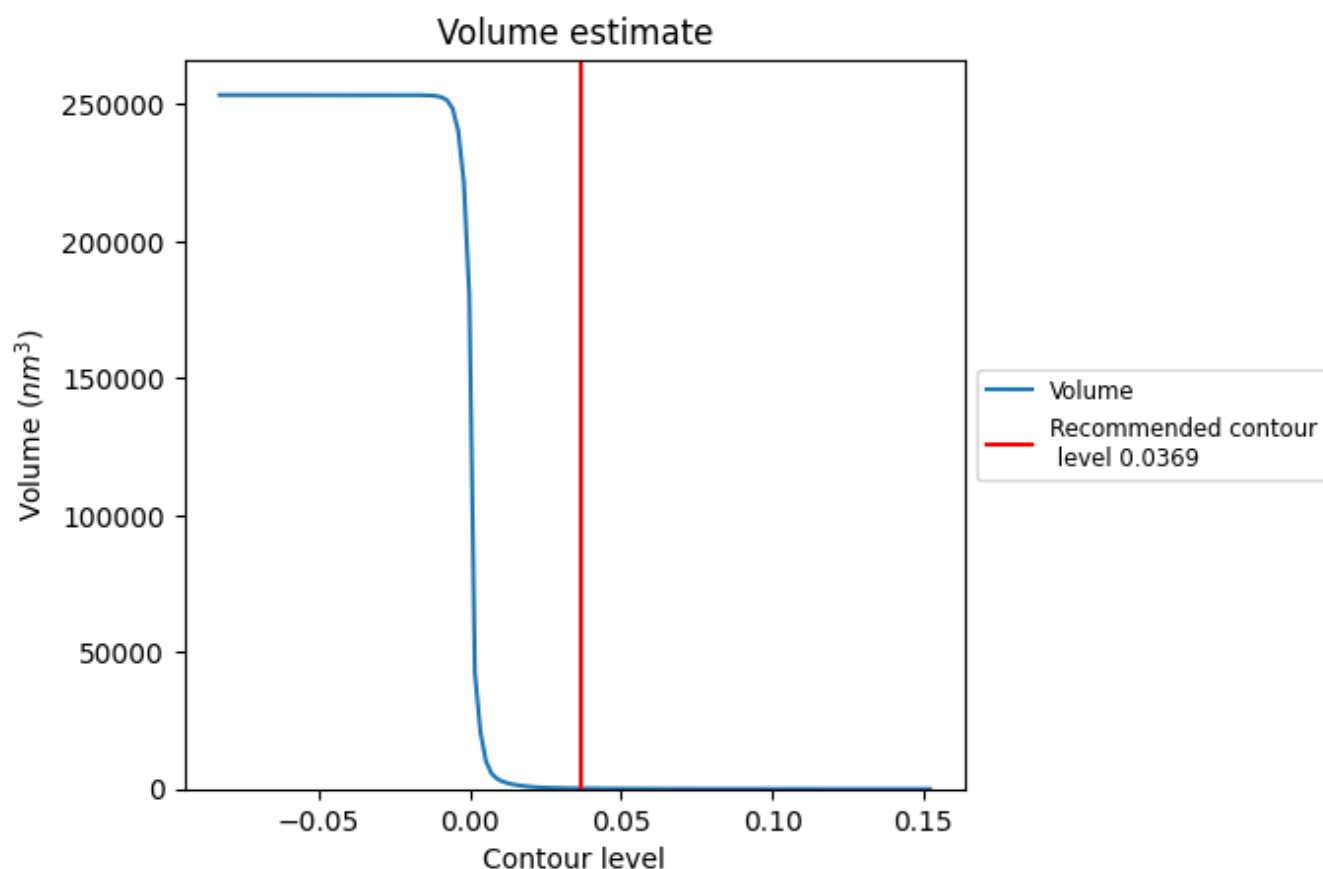
This section contains the results of statistical analysis of the map.

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.

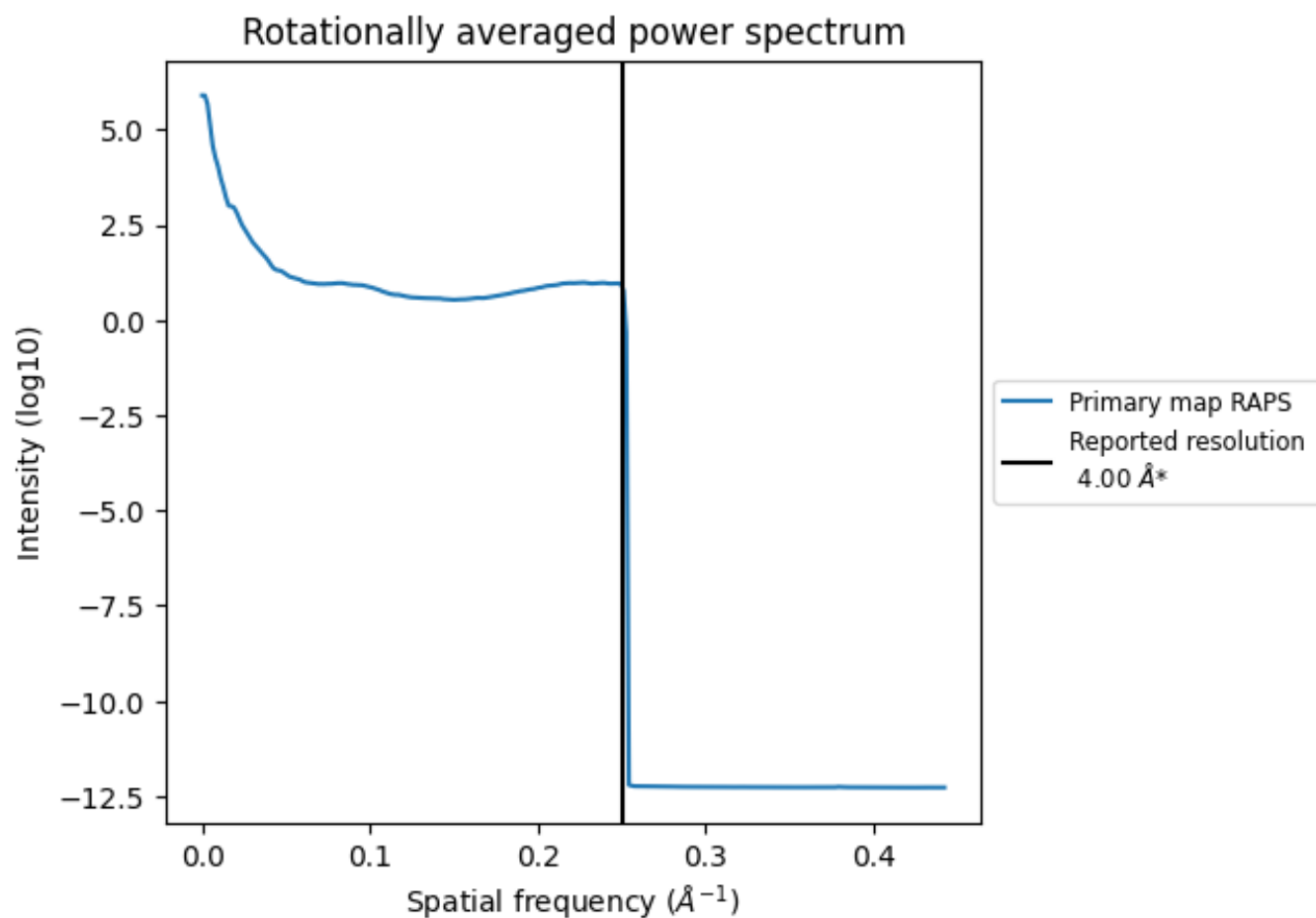
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 189 nm³; this corresponds to an approximate mass of 171 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 0.250 Å⁻¹

8 Fourier-Shell correlation

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

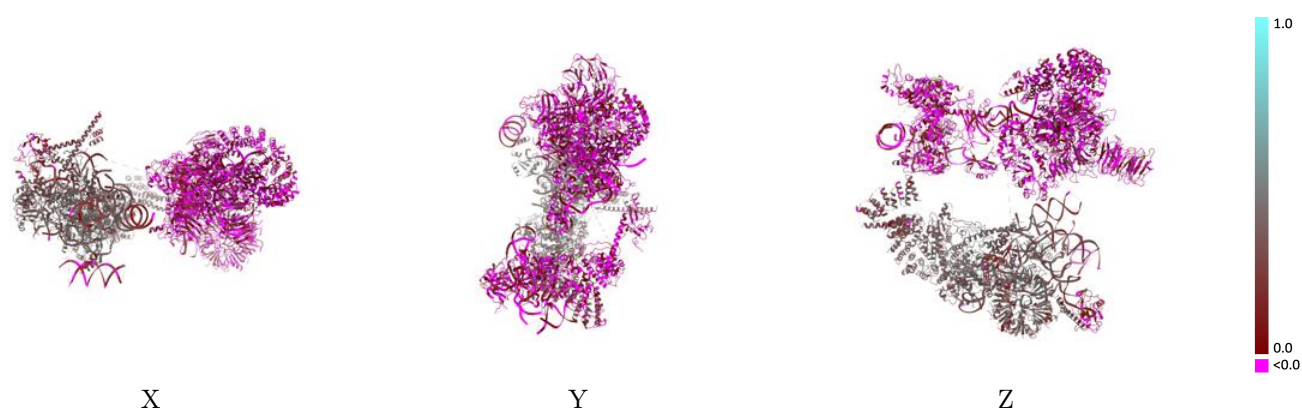
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4364 and PDB model 6G90. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

This section was not generated.

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

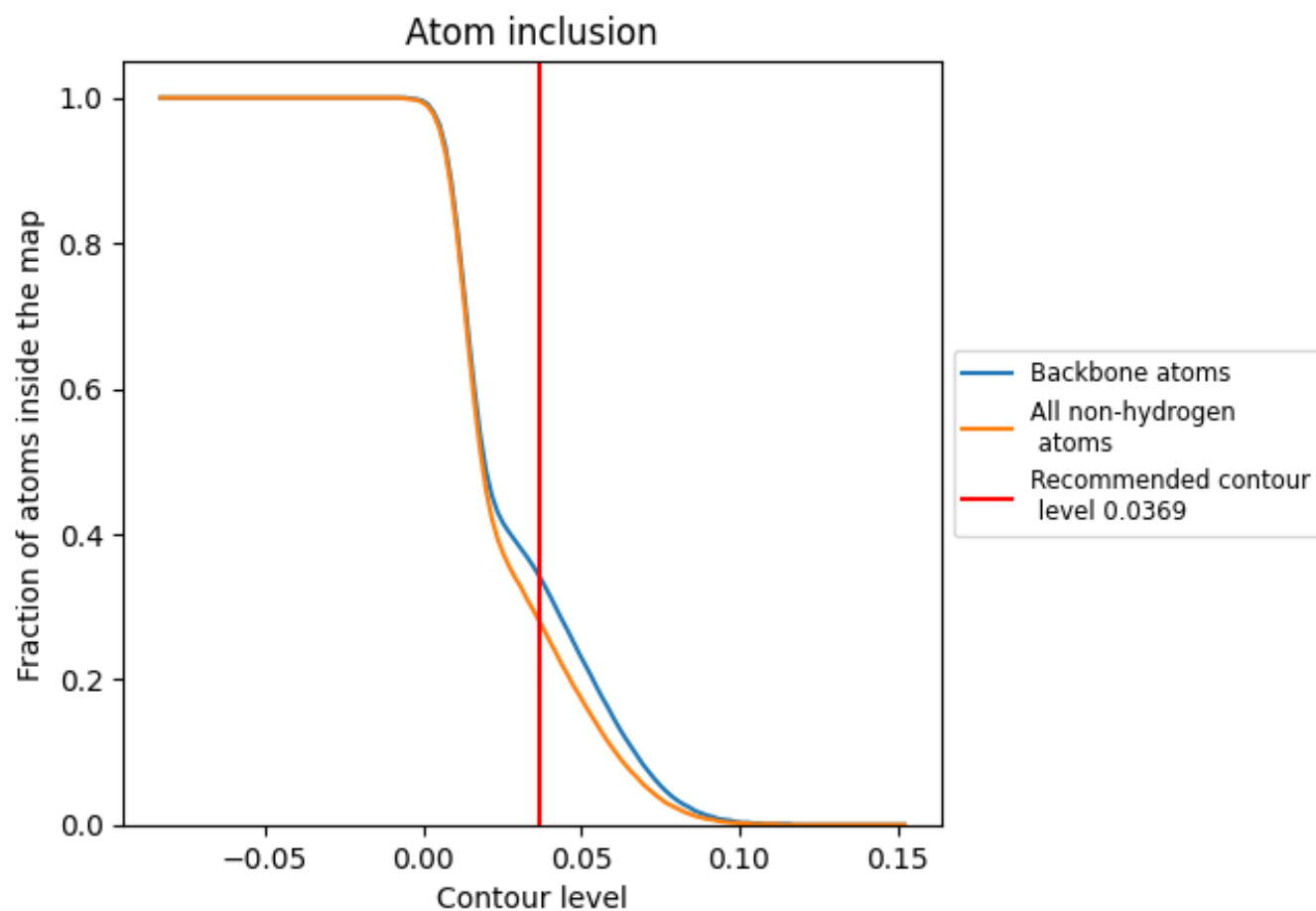


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 34% of all backbone atoms, 28% 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 (0.0369) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2790	 0.1520
1	 0.6780	 0.2970
2	 0.0000	 0.0010
A	 0.7990	 0.3950
B	 0.3390	 0.1890
C	 0.6650	 0.4050
D	 0.6580	 0.3440
E	 0.6800	 0.3970
F	 0.6370	 0.3920
G	 0.6570	 0.3800
H	 0.5710	 0.3040
I	 0.2190	 0.0990
J	 0.7040	 0.4150
O	 0.0000	 -0.0020
P	 0.0000	 0.0010
Q	 0.0000	 -0.0020
R	 0.0000	 0.0120
S	 0.0000	 0.0090
T	 0.0000	 0.0070
U	 0.0000	 0.0040
V	 0.0000	 -0.0060
W	 0.0310	 0.0250
X	 0.6120	 0.3000
Y	 0.0210	 0.0230
Z	 0.0000	 0.0080
b	 0.6260	 0.4070
d	 0.6770	 0.4380
e	 0.6250	 0.3770
f	 0.6290	 0.3320
g	 0.6440	 0.4250
h	 0.6390	 0.3970
i	 0.6240	 0.3460
s	 0.0000	 -0.0080
t	 0.0000	 -0.0400
u	 0.0000	 0.0300



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Chain	Atom inclusion	Q-score
v	 0.0000	 0.0160
w	 0.0000	 -0.0150
x	 0.0000	 0.0370
y	 0.0000	 0.0090