



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 06:50 AM UTC

PDB ID : 8H6E / pdb_00008h6e
EMDB ID : EMD-34500
Title : Cryo-EM structure of human exon-defined spliceosome in the late pre-B state.
Authors : Zhang, W.; Zhan, X.; Zhang, X.; Bai, R.; Lei, J.; Yan, C.; Shi, Y.
Deposited on : 2022-10-17
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

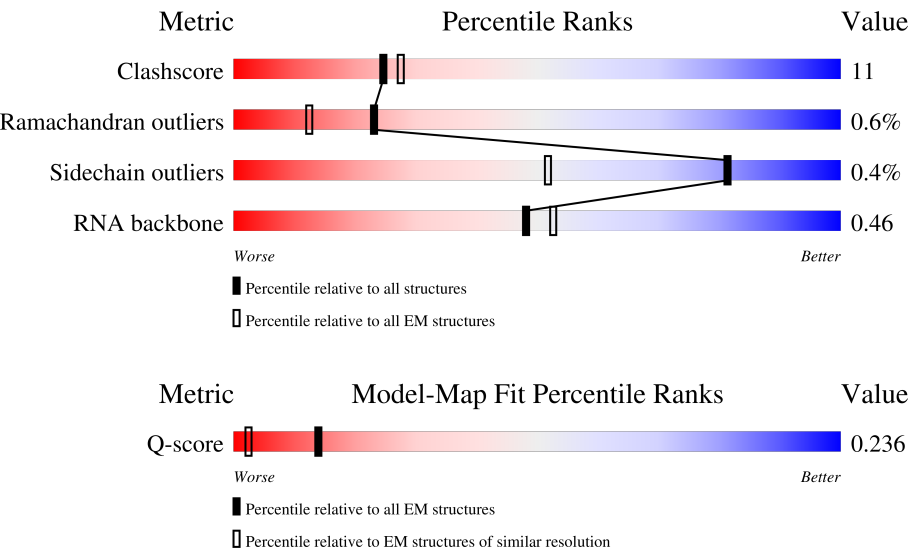
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	A	144	
2	6A	107	
3	6a	95	

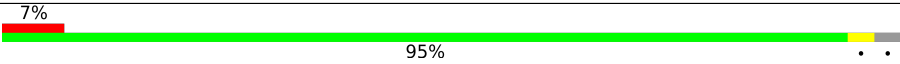
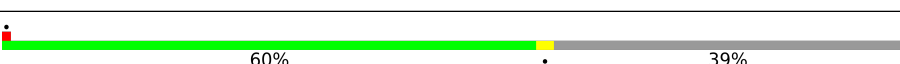
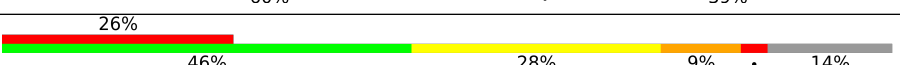
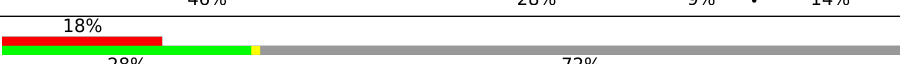
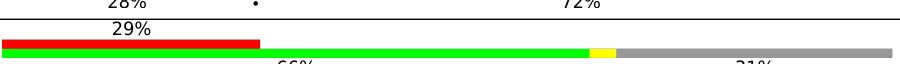
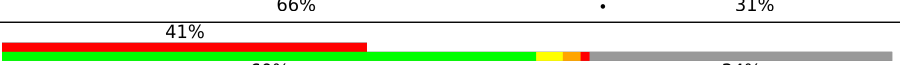
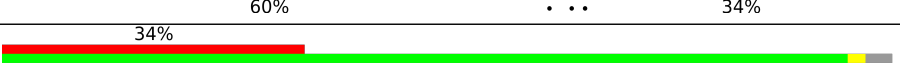
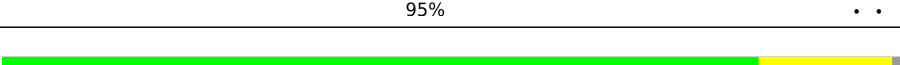
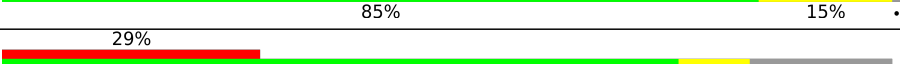
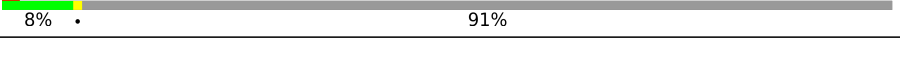
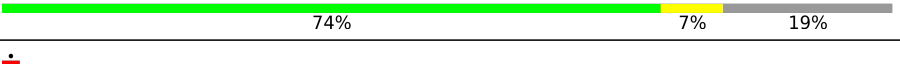
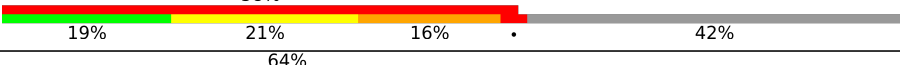
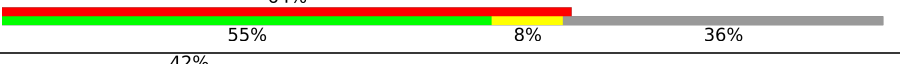
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Mol	Chain	Length	Quality of chain
4	6b	102	
5	6c	139	
6	6d	91	
7	6e	80	
8	6f	103	
9	6g	96	
10	5A	117	
11	5B	2335	
12	5C	972	
13	5D	2136	
14	5E	357	
15	2a	231	
15	4a	231	
15	5a	231	
16	2b	119	
16	4b	119	
16	5b	119	
17	2c	118	
17	4c	118	
17	5c	118	
18	2d	86	
18	4d	86	
18	5d	86	
19	2e	92	
19	4e	92	

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Mol	Chain	Length	Quality of chain
19	5e	92	
20	2f	76	
20	4f	76	
20	5f	76	
21	2g	126	
21	4g	126	
21	5g	126	
22	4A	146	
23	4B	683	
24	4C	522	
25	4D	499	
26	4E	128	
27	4F	142	
28	4G	941	
29	4R	480	
30	4S	800	
31	4T	565	
32	4U	820	
33	4X	155	
34	4Y	1007	
35	2A	188	
36	2B	255	
37	2C	225	
38	2D	793	
39	2E	464	

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Mol	Chain	Length	Quality of chain
40	2F	501	84% 5% 16%
41	2G	1304	80% 50% 28% 20%
42	2H	895	20% 18% 80%
43	2I	1217	96% 83% 13%
44	2J	424	18% 17% 82%
45	2K	125	86% 74% 12% 14%
46	2L	110	80% 73% 8% 19%
47	2M	86	77% 52% 23% 23%

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 96125 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 pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	59	Total	C	N	O	P	0	0
			1232	551	193	429	59		

- Molecule 2 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	6A	59	Total	C	N	O	P	0	0
			1251	558	230	404	59		

- Molecule 3 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	6a	89	Total	C	N	O	0	0
			356	178	89	89		

- Molecule 4 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	6b	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 5 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	6c	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 6 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	6d	72	Total	C	N	O	0	0
			288	144	72	72		

- Molecule 7 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	6e	70	Total	C	N	O	0	0
			280	140	70	70		

- Molecule 8 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	6f	65	Total	C	N	O	0	0
			260	130	65	65		

- Molecule 9 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	6g	61	Total	C	N	O	0	0
			244	122	61	61		

- Molecule 10 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	5A	114	Total	C	N	O	P	0	0
			2398	1074	398	812	114		

- Molecule 11 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	5B	2214	Total	C	N	O	S	0	0
			18281	11782	3177	3243	79		

- Molecule 12 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	5C	852	Total	C	N	O	S	0	0
			6727	4300	1127	1266	34		

- Molecule 13 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	5D	2001	Total	C	N	O	S	0	0
			16077	10235	2767	2991	84		

- Molecule 14 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	5E	304	Total	C	N	O	0	0
			1497	888	304	305		

- Molecule 15 is a protein called Isoform SM-B of Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	5a	85	Total	C	N	O	0	0
			340	170	85	85		
15	4a	82	Total	C	N	O	0	0
			405	241	82	82		
15	2a	85	Total	C	N	O	0	0
			340	170	85	85		

- Molecule 16 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	5b	82	Total	C	N	O	0	0
			328	164	82	82		
16	4b	81	Total	C	N	O	0	0
			401	239	81	81		
16	2b	82	Total	C	N	O	0	0
			328	164	82	82		

- Molecule 17 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	5c	97	Total	C	N	O	0	0
			388	194	97	97		
17	4c	92	Total	C	N	O	0	0
			455	271	92	92		
17	2c	85	Total	C	N	O	0	0
			340	170	85	85		

- Molecule 18 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	5d	73	Total	C	N	O	0	0
			292	146	73	73		
18	4d	72	Total	C	N	O	0	0
			351	207	72	72		
18	2d	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 19 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	5e	79	Total	C	N	O	0	0
			316	158	79	79		
19	4e	76	Total	C	N	O	0	0
			376	224	76	76		
19	2e	79	Total	C	N	O	0	0
			316	158	79	79		

- Molecule 20 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	5f	74	Total	C	N	O	0	0
			296	148	74	74		
20	4f	73	Total	C	N	O	0	0
			358	212	73	73		
20	2f	67	Total	C	N	O	0	0
			268	134	67	67		

- Molecule 21 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	5g	77	Total	C	N	O	0	0
			308	154	77	77		
21	4g	83	Total	C	N	O	0	0
			409	243	83	83		
21	2g	80	Total	C	N	O	0	0
			320	160	80	80		

- Molecule 22 is a RNA chain called U4 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	4A	125	Total	C	N	O	P	0	0
			2653	1187	471	872	123		

- Molecule 23 is a protein called U4/U6 small nuclear ribonucleoprotein Prp3.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	4B	193	Total	C	N	O	0	0
			954	568	193	193		

- Molecule 24 is a protein called U4/U6 small nuclear ribonucleoprotein Prp4.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	4C	359	Total	C	N	O	0	0
			1765	1047	359	359		

- Molecule 25 is a protein called U4/U6 small nuclear ribonucleoprotein Prp31.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	4D	327	Total	C	N	O	S	0	0
			1764	1057	357	348	2		

- Molecule 26 is a protein called NHP2-like protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	4E	124	Total	C	N	O	0	0
			615	367	124	124		

- Molecule 27 is a protein called Thioredoxin-like protein 4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	4F	141	Total	C	N	O	S	0	0
			1169	751	194	214	10		

- Molecule 28 is a protein called Pre-mRNA-processing factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	4G	794	Total	C	N	O	S	0	0
			4803	2915	933	943	12		

- Molecule 29 is a protein called RNA-binding protein 42.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	4R	106	Total	C	N	O	S	0	0
			874	553	160	157	4		

- Molecule 30 is a protein called U4/U6.U5 tri-snRNP-associated protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4S	70	Total	C	N	O	S	0	0
			549	343	103	100	3		

- Molecule 31 is a protein called U4/U6.U5 tri-snRNP-associated protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4T	456	Total	C	N	O	S	0	0
			3749	2427	635	673	14		

- Molecule 32 is a protein called Probable ATP-dependent RNA helicase DDX23.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	4U	153	Total	C	N	O	S	0	0
			1338	831	262	243	2		

- Molecule 33 is a protein called U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	4X	21	Total	C	N	O	S	0	0
			184	115	40	28	1		

- Molecule 34 is a protein called Serine/threonine-protein kinase PRP4 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	4Y	322	Total	C	N	O		0	0
			1595	951	322	322			

- Molecule 35 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	2A	109	Total	C	N	O	P	0	0
			2311	1032	396	774	109		

- Molecule 36 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	2B	162	Total	C	N	O		0	0
			648	324	162	162			

- Molecule 37 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	2C	94	Total	C	N	O		0	0
			376	188	94	94			

- Molecule 38 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	2D	181	Total	C	N	O	S	0	0
			969	546	206	216	1		

- Molecule 39 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	2E	94	Total	C	N	O	0	0
			376	188	94	94		

- Molecule 40 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	2F	423	Total	C	N	O	0	0
			1693	847	423	423		

- Molecule 41 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	2G	1048	Total	C	N	O	0	0
			4192	2096	1048	1048		

- Molecule 42 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	2H	182	Total	C	N	O	0	0
			728	364	182	182		

- Molecule 43 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	2I	1168	Total	C	N	O	0	0
			4672	2336	1168	1168		

- Molecule 44 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	2J	78	Total	C	N	O	0	0
			312	156	78	78		

- Molecule 45 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	2K	108	Total	C	N	O	0	0
			432	216	108	108		

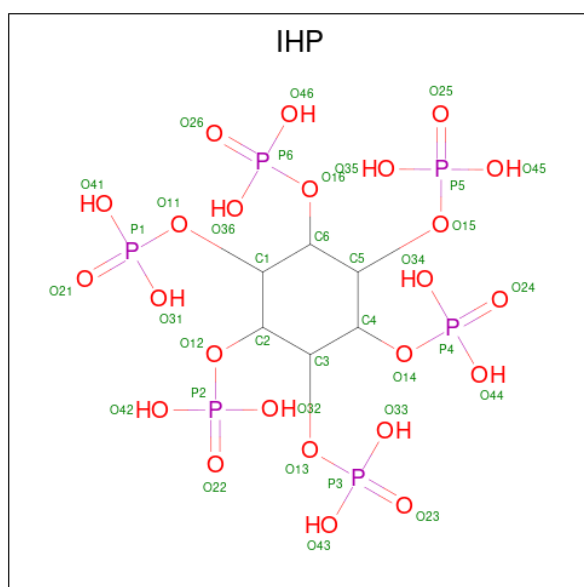
- Molecule 46 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	2L	89	Total	C	N	O	0	0
			356	178	89	89		

- Molecule 47 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	2M	66	Total	C	N	O	0	0
			264	132	66	66		

- Molecule 48 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$) (labeled as "Ligand of Interest" by depositor).

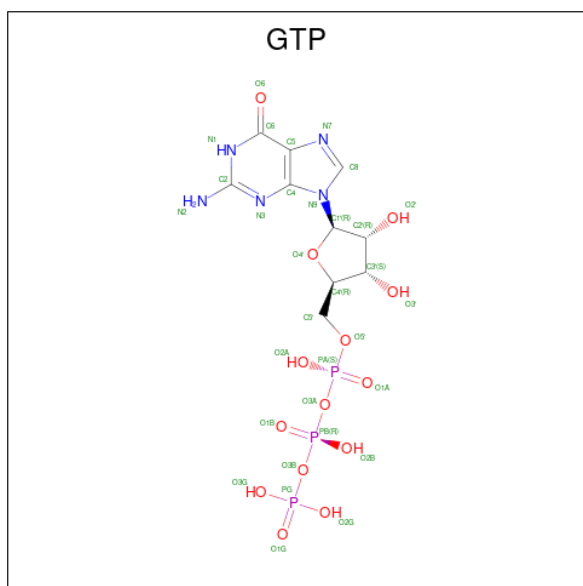


Mol	Chain	Residues	Atoms				AltConf
48	5B	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 49 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
49	5C	1	Total	Mg	0
			1	1	

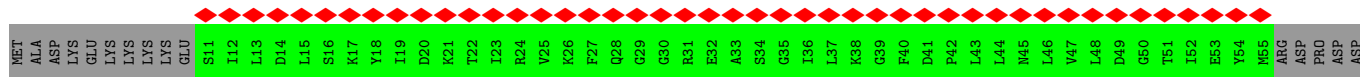
- Molecule 50 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
50	5C	1	Total	C	N	O	P	0
			32	10	5	14	3	

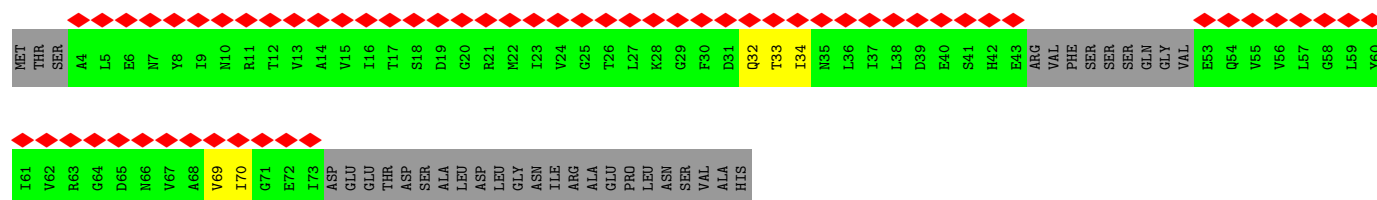
- Molecule 51 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
51	4T	1	Total	Zn	0
			1	1	

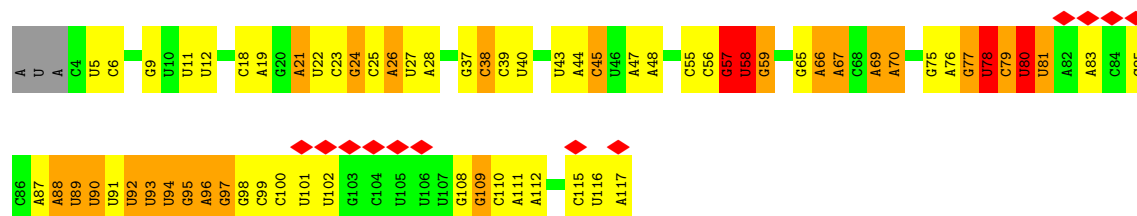




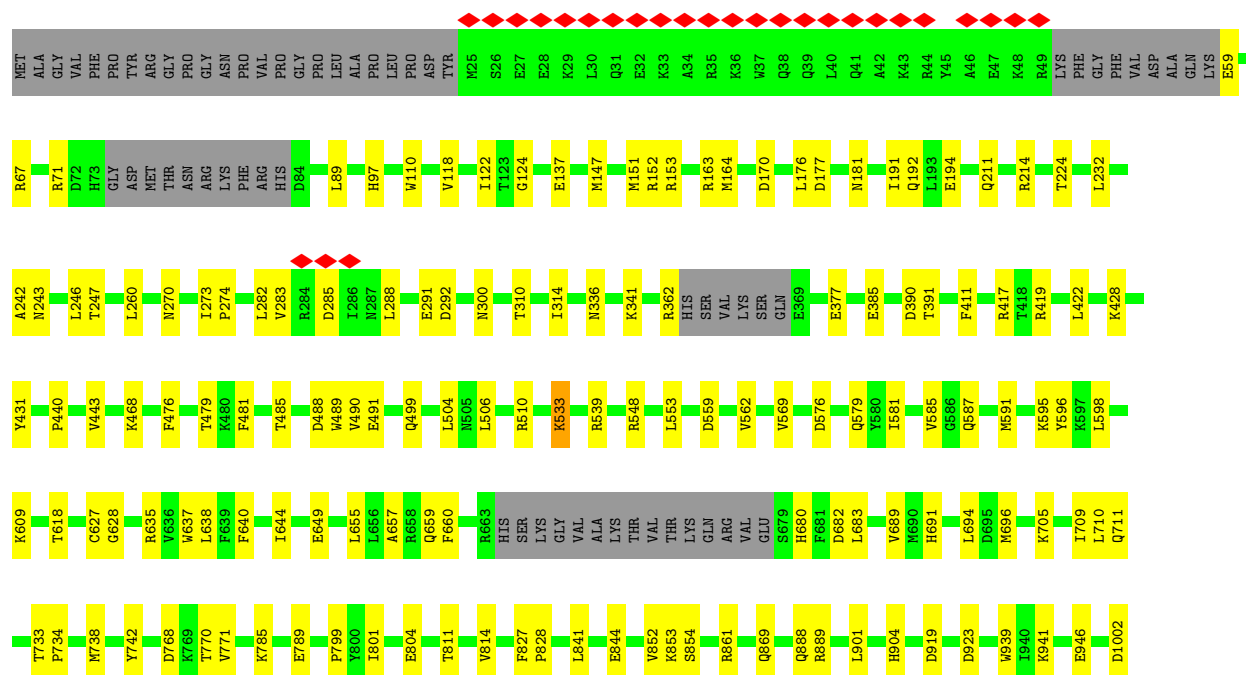
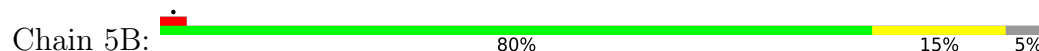
• Molecule 9: U6 snRNA-associated Sm-like protein LSm8

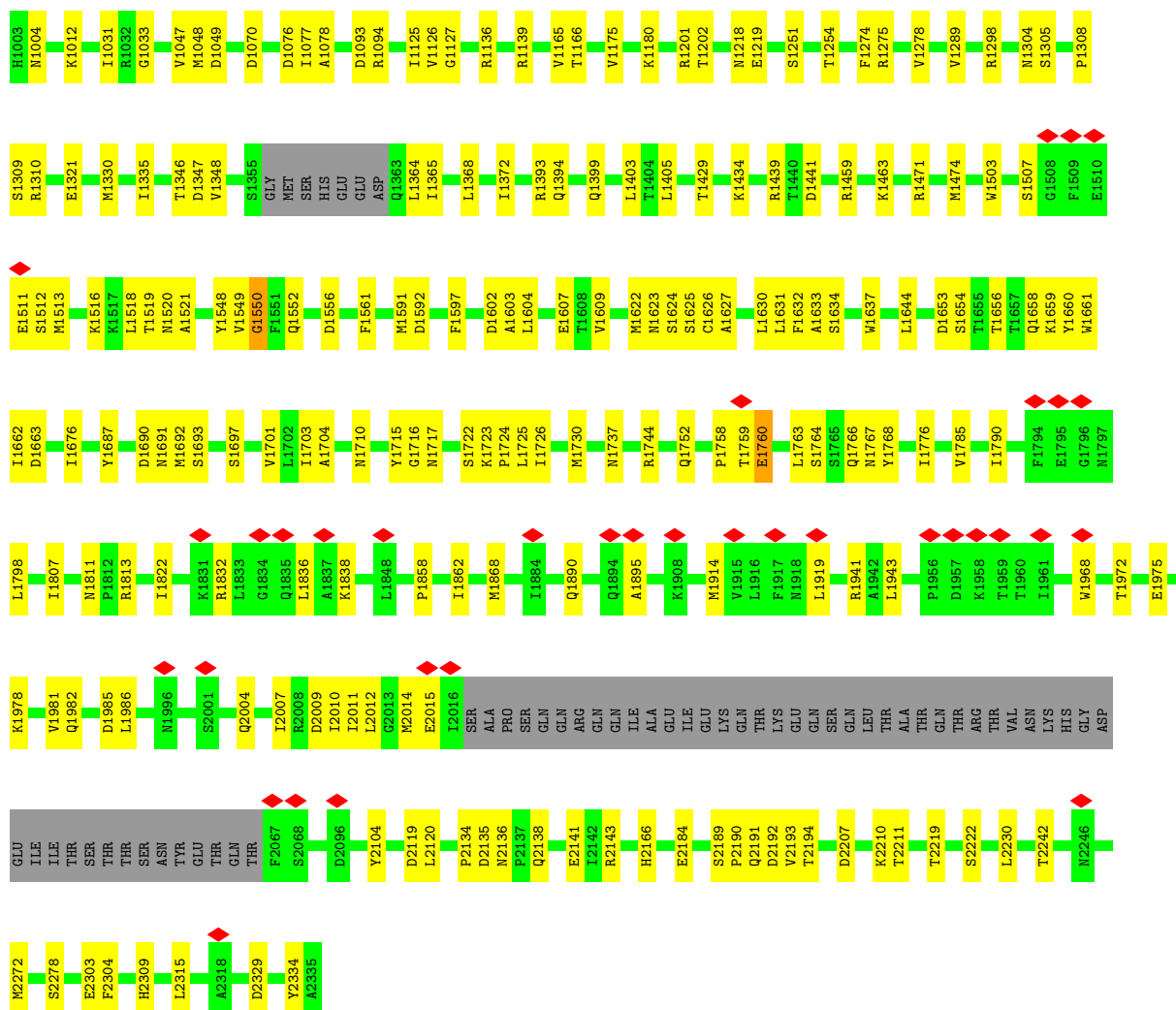


• Molecule 10: U5 snRNA



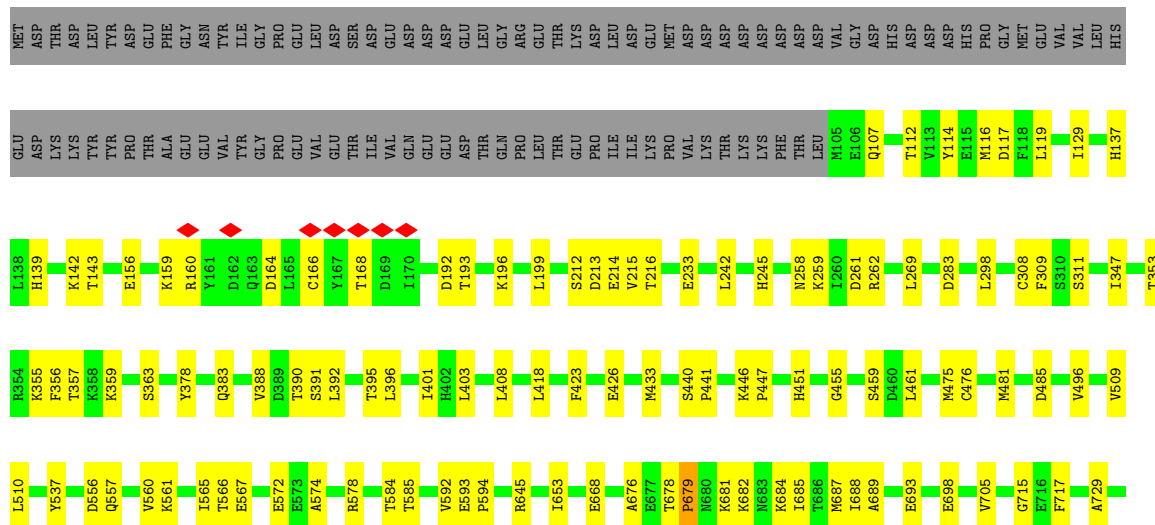
• Molecule 11: Pre-mRNA-processing-splicing factor 8

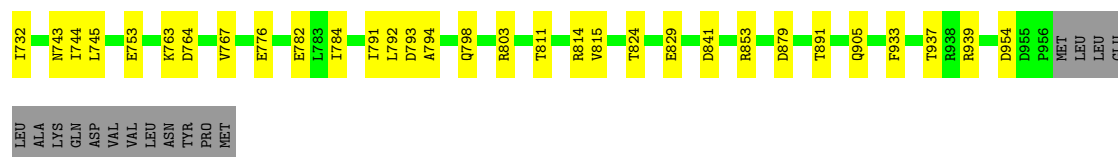




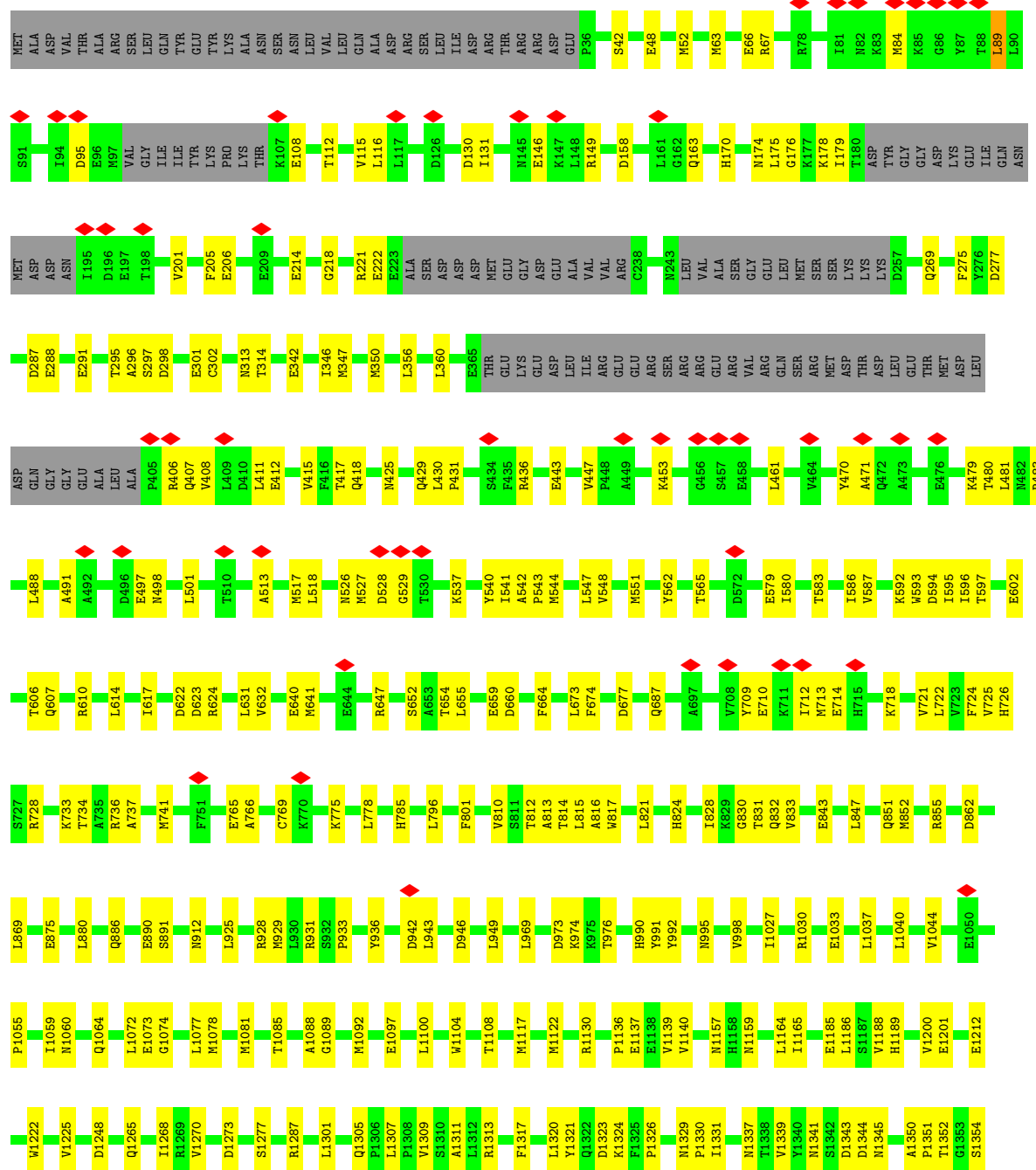
- Molecule 12: 116 kDa U5 small nuclear ribonucleoprotein component

Chain 5C:

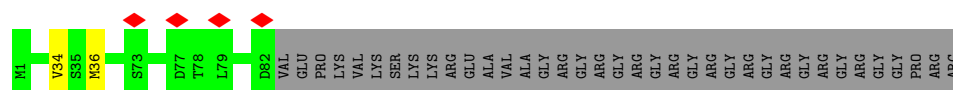




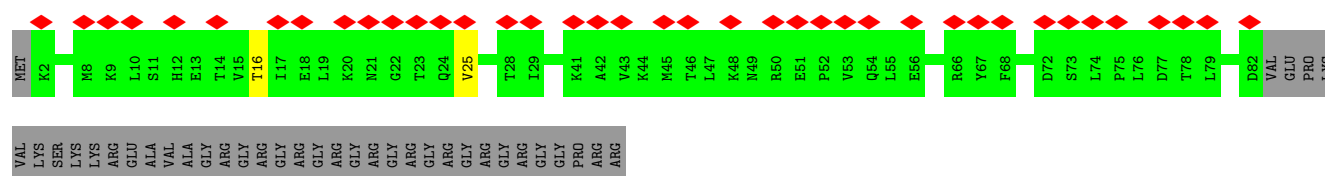
- Molecule 13: U5 small nuclear ribonucleoprotein 200 kDa helicase



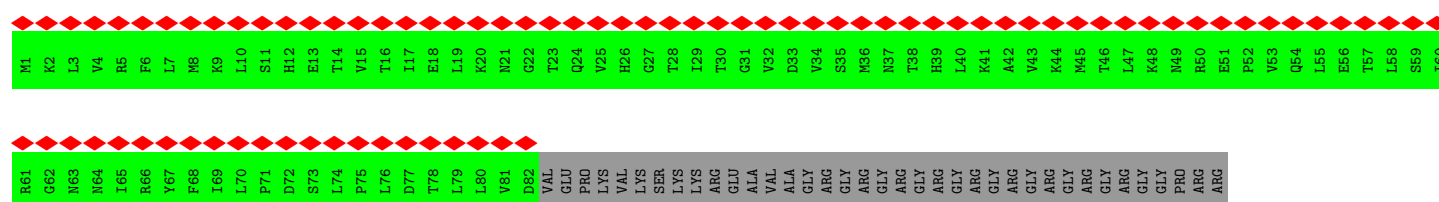
- Molecule 16: Small nuclear ribonucleoprotein Sm D1



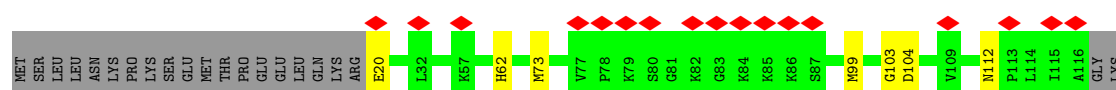
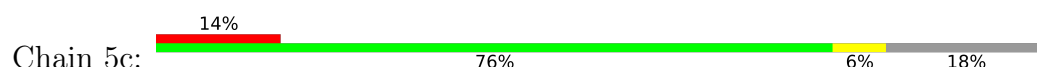
- Molecule 16: Small nuclear ribonucleoprotein Sm D1



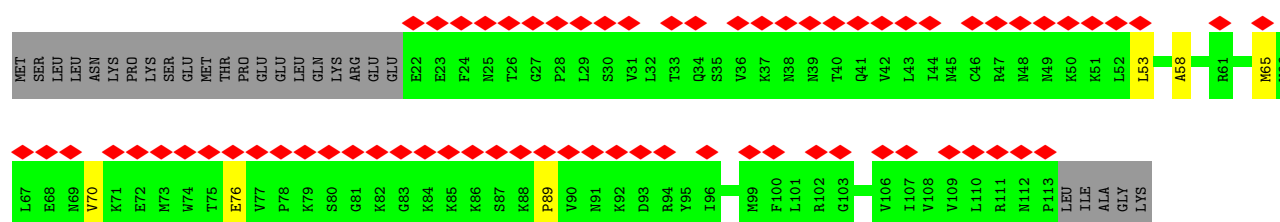
- Molecule 16: Small nuclear ribonucleoprotein Sm D1



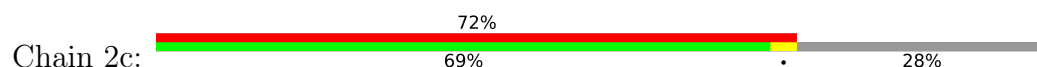
- Molecule 17: Small nuclear ribonucleoprotein Sm D2



- Molecule 17: Small nuclear ribonucleoprotein Sm D2

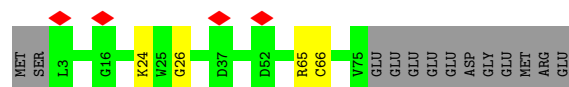
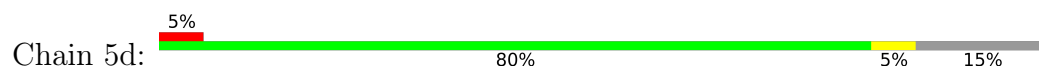


- Molecule 17: Small nuclear ribonucleoprotein Sm D2

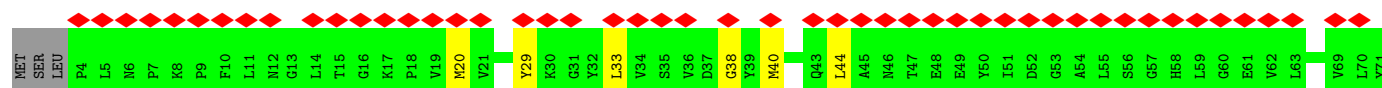
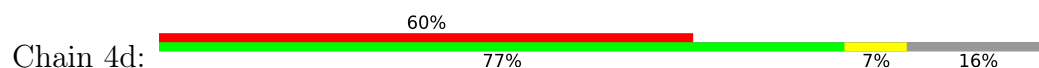




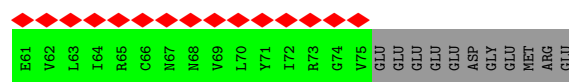
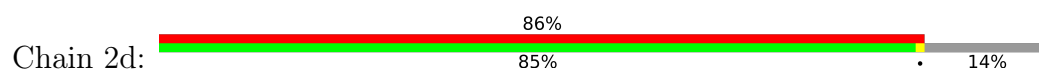
- Molecule 18: Small nuclear ribonucleoprotein F



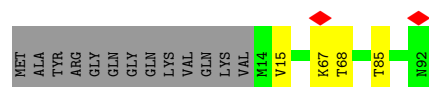
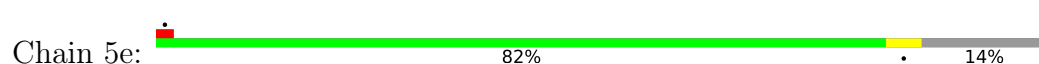
- Molecule 18: Small nuclear ribonucleoprotein F



- Molecule 18: Small nuclear ribonucleoprotein F

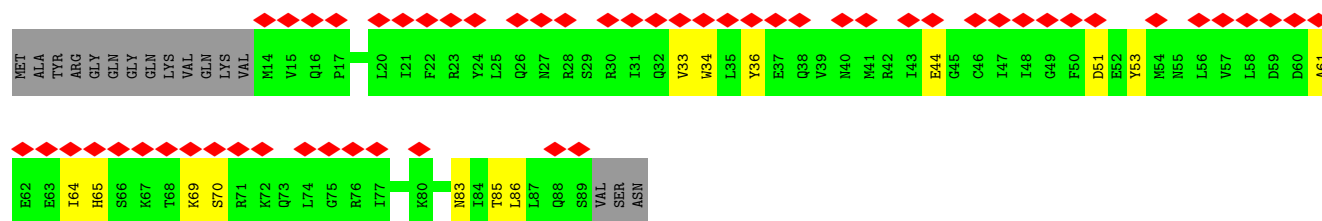


- Molecule 19: Small nuclear ribonucleoprotein E

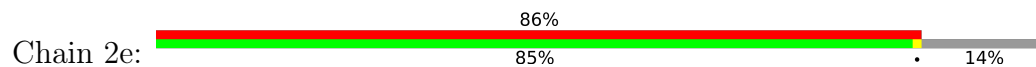


- Molecule 19: Small nuclear ribonucleoprotein E

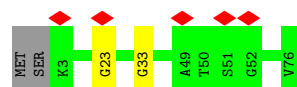




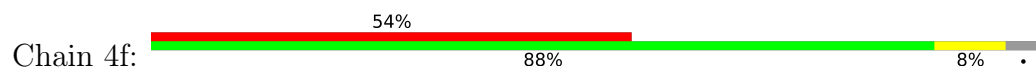
• Molecule 19: Small nuclear ribonucleoprotein E



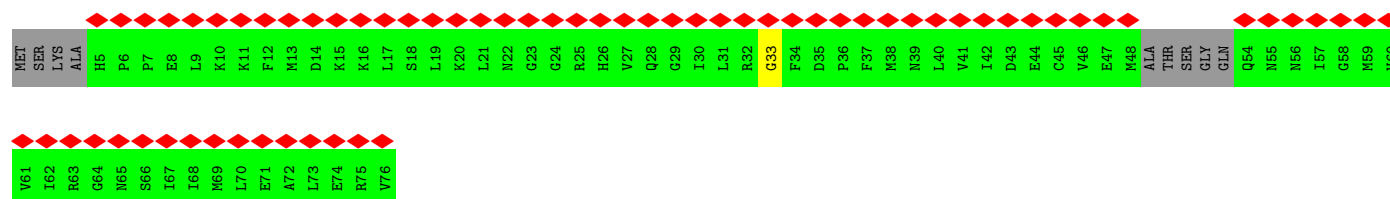
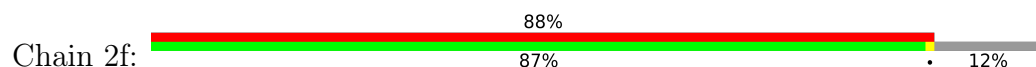
• Molecule 20: Small nuclear ribonucleoprotein G



• Molecule 20: Small nuclear ribonucleoprotein G

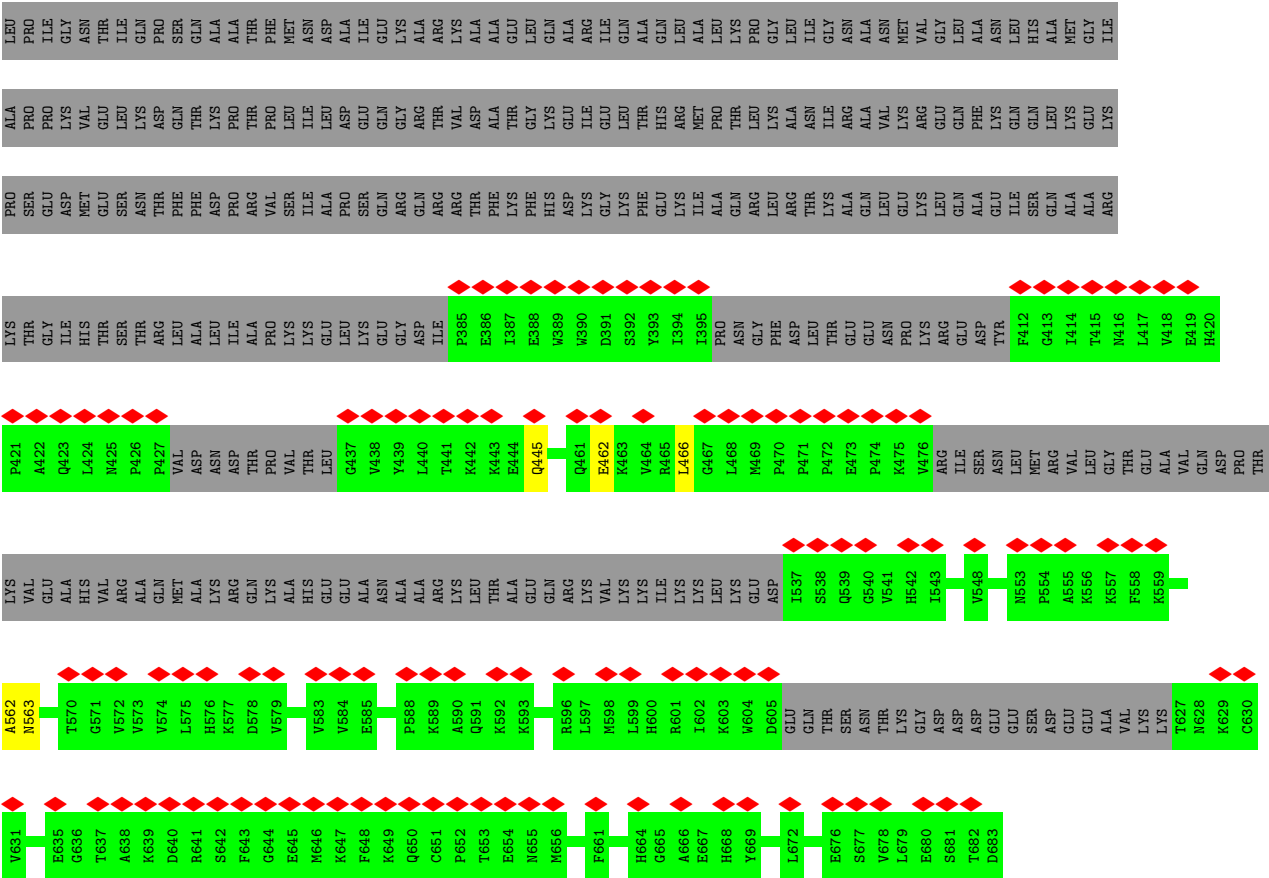


• Molecule 20: Small nuclear ribonucleoprotein G

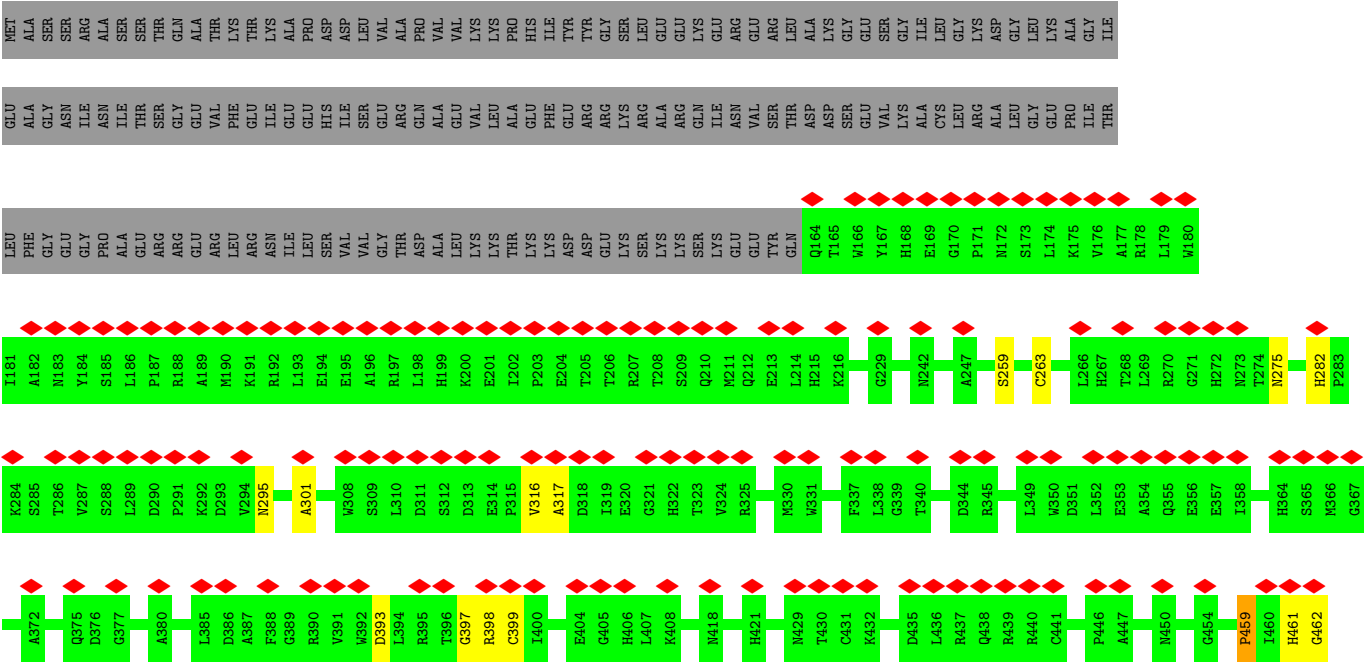


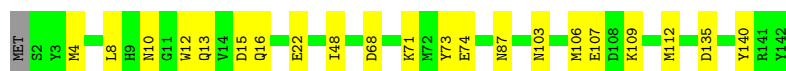
• Molecule 21: Small nuclear ribonucleoprotein Sm D3



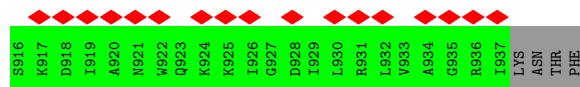
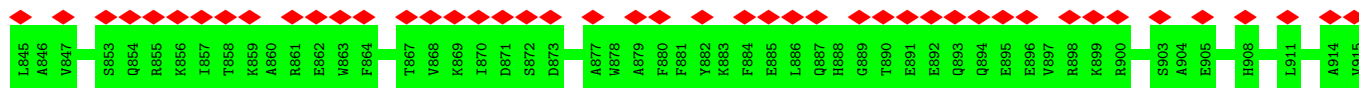
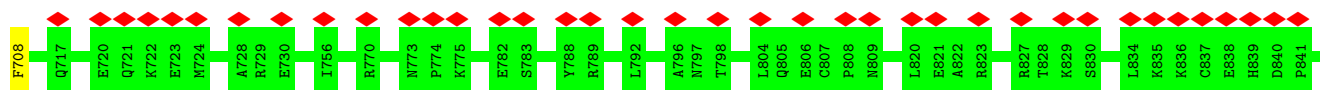
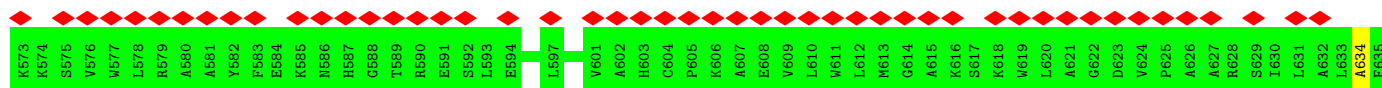
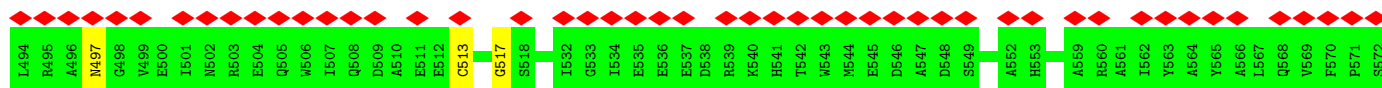
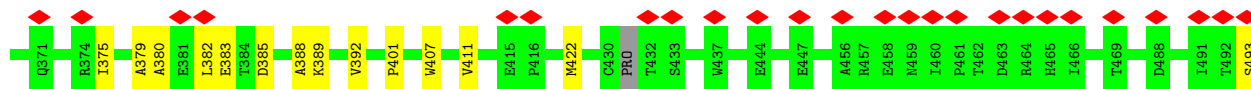
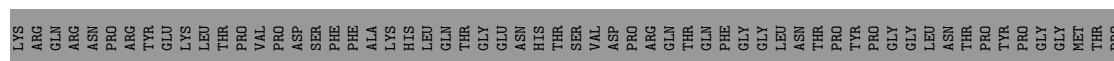
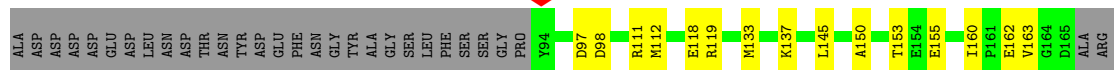
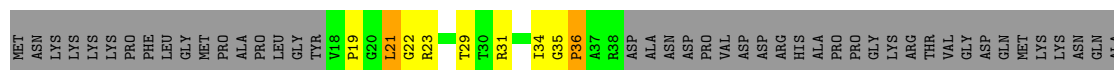
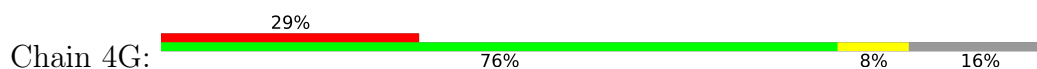


● Molecule 24: U4/U6 small nuclear ribonucleoprotein Prp4





• Molecule 28: Pre-mRNA-processing factor 6



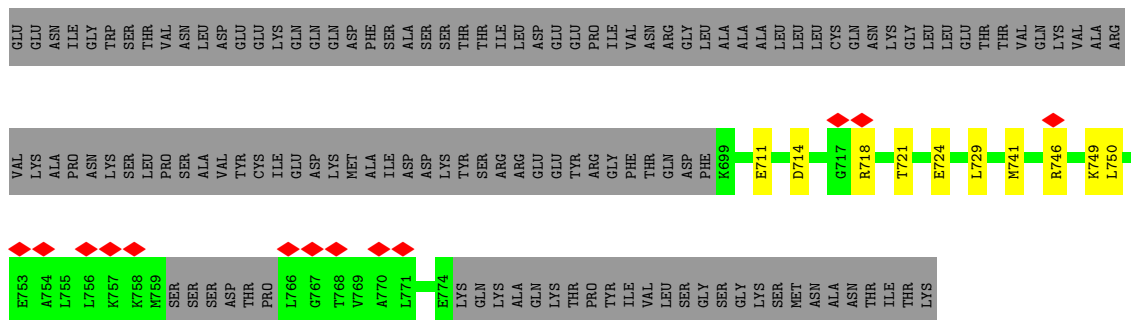
• Molecule 29: RNA-binding protein 42



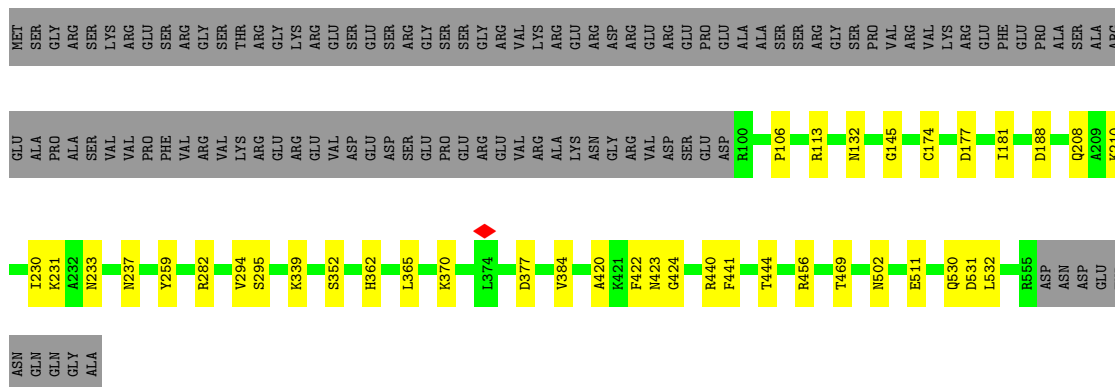
ARG

- Chain 4S: 8% 91%

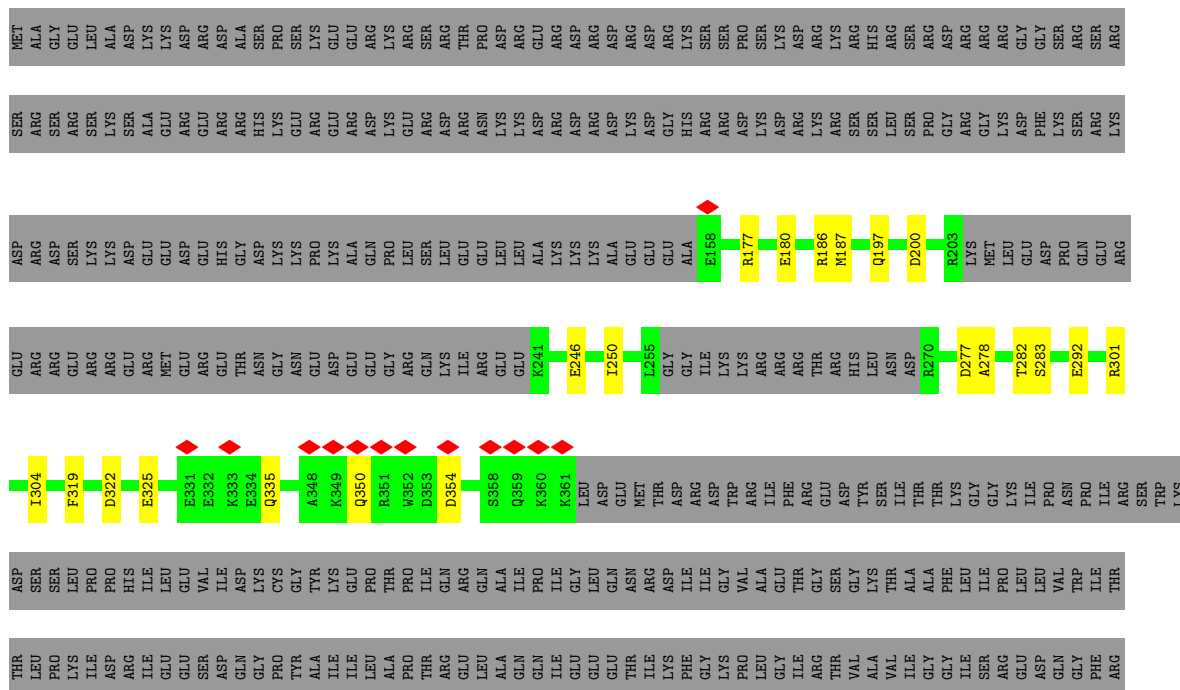
[illegible]



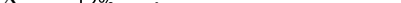
- Molecule 31: U4/U6.U5 tri-snRNP-associated protein 2



- Molecule 32: Probable ATP-dependent RNA helicase DDX23

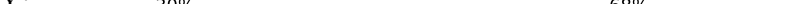


- Molecule 33: U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein

Chain 4X:  12% 86%

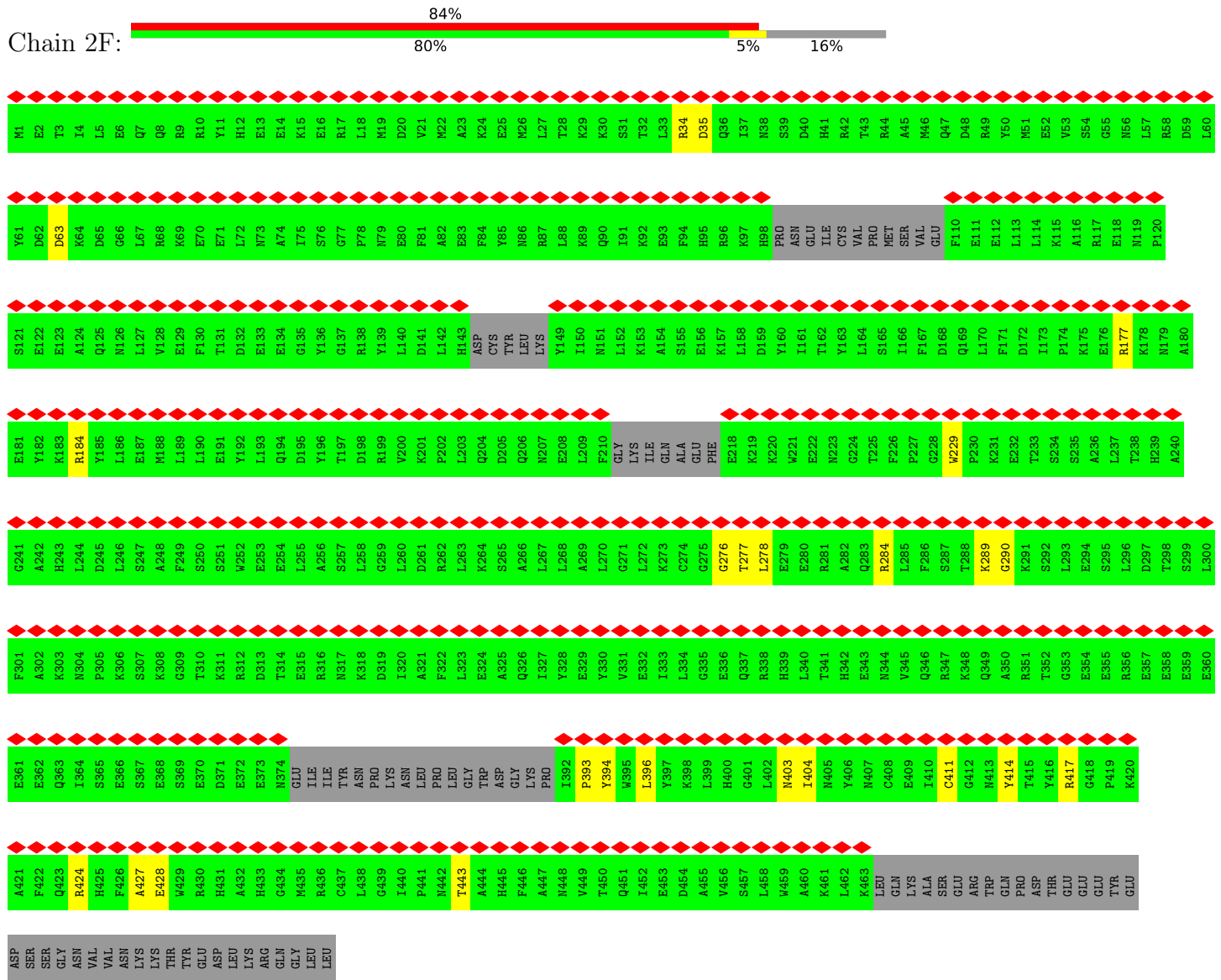
[illegible]

- Molecule 34: Serine/threonine-protein kinase PRP4 homolog

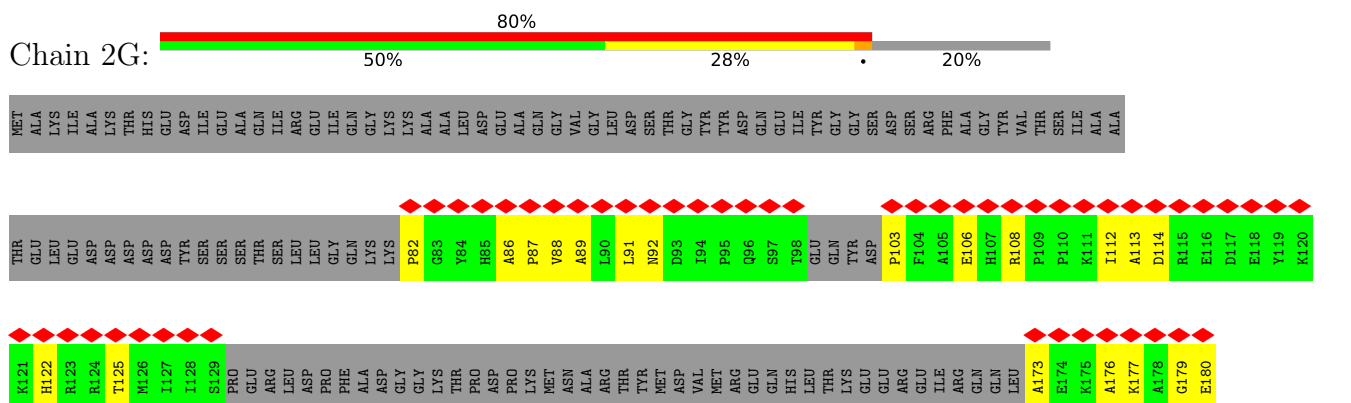
Chain 4Y: 

[illegible]

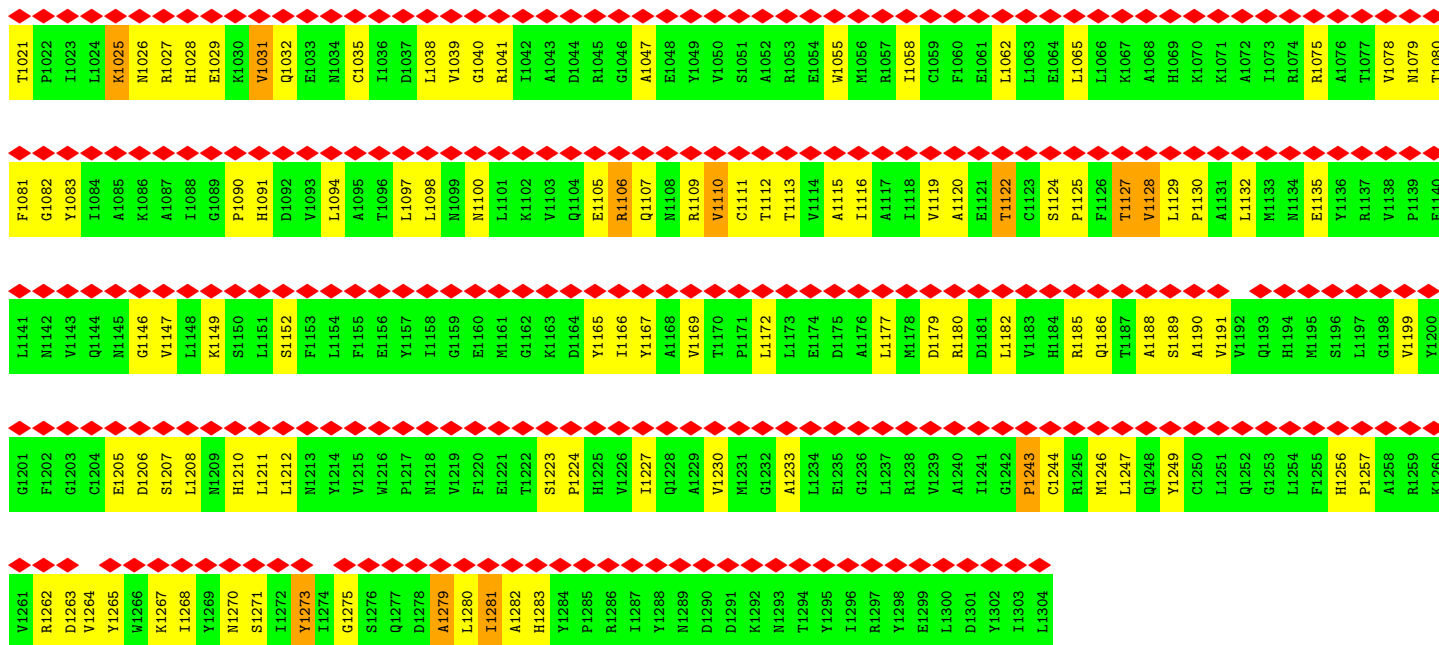
- Molecule 40: Splicing factor 3A subunit 3



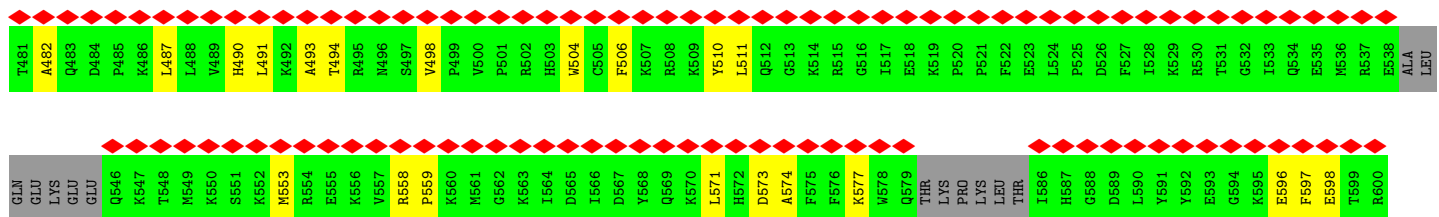
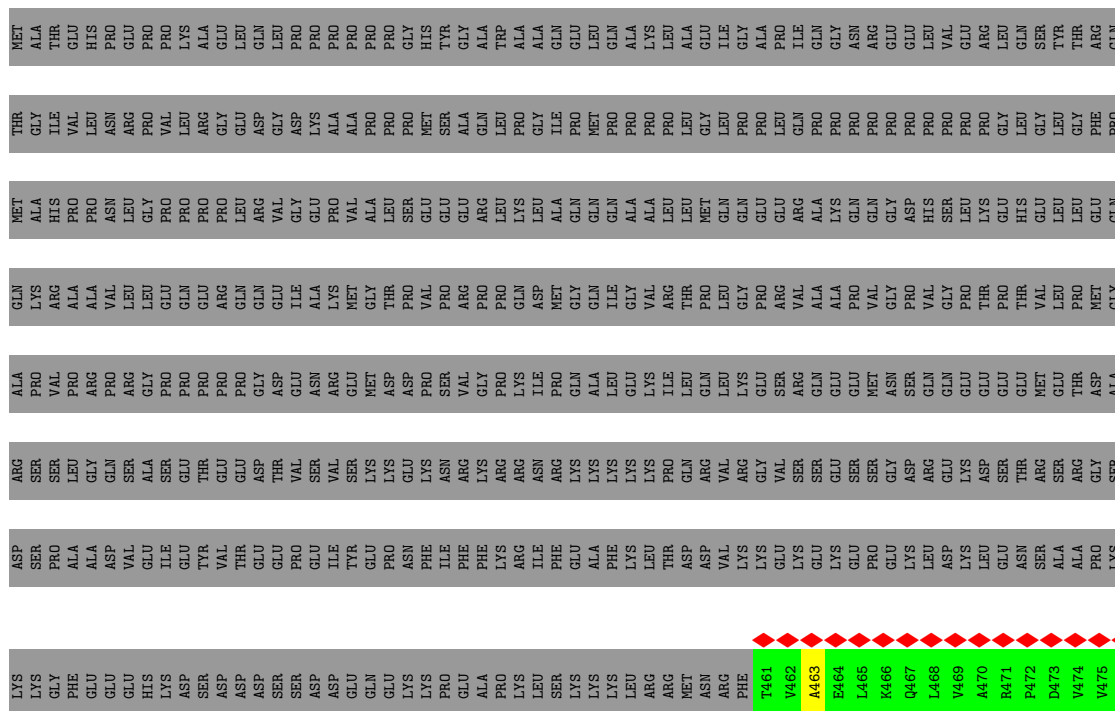
- Molecule 41: Splicing factor 3B subunit 1



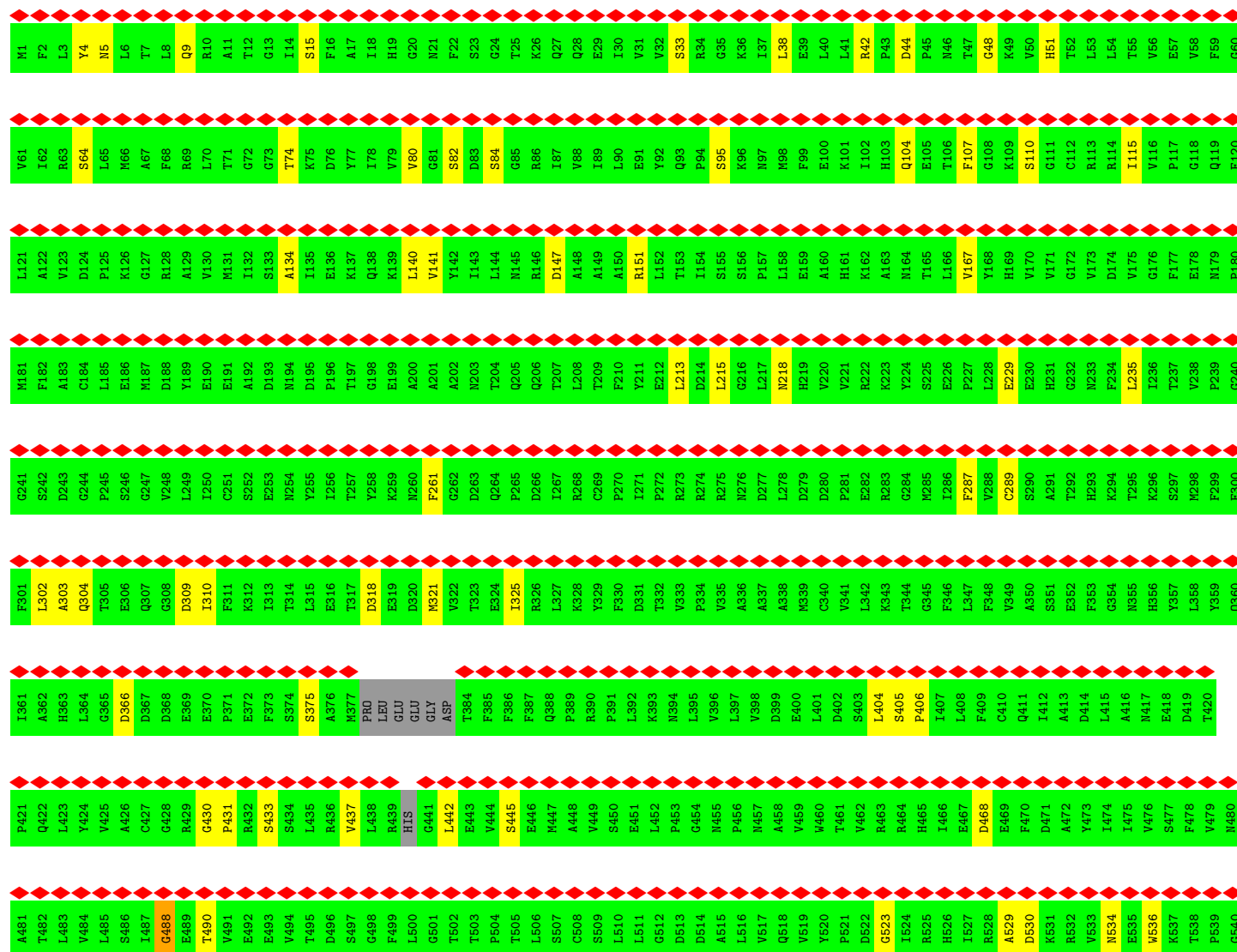
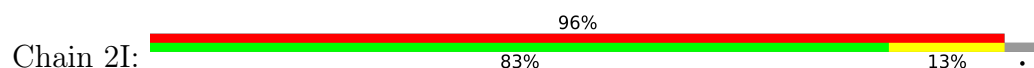
V961	Q901	A941	D781	I721	R661	A601	S541	D481	Y421	GLY	R301	G241	L181
M962	E902	M942	E782	E722	H662	K602	P542	V482	V422	THR	D302	S242	K182
K963	Q903	K963	E783	F723	G664	A603	T663	V482	I424	ALA	T303	E243	V183
T964	T904	V844	M784	S723	G664	A604	L544	E484	I424	MET	P304	T244	V184
C965	T905	G845	K785	D725	I665	G605	E545	S485	R425	ASN	G305	P245	N185
Q966	E906	A846	K786	S726	K666	L606	D546	THR	T426	MET	H306	G246	G186
E967	D907	A847	T787	V727	I667	A607	Q547	SER	T426	ALA	G307	A247	A187
E968	S908	E948	V788	L728	V668	T608	E548	PRO	A428	THR	S308	T248	A188
K969	V909	L849	L789	K729	Q669	M609	R549	E490	R429	THR	G309	T249	A189
L970	H910	T850	K790	P730	Q670	I610	H550	E491	R429	PRO	W310	G250	S190
M971	L911	S851	V791	L731	I671	S611	L551	E491	K430	GLY	A311	G250	S190
G972	N912	R852	V792	K732	A672	T612	L552	Q492	L431	ILE	E312	S251	GLN
H973	G913	K793	K793	L673	I673	M613	V553	K493	T432	HIS	T313	K252	PRO
L974	F914	V854	Q794	G734	L674	R614	K554	E494	A433	SER	P314	W254	LYS
G975	G915	D855	C795	I735	M675	P615	V555	K495	T434	MET	R315	D255	ARG
V976	T916	D856	C796	K736	G676	D616	I556	K496	P435	THR	T316	P256	LYS
V977	V917	L857	G797	T737	C677	I617	D557	L497	T436	GLU	D317	T257	ARG
L978	V918	K958	T798	H738	A678	D618	R558	K499	L438	LEU	R318	P258	TRP
Y979	N919	D859	D799	R739	I679	M619	L559	L500	G439	GLN	G319	S259	ASP
E980	A920	E860	G800	G740	L680	M620	L560	L501	G440	ALA	G320	HIS	GLN
Y981	L921	A861	V801	K741	P681	D621	Y561	L502	M441	THR	D321	THR	THR
L982	G922	E862	E802	G742	H682	E622	K362	K503	T442	TRP	S322	ALA	D205
G983	K923	Q863	L743	L743	L683	Y623	L563	I504	G443	GLY	G324	GLY	Q206
E984	R924	Y864	N804	A744	R684	V624	D564	K505	F444	GLU	E325	ALA	T207
E985	V925	R865	Y805	A745	S685	R625	D565	N506	H445	ILE	T326	THR	P208
Y986	K926	K866	I806	F746	L686	N626	L566	G507	M446	ASP	G209	PRO	G209
P987	P927	M867	K807	T747	V687	T627	V567	T508	Q447	E394	P327	GLY	A210
E988	Y928	V868	T808	K748	E888	T628	R568	P509	THR	R395	T328	ARG	T211
V989	L929	M869	E809	A749	P689	A629	P569	P510	GLU	N396	GLY	GLY	P212
L990	P930	E870	I810	I750	I690	R630	Y570	M511	ASP	R397	THR	THR	K213
G991	Q931	T871	L811	G751	E691	A631	V571	R512	ARG	P398	ALA	PRO	K214
S992	I932	L872	P812	Y752	H692	F632	H572	K513	MET	L399	LYS	GLY	L215
L994	G934	K874	F814	L754	L694	V634	A574	A514	K454	S400	ARG	ALA	S216
G995	T935	I875	R815	P755	V695	V635	L575	A515	S455	D401	LYS	THR	S217
A996	V936	M876	K816	L756	D696	A636	V576	R517	V456	E402	ARG	GLY	W218
L997	T937	G877	H817	T757	E697	S637	V577	Q518	M457	L404	ASP	GLY	D219
K998	W938	M878	F818	D758	Q698	A638	I578	I519	D458	D405	GLU	GLY	Q220
A999	R939	L879	W819	A759	K699	L639	E579	T520	Q459	A406	THR	ALA	A221
I1000	L940	G980	Q820	E760	Q700	G640	P580	D521	P460	M407	PRO	ALA	E222
V1001	N941	A881	H821	Y761	V701	I641	L581	D521	S461	ALA	ALA	SER	T223
N1002	N942	A882	R822	A762	R702	P642	L582	A523	G462	K522	SER	SER	G225
K1003	K943	D883	M823	K763	I703	S643	D583	R524	M464	P409	GLN	ALA	G225
I1004	L884	I884	A824	Y764	I704	L644	D584	E525	P465	G411	GLY	ARG	H226
G1005	D885	D885	L825	Y765	S705	L645	E585	F526	F466	Y412	GLY	ASN	T227
M1006	K946	H886	D826	T766	A706	P646	D586	G527	L467	K413	THR	ARG	P228
V947	V947	K887	R827	R767	A707	F647	Y587	A528	K468	V414	VAL	LYS	S229
H1007	K948	L888	E828	E768	A708	L648	V588	G529	P469	L415	LEU	GLU	L230
K1008	Q948	E889	R829	V769	I709	K649	Y589	P530	D470	THR	THR	PRO	W231
M1009	Q949	E890	N829	V769	A709	A650	A589	P530	P416	THR	PRO	LYS	R231
T1010	Q950	E890	Y830	M770	A710	V651	R590	L531	D471	GLY	LYS	THR	D232
P1011	A951	Q891	R831	L771	A711	C651	V591	F532	I472	P418	E234	E300	D233
P1012	A952	L892	Q832	I772	L712	K652	E592	N532	Q473	A419	THR	THR	E234
I1013	D953	I893	L833	T773	L713	K653	G593	Q534	Y474	G420	PRO	THR	T235
K1014	L954	D894	V834	I774	E714	S654	R594	I535	F475		ILE		P236
D1015	P955	G995	D835	R775	A715	K655	E595	L536	D476				G237
L1016	S956	I896	T836	E776	A716	K656	I596	P537	K477				R238
L1017	R957	L897	T837	F777	T717	S657	I597	L538	L478				A239
P1018	T958	Y898	V838	Q778	P718	W658	S598	L539	L479				K240
R1019	V960	F900	E839	S779	G720	Q659	N599	M540	V480				



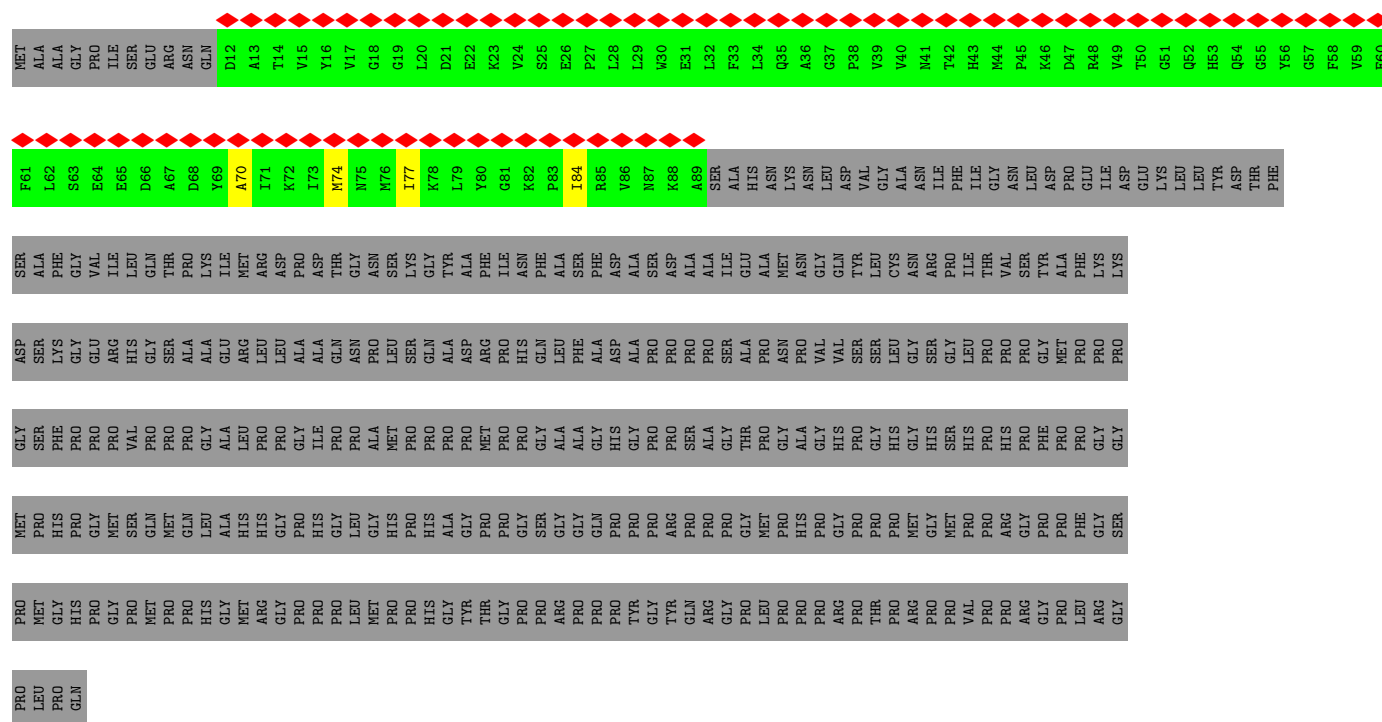
- Molecule 42: Splicing factor 3B subunit 2



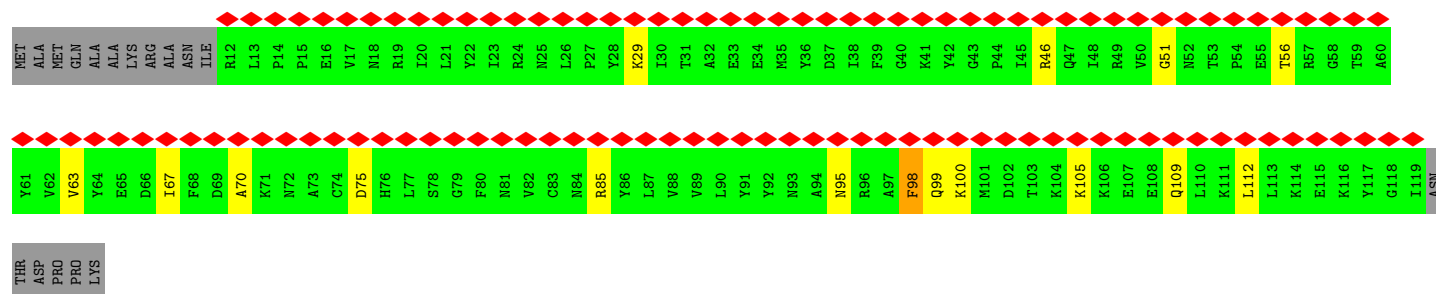
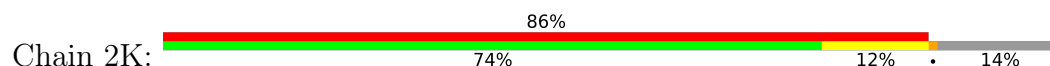
- Molecule 43: Splicing factor 3B subunit 3



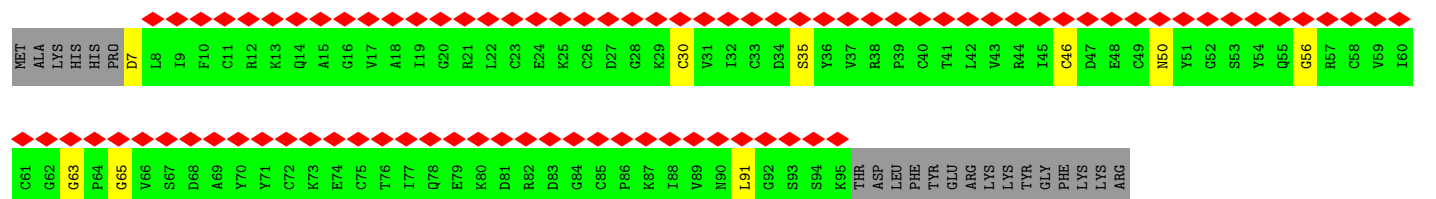
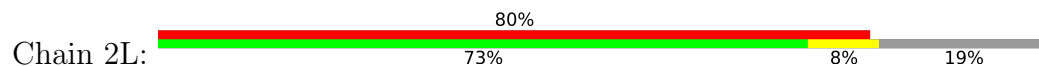




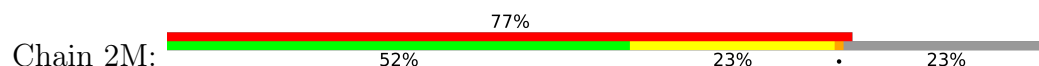
• Molecule 45: Splicing factor 3B subunit 6



• Molecule 46: PHD finger-like domain-containing protein 5A



• Molecule 47: Splicing factor 3B subunit 5



K61	A62	R63	Y64	R65	F66	N67	L68	M69	E70	K71	M72	L73	Q74	P75	C76	G77	P78	P79	A80	ASP	LYS	PRO	GLU	GLU	ASN
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	140426	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.381	Depositor
Minimum map value	-1.074	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.065	Depositor
Recommended contour level	0.25	Depositor
Map size ($\text{\AA}$)	563.2, 563.2, 563.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.62	6/1368 (0.4%)	0.69	2/2122 (0.1%)
2	6A	0.34	2/1398 (0.1%)	0.53	6/2172 (0.3%)
3	6a	0.70	0/355	1.27	0/442
4	6b	0.75	0/294	1.37	3/364 (0.8%)
5	6c	0.59	0/294	1.32	3/364 (0.8%)
6	6d	0.71	0/286	1.28	2/354 (0.6%)
7	6e	0.71	0/279	1.40	2/347 (0.6%)
8	6f	0.60	0/258	1.14	0/319
9	6g	0.68	0/242	1.21	1/299 (0.3%)
10	5A	0.23	0/2673	0.55	10/4156 (0.2%)
11	5B	0.16	0/18786	0.33	1/25502 (0.0%)
12	5C	0.16	0/6879	0.36	1/9344 (0.0%)
13	5D	0.13	0/16393	0.33	0/22174
14	5E	0.26	0/1495	0.66	0/2074
15	2a	0.86	0/339	1.19	2/422 (0.5%)
15	4a	0.30	0/404	0.71	0/561
15	5a	0.86	0/339	1.18	2/422 (0.5%)
16	2b	0.89	0/327	1.10	0/407
16	4b	0.32	0/400	0.78	0/556
16	5b	0.89	0/327	1.11	0/407
17	2c	1.18	0/338	1.20	1/419 (0.2%)
17	4c	0.34	0/454	0.78	0/631
17	5c	1.14	1/387 (0.3%)	1.22	1/482 (0.2%)
18	2d	1.24	1/295 (0.3%)	1.26	0/367
18	4d	0.39	0/350	0.78	0/483
18	5d	1.24	0/291	1.26	0/362
19	2e	1.02	0/315	1.26	0/392
19	4e	0.33	0/375	0.91	2/521 (0.4%)
19	5e	1.03	0/315	1.27	1/392 (0.3%)
20	2f	0.85	0/266	1.03	0/329
20	4f	0.34	0/357	0.81	0/494
20	5f	0.86	0/295	1.05	0/367

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
21	2g	0.81	0/318	1.01	0/394
21	4g	0.30	0/408	0.72	0/566
21	5g	0.78	0/307	1.01	0/382
22	4A	0.38	1/2960 (0.0%)	0.58	11/4599 (0.2%)
23	4B	0.17	0/949	0.40	0/1314
24	4C	0.13	0/1764	0.36	0/2450
25	4D	0.29	0/1767	0.57	4/2434 (0.2%)
26	4E	0.11	0/614	0.29	0/855
27	4F	0.14	0/1198	0.31	0/1620
28	4G	0.16	0/4833	0.37	2/6625 (0.0%)
29	4R	0.22	0/891	0.45	0/1188
30	4S	0.12	0/555	0.33	0/731
31	4T	0.15	0/3845	0.34	0/5208
32	4U	0.13	0/1356	0.30	0/1790
33	4X	0.10	0/187	0.27	0/245
34	4Y	0.49	0/1592	0.99	2/2215 (0.1%)
35	2A	0.71	12/2576 (0.5%)	1.11	27/4003 (0.7%)
36	2B	0.99	0/647	2.34	33/807 (4.1%)
37	2C	0.96	0/375	1.97	7/467 (1.5%)
38	2D	0.29	0/972	0.73	2/1260 (0.2%)
39	2E	0.47	0/373	1.09	2/461 (0.4%)
40	2F	0.39	0/1688	0.92	2/2102 (0.1%)
41	2G	1.72	36/4184 (0.9%)	1.43	29/5216 (0.6%)
42	2H	1.17	0/722	1.25	3/892 (0.3%)
43	2I	1.39	24/4664 (0.5%)	1.20	10/5816 (0.2%)
44	2J	1.02	0/311	0.99	0/387
45	2K	1.27	2/431 (0.5%)	1.27	1/537 (0.2%)
46	2L	1.16	0/355	1.12	0/442
47	2M	1.59	1/263 (0.4%)	1.24	0/327
All	All	0.61	86/98279 (0.1%)	0.72	175/133380 (0.1%)

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
15	4a	0	1
17	2c	0	1
17	5c	0	1
18	4d	0	1
19	4e	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
22	4A	0	1
24	4C	0	1
40	2F	0	1
41	2G	0	11
42	2H	0	3
43	2I	0	11
45	2K	0	1
47	2M	0	1
All	All	0	35

All (86) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	2G	407	MET	N-CA	22.59	1.71	1.46
41	2G	406	ALA	C-N	14.97	1.52	1.33
41	2G	1243	PRO	N-CA	-9.49	1.35	1.47
22	4A	87	C	O3'-P	9.24	1.75	1.61
41	2G	944	SER	N-CA	-8.47	1.34	1.46
43	2I	84	SER	CA-C	-7.80	1.42	1.53
35	2A	142	C	C1'-N1	7.45	1.59	1.48
41	2G	868	VAL	CA-C	-7.21	1.42	1.52
43	2I	82	SER	CA-C	-7.19	1.43	1.52
43	2I	110	SER	C-O	-7.19	1.15	1.23
43	2I	1101	VAL	CA-C	-7.12	1.44	1.52
35	2A	182	U	C1'-N1	7.09	1.59	1.48
43	2I	1101	VAL	C-O	-7.04	1.16	1.24
35	2A	150	U	C1'-N1	7.01	1.58	1.48
41	2G	1273	TYR	CA-C	-6.74	1.43	1.52
35	2A	151	C	C1'-N1	6.71	1.58	1.48
41	2G	939	ARG	CA-C	-6.68	1.44	1.52
35	2A	97	G	C1'-N9	-6.67	1.38	1.48
35	2A	141	C	C1'-N1	6.60	1.58	1.48
43	2I	141	VAL	C-O	-6.55	1.17	1.24
43	2I	289	CYS	C-O	-6.54	1.15	1.23
35	2A	184	C	C1'-N1	6.54	1.58	1.48
43	2I	64	SER	N-CA	-6.54	1.38	1.46
35	2A	148	C	C1'-N1	6.53	1.58	1.48
45	2K	98	PHE	N-CA	-6.48	1.37	1.46
41	2G	814	PHE	CA-C	-6.21	1.45	1.52
2	6A	59	G	O5'-C5'	6.12	1.51	1.42
43	2I	213	LEU	CA-C	-6.04	1.45	1.52
41	2G	678	ALA	N-CA	-6.04	1.38	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	2I	64	SER	C-O	-6.04	1.16	1.23
1	A	8	U	C1'-N1	6.02	1.56	1.47
1	A	9	U	C1'-N1	6.01	1.56	1.47
1	A	7	U	C1'-N1	5.98	1.56	1.47
43	2I	140	LEU	CA-C	-5.95	1.45	1.52
41	2G	1167	TYR	CA-C	-5.92	1.45	1.52
41	2G	945	ALA	CA-C	-5.91	1.44	1.52
35	2A	48	A	C1'-N9	-5.90	1.39	1.48
43	2I	302	LEU	C-O	-5.85	1.17	1.24
41	2G	940	LEU	CA-C	-5.85	1.45	1.52
43	2I	167	VAL	CA-C	-5.84	1.46	1.52
41	2G	571	VAL	CA-C	-5.84	1.46	1.52
2	6A	59	G	P-O5'	5.80	1.68	1.59
41	2G	893	ILE	N-CA	-5.78	1.39	1.46
43	2I	115	ILE	N-CA	-5.77	1.40	1.46
45	2K	95	ASN	N-CA	-5.70	1.38	1.46
35	2A	65	U	C1'-N1	5.70	1.56	1.48
43	2I	235	LEU	C-O	-5.67	1.16	1.23
41	2G	989	VAL	CA-C	-5.66	1.45	1.52
41	2G	482	VAL	C-O	-5.65	1.17	1.24
43	2I	104	GLN	CA-C	-5.64	1.46	1.52
43	2I	1153	PRO	C-O	-5.61	1.18	1.24
41	2G	233	ASP	CA-C	-5.60	1.45	1.52
41	2G	1177	LEU	C-O	-5.59	1.17	1.24
43	2I	80	VAL	C-O	-5.58	1.18	1.24
41	2G	439	GLY	CA-C	5.54	1.56	1.52
41	2G	838	VAL	N-CA	-5.54	1.40	1.46
35	2A	110	A	C1'-N9	-5.53	1.39	1.48
1	A	10	C	C1'-N1	5.53	1.55	1.47
1	A	11	C	C1'-N1	5.53	1.55	1.47
41	2G	235	THR	C-O	-5.48	1.19	1.24
43	2I	1123	SER	CA-C	-5.47	1.45	1.52
41	2G	738	HIS	N-CA	-5.44	1.39	1.45
43	2I	134	ALA	C-O	-5.43	1.18	1.23
43	2I	107	PHE	CA-C	-5.36	1.45	1.52
41	2G	627	THR	N-CA	-5.35	1.40	1.46
43	2I	941	HIS	C-O	5.33	1.30	1.23
43	2I	38	LEU	CA-C	-5.33	1.46	1.52
41	2G	898	TYR	C-N	-5.28	1.27	1.33
1	A	46	U	C1'-N1	5.27	1.55	1.47
41	2G	672	ALA	CA-C	-5.26	1.46	1.52
41	2G	721	ILE	N-CA	-5.26	1.40	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	2G	864	TYR	CA-C	-5.24	1.46	1.52
47	2M	44	MET	C-O	-5.23	1.18	1.24
41	2G	601	ALA	N-CA	-5.23	1.40	1.46
41	2G	680	LEU	C-O	-5.23	1.19	1.24
41	2G	415	LEU	C-N	5.19	1.39	1.33
43	2I	1034	THR	CA-C	-5.19	1.47	1.53
41	2G	944	SER	CA-C	5.17	1.59	1.53
41	2G	407	MET	C-O	-5.14	1.18	1.23
41	2G	776	GLU	CA-C	-5.14	1.45	1.52
41	2G	1281	ILE	CA-C	-5.13	1.46	1.52
35	2A	60	U	C1'-N1	5.12	1.56	1.48
41	2G	1279	ALA	CA-C	-5.09	1.46	1.52
18	2d	14	LEU	CA-C	5.07	1.59	1.52
17	5c	73	MET	CA-C	-5.04	1.46	1.52
41	2G	899	ALA	N-CA	-5.04	1.40	1.46

All (175) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	2G	406	ALA	CA-C-N	17.64	147.35	120.89
41	2G	406	ALA	C-N-CA	17.64	147.35	120.89
41	2G	406	ALA	CA-C-O	-13.03	105.77	120.24
41	2G	108	ARG	CA-C-N	12.17	132.92	120.38
41	2G	108	ARG	C-N-CA	12.17	132.92	120.38
10	5A	78	U	P-O3'-C3'	-10.45	104.52	120.20
10	5A	57	G	P-O3'-C3'	-10.41	104.58	120.20
22	4A	87	C	O3'-P-O5'	10.23	119.35	104.00
43	2I	916	ASN	CA-C-N	9.50	131.72	119.84
43	2I	916	ASN	C-N-CA	9.50	131.72	119.84
41	2G	114	ASP	N-CA-C	9.44	121.33	111.14
35	2A	149	A	O3'-P-O5'	-8.65	91.02	104.00
35	2A	180	G	O3'-P-O5'	-8.62	91.07	104.00
35	2A	182	U	O3'-P-O5'	-8.62	91.08	104.00
35	2A	183	G	O3'-P-O5'	-8.62	91.08	104.00
35	2A	148	C	O3'-P-O5'	-8.59	91.12	104.00
35	2A	141	C	O3'-P-O5'	-8.57	91.15	104.00
35	2A	181	G	O3'-P-O5'	-8.56	91.16	104.00
7	6e	45	LEU	N-CA-C	8.56	123.58	112.12
35	2A	114	A	O3'-P-O5'	-8.55	91.18	104.00
35	2A	113	G	O3'-P-O5'	-8.54	91.19	104.00
35	2A	150	U	O3'-P-O5'	-8.54	91.20	104.00
10	5A	77	G	P-O3'-C3'	-8.49	107.46	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	4A	76	C	P-O3'-C3'	-8.19	107.92	120.20
28	4G	707	ASP	CA-C-N	8.19	136.44	121.70
28	4G	707	ASP	C-N-CA	8.19	136.44	121.70
22	4A	77	A	P-O3'-C3'	-8.07	108.09	120.20
36	2B	16	THR	CA-C-O	-8.03	111.77	120.36
36	2B	99	SER	N-CA-C	8.03	122.85	112.26
22	4A	55	U	P-O3'-C3'	-7.96	108.26	120.20
12	5C	679	PRO	CA-N-CD	-7.91	100.93	112.00
22	4A	79	U	P-O3'-C3'	-7.91	108.34	120.20
36	2B	117	TYR	CA-C-O	7.73	128.52	120.40
35	2A	168	A	P-O5'-C5'	-7.63	109.45	120.90
22	4A	78	A	P-O3'-C3'	-7.49	108.97	120.20
35	2A	167	U	O3'-P-O5'	-7.30	93.05	104.00
22	4A	74	C	P-O3'-C3'	-7.29	109.26	120.20
22	4A	75	C	P-O3'-C3'	-7.25	109.32	120.20
25	4D	350	GLN	N-CA-C	-7.20	103.51	111.36
41	2G	1100	ASN	N-CA-C	7.17	119.23	110.41
36	2B	71	VAL	CA-C-N	7.15	131.55	120.75
36	2B	71	VAL	C-N-CA	7.15	131.55	120.75
41	2G	613	MET	N-CA-C	7.15	121.71	112.92
41	2G	407	MET	N-CA-C	7.03	121.93	111.04
34	4Y	965	LEU	CA-C-N	7.01	126.94	120.21
34	4Y	965	LEU	C-N-CA	7.01	126.94	120.21
35	2A	170	C	C3'-C2'-O2'	-6.99	104.11	114.60
40	2F	290	GLY	N-CA-C	6.89	121.00	112.73
36	2B	121	LEU	CA-C-O	6.88	128.87	121.44
38	2D	199	ARG	CA-C-N	6.87	127.82	120.47
38	2D	199	ARG	C-N-CA	6.87	127.82	120.47
36	2B	4	LEU	N-CA-C	-6.86	98.04	108.67
37	2C	53	PHE	CA-C-O	-6.77	112.87	120.32
41	2G	1120	ALA	CA-C-N	-6.72	111.30	120.44
41	2G	1120	ALA	C-N-CA	-6.72	111.30	120.44
39	2E	158	ARG	N-CA-C	6.71	118.68	111.36
35	2A	164	C	C5'-C4'-O4'	-6.61	99.19	109.10
2	6A	59	G	C2'-C3'-O3'	-6.59	103.81	113.70
45	2K	85	ARG	N-CA-C	6.51	120.02	109.40
36	2B	87	LEU	CA-C-N	6.43	126.19	119.05
36	2B	87	LEU	C-N-CA	6.43	126.19	119.05
10	5A	80	U	C4'-C3'-O3'	6.43	119.04	109.40
41	2G	406	ALA	O-C-N	6.42	130.57	122.23
10	5A	56	C	P-O3'-C3'	-6.37	110.65	120.20
35	2A	168	A	C5'-C4'-C3'	-6.34	106.50	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	2A	169	C	P-O3'-C3'	6.26	129.60	120.20
36	2B	40	THR	CA-C-N	6.24	131.45	122.40
36	2B	40	THR	C-N-CA	6.24	131.45	122.40
41	2G	406	ALA	N-CA-C	6.24	119.36	111.69
2	6A	58	G	P-O3'-C3'	-6.18	110.92	120.20
41	2G	1180	ARG	N-CA-C	-6.16	103.28	111.96
36	2B	73	ASN	N-CA-C	6.15	119.84	111.17
22	4A	87	C	P-O3'-C3'	-6.12	111.01	120.20
42	2H	559	PRO	N-CA-C	6.10	120.05	111.33
41	2G	1275	GLY	N-CA-C	-6.08	104.94	111.93
10	5A	58	U	O3'-P-O5'	-6.06	94.91	104.00
22	4A	73	U	P-O3'-C3'	-6.06	111.12	120.20
36	2B	79	ILE	CA-C-N	6.03	125.83	120.10
36	2B	79	ILE	C-N-CA	6.03	125.83	120.10
41	2G	415	LEU	O-C-N	-6.03	114.38	121.32
2	6A	56	A	P-O3'-C3'	-5.99	111.22	120.20
2	6A	59	G	OP2-P-O3'	-5.98	90.05	108.00
37	2C	46	MET	N-CA-C	-5.92	104.74	111.07
41	2G	465	PRO	N-CA-C	-5.87	106.46	114.80
2	6A	57	U	P-O3'-C3'	-5.86	111.41	120.20
10	5A	58	U	C2'-C3'-O3'	5.85	122.48	113.70
36	2B	113	LYS	N-CA-C	5.85	118.41	111.33
35	2A	163	G	O3'-P-O5'	-5.85	95.22	104.00
22	4A	87	C	OP2-P-O3'	-5.84	90.49	108.00
2	6A	59	G	C4'-C3'-O3'	5.83	121.74	113.00
5	6c	2	LEU	CA-C-N	5.82	127.11	119.84
5	6c	2	LEU	C-N-CA	5.82	127.11	119.84
6	6d	13	LEU	CA-C-N	5.81	125.95	119.32
6	6d	13	LEU	C-N-CA	5.81	125.95	119.32
36	2B	50	SER	CA-C-O	5.80	127.70	121.55
25	4D	380	PHE	CA-CB-CG	5.77	119.57	113.80
10	5A	76	A	P-O3'-C3'	-5.76	111.56	120.20
43	2I	679	LEU	N-CA-C	5.75	119.46	110.32
36	2B	27	ARG	CA-C-N	5.74	128.78	120.11
36	2B	27	ARG	C-N-CA	5.74	128.78	120.11
7	6e	63	ALA	N-CA-C	5.69	118.04	109.23
35	2A	164	C	P-O3'-C3'	5.68	128.72	120.20
41	2G	942	ASN	CA-C-N	-5.66	114.75	124.82
41	2G	942	ASN	C-N-CA	-5.66	114.75	124.82
43	2I	887	ALA	N-CA-C	-5.64	101.69	110.10
35	2A	160	A	P-O5'-C5'	-5.61	112.49	120.90
15	2a	52	LYS	CA-C-N	-5.61	114.15	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	2a	52	LYS	C-N-CA	-5.61	114.15	119.76
10	5A	80	U	O3'-P-O5'	-5.61	95.59	104.00
36	2B	71	VAL	O-C-N	-5.60	115.58	122.57
36	2B	32	PRO	CA-C-N	5.59	130.76	122.99
36	2B	32	PRO	C-N-CA	5.59	130.76	122.99
41	2G	942	ASN	N-CA-C	-5.58	98.91	110.80
11	5B	1550	GLY	N-CA-C	5.58	120.21	112.57
15	5a	52	LYS	CA-C-N	-5.56	114.20	119.76
15	5a	52	LYS	C-N-CA	-5.56	114.20	119.76
35	2A	168	A	O4'-C1'-C2'	-5.54	102.06	107.60
35	2A	165	A	N9-C1'-C2'	5.54	120.31	112.00
35	2A	157	G	P-O5'-C5'	-5.51	112.63	120.90
36	2B	34	ILE	CA-C-O	-5.50	114.25	120.74
36	2B	159	GLU	N-CA-C	-5.47	104.96	111.69
36	2B	16	THR	O-C-N	5.47	129.46	123.22
41	2G	1128	VAL	N-CA-C	5.46	117.92	111.09
4	6b	49	HIS	N-CA-C	-5.46	106.70	113.19
42	2H	511	LEU	N-CA-C	5.45	117.55	108.99
41	2G	1105	GLU	N-CA-C	5.42	117.56	108.73
1	A	28	G	C2'-C3'-O3'	-5.42	105.58	113.70
43	2I	488	GLY	N-CA-C	-5.42	106.38	115.80
25	4D	357	ARG	CB-CA-C	-5.40	109.88	117.23
1	A	28	G	C4'-C3'-O3'	-5.40	104.91	113.00
41	2G	751	GLY	CA-C-N	-5.38	111.74	120.72
41	2G	751	GLY	C-N-CA	-5.38	111.74	120.72
36	2B	40	THR	N-CA-C	-5.38	106.22	112.89
10	5A	78	U	C3'-C2'-C1'	-5.36	95.94	101.30
36	2B	125	VAL	CA-C-N	5.34	127.97	120.28
36	2B	125	VAL	C-N-CA	5.34	127.97	120.28
39	2E	199	TRP	N-CA-C	5.33	117.32	107.73
25	4D	355	GLY	N-CA-C	5.32	118.89	110.96
4	6b	92	VAL	N-CA-C	5.28	115.90	109.30
41	2G	1106	ARG	N-CA-C	5.26	118.84	111.74
35	2A	171	U	C2'-C3'-O3'	-5.26	105.81	113.70
40	2F	289	LYS	N-CA-C	5.26	122.00	110.80
36	2B	146	ASP	CA-C-N	5.25	130.02	122.40
36	2B	146	ASP	C-N-CA	5.25	130.02	122.40
5	6c	30	VAL	N-CA-C	5.25	116.15	111.90
43	2I	4	TYR	N-CA-C	-5.23	102.55	110.28
35	2A	170	C	O4'-C1'-C2'	-5.22	100.58	105.80
9	6g	69	VAL	N-CA-C	5.21	115.40	108.27
37	2C	20	LYS	N-CA-C	5.20	117.35	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	2C	51	GLN	N-CA-C	5.17	117.53	109.52
4	6b	44	HIS	N-CA-C	-5.17	107.04	113.55
17	5c	99	MET	N-CA-C	5.15	116.89	108.76
41	2G	415	LEU	CA-C-N	5.14	125.67	120.38
41	2G	415	LEU	C-N-CA	5.14	125.67	120.38
35	2A	160	A	N9-C1'-C2'	5.11	119.67	112.00
37	2C	83	TYR	CA-C-O	-5.11	115.22	121.05
36	2B	90	LEU	O-C-N	5.11	129.38	122.59
36	2B	90	LEU	CA-C-O	-5.10	113.22	120.51
19	4e	53	TYR	CA-C-N	5.09	129.78	122.40
19	4e	53	TYR	C-N-CA	5.09	129.78	122.40
35	2A	155	C	P-O3'-C3'	5.08	127.82	120.20
43	2I	404	LEU	N-CA-C	-5.08	105.82	111.36
19	5e	85	THR	N-CA-C	-5.08	105.93	112.68
36	2B	83	LEU	N-CA-C	5.08	117.47	111.33
17	2c	99	MET	N-CA-C	5.08	116.78	108.76
37	2C	38	VAL	O-C-N	5.07	127.05	121.83
37	2C	48	MET	N-CA-C	5.07	119.46	113.28
35	2A	156	U	C4'-C3'-C2'	5.06	107.66	102.60
43	2I	9	GLN	N-CA-C	-5.05	101.52	109.25
41	2G	1002	ASN	CA-C-N	-5.04	118.03	122.97
41	2G	1002	ASN	C-N-CA	-5.04	118.03	122.97
43	2I	445	SER	N-CA-C	-5.03	104.04	110.53
36	2B	81	GLU	N-CA-C	5.02	118.56	112.23
42	2H	498	VAL	N-CA-C	5.01	113.35	107.89
43	2I	213	LEU	N-CA-C	-5.01	103.54	110.35

There are no chirality outliers.

All (35) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
40	2F	443	THR	Peptide
41	2G	1025	LYS	Peptide
41	2G	1122	THR	Peptide
41	2G	1127	THR	Peptide
41	2G	1179	ASP	Peptide
41	2G	1199	VAL	Peptide
41	2G	220	GLN	Peptide
41	2G	415	LEU	Mainchain,Peptide
41	2G	689	ILE	Peptide
41	2G	941	ASN	Peptide
41	2G	944	SER	Peptide

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Mol	Chain	Res	Type	Group
42	2H	553	MET	Peptide
42	2H	558	ARG	Peptide
42	2H	571	LEU	Peptide
43	2I	261	PHE	Peptide
43	2I	366	ASP	Peptide
43	2I	468	ASP	Peptide
43	2I	530	ASP	Peptide
43	2I	534	ASN	Peptide
43	2I	552	ARG	Peptide
43	2I	670	GLN	Peptide
43	2I	678	VAL	Peptide
43	2I	74	THR	Peptide
43	2I	980	LYS	Peptide
43	2I	986	ILE	Peptide
45	2K	29	LYS	Peptide
47	2M	74	GLN	Peptide
17	2c	112	ASN	Peptide
22	4A	90	G	Sidechain
24	4C	459	PRO	Peptide
15	4a	53	PRO	Peptide
18	4d	40	MET	Peptide
19	4e	51	ASP	Peptide
17	5c	112	ASN	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1232	0	627	152	0
2	6A	1251	0	630	48	0
3	6a	356	0	94	2	0
4	6b	296	0	76	5	0
5	6c	296	0	77	0	0
6	6d	288	0	78	0	0
7	6e	280	0	81	8	0
8	6f	260	0	75	0	0
9	6g	244	0	71	3	0
10	5A	2398	0	1215	96	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	5B	18281	0	18097	256	0
12	5C	6727	0	6735	92	0
13	5D	16077	0	16192	329	0
14	5E	1497	0	678	1	0
15	2a	340	0	90	4	0
15	4a	405	0	170	4	0
15	5a	340	0	90	0	0
16	2b	328	0	89	0	0
16	4b	401	0	165	1	0
16	5b	328	0	89	5	0
17	2c	340	0	87	1	0
17	4c	455	0	187	3	0
17	5c	388	0	102	7	0
18	2d	296	0	87	0	0
18	4d	351	0	155	3	0
18	5d	292	0	86	10	0
19	2e	316	0	85	1	0
19	4e	376	0	157	6	0
19	5e	316	0	85	4	0
20	2f	268	0	74	1	0
20	4f	358	0	158	3	0
20	5f	296	0	84	5	0
21	2g	320	0	88	0	0
21	4g	409	0	180	3	0
21	5g	308	0	86	4	0
22	4A	2653	0	1346	81	0
23	4B	954	0	412	10	0
24	4C	1765	0	801	8	0
25	4D	1764	0	1004	47	0
26	4E	615	0	279	4	0
27	4F	1169	0	1141	23	0
28	4G	4803	0	3533	67	0
29	4R	874	0	883	19	0
30	4S	549	0	551	8	0
31	4T	3749	0	3768	29	0
32	4U	1338	0	1355	15	0
33	4X	184	0	192	2	0
34	4Y	1595	0	694	11	0
35	2A	2311	0	1170	143	0
36	2B	648	0	167	0	0
37	2C	376	0	102	0	0
38	2D	969	0	621	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
39	2E	376	0	85	1	0
40	2F	1693	0	454	22	0
41	2G	4192	0	1110	233	0
42	2H	728	0	183	9	0
43	2I	4672	0	1260	71	0
44	2J	312	0	87	3	0
45	2K	432	0	114	6	0
46	2L	356	0	105	5	0
47	2M	264	0	70	12	0
48	5B	36	0	6	1	0
49	5C	1	0	0	0	0
50	5C	32	0	12	1	0
51	4T	1	0	0	0	0
All	All	96125	0	68625	1746	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (1746) 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)
41:2G:407:MET:N	41:2G:407:MET:CA	1.71	1.51
2:6A:76:A:N1	23:4B:562:ALA:HB1	1.21	1.50
2:6A:36:A:C8	38:2D:506:SER:HB3	1.54	1.43
1:A:30:C:C2'	1:A:31:C:H5''	1.54	1.38
10:5A:79:C:O5'	10:5A:80:U:H5	1.12	1.28
2:6A:76:A:N1	23:4B:562:ALA:CB	2.03	1.22
1:A:30:C:N4	1:A:31:C:C4	2.10	1.20
2:6A:37:C:H41	38:2D:504:GLY:C	1.49	1.20
10:5A:79:C:O5'	10:5A:80:U:C5	1.98	1.17
1:A:34:G:C8	1:A:35:U:C5	2.34	1.15
1:A:30:C:C4	1:A:31:C:C5	2.34	1.15
1:A:22:C:O2'	1:A:23:G:H5'	1.45	1.14
1:A:30:C:H2'	1:A:31:C:C5'	1.78	1.13
35:2A:156:U:H6	35:2A:156:U:H5''	1.09	1.13
2:6A:76:A:C2	23:4B:562:ALA:HB1	1.85	1.11
25:4D:357:ARG:HG3	25:4D:358:ARG:H	1.08	1.10
1:A:38:C:H4'	1:A:39:U:OP1	1.42	1.06
10:5A:79:C:H3'	10:5A:80:U:C6	1.92	1.05
35:2A:105:G:H2'	35:2A:106:G:H5''	1.37	1.05
1:A:30:C:C3'	1:A:31:C:H5''	1.84	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:6A:36:A:C8	38:2D:506:SER:CB	2.39	1.05
23:4B:462:GLU:CB	29:4R:432:PRO:HG2	1.86	1.05
10:5A:90:U:C5	21:5g:38:ASN:O	2.09	1.04
2:6A:36:A:N7	38:2D:506:SER:CB	2.20	1.04
1:A:34:G:C8	1:A:35:U:C4	2.47	1.02
1:A:40:U:H4'	1:A:41:U:H5'	1.38	1.02
22:4A:31:U:O4	26:4E:61:GLU:N	1.93	1.02
22:4A:79:U:H3'	22:4A:80:A:H8	1.23	1.01
1:A:30:C:C2'	1:A:31:C:C5'	2.38	1.00
1:A:30:C:H2'	1:A:31:C:H5''	1.03	0.99
10:5A:95:G:H1'	18:5d:24:LYS:CA	1.91	0.99
1:A:30:C:C3'	1:A:31:C:C5'	2.40	0.98
35:2A:168:A:H5''	35:2A:168:A:C8	1.98	0.98
27:4F:71:LYS:HE3	38:2D:501:THR:OG1	1.65	0.97
10:5A:79:C:H3'	10:5A:80:U:C5	2.00	0.97
1:A:31:C:C2	35:2A:33:G:C6	2.53	0.97
1:A:31:C:C2	35:2A:33:G:N1	2.32	0.97
25:4D:350:GLN:O	25:4D:351:ARG:HB2	1.64	0.96
22:4A:79:U:H3'	22:4A:80:A:C8	2.01	0.95
41:2G:501:LEU:O	41:2G:504:ILE:N	1.98	0.95
2:6A:76:A:C6	23:4B:562:ALA:CB	2.50	0.95
25:4D:357:ARG:HG3	25:4D:358:ARG:N	1.80	0.94
35:2A:156:U:H5''	35:2A:156:U:C6	2.02	0.94
2:6A:36:A:N7	38:2D:506:SER:OG	1.98	0.94
1:A:31:C:O2	35:2A:33:G:C6	2.20	0.94
2:6A:58:G:H1	25:4D:357:ARG:HH12	0.95	0.94
10:5A:93:U:H1'	17:5c:104:ASP:CA	1.96	0.94
27:4F:68:ASP:HA	38:2D:501:THR:HG21	1.51	0.93
2:6A:36:A:N7	38:2D:506:SER:HB3	1.83	0.92
41:2G:86:ALA:O	41:2G:89:ALA:N	2.02	0.92
10:5A:95:G:H21	10:5A:96:A:H5''	1.36	0.91
1:A:40:U:O2'	1:A:41:U:OP2	1.89	0.91
35:2A:54:U:OP1	40:2F:428:GLU:CA	2.20	0.90
1:A:34:G:N7	1:A:35:U:C4	2.40	0.89
2:6A:37:C:N4	38:2D:504:GLY:C	2.30	0.89
35:2A:168:A:H5''	35:2A:168:A:H8	1.36	0.88
10:5A:90:U:H5	21:5g:38:ASN:O	1.53	0.88
41:2G:793:LYS:O	41:2G:797:GLY:HA3	1.73	0.88
1:A:30:C:H3'	1:A:31:C:C5'	2.04	0.88
2:6A:76:A:C6	23:4B:562:ALA:HB3	2.07	0.88
10:5A:93:U:C1'	17:5c:104:ASP:CA	2.52	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:5A:93:U:O4	18:5d:66:CYS:N	2.06	0.88
28:4G:21:LEU:HD23	28:4G:22:GLY:N	1.89	0.87
35:2A:154:C:O2	35:2A:176:G:N2	2.07	0.87
1:A:23:G:H1	35:2A:39:U:H3	1.20	0.86
1:A:38:C:OP1	1:A:39:U:P	2.34	0.86
1:A:12:U:H2'	1:A:12:U:OP2	1.74	0.86
35:2A:156:U:H6	35:2A:156:U:C5'	1.89	0.85
13:5D:84:MET:HA	13:5D:84:MET:HE3	1.57	0.85
13:5D:1732:MET:HE1	13:5D:1755:LEU:HD11	1.58	0.85
35:2A:40:C:H6	35:2A:40:C:H5''	1.39	0.85
10:5A:79:C:C3'	10:5A:80:U:C6	2.58	0.85
28:4G:19:PRO:HG2	28:4G:21:LEU:HD22	1.57	0.84
1:A:11:C:O2	1:A:11:C:H2'	1.75	0.84
11:5B:682:ASP:OD1	11:5B:683:LEU:N	2.09	0.84
11:5B:1972:THR:OG1	11:5B:1975:GLU:OE1	1.95	0.84
13:5D:1891:THR:HG22	13:5D:1915:ILE:HD11	1.57	0.84
27:4F:71:LYS:CE	38:2D:501:THR:OG1	2.24	0.84
25:4D:357:ARG:HG3	25:4D:358:ARG:HG3	1.59	0.84
41:2G:728:LEU:O	41:2G:731:LEU:N	2.10	0.83
1:A:36:C:H1'	1:A:37:C:OP1	1.78	0.83
35:2A:152:G:N2	35:2A:153:A:N7	2.26	0.83
31:4T:362:HIS:O	31:4T:370:LYS:NZ	2.12	0.83
13:5D:579:GLU:OE2	13:5D:583:THR:OG1	1.97	0.83
1:A:36:C:H4'	1:A:37:C:H5	1.44	0.82
13:5D:48:GLU:N	13:5D:48:GLU:OE1	2.12	0.82
13:5D:1430:GLU:OE2	13:5D:1463:ASN:ND2	2.12	0.82
31:4T:208:GLN:NE2	31:4T:210:LYS:O	2.11	0.82
46:2L:56:GLY:O	46:2L:65:GLY:N	2.12	0.82
1:A:31:C:O2	35:2A:33:G:N1	2.13	0.82
1:A:30:C:C5	1:A:31:C:C5	2.67	0.82
7:6e:46:GLU:CA	7:6e:63:ALA:N	2.43	0.82
13:5D:602:GLU:OE1	13:5D:606:THR:OG1	1.98	0.82
22:4A:74:C:H2'	22:4A:75:C:C6	2.14	0.82
35:2A:105:G:C2'	35:2A:106:G:H5''	2.10	0.82
22:4A:76:C:H2'	22:4A:77:A:O4'	1.80	0.82
35:2A:152:G:H5''	35:2A:153:A:OP2	1.80	0.81
11:5B:362:ARG:NH2	12:5C:283:ASP:OD2	2.14	0.81
13:5D:1753:ASP:O	13:5D:1756:THR:OG1	1.98	0.81
1:A:23:G:N2	35:2A:39:U:O2	2.14	0.81
13:5D:1588:ARG:NH1	13:5D:1588:ARG:O	2.14	0.81
41:2G:648:LEU:O	41:2G:651:VAL:N	2.13	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:G:H5'	1:A:28:G:H8	1.45	0.81
10:5A:92:U:H3	16:5b:36:MET:CA	1.93	0.80
11:5B:476:PHE:O	11:5B:479:THR:OG1	1.98	0.80
11:5B:1604:LEU:HD11	11:5B:1725:LEU:HD22	1.62	0.80
25:4D:357:ARG:CG	25:4D:358:ARG:H	1.83	0.80
27:4F:68:ASP:HA	38:2D:501:THR:CG2	2.10	0.80
13:5D:287:ASP:OD1	13:5D:288:GLU:N	2.15	0.80
13:5D:1568:GLN:OE1	13:5D:1572:THR:OG1	1.99	0.80
1:A:34:G:N9	1:A:35:U:C5	2.49	0.80
43:2I:839:ALA:O	43:2I:843:LEU:N	2.13	0.80
1:A:27:U:OP2	41:2G:1106:ARG:CA	2.29	0.80
10:5A:94:U:H1'	10:5A:95:G:OP1	1.82	0.80
11:5B:1076:ASP:OD1	11:5B:1077:ILE:N	2.15	0.80
11:5B:2303:GLU:OE1	11:5B:2304:PHE:N	2.14	0.79
10:5A:12:U:OP1	11:5B:224:THR:OG1	1.99	0.79
13:5D:1741:VAL:O	13:5D:1743:LYS:NZ	2.15	0.79
35:2A:101:U:H5''	35:2A:102:U:H5'	1.65	0.79
1:A:34:G:C2	1:A:35:U:H2'	2.16	0.79
27:4F:107:GLU:OE1	27:4F:107:GLU:N	2.15	0.79
12:5C:116:MET:SD	12:5C:117:ASP:N	2.56	0.79
1:A:20:U:O2	35:2A:42:G:C2	2.35	0.79
13:5D:1265:GLN:OE1	13:5D:1287:ARG:NH2	2.16	0.79
11:5B:1321:GLU:OE2	11:5B:1471:ARG:NH2	2.15	0.79
12:5C:811:THR:O	12:5C:815:VAL:HG23	1.81	0.79
35:2A:54:U:OP1	40:2F:424:ARG:O	2.00	0.79
1:A:30:C:N4	1:A:31:C:N4	2.31	0.78
22:4A:68:A:O2'	22:4A:69:C:OP1	2.01	0.78
41:2G:669:GLN:O	41:2G:672:ALA:N	2.16	0.78
43:2I:523:GLY:HA3	43:2I:536:TRP:O	1.83	0.78
1:A:28:G:H5'	1:A:28:G:C8	2.18	0.78
1:A:31:C:H1'	35:2A:33:G:N2	1.99	0.78
1:A:36:C:H4'	1:A:37:C:C5	2.18	0.78
25:4D:351:ARG:HA	25:4D:351:ARG:CZ	2.14	0.78
13:5D:1693:ARG:NH1	13:5D:1696:GLN:OE1	2.15	0.78
1:A:34:G:H2'	1:A:35:U:C6	2.19	0.78
1:A:40:U:H4'	1:A:41:U:C5'	2.13	0.78
1:A:31:C:O2	35:2A:33:G:C2	2.37	0.77
43:2I:914:ILE:O	43:2I:918:ARG:CA	2.32	0.77
41:2G:428:ALA:O	41:2G:432:THR:N	2.17	0.77
1:A:32:C:O2	35:2A:31:G:N1	2.11	0.77
12:5C:137:HIS:O	12:5C:142:LYS:NZ	2.17	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2A:153:A:H2'	35:2A:154:C:H5'	1.65	0.77
12:5C:192:ASP:OD1	12:5C:193:THR:N	2.17	0.77
41:2G:531:LEU:O	41:2G:534:GLN:N	2.18	0.77
11:5B:579:GLN:NE2	11:5B:627:CYS:O	2.18	0.76
1:A:31:C:H1'	35:2A:33:G:C2	2.20	0.76
13:5D:479:LYS:HG3	13:5D:480:THR:HG23	1.67	0.76
30:4S:711:GLU:OE1	30:4S:711:GLU:N	2.18	0.76
35:2A:177:A:H5''	35:2A:178:A:OP1	1.84	0.76
40:2F:276:GLY:C	40:2F:278:LEU:H	1.92	0.76
41:2G:1246:MET:O	41:2G:1249:TYR:N	2.18	0.76
11:5B:1637:TRP:O	11:5B:1656:THR:OG1	2.02	0.76
13:5D:470:TYR:O	13:5D:562:TYR:OH	2.01	0.76
31:4T:420:ALA:O	31:4T:423:ASN:ND2	2.18	0.76
1:A:8:U:O2	1:A:8:U:H2'	1.84	0.76
11:5B:1520:ASN:OD1	11:5B:1521:ALA:N	2.18	0.76
12:5C:426:GLU:OE1	12:5C:426:GLU:N	2.19	0.76
13:5D:1845:LEU:HD23	13:5D:1945:LEU:HD12	1.68	0.75
13:5D:1900:SER:OG	13:5D:1902:MET:SD	2.45	0.75
25:4D:383:ILE:O	25:4D:384:GLU:HG2	1.85	0.75
19:4e:64:ILE:HA	19:4e:70:SER:O	1.86	0.75
11:5B:71:ARG:NH1	11:5B:177:ASP:OD2	2.19	0.75
28:4G:380:ALA:O	28:4G:389:LYS:NZ	2.18	0.75
35:2A:143:A:H3'	35:2A:143:A:N3	2.01	0.75
1:A:34:G:H2'	1:A:35:U:H6	1.52	0.75
13:5D:973:ASP:OD2	13:5D:976:THR:OG1	2.05	0.75
11:5B:1592:ASP:OD2	11:5B:1737:ASN:ND2	2.19	0.75
1:A:34:G:H3'	1:A:35:U:H5''	1.67	0.74
11:5B:291:GLU:OE1	11:5B:291:GLU:N	2.20	0.74
11:5B:804:GLU:OE1	11:5B:804:GLU:N	2.20	0.74
41:2G:1016:LEU:O	41:2G:1019:ARG:N	2.19	0.74
11:5B:2219:THR:OG1	11:5B:2222:SER:OG	2.03	0.74
11:5B:2184:GLU:OE1	11:5B:2184:GLU:N	2.20	0.74
41:2G:874:LYS:O	41:2G:877:GLY:N	2.20	0.74
25:4D:357:ARG:CG	25:4D:358:ARG:N	2.44	0.74
43:2I:304:GLN:CA	43:2I:309:ASP:O	2.36	0.74
1:A:17:G:H1	35:2A:44:U:H3	1.33	0.74
10:5A:93:U:O4	18:5d:65:ARG:CA	2.35	0.74
15:4a:28:ILE:O	15:4a:45:CYS:HA	1.86	0.73
43:2I:753:GLY:HA3	43:2I:765:LEU:O	1.88	0.73
13:5D:1901:ARG:NH2	13:5D:1952:ALA:O	2.20	0.73
1:A:31:C:O2	35:2A:33:G:C5	2.41	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:C:C4	1:A:31:C:C6	2.76	0.73
40:2F:184:ARG:O	15:2a:85:PRO:N	2.21	0.73
7:6e:46:GLU:N	7:6e:63:ALA:H	1.87	0.73
35:2A:106:G:H4'	35:2A:107:A:O4'	1.89	0.73
35:2A:153:A:C2'	35:2A:154:C:H5'	2.17	0.73
35:2A:179:C:H2'	35:2A:180:G:H8	1.54	0.73
13:5D:769:CYS:O	13:5D:775:LYS:NZ	2.22	0.73
1:A:38:C:OP1	1:A:39:U:OP1	2.05	0.73
43:2I:442:LEU:O	43:2I:735:SER:N	2.19	0.73
10:5A:117:A:N1	18:5d:26:GLY:HA3	2.03	0.72
13:5D:1538:ARG:NH1	13:5D:1665:ASP:OD1	2.21	0.72
25:4D:380:PHE:CD1	25:4D:380:PHE:C	2.67	0.72
28:4G:19:PRO:CG	28:4G:21:LEU:HD22	2.18	0.72
40:2F:276:GLY:O	40:2F:278:LEU:N	2.20	0.72
41:2G:994:LEU:O	41:2G:997:LEU:N	2.22	0.72
12:5C:383:GLN:HG2	12:5C:395:THR:HG21	1.72	0.72
22:4A:114:U:H4'	22:4A:115:G:OP1	1.87	0.72
20:4f:42:ILE:O	20:4f:59:MET:HA	1.89	0.72
41:2G:660:ALA:O	41:2G:663:THR:N	2.22	0.72
1:A:30:C:C4	1:A:31:C:C4	2.69	0.72
7:6e:46:GLU:N	7:6e:63:ALA:N	2.37	0.72
41:2G:1055:TRP:O	41:2G:1058:ILE:N	2.22	0.72
41:2G:1270:ASN:O	41:2G:1273:TYR:N	2.21	0.72
1:A:19:U:H3	35:2A:42:G:H1	1.37	0.72
13:5D:297:SER:N	13:5D:301:GLU:OE2	2.23	0.72
32:4U:186:ARG:NH1	32:4U:187:MET:SD	2.63	0.72
35:2A:153:A:H2'	35:2A:154:C:C5'	2.19	0.72
1:A:15:A:H2'	1:A:16:A:O4'	1.89	0.72
10:5A:92:U:N3	16:5b:36:MET:CA	2.53	0.72
28:4G:153:THR:OG1	28:4G:155:GLU:OE1	2.08	0.71
2:6A:76:A:C2	23:4B:562:ALA:CB	2.64	0.71
13:5D:488:LEU:HD21	13:5D:501:LEU:HD22	1.71	0.71
1:A:21:U:H1'	1:A:22:C:OP1	1.90	0.71
1:A:38:C:OP1	1:A:39:U:OP2	2.09	0.71
12:5C:668:GLU:OE2	12:5C:824:THR:OG1	2.03	0.71
13:5D:429:GLN:N	13:5D:886:GLN:OE1	2.24	0.71
41:2G:791:VAL:O	41:2G:794:GLN:N	2.23	0.71
13:5D:1212:GLU:N	13:5D:1212:GLU:OE1	2.23	0.71
31:4T:531:ASP:OD1	31:4T:532:LEU:N	2.24	0.71
10:5A:94:U:C1'	10:5A:95:G:OP1	2.39	0.71
10:5A:96:A:H4'	10:5A:97:G:H5''	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:1845:LEU:HD23	13:5D:1945:LEU:CD1	2.20	0.71
35:2A:106:G:H21	35:2A:107:A:N6	1.87	0.71
41:2G:535:ILE:O	41:2G:538:LEU:N	2.23	0.71
2:6A:36:A:C5	38:2D:506:SER:OG	2.40	0.71
10:5A:87:A:N6	10:5A:92:U:P	2.64	0.70
43:2I:558:LEU:O	43:2I:561:GLY:N	2.24	0.70
11:5B:1914:MET:N	11:5B:1914:MET:SD	2.64	0.70
13:5D:406:ARG:NH2	13:5D:974:LYS:O	2.24	0.70
11:5B:152:ARG:NH2	11:5B:618:THR:O	2.24	0.70
46:2L:7:ASP:O	46:2L:91:LEU:N	2.25	0.70
2:6A:86:U:H3	35:2A:12:G:H1	1.39	0.70
13:5D:407:GLN:NE2	13:5D:408:VAL:O	2.24	0.70
41:2G:700:LYS:O	41:2G:703:THR:N	2.24	0.70
13:5D:1462:GLU:N	13:5D:1462:GLU:OE2	2.25	0.70
35:2A:153:A:N6	35:2A:177:A:C2	2.60	0.70
42:2H:479:ASP:O	42:2H:482:ALA:N	2.25	0.70
43:2I:545:VAL:N	43:2I:557:ALA:O	2.25	0.70
11:5B:1048:MET:HE2	11:5B:1048:MET:N	2.07	0.69
35:2A:54:U:OP1	40:2F:427:ALA:O	2.10	0.69
10:5A:79:C:C3'	10:5A:80:U:H6	2.05	0.69
10:5A:96:A:H61	20:5f:23:GLY:H	1.38	0.69
13:5D:1072:LEU:HD22	13:5D:1077:LEU:HD23	1.74	0.69
27:4F:87:ASN:OD1	28:4G:23:ARG:NH1	2.25	0.69
13:5D:660:ASP:OD1	13:5D:931:ARG:NH1	2.26	0.69
35:2A:40:C:H6	35:2A:40:C:C5'	2.05	0.69
13:5D:1073:GLU:N	13:5D:1073:GLU:OE2	2.25	0.69
35:2A:154:C:H2'	35:2A:155:C:C6	2.27	0.69
2:6A:102:A:O2'	9:6g:33:THR:CA	2.41	0.69
2:6A:103:U:O4	9:6g:32:GLN:O	2.10	0.69
1:A:22:C:HO2'	1:A:23:G:H5'	1.54	0.69
12:5C:698:GLU:OE1	12:5C:698:GLU:N	2.25	0.69
13:5D:1313:ARG:NH1	13:5D:1313:ARG:O	2.26	0.69
31:4T:259:TYR:OH	31:4T:282:ARG:NH2	2.26	0.69
1:A:31:C:H6	1:A:31:C:H5'	1.58	0.69
10:5A:79:C:C4'	10:5A:80:U:H6	2.06	0.69
11:5B:377:GLU:OE1	11:5B:377:GLU:N	2.26	0.69
10:5A:97:G:H1	10:5A:116:U:H3	1.41	0.69
42:2H:596:GLU:C	42:2H:598:GLU:H	2.00	0.69
11:5B:67:ARG:NH2	11:5B:491:GLU:OE1	2.26	0.68
10:5A:95:G:H21	10:5A:96:A:C5'	2.06	0.68
11:5B:2014:MET:SD	11:5B:2015:GLU:N	2.66	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:1854:GLU:OE1	13:5D:1854:GLU:N	2.26	0.68
28:4G:118:GLU:OE2	28:4G:119:ARG:NH1	2.27	0.68
11:5B:1985:ASP:OD1	11:5B:1986:LEU:N	2.26	0.68
12:5C:455:GLY:O	12:5C:459:SER:OG	2.11	0.68
11:5B:1251:SER:OG	11:5B:1298:ARG:NH2	2.26	0.68
13:5D:222:GLU:OE1	13:5D:222:GLU:N	2.26	0.68
28:4G:21:LEU:HD12	38:2D:509:MET:HG3	1.76	0.68
35:2A:30:A:H2'	35:2A:30:A:N3	2.06	0.68
11:5B:1304:ASN:OD1	11:5B:1305:SER:N	2.27	0.68
10:5A:87:A:N6	10:5A:92:U:OP2	2.26	0.68
11:5B:1687:TYR:O	11:5B:1693:SER:OG	2.11	0.68
30:4S:741:MET:SD	30:4S:741:MET:N	2.66	0.68
2:6A:58:G:H1	25:4D:357:ARG:NH1	1.80	0.68
10:5A:93:U:O4	18:5d:65:ARG:C	2.36	0.68
11:5B:147:MET:HE1	11:5B:191:ILE:HB	1.76	0.68
13:5D:2109:MET:HA	13:5D:2109:MET:HE3	1.76	0.68
32:4U:292:GLU:OE1	32:4U:292:GLU:N	2.24	0.68
10:5A:93:U:O4'	17:5c:104:ASP:CA	2.42	0.68
35:2A:151:C:H2'	35:2A:152:G:H8	1.60	0.67
13:5D:832:GLN:NE2	13:5D:843:GLU:OE2	2.27	0.67
35:2A:152:G:O3'	35:2A:153:A:O4'	2.11	0.67
2:6A:103:U:H3'	2:6A:104:U:H5''	1.75	0.67
12:5C:853:ARG:NH1	12:5C:879:ASP:O	2.26	0.67
13:5D:342:GLU:N	13:5D:342:GLU:OE1	2.27	0.67
11:5B:341:LYS:O	32:4U:301:ARG:NH1	2.28	0.67
11:5B:1764:SER:OG	11:5B:1767:ASN:OD1	2.11	0.67
35:2A:143:A:H2'	35:2A:144:C:H6	1.59	0.67
2:6A:103:U:H4'	2:6A:104:U:OP2	1.95	0.67
13:5D:1633:GLU:OE2	13:5D:1655:ASN:N	2.27	0.67
28:4G:513:CYS:O	28:4G:517:GLY:N	2.27	0.67
28:4G:338:MET:HA	28:4G:338:MET:HE3	1.76	0.67
22:4A:109:G:H2'	22:4A:110:G:C8	2.30	0.67
22:4A:114:U:P	22:4A:114:U:H6	2.18	0.67
35:2A:151:C:O2	35:2A:152:G:C8	2.48	0.67
42:2H:487:LEU:O	42:2H:490:HIS:N	2.28	0.67
11:5B:1633:ALA:O	11:5B:1634:SER:OG	2.08	0.67
12:5C:814:ARG:NH1	12:5C:954:ASP:OD1	2.28	0.67
25:4D:351:ARG:O	25:4D:352:LYS:C	2.38	0.67
35:2A:153:A:C3'	35:2A:154:C:H5'	2.25	0.67
1:A:30:C:N4	1:A:31:C:C5	2.50	0.67
11:5B:147:MET:HE3	11:5B:147:MET:HA	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:869:GLN:NE2	11:5B:869:GLN:O	2.28	0.66
22:4A:77:A:H2'	22:4A:78:A:O4'	1.95	0.66
1:A:30:C:H41	1:A:31:C:N4	1.91	0.66
11:5B:1180:LYS:O	11:5B:1201:ARG:NH2	2.28	0.66
43:2I:753:GLY:CA	43:2I:765:LEU:O	2.44	0.66
1:A:22:C:O5'	1:A:22:C:H6	1.78	0.66
1:A:36:C:C4'	1:A:37:C:H5	2.07	0.66
35:2A:150:U:H3	35:2A:181:G:H1	1.41	0.66
41:2G:87:PRO:O	41:2G:91:LEU:N	2.21	0.66
13:5D:1855:TYR:HB3	13:5D:1891:THR:HG21	1.78	0.66
35:2A:151:C:C2	35:2A:152:G:C8	2.83	0.66
35:2A:54:U:OP1	40:2F:427:ALA:C	2.39	0.66
13:5D:1388:GLN:NE2	13:5D:1655:ASN:OD1	2.29	0.66
41:2G:400:SER:O	41:2G:404:LEU:N	2.28	0.66
11:5B:2141:GLU:OE1	11:5B:2143:ARG:NH2	2.29	0.66
1:A:8:U:O2	1:A:8:U:C2'	2.44	0.65
1:A:36:C:C4'	1:A:37:C:C5	2.79	0.65
2:6A:44:G:N1	11:5B:1556:ASP:OD2	2.29	0.65
22:4A:78:A:H2'	22:4A:79:U:C6	2.31	0.65
43:2I:550:ASN:N	43:2I:553:GLN:O	2.27	0.65
11:5B:1289:VAL:HG11	13:5D:42:SER:HA	1.78	0.65
25:4D:357:ARG:HG3	25:4D:358:ARG:CG	2.26	0.65
1:A:32:C:H3'	1:A:32:C:OP2	1.96	0.65
11:5B:2119:ASP:OD1	11:5B:2120:LEU:N	2.30	0.65
41:2G:122:HIS:O	41:2G:125:THR:N	2.22	0.65
41:2G:1280:LEU:O	41:2G:1283:HIS:N	2.22	0.65
11:5B:2138:GLN:N	11:5B:2138:GLN:OE1	2.29	0.65
43:2I:1148:LEU:O	43:2I:1152:HIS:N	2.27	0.65
1:A:36:C:H1'	1:A:37:C:P	2.36	0.65
27:4F:15:ASP:OD1	27:4F:16:GLN:N	2.29	0.65
35:2A:156:U:C6	35:2A:156:U:C5'	2.72	0.65
35:2A:168:A:C8	35:2A:168:A:C5'	2.75	0.65
41:2G:1243:PRO:O	41:2G:1246:MET:N	2.29	0.65
11:5B:1661:TRP:NE1	11:5B:1697:SER:O	2.28	0.65
35:2A:114:A:H61	35:2A:142:C:H42	1.44	0.65
42:2H:491:LEU:O	42:2H:494:THR:N	2.30	0.65
43:2I:868:VAL:O	43:2I:877:LEU:N	2.30	0.65
41:2G:658:TRP:O	41:2G:661:ARG:N	2.30	0.65
41:2G:1018:PRO:O	41:2G:1021:THR:N	2.30	0.64
1:A:11:C:O2	1:A:11:C:C2'	2.45	0.64
41:2G:758:ASP:O	41:2G:762:ALA:N	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2G:886:HIS:O	41:2G:889:GLU:N	2.30	0.64
13:5D:1475:ARG:NH1	13:5D:1503:TRP:O	2.31	0.64
32:4U:350:GLN:NE2	32:4U:354:ASP:OD2	2.30	0.64
25:4D:388:TYR:N	25:4D:388:TYR:CD1	2.66	0.64
11:5B:1275:ARG:O	13:5D:52:MET:HE1	1.97	0.64
22:4A:18:G:C2	25:4D:361:LYS:HE2	2.33	0.64
25:4D:351:ARG:HA	25:4D:351:ARG:NH2	2.11	0.64
31:4T:456:ARG:NH1	31:4T:469:THR:O	2.30	0.64
1:A:35:U:OP1	46:2L:63:GLY:HA3	1.98	0.64
10:5A:85:C:OP1	17:5c:20:GLU:CA	2.46	0.64
11:5B:1626:CYS:SG	11:5B:1627:ALA:N	2.71	0.64
13:5D:206:GLU:OE1	13:5D:206:GLU:N	2.31	0.64
10:5A:79:C:C6	10:5A:79:C:H5'	2.32	0.64
11:5B:1093:ASP:OD1	11:5B:1094:ARG:NH1	2.31	0.64
11:5B:1623:ASN:OD1	11:5B:1624:SER:N	2.31	0.64
10:5A:24:G:OP2	11:5B:417:ARG:NH2	2.30	0.64
10:5A:89:U:H2'	10:5A:90:U:H5''	1.79	0.64
28:4G:162:GLU:OE1	28:4G:162:GLU:N	2.30	0.64
1:A:35:U:H4'	1:A:36:C:OP2	1.98	0.63
13:5D:607:GLN:O	13:5D:610:ARG:NH1	2.29	0.63
28:4G:493:SER:O	28:4G:497:ASN:N	2.31	0.63
35:2A:164:C:H6	35:2A:164:C:H5'	1.63	0.63
12:5C:143:THR:HG23	12:5C:168:THR:OG1	1.99	0.63
13:5D:733:LYS:O	13:5D:736:ARG:NH2	2.32	0.63
41:2G:749:ALA:O	41:2G:752:TYR:N	2.31	0.63
1:A:31:C:C2	1:A:32:C:C5	2.87	0.63
10:5A:90:U:H5	21:5g:38:ASN:C	2.06	0.63
10:5A:95:G:N2	10:5A:96:A:H5''	2.13	0.63
22:4A:79:U:C3'	22:4A:80:A:H8	2.05	0.63
35:2A:147:G:H2'	35:2A:148:C:H6	1.63	0.63
35:2A:154:C:H2'	35:2A:155:C:H6	1.63	0.63
43:2I:325:ILE:O	43:2I:375:SER:N	2.30	0.63
1:A:20:U:H5'	1:A:21:U:OP2	1.99	0.63
12:5C:753:GLU:OE1	12:5C:753:GLU:N	2.32	0.63
13:5D:821:LEU:HD12	13:5D:821:LEU:O	1.99	0.63
35:2A:152:G:C2	35:2A:153:A:C5	2.87	0.63
1:A:22:C:C2'	1:A:23:G:H5'	2.28	0.63
13:5D:1225:VAL:HG22	13:5D:1268:ILE:HG22	1.80	0.63
41:2G:1109:ARG:O	41:2G:1110:VAL:C	2.41	0.63
43:2I:1191:LYS:O	43:2I:1194:SER:N	2.32	0.63
47:2M:40:TYR:O	47:2M:43:TYR:N	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:C:N3	35:2A:33:G:C6	2.65	0.63
25:4D:383:ILE:HD11	25:4D:386:ASP:O	1.99	0.63
11:5B:1503:TRP:CD1	25:4D:380:PHE:HB2	2.34	0.62
12:5C:676:ALA:HB3	12:5C:815:VAL:HG22	1.80	0.62
13:5D:537:LYS:NZ	13:5D:583:THR:O	2.32	0.62
35:2A:153:A:H3'	35:2A:154:C:H5'	1.79	0.62
41:2G:491:GLU:O	41:2G:494:GLU:N	2.32	0.62
44:2J:77:ILE:O	44:2J:84:ILE:N	2.32	0.62
29:4R:391:GLU:OE2	29:4R:391:GLU:N	2.32	0.62
41:2G:914:PHE:O	41:2G:917:VAL:N	2.32	0.62
43:2I:931:VAL:O	43:2I:936:LYS:N	2.31	0.62
41:2G:1264:VAL:O	41:2G:1267:LYS:N	2.32	0.62
11:5B:1630:LEU:HD21	11:5B:1659:LYS:HB3	1.80	0.62
1:A:31:C:H2'	1:A:32:C:H6	1.65	0.62
41:2G:179:GLY:O	41:2G:182:LYS:N	2.33	0.62
43:2I:973:GLY:HA3	43:2I:976:LYS:O	2.00	0.62
13:5D:1914:GLU:O	13:5D:1917:SER:OG	2.14	0.62
29:4R:375:GLU:OE1	29:4R:375:GLU:N	2.33	0.62
13:5D:1040:LEU:O	13:5D:1044:VAL:HG13	1.99	0.62
29:4R:374:LEU:HD23	29:4R:374:LEU:H	1.62	0.62
27:4F:4:MET:SD	27:4F:4:MET:N	2.67	0.62
43:2I:586:ASP:O	43:2I:610:VAL:N	2.32	0.62
1:A:31:C:O2'	1:A:32:C:H5'	2.00	0.61
35:2A:157:G:H5''	35:2A:157:G:H8	1.65	0.61
41:2G:862:GLU:O	41:2G:865:ARG:N	2.33	0.61
10:5A:95:G:H2'	10:5A:95:G:N3	2.15	0.61
13:5D:890:GLU:OE1	13:5D:928:ARG:NE	2.33	0.61
13:5D:1822:TYR:HB2	13:5D:1824:ILE:HD11	1.82	0.61
25:4D:387:ALA:HB1	25:4D:388:TYR:CD1	2.34	0.61
41:2G:88:VAL:CA	41:2G:92:ASN:H	2.13	0.61
22:4A:77:A:H2'	22:4A:78:A:C8	2.35	0.61
27:4F:74:GLU:HG2	28:4G:34:ILE:HG21	1.80	0.61
1:A:40:U:H5''	1:A:41:U:H5''	1.82	0.61
35:2A:143:A:H2'	35:2A:144:C:C6	2.35	0.61
41:2G:551:LEU:O	41:2G:554:LYS:N	2.34	0.61
41:2G:895:GLY:O	41:2G:898:TYR:N	2.34	0.61
1:A:31:C:C2'	1:A:32:C:H5'	2.30	0.61
10:5A:88:A:H2'	10:5A:88:A:N3	2.14	0.61
35:2A:106:G:N2	35:2A:107:A:C6	2.67	0.61
41:2G:897:LEU:O	41:2G:900:PHE:N	2.34	0.61
1:A:31:C:H2'	1:A:32:C:C6	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:4D:383:ILE:HD11	25:4D:386:ASP:C	2.26	0.61
41:2G:784:MET:O	41:2G:787:ILE:N	2.33	0.61
1:A:13:U:H2'	1:A:14:G:H8	1.66	0.61
1:A:21:U:H1'	1:A:22:C:P	2.41	0.61
13:5D:1040:LEU:HD11	13:5D:1072:LEU:HD21	1.83	0.61
35:2A:112:G:H2'	35:2A:113:G:H8	1.65	0.61
35:2A:142:C:C2'	35:2A:143:A:H5'	2.31	0.61
35:2A:153:A:N6	35:2A:177:A:H2	1.98	0.61
1:A:30:C:H3'	1:A:31:C:H5'	1.83	0.61
11:5B:1838:LYS:NZ	13:5D:205:PHE:O	2.33	0.61
41:2G:929:LEU:O	41:2G:932:ILE:N	2.34	0.61
13:5D:1433:ASP:OD1	13:5D:1473:ARG:NH2	2.32	0.60
22:4A:76:C:H2'	22:4A:77:A:C8	2.36	0.60
13:5D:497:GLU:OE1	13:5D:498:ASN:N	2.34	0.60
41:2G:610:ILE:O	41:2G:613:MET:N	2.34	0.60
12:5C:679:PRO:O	12:5C:681:LYS:NZ	2.27	0.60
13:5D:592:LYS:O	13:5D:596:ILE:HG23	2.00	0.60
38:2D:252:PHE:CA	40:2F:63:ASP:CA	2.79	0.60
7:6e:46:GLU:CA	7:6e:62:ASP:C	2.74	0.60
2:6A:103:U:C3'	2:6A:104:U:H5''	2.31	0.60
11:5B:390:ASP:OD1	11:5B:391:THR:N	2.34	0.60
28:4G:332:ILE:HG21	28:4G:349:ALA:HA	1.83	0.60
1:A:10:C:O2'	1:A:11:C:OP2	2.16	0.60
12:5C:112:THR:HG23	12:5C:114:TYR:O	2.02	0.60
43:2I:638:GLU:N	43:2I:668:GLY:O	2.32	0.60
1:A:13:U:H6	1:A:13:U:O5'	1.84	0.60
11:5B:2009:ASP:OD1	11:5B:2010:ILE:N	2.34	0.60
13:5D:425:ASN:ND2	13:5D:886:GLN:O	2.33	0.60
13:5D:67:ARG:NH1	13:5D:214:GLU:OE2	2.35	0.60
11:5B:67:ARG:NE	11:5B:491:GLU:OE2	2.35	0.60
11:5B:1763:LEU:HD22	11:5B:1862:ILE:HD13	1.84	0.60
13:5D:565:THR:HG21	13:5D:583:THR:HG22	1.84	0.60
32:4U:282:THR:O	32:4U:283:SER:OG	2.16	0.60
43:2I:563:LEU:N	43:2I:581:LYS:O	2.27	0.60
31:4T:233:ASN:O	31:4T:233:ASN:OD1	2.19	0.59
41:2G:173:ALA:C	41:2G:176:ALA:H	2.09	0.59
41:2G:1125:PRO:O	41:2G:1128:VAL:N	2.35	0.59
11:5B:97:HIS:ND1	11:5B:649:GLU:OE2	2.35	0.59
13:5D:295:THR:HG23	13:5D:295:THR:O	2.01	0.59
13:5D:1732:MET:CE	13:5D:1755:LEU:HD11	2.30	0.59
13:5D:1856:GLU:OE1	13:5D:1856:GLU:N	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:4D:385:GLU:HG3	25:4D:386:ASP:O	2.02	0.59
18:4d:20:MET:HA	18:4d:29:TYR:O	2.02	0.59
41:2G:953:ASP:O	41:2G:956:SER:N	2.34	0.59
43:2I:645:MET:N	43:2I:662:PHE:O	2.28	0.59
10:5A:87:A:N6	10:5A:91:U:O3'	2.36	0.59
30:4S:729:LEU:HD23	30:4S:729:LEU:C	2.27	0.59
43:2I:523:GLY:CA	43:2I:536:TRP:O	2.51	0.59
43:2I:664:TYR:CA	43:2I:677:THR:O	2.50	0.59
1:A:118:A:H62	38:2D:507:GLY:HA2	1.67	0.59
11:5B:110:TRP:O	11:5B:192:GLN:NE2	2.35	0.59
11:5B:282:LEU:HD23	11:5B:283:VAL:HG13	1.85	0.59
13:5D:1665:ASP:O	13:5D:1667:GLN:N	2.34	0.59
28:4G:21:LEU:HB2	38:2D:502:TRP:CE3	2.38	0.59
13:5D:1507:SER:O	13:5D:1511:THR:HG23	2.02	0.59
41:2G:1182:LEU:O	41:2G:1185:ARG:N	2.35	0.59
13:5D:1222:TRP:NE1	13:5D:1273:ASP:OD2	2.34	0.59
13:5D:1185:GLU:OE1	13:5D:1185:GLU:HA	2.03	0.59
11:5B:300:ASN:O	12:5C:939:ARG:NH1	2.35	0.58
13:5D:453:LYS:O	13:5D:483:ARG:NH1	2.32	0.58
28:4G:307:HIS:ND1	28:4G:307:HIS:O	2.35	0.58
22:4A:73:U:H2'	22:4A:74:C:C6	2.38	0.58
40:2F:276:GLY:C	40:2F:278:LEU:N	2.60	0.58
41:2G:308:SER:O	41:2G:311:ALA:N	2.35	0.58
41:2G:745:ALA:O	41:2G:748:LYS:N	2.36	0.58
10:5A:95:G:O2'	18:5d:24:LYS:C	2.46	0.58
10:5A:96:A:N6	20:5f:23:GLY:H	2.02	0.58
11:5B:336:ASN:O	12:5C:262:ARG:NH2	2.36	0.58
41:2G:811:LEU:O	41:2G:814:PHE:N	2.36	0.58
1:A:30:C:N3	1:A:31:C:C6	2.72	0.58
1:A:31:C:O2	35:2A:33:G:C4	2.56	0.58
18:4d:33:LEU:HA	18:4d:44:LEU:HA	1.86	0.58
47:2M:48:ASP:O	47:2M:51:ASN:N	2.37	0.58
11:5B:705:LYS:NZ	28:4G:160:ILE:O	2.33	0.58
1:A:34:G:N9	1:A:35:U:C6	2.72	0.58
1:A:38:C:C4'	1:A:39:U:OP1	2.34	0.58
45:2K:67:ILE:O	45:2K:70:ALA:N	2.36	0.58
7:6e:46:GLU:H	7:6e:63:ALA:N	2.01	0.58
11:5B:1607:GLU:N	11:5B:1632:PHE:O	2.35	0.58
13:5D:1309:VAL:HG23	13:5D:1326:PRO:O	2.03	0.58
41:2G:1149:LYS:O	41:2G:1152:SER:N	2.36	0.58
11:5B:1776:ILE:HG23	11:5B:1858:PRO:HA	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2A:154:C:O2'	35:2A:155:C:H5'	2.04	0.57
10:5A:79:C:C5'	10:5A:80:U:C5	2.86	0.57
29:4R:465:ASP:OD1	29:4R:466:VAL:N	2.37	0.57
41:2G:929:LEU:O	41:2G:930:PRO:C	2.46	0.57
12:5C:891:THR:O	12:5C:891:THR:HG22	2.05	0.57
13:5D:214:GLU:OE1	13:5D:214:GLU:N	2.35	0.57
41:2G:981:TYR:O	41:2G:984:GLU:N	2.21	0.57
43:2I:1204:VAL:O	43:2I:1207:LYS:N	2.37	0.57
1:A:35:U:O2	1:A:35:U:O2'	2.22	0.57
12:5C:776:GLU:O	12:5C:782:GLU:N	2.38	0.57
41:2G:424:ILE:O	41:2G:428:ALA:N	2.36	0.57
27:4F:73:TYR:OH	28:4G:23:ARG:NH2	2.38	0.57
10:5A:81:U:H2'	10:5A:81:U:O2	2.05	0.57
11:5B:1274:PHE:O	11:5B:1278:VAL:HG23	2.04	0.57
22:4A:79:U:H2'	22:4A:80:A:O4'	2.05	0.57
35:2A:152:G:N2	35:2A:153:A:C5	2.73	0.57
11:5B:1604:LEU:CD1	11:5B:1725:LEU:HD22	2.34	0.57
13:5D:1092:MET:HA	13:5D:1092:MET:HE3	1.87	0.57
22:4A:74:C:C2'	22:4A:75:C:C6	2.86	0.57
10:5A:79:C:C4'	10:5A:80:U:C6	2.87	0.57
10:5A:79:C:H5'	10:5A:79:C:H6	1.70	0.57
22:4A:37:C:H1'	22:4A:38:U:H2'	1.85	0.57
40:2F:184:ARG:CA	15:2a:85:PRO:CA	2.82	0.57
43:2I:15:SER:N	43:2I:33:SER:O	2.35	0.57
1:A:12:U:H2'	1:A:12:U:P	2.45	0.57
1:A:34:G:C4	1:A:35:U:C6	2.93	0.57
1:A:34:G:C2'	1:A:35:U:C6	2.88	0.56
22:4A:31:U:O4	26:4E:60:ALA:CA	2.53	0.56
42:2H:596:GLU:O	42:2H:598:GLU:N	2.37	0.56
43:2I:914:ILE:O	43:2I:918:ARG:C	2.47	0.56
12:5C:233:GLU:OE1	12:5C:233:GLU:N	2.36	0.56
43:2I:430:GLY:O	43:2I:433:SER:N	2.31	0.56
43:2I:931:VAL:O	43:2I:935:GLU:N	2.39	0.56
1:A:31:C:C1'	35:2A:33:G:N2	2.68	0.56
13:5D:1060:ASN:OD1	13:5D:1064:GLN:NE2	2.37	0.56
13:5D:1903:GLN:OE1	13:5D:1903:GLN:N	2.34	0.56
35:2A:152:G:N2	35:2A:153:A:C8	2.73	0.56
40:2F:184:ARG:O	15:2a:85:PRO:CA	2.53	0.56
41:2G:892:LEU:O	41:2G:895:GLY:N	2.37	0.56
43:2I:287:PHE:CA	43:2I:304:GLN:O	2.53	0.56
1:A:20:U:O2	35:2A:42:G:N2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:288:LEU:O	11:5B:1136:ARG:NH2	2.38	0.56
12:5C:159:LYS:NZ	12:5C:160:ARG:O	2.35	0.56
12:5C:678:THR:OG1	12:5C:682:LYS:O	2.21	0.56
13:5D:1464:GLY:N	13:5D:1465:PRO:HD2	2.21	0.56
1:A:36:C:C5'	1:A:37:C:H5	2.17	0.56
1:A:106:A:OP1	1:A:106:A:H4'	2.05	0.56
2:6A:37:C:N4	38:2D:504:GLY:CA	2.69	0.56
13:5D:89:LEU:HD13	13:5D:95:ASP:CB	2.35	0.56
13:5D:1518:VAL:O	13:5D:1518:VAL:HG12	2.05	0.56
1:A:36:C:O2'	1:A:37:C:OP1	2.24	0.56
10:5A:110:C:H2'	10:5A:111:A:H8	1.70	0.56
13:5D:1887:PRO:O	13:5D:1891:THR:HG23	2.06	0.56
35:2A:141:C:C2	35:2A:142:C:C5	2.93	0.56
38:2D:174:VAL:O	38:2D:178:GLY:HA2	2.05	0.56
41:2G:86:ALA:C	41:2G:89:ALA:H	2.11	0.56
13:5D:411:LEU:O	13:5D:415:VAL:HG13	2.05	0.56
13:5D:593:TRP:CZ3	13:5D:597:THR:HG21	2.40	0.56
25:4D:351:ARG:HA	25:4D:351:ARG:NE	2.17	0.56
41:2G:849:ILE:O	41:2G:852:ARG:N	2.38	0.56
41:2G:874:LYS:O	41:2G:877:GLY:CA	2.54	0.56
41:2G:1124:SER:O	41:2G:1127:THR:N	2.34	0.56
13:5D:1027:ILE:HG21	13:5D:1059:ILE:HD11	1.87	0.56
13:5D:1361:GLU:OE2	13:5D:1393:TRP:NE1	2.39	0.56
22:4A:31:U:O4	26:4E:60:ALA:C	2.49	0.56
35:2A:150:U:C2	35:2A:151:C:C5	2.94	0.56
41:2G:937:LEU:O	41:2G:940:LEU:N	2.38	0.56
11:5B:941:LYS:NZ	11:5B:946:GLU:OE2	2.31	0.56
12:5C:476:CYS:SG	12:5C:496:VAL:HG22	2.46	0.56
13:5D:1323:ASP:OD1	13:5D:1324:LYS:NZ	2.39	0.56
25:4D:387:ALA:HB1	25:4D:388:TYR:CE1	2.41	0.56
35:2A:150:U:H2'	35:2A:151:C:H6	1.71	0.56
35:2A:183:G:H2'	35:2A:184:C:H6	1.71	0.56
43:2I:488:GLY:C	43:2I:490:THR:H	2.14	0.56
43:2I:1160:HIS:O	43:2I:1163:PHE:N	2.37	0.56
1:A:31:C:N4	1:A:32:C:H41	2.03	0.56
12:5C:258:ASN:OD1	12:5C:259:LYS:N	2.39	0.56
22:4A:78:A:H2'	22:4A:79:U:O4'	2.06	0.56
28:4G:411:VAL:HG22	28:4G:422:MET:HG3	1.88	0.56
31:4T:230:ILE:HG22	31:4T:231:LYS:H	1.71	0.56
41:2G:578:ILE:O	41:2G:581:LEU:N	2.39	0.56
41:2G:968:GLU:O	41:2G:971:MET:N	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2I:303:ALA:O	43:2I:310:ILE:CA	2.54	0.56
43:2I:973:GLY:HA3	43:2I:976:LYS:C	2.31	0.56
10:5A:110:C:H2'	10:5A:111:A:C8	2.41	0.55
12:5C:557:GLN:C	12:5C:557:GLN:OE1	2.49	0.55
28:4G:329:ARG:O	28:4G:333:MET:HG3	2.06	0.55
35:2A:181:G:C4	35:2A:182:U:C5	2.95	0.55
1:A:22:C:O2'	1:A:23:G:C5'	2.37	0.55
10:5A:117:A:C2	18:5d:26:GLY:HA3	2.41	0.55
25:4D:374:GLN:H	25:4D:377:ARG:HD2	1.71	0.55
35:2A:183:G:C4	35:2A:184:C:C5	2.94	0.55
1:A:21:U:C1'	1:A:22:C:P	2.94	0.55
4:6b:48:GLN:C	4:6b:50:LEU:H	2.15	0.55
7:6e:46:GLU:CA	7:6e:62:ASP:CA	2.85	0.55
10:5A:87:A:C6	10:5A:92:U:OP2	2.59	0.55
11:5B:1653:ASP:OD1	11:5B:1654:SER:N	2.39	0.55
30:4S:721:THR:OG1	30:4S:724:GLU:OE1	2.22	0.55
35:2A:147:G:C4	35:2A:148:C:C5	2.95	0.55
35:2A:149:A:H2'	35:2A:150:U:H6	1.70	0.55
41:2G:1109:ARG:O	41:2G:1112:THR:N	2.36	0.55
2:6A:56:A:C6	2:6A:57:U:C4	2.94	0.55
29:4R:383:ILE:HD12	29:4R:455:ARG:O	2.05	0.55
35:2A:141:C:H2'	35:2A:142:C:H6	1.71	0.55
1:A:36:C:C1'	1:A:37:C:P	2.94	0.55
11:5B:1346:THR:HG23	11:5B:1348:VAL:HG12	1.88	0.55
11:5B:1622:MET:O	11:5B:1687:TYR:OH	2.24	0.55
13:5D:1186:LEU:HD21	13:5D:1270:VAL:HG13	1.87	0.55
22:4A:114:U:O2	22:4A:114:U:H2'	2.06	0.55
45:2K:109:GLN:O	45:2K:112:LEU:N	2.39	0.55
1:A:10:C:O2'	1:A:11:C:P	2.64	0.55
13:5D:544:MET:N	13:5D:544:MET:SD	2.80	0.55
22:4A:56:U:C5	25:4D:354:ARG:CZ	2.89	0.55
28:4G:97:ASP:OD1	28:4G:98:ASP:N	2.39	0.55
35:2A:181:G:H2'	35:2A:182:U:H6	1.71	0.55
11:5B:270:ASN:ND2	11:5B:285:ASP:OD1	2.40	0.55
45:2K:98:PHE:O	45:2K:100:LYS:N	2.39	0.55
11:5B:1710:ASN:OD1	11:5B:1744:ARG:NH2	2.36	0.55
11:5B:2189:SER:OG	11:5B:2191:GLN:OE1	2.25	0.55
12:5C:212:SER:O	12:5C:216:THR:HG23	2.06	0.55
1:A:31:C:N3	35:2A:33:G:O6	2.40	0.55
12:5C:693:GLU:OE1	12:5C:693:GLU:N	2.40	0.55
13:5D:89:LEU:CD2	28:4G:363:ALA:HB3	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:801:PHE:CD2	13:5D:821:LEU:HD13	2.42	0.55
35:2A:153:A:H3'	35:2A:154:C:C5'	2.37	0.55
11:5B:270:ASN:OD1	11:5B:270:ASN:O	2.25	0.55
13:5D:108:GLU:N	13:5D:108:GLU:OE1	2.39	0.55
13:5D:412:GLU:O	13:5D:415:VAL:HG22	2.07	0.55
30:4S:711:GLU:O	33:4X:135:ARG:NH2	2.37	0.55
31:4T:188:ASP:OD1	31:4T:188:ASP:N	2.38	0.55
11:5B:888:GLN:O	11:5B:889:ARG:NH1	2.39	0.54
13:5D:1986:MET:O	13:5D:1993:ARG:NH2	2.38	0.54
35:2A:149:A:C4	35:2A:150:U:C5	2.95	0.54
1:A:31:C:C2	35:2A:33:G:C2	2.95	0.54
11:5B:1076:ASP:OD1	11:5B:1078:ALA:N	2.36	0.54
13:5D:342:GLU:O	13:5D:346:ILE:HG12	2.07	0.54
22:4A:74:C:H2'	22:4A:75:C:H6	1.69	0.54
22:4A:74:C:H2'	22:4A:75:C:O4'	2.07	0.54
41:2G:517:ARG:O	41:2G:520:THR:N	2.41	0.54
1:A:36:C:O2'	1:A:36:C:O2	2.24	0.54
22:4A:55:U:H5	25:4D:358:ARG:NH2	2.05	0.54
2:6A:51:U:OP2	25:4D:351:ARG:HG2	2.08	0.54
12:5C:353:THR:HG22	12:5C:355:LYS:HG3	1.89	0.54
28:4G:634:ALA:O	28:4G:638:ASN:N	2.40	0.54
41:2G:557:ASP:O	41:2G:560:LEU:N	2.40	0.54
41:2G:1205:GLU:O	41:2G:1208:LEU:N	2.41	0.54
1:A:10:C:HO2'	1:A:11:C:P	2.29	0.54
11:5B:310:THR:O	11:5B:314:ILE:HD12	2.07	0.54
12:5C:933:PHE:O	12:5C:937:THR:HG22	2.07	0.54
43:2I:1195:GLU:C	43:2I:1198:ASP:H	2.14	0.54
11:5B:385:GLU:OE1	11:5B:385:GLU:N	2.40	0.54
11:5B:504:LEU:HD11	11:5B:548:ARG:HA	1.89	0.54
11:5B:694:LEU:HD21	11:5B:709:ILE:HD11	1.90	0.54
13:5D:287:ASP:OD1	13:5D:287:ASP:C	2.50	0.54
7:6e:46:GLU:H	7:6e:63:ALA:CA	2.21	0.54
1:A:38:C:O2	1:A:38:C:H2'	2.08	0.54
11:5B:1625:SER:OG	11:5B:1663:ASP:OD2	2.26	0.54
41:2G:747:LEU:O	41:2G:748:LYS:C	2.48	0.54
13:5D:816:ALA:O	13:5D:855:ARG:NH2	2.41	0.54
13:5D:1982:VAL:O	13:5D:1986:MET:HG2	2.08	0.54
13:5D:2084:LEU:HD23	13:5D:2084:LEU:H	1.73	0.54
10:5A:108:G:H3'	10:5A:109:G:H8	1.73	0.54
11:5B:1785:VAL:HG22	11:5B:1807:ILE:HG13	1.90	0.54
35:2A:153:A:C3'	35:2A:154:C:C5'	2.85	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2I:785:PRO:CA	43:2I:800:ILE:O	2.56	0.54
13:5D:543:PRO:O	13:5D:624:ARG:NH2	2.38	0.53
27:4F:22:GLU:OE1	27:4F:22:GLU:N	2.42	0.53
39:2E:145:ILE:O	39:2E:146:MET:C	2.51	0.53
1:A:118:A:H5''	1:A:119:U:H5	1.73	0.53
10:5A:99:C:H2'	10:5A:100:C:C6	2.43	0.53
11:5B:2134:PRO:O	11:5B:2135:ASP:OD1	2.27	0.53
13:5D:1367:MET:SD	13:5D:1367:MET:C	2.92	0.53
13:5D:1391:MET:HA	13:5D:1391:MET:HE3	1.90	0.53
22:4A:68:A:O2'	22:4A:69:C:P	2.66	0.53
27:4F:71:LYS:HE2	38:2D:501:THR:OG1	2.04	0.53
28:4G:707:ASP:HA	28:4G:708:PHE:C	2.33	0.53
41:2G:978:LEU:O	41:2G:979:TYR:C	2.51	0.53
13:5D:659:GLU:OE1	13:5D:659:GLU:N	2.34	0.53
13:5D:1842:VAL:HG12	13:5D:1945:LEU:HG	1.89	0.53
25:4D:389:GLN:O	25:4D:390:GLU:C	2.52	0.53
35:2A:54:U:P	40:2F:424:ARG:O	2.67	0.53
1:A:106:A:OP1	11:5B:539:ARG:HD3	2.09	0.53
10:5A:45:C:OP2	11:5B:595:LYS:NZ	2.39	0.53
13:5D:1137:GLU:HA	13:5D:1140:VAL:HG22	1.89	0.53
13:5D:1188:VAL:HG23	13:5D:1200:VAL:HG13	1.91	0.53
41:2G:699:GLN:O	41:2G:700:LYS:C	2.48	0.53
1:A:22:C:C2'	1:A:23:G:C5'	2.87	0.53
41:2G:1026:ASN:O	41:2G:1028:HIS:N	2.41	0.53
1:A:36:C:C5'	1:A:37:C:C5	2.92	0.53
13:5D:63:MET:HG3	13:5D:63:MET:O	2.07	0.53
13:5D:765:GLU:HG3	13:5D:796:LEU:HD11	1.88	0.53
13:5D:1030:ARG:NH2	13:5D:1033:GLU:OE1	2.41	0.53
13:5D:1351:PRO:O	13:5D:1354:SER:OG	2.11	0.53
1:A:15:A:O2'	1:A:16:A:H5'	2.09	0.53
10:5A:19:A:N3	10:5A:21:A:N6	2.57	0.53
11:5B:1919:LEU:O	11:5B:1968:TRP:NE1	2.39	0.53
35:2A:179:C:H2'	35:2A:180:G:C8	2.39	0.53
41:2G:1132:LEU:O	41:2G:1135:GLU:N	2.42	0.53
41:2G:1280:LEU:O	41:2G:1282:ALA:N	2.42	0.53
13:5D:737:ALA:O	13:5D:741:MET:HG3	2.08	0.53
19:4e:33:VAL:HA	19:4e:86:LEU:O	2.09	0.53
1:A:41:U:O2	1:A:41:U:H2'	2.08	0.53
41:2G:663:THR:O	41:2G:666:LYS:N	2.42	0.53
42:2H:596:GLU:C	42:2H:598:GLU:N	2.67	0.53
11:5B:124:GLY:O	11:5B:499:GLN:NE2	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:711:GLN:HB3	28:4G:163:VAL:HG11	1.91	0.53
12:5C:392:LEU:O	12:5C:396:LEU:HG	2.09	0.53
41:2G:1280:LEU:O	41:2G:1281:ILE:C	2.51	0.53
11:5B:2278:SER:HG	11:5B:2309:HIS:CD2	2.22	0.52
24:4C:393:ASP:O	24:4C:397:GLY:N	2.42	0.52
1:A:34:G:C3'	1:A:35:U:H5''	2.35	0.52
13:5D:1834:MET:HE2	13:5D:1834:MET:HA	1.92	0.52
22:4A:78:A:H3'	22:4A:79:U:C6	2.45	0.52
25:4D:380:PHE:C	25:4D:380:PHE:HD1	2.16	0.52
30:4S:746:ARG:O	30:4S:750:LEU:HG	2.08	0.52
11:5B:260:LEU:H	11:5B:260:LEU:HD23	1.73	0.52
11:5B:1602:ASP:OD1	11:5B:1603:ALA:N	2.42	0.52
25:4D:383:ILE:C	25:4D:384:GLU:HG2	2.33	0.52
28:4G:651:LEU:O	28:4G:655:ASN:N	2.42	0.52
31:4T:511:GLU:OE1	31:4T:511:GLU:O	2.27	0.52
41:2G:244:THR:O	41:2G:247:ALA:N	2.43	0.52
41:2G:841:ALA:O	41:2G:843:LYS:N	2.41	0.52
11:5B:1941:ARG:NE	11:5B:2011:ILE:O	2.39	0.52
12:5C:196:LYS:HE2	21:5g:14:GLU:O	2.09	0.52
13:5D:925:LEU:O	13:5D:929:MET:HG3	2.09	0.52
13:5D:1628:GLU:O	13:5D:1632:VAL:HG23	2.10	0.52
31:4T:424:GLY:O	31:4T:440:ARG:NH1	2.41	0.52
11:5B:939:TRP:NE1	11:5B:1049:ASP:OD2	2.42	0.52
11:5B:1434:LYS:O	11:5B:1439:ARG:NH2	2.42	0.52
13:5D:537:LYS:NZ	13:5D:580:ILE:O	2.29	0.52
13:5D:548:VAL:HG13	13:5D:587:VAL:HG12	1.92	0.52
13:5D:1795:ASP:OD1	13:5D:1826:TYR:OH	2.21	0.52
43:2I:546:LYS:O	43:2I:556:ILE:CA	2.58	0.52
12:5C:509:VAL:HG22	12:5C:565:ILE:HD12	1.92	0.52
13:5D:1320:LEU:HD11	13:5D:1321:TYR:CZ	2.45	0.52
41:2G:1025:LYS:O	41:2G:1027:ARG:N	2.42	0.52
43:2I:42:ARG:N	43:2I:51:HIS:O	2.32	0.52
11:5B:768:ASP:OD1	11:5B:768:ASP:N	2.41	0.52
34:4Y:957:ALA:C	34:4Y:958:ASP:O	2.50	0.52
41:2G:423:PRO:O	41:2G:427:PRO:N	2.43	0.52
10:5A:96:A:N6	20:5f:23:GLY:N	2.58	0.52
12:5C:841:ASP:C	12:5C:841:ASP:OD1	2.53	0.52
13:5D:430:LEU:HD23	13:5D:880:LEU:HD12	1.92	0.52
13:5D:2098:ALA:O	13:5D:2099:THR:HG22	2.09	0.52
10:5A:95:G:N3	10:5A:95:G:C2'	2.73	0.52
12:5C:139:HIS:ND1	50:5C:1002:GTP:H5''	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:89:LEU:HD13	13:5D:95:ASP:HB2	1.92	0.52
22:4A:91:A:H2	22:4A:110:G:H22	1.58	0.52
28:4G:35:GLY:O	28:4G:36:PRO:O	2.27	0.52
1:A:108:G:O6	11:5B:1550:GLY:O	2.28	0.51
11:5B:901:LEU:O	11:5B:904:HIS:N	2.39	0.51
13:5D:1378:TYR:OH	13:5D:1454:ASP:OD1	2.21	0.51
13:5D:1980:GLU:N	13:5D:1980:GLU:OE1	2.43	0.51
22:4A:114:U:P	22:4A:114:U:C6	3.02	0.51
32:4U:282:THR:HG22	32:4U:283:SER:H	1.75	0.51
41:2G:720:GLY:O	41:2G:721:ILE:C	2.54	0.51
1:A:31:C:H2'	1:A:32:C:H5'	1.91	0.51
11:5B:696:MET:CE	28:4G:150:ALA:HB2	2.39	0.51
13:5D:1608:THR:O	13:5D:1612:THR:HG23	2.10	0.51
41:2G:771:LEU:O	41:2G:774:ILE:N	2.44	0.51
43:2I:699:VAL:CA	43:2I:715:MET:O	2.59	0.51
10:5A:85:C:OP1	17:5c:20:GLU:N	2.44	0.51
13:5D:488:LEU:CD2	13:5D:501:LEU:HD22	2.40	0.51
28:4G:21:LEU:HD23	28:4G:21:LEU:C	2.34	0.51
31:4T:177:ASP:OD1	31:4T:177:ASP:N	2.40	0.51
35:2A:107:A:C6	35:2A:108:G:C5	2.98	0.51
35:2A:111:G:O3'	35:2A:112:G:O4'	2.29	0.51
10:5A:79:C:C5'	10:5A:80:U:C6	2.93	0.51
11:5B:1552:GLN:OE1	11:5B:1561:PHE:CD1	2.64	0.51
11:5B:1591:MET:N	11:5B:1591:MET:SD	2.83	0.51
13:5D:1339:VAL:HG11	13:5D:1359:CYS:O	2.11	0.51
13:5D:1360:ALA:O	13:5D:1364:ILE:HG13	2.09	0.51
41:2G:103:PRO:C	41:2G:106:GLU:H	2.18	0.51
1:A:34:G:C2'	1:A:35:U:H6	2.23	0.51
2:6A:59:G:H2'	2:6A:59:G:N3	2.25	0.51
11:5B:799:PRO:HD3	28:4G:248:ASN:OD1	2.11	0.51
27:4F:68:ASP:N	27:4F:68:ASP:OD1	2.43	0.51
35:2A:164:C:H5'	35:2A:164:C:C6	2.44	0.51
41:2G:1110:VAL:O	41:2G:1113:THR:N	2.43	0.51
13:5D:347:MET:HG3	13:5D:360:LEU:HD21	1.92	0.51
14:5E:160:ALA:HB3	14:5E:166:LEU:H	1.74	0.51
25:4D:383:ILE:C	25:4D:384:GLU:CG	2.83	0.51
41:2G:939:ARG:O	41:2G:940:LEU:C	2.51	0.51
41:2G:1035:CYS:O	41:2G:1038:LEU:N	2.44	0.51
10:5A:100:C:H2'	10:5A:101:U:C6	2.46	0.51
13:5D:429:GLN:O	13:5D:886:GLN:NE2	2.40	0.51
23:4B:466:LEU:CB	29:4R:379:ASP:HB3	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4T:530:GLN:O	31:4T:531:ASP:C	2.54	0.51
19:4e:36:TYR:N	19:4e:83:ASN:O	2.41	0.51
41:2G:1207:SER:O	41:2G:1210:HIS:N	2.43	0.51
11:5B:1076:ASP:OD1	11:5B:1076:ASP:C	2.53	0.51
13:5D:1736:PHE:HZ	13:5D:1751:ALA:HB1	1.75	0.51
28:4G:358:ALA:O	28:4G:362:VAL:HG23	2.11	0.51
10:5A:87:A:H61	10:5A:92:U:P	2.32	0.51
12:5C:213:ASP:OD1	12:5C:214:GLU:N	2.44	0.51
21:4g:19:THR:HA	21:4g:28:TYR:O	2.11	0.51
35:2A:30:A:N3	35:2A:30:A:C2'	2.73	0.51
41:2G:641:ILE:O	41:2G:644:LEU:N	2.40	0.51
41:2G:1109:ARG:O	41:2G:1111:CYS:N	2.43	0.51
13:5D:491:ALA:O	13:5D:647:ARG:NH2	2.43	0.51
13:5D:1589:PHE:N	13:5D:1589:PHE:CD1	2.76	0.51
12:5C:485:ASP:OD1	12:5C:485:ASP:N	2.42	0.50
13:5D:713:MET:SD	13:5D:713:MET:C	2.94	0.50
13:5D:1092:MET:HE3	13:5D:1092:MET:CA	2.41	0.50
13:5D:1897:ALA:HB1	13:5D:1904:LEU:HD21	1.93	0.50
31:4T:113:ARG:NH1	31:4T:188:ASP:OD2	2.43	0.50
41:2G:660:ALA:O	41:2G:661:ARG:C	2.53	0.50
41:2G:667:ILE:O	41:2G:668:VAL:C	2.53	0.50
11:5B:640:PHE:CZ	11:5B:644:ILE:HG13	2.46	0.50
13:5D:1890:LYS:O	13:5D:1894:LEU:HG	2.11	0.50
28:4G:21:LEU:HB2	38:2D:502:TRP:CZ3	2.47	0.50
45:2K:46:ARG:N	45:2K:63:VAL:O	2.44	0.50
11:5B:422:LEU:O	11:5B:635:ARG:NE	2.34	0.50
12:5C:156:GLU:OE1	12:5C:156:GLU:N	2.44	0.50
13:5D:622:ASP:OD1	13:5D:623:ASP:N	2.45	0.50
43:2I:673:VAL:CA	43:2I:691:THR:H	2.24	0.50
1:A:37:C:H3'	1:A:37:C:H6	1.75	0.50
11:5B:689:VAL:HG21	11:5B:742:TYR:HB2	1.93	0.50
11:5B:1763:LEU:HD22	11:5B:1862:ILE:CD1	2.41	0.50
13:5D:479:LYS:CG	13:5D:480:THR:HG23	2.40	0.50
13:5D:513:ALA:HB1	13:5D:517:MET:HE3	1.93	0.50
13:5D:1104:TRP:O	13:5D:1108:THR:HG22	2.11	0.50
27:4F:8:LEU:HD12	27:4F:13:GLN:HB3	1.93	0.50
34:4Y:956:LEU:O	34:4Y:958:ASP:O	2.30	0.50
17:4c:53:LEU:O	17:4c:70:VAL:HA	2.11	0.50
41:2G:849:ILE:O	41:2G:850:ILE:C	2.54	0.50
11:5B:170:ASP:C	11:5B:170:ASP:OD1	2.54	0.50
12:5C:743:ASN:ND2	12:5C:784:ILE:O	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:1277:SER:O	13:5D:1277:SER:OG	2.27	0.50
13:5D:1493:SER:OG	13:5D:1514:PHE:O	2.29	0.50
13:5D:2062:GLU:OE1	13:5D:2064:TRP:NE1	2.45	0.50
35:2A:147:G:H2'	35:2A:148:C:C6	2.43	0.50
41:2G:1129:LEU:O	41:2G:1132:LEU:N	2.44	0.50
42:2H:573:ASP:O	42:2H:577:LYS:N	2.44	0.50
19:2e:15:VAL:O	20:2f:33:GLY:HA3	2.12	0.50
10:5A:98:G:H2'	10:5A:99:C:H6	1.77	0.50
11:5B:488:ASP:OD1	11:5B:489:TRP:N	2.45	0.50
13:5D:1378:TYR:CE2	13:5D:1389:VAL:HG11	2.46	0.50
41:2G:528:ALA:O	41:2G:531:LEU:N	2.44	0.50
41:2G:629:ALA:O	41:2G:632:PHE:N	2.45	0.50
41:2G:804:ASN:O	41:2G:807:LYS:N	2.44	0.50
43:2I:1194:SER:O	43:2I:1199:ARG:N	2.35	0.50
47:2M:48:ASP:O	47:2M:49:LEU:C	2.54	0.50
1:A:36:C:C1'	1:A:37:C:OP1	2.55	0.50
1:A:37:C:O2'	1:A:38:C:O5'	2.30	0.50
10:5A:92:U:H3'	10:5A:92:U:H6	1.77	0.50
11:5B:490:VAL:HG22	11:5B:562:VAL:HG12	1.94	0.50
11:5B:609:LYS:NZ	48:5B:2401:IHP:O41	2.40	0.50
12:5C:261:ASP:OD2	12:5C:311:SER:OG	2.30	0.50
28:4G:21:LEU:CB	38:2D:502:TRP:CE3	2.94	0.50
28:4G:353:GLN:HB3	28:4G:357:THR:HG23	1.93	0.50
41:2G:862:GLU:O	41:2G:863:GLN:C	2.55	0.50
41:2G:1268:ILE:O	41:2G:1271:SER:N	2.44	0.50
47:2M:37:ARG:O	47:2M:40:TYR:N	2.44	0.50
1:A:109:U:O2	11:5B:533:LYS:HE2	2.12	0.50
13:5D:1360:ALA:HB2	13:5D:1490:LEU:HD11	1.94	0.50
32:4U:277:ASP:OD1	32:4U:278:ALA:N	2.45	0.50
38:2D:482:THR:O	38:2D:483:ALA:CB	2.59	0.50
41:2G:708:ALA:O	41:2G:709:ILE:C	2.54	0.50
13:5D:84:MET:HA	13:5D:84:MET:CE	2.38	0.50
34:4Y:695:GLN:O	34:4Y:696:GLY:C	2.55	0.50
47:2M:36:HIS:O	47:2M:37:ARG:C	2.53	0.50
10:5A:115:C:OP1	19:5e:67:LYS:O	2.30	0.49
13:5D:1136:PRO:O	13:5D:1139:VAL:HG12	2.12	0.49
29:4R:458:MET:HE2	29:4R:458:MET:HA	1.94	0.49
41:2G:237:GLY:O	41:2G:239:ALA:N	2.45	0.49
41:2G:705:SER:O	41:2G:706:ALA:C	2.54	0.49
41:2G:1188:ALA:O	41:2G:1191:VAL:N	2.45	0.49
12:5C:451:HIS:O	12:5C:578:ARG:NH1	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:59:GLU:OE1	11:5B:59:GLU:N	2.45	0.49
11:5B:1218:ASN:OD1	11:5B:1219:GLU:N	2.44	0.49
11:5B:1811:ASN:OD1	11:5B:1813:ARG:N	2.41	0.49
11:5B:2190:PRO:HA	11:5B:2193:VAL:HG12	1.93	0.49
12:5C:116:MET:H	12:5C:116:MET:HE3	1.76	0.49
13:5D:812:THR:HG23	13:5D:814:THR:HG22	1.92	0.49
13:5D:1402:ASN:O	13:5D:1402:ASN:ND2	2.43	0.49
41:2G:793:LYS:O	41:2G:797:GLY:CA	2.54	0.49
1:A:34:G:H21	1:A:35:U:H5'	1.77	0.49
11:5B:1165:VAL:HG23	11:5B:1166:THR:N	2.27	0.49
28:4G:385:ASP:OD1	28:4G:385:ASP:N	2.45	0.49
30:4S:714:ASP:OD1	30:4S:718:ARG:N	2.43	0.49
41:2G:892:LEU:O	41:2G:893:ILE:C	2.54	0.49
41:2G:1080:THR:O	41:2G:1083:TYR:N	2.45	0.49
43:2I:1195:GLU:O	43:2I:1198:ASP:N	2.41	0.49
11:5B:1031:ILE:HG22	11:5B:1033:GLY:H	1.77	0.49
11:5B:1868:MET:HA	11:5B:1868:MET:HE2	1.95	0.49
29:4R:414:ARG:NH1	29:4R:421:THR:OG1	2.45	0.49
41:2G:1243:PRO:O	41:2G:1244:CYS:C	2.55	0.49
1:A:25:G:H1	35:2A:37:U:H3	1.60	0.49
2:6A:36:A:H4'	2:6A:37:C:OP1	2.13	0.49
11:5B:1275:ARG:C	13:5D:52:MET:HE1	2.37	0.49
13:5D:291:GLU:O	13:5D:295:THR:HG22	2.12	0.49
13:5D:429:GLN:NE2	13:5D:430:LEU:O	2.45	0.49
13:5D:991:TYR:OH	13:5D:1097:GLU:OE2	2.21	0.49
28:4G:401:PRO:O	28:4G:407:TRP:NE1	2.45	0.49
4:6b:48:GLN:C	4:6b:50:LEU:N	2.69	0.49
11:5B:733:THR:HG23	11:5B:734:PRO:HD3	1.95	0.49
12:5C:560:VAL:HG23	12:5C:561:LYS:N	2.27	0.49
41:2G:803:ALA:O	41:2G:804:ASN:C	2.54	0.49
10:5A:98:G:H2'	10:5A:99:C:C6	2.46	0.49
11:5B:801:ILE:HG23	11:5B:801:ILE:O	2.13	0.49
13:5D:1248:ASP:N	13:5D:1248:ASP:OD1	2.45	0.49
13:5D:1301:LEU:HD21	13:5D:1330:PRO:HB2	1.94	0.49
29:4R:421:THR:HG22	29:4R:423:GLY:H	1.78	0.49
41:2G:553:VAL:O	41:2G:556:ILE:N	2.46	0.49
11:5B:1895:ALA:HB1	11:5B:1943:LEU:HD22	1.94	0.49
12:5C:688:ILE:HD11	12:5C:792:LEU:HD13	1.94	0.49
15:4a:17:MET:O	15:4a:28:ILE:HA	2.12	0.49
43:2I:930:LEU:C	43:2I:934:GLY:HA2	2.38	0.49
10:5A:69:A:H2'	10:5A:70:A:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:1347:ASP:OD1	11:5B:1348:VAL:N	2.46	0.49
13:5D:277:ASP:OD1	13:5D:277:ASP:N	2.44	0.49
13:5D:677:ASP:OD1	13:5D:677:ASP:N	2.45	0.49
41:2G:625:ARG:O	41:2G:628:THR:N	2.46	0.49
11:5B:1365:ILE:CG2	11:5B:1474:MET:HE1	2.43	0.48
12:5C:461:LEU:HD13	12:5C:475:MET:HE3	1.94	0.48
19:5e:15:VAL:O	20:5f:33:GLY:HA3	2.12	0.48
22:4A:20:A:H2'	22:4A:21:U:C6	2.48	0.48
35:2A:107:A:C2	35:2A:108:G:C4	3.01	0.48
46:2L:46:CYS:O	46:2L:50:ASN:N	2.43	0.48
1:A:31:C:C2	1:A:32:C:H5	2.30	0.48
1:A:106:A:N6	1:A:107:G:O6	2.46	0.48
11:5B:1520:ASN:OD1	11:5B:1520:ASN:C	2.56	0.48
13:5D:417:THR:OG1	13:5D:418:GLN:OE1	2.31	0.48
13:5D:1320:LEU:HD13	13:5D:1396:LYS:CG	2.43	0.48
25:4D:383:ILE:CD1	25:4D:387:ALA:HA	2.43	0.48
35:2A:40:C:C5'	35:2A:40:C:C6	2.92	0.48
43:2I:596:PRO:O	43:2I:598:GLY:N	2.46	0.48
43:2I:672:GLY:O	43:2I:695:GLY:N	2.46	0.48
10:5A:18:C:OP2	11:5B:468:LYS:NZ	2.42	0.48
11:5B:270:ASN:O	11:5B:270:ASN:CG	2.55	0.48
11:5B:581:ILE:O	11:5B:585:VAL:HG23	2.13	0.48
11:5B:598:LEU:HD21	11:5B:640:PHE:CZ	2.48	0.48
11:5B:1364:LEU:N	11:5B:1364:LEU:HD23	2.28	0.48
13:5D:593:TRP:HE3	13:5D:631:LEU:HD22	1.77	0.48
22:4A:94:A:O2'	22:4A:95:C:H5'	2.12	0.48
22:4A:110:G:O2'	22:4A:111:C:H5'	2.13	0.48
29:4R:392:VAL:HG22	29:4R:393:ASN:H	1.77	0.48
19:4e:65:HIS:O	19:4e:69:LYS:N	2.45	0.48
41:2G:226:HIS:O	41:2G:229:SER:N	2.46	0.48
41:2G:665:ILE:O	41:2G:666:LYS:C	2.56	0.48
43:2I:318:ASP:N	43:2I:321:MET:O	2.27	0.48
13:5D:594:ASP:HB2	13:5D:631:LEU:HD21	1.95	0.48
13:5D:847:LEU:HD23	13:5D:847:LEU:H	1.77	0.48
13:5D:1671:GLY:N	13:5D:1860:ILE:O	2.41	0.48
20:4f:6:PRO:HA	20:4f:36:PRO:HA	1.96	0.48
21:4g:31:LYS:O	21:4g:44:SER:N	2.47	0.48
35:2A:54:U:C5'	40:2F:424:ARG:O	2.62	0.48
41:2G:177:LYS:O	41:2G:180:GLU:N	2.46	0.48
41:2G:501:LEU:O	41:2G:502:LEU:C	2.55	0.48
41:2G:1094:LEU:O	41:2G:1098:LEU:N	2.41	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:6b:47:ASP:O	4:6b:50:LEU:N	2.39	0.48
11:5B:2193:VAL:HG23	11:5B:2230:LEU:CD1	2.43	0.48
41:2G:693:GLY:O	41:2G:694:LEU:C	2.56	0.48
41:2G:993:ILE:O	41:2G:994:LEU:C	2.56	0.48
42:2H:491:LEU:O	42:2H:493:ALA:N	2.46	0.48
22:4A:78:A:C2'	22:4A:79:U:C6	2.96	0.48
22:4A:92:C:O2'	22:4A:93:G:H5'	2.14	0.48
27:4F:135:ASP:OD1	27:4F:140:TYR:OH	2.15	0.48
11:5B:841:LEU:HD21	11:5B:1429:THR:HG22	1.95	0.48
11:5B:1597:PHE:HE2	11:5B:1662:ILE:HD12	1.78	0.48
13:5D:1620:LEU:HA	13:5D:1624:LEU:HD12	1.94	0.48
22:4A:56:U:O5'	22:4A:56:U:H6	1.96	0.48
22:4A:78:A:C3'	22:4A:79:U:H6	2.25	0.48
41:2G:1227:ILE:O	41:2G:1230:VAL:N	2.46	0.48
2:6A:78:A:H2'	2:6A:78:A:N3	2.29	0.48
12:5C:592:VAL:HG13	12:5C:653:ILE:CG2	2.44	0.48
22:4A:73:U:H2'	22:4A:74:C:H6	1.77	0.48
41:2G:578:ILE:O	41:2G:579:GLU:C	2.57	0.48
41:2G:865:ARG:O	41:2G:866:LYS:C	2.56	0.48
41:2G:974:LEU:O	41:2G:975:GLY:C	2.54	0.48
45:2K:98:PHE:C	45:2K:100:LYS:N	2.72	0.48
3:6a:61:PHE:N	9:6g:70:ILE:O	2.45	0.48
11:5B:147:MET:HE1	11:5B:191:ILE:CB	2.43	0.48
11:5B:801:ILE:HD12	11:5B:1165:VAL:HG12	1.96	0.48
13:5D:526:ASN:O	13:5D:529:GLY:N	2.47	0.48
13:5D:595:ILE:HD11	13:5D:990:HIS:O	2.14	0.48
41:2G:629:ALA:O	41:2G:630:ARG:C	2.56	0.48
41:2G:631:ALA:O	41:2G:634:VAL:N	2.46	0.48
2:6A:76:A:H61	23:4B:563:ASN:N	2.12	0.48
10:5A:95:G:C1'	18:5d:24:LYS:CA	2.80	0.48
13:5D:1651:CYS:HB3	13:5D:1687:MET:HE2	1.95	0.48
22:4A:79:U:C3'	22:4A:80:A:C8	2.84	0.48
22:4A:108:C:H2'	22:4A:109:G:C8	2.49	0.48
34:4Y:680:GLY:O	34:4Y:681:GLU:C	2.56	0.48
41:2G:833:LEU:O	41:2G:834:VAL:C	2.56	0.48
41:2G:1264:VAL:O	41:2G:1265:TYR:C	2.56	0.48
43:2I:589:CYS:O	43:2I:608:GLY:N	2.30	0.48
1:A:17:G:H2'	1:A:18:C:H6	1.78	0.47
12:5C:107:GLN:OE1	12:5C:107:GLN:N	2.37	0.47
12:5C:537:TYR:CD1	12:5C:537:TYR:C	2.91	0.47
13:5D:436:ARG:NE	13:5D:443:GLU:OE2	2.38	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:710:GLU:O	13:5D:713:MET:HE3	2.14	0.47
13:5D:1305:GLN:N	13:5D:1305:GLN:OE1	2.47	0.47
13:5D:1561:VAL:HB	13:5D:1645:VAL:HG22	1.95	0.47
22:4A:9:G:OP1	23:4B:445:GLN:CB	2.62	0.47
29:4R:374:LEU:HD23	29:4R:374:LEU:N	2.29	0.47
11:5B:919:ASP:OD2	11:5B:1012:LYS:NZ	2.46	0.47
11:5B:1985:ASP:OD1	11:5B:1985:ASP:C	2.57	0.47
13:5D:221:ARG:O	13:5D:221:ARG:NH1	2.45	0.47
13:5D:617:ILE:HG22	13:5D:652:SER:HB2	1.96	0.47
13:5D:1122:MET:HE3	13:5D:1130:ARG:HD2	1.95	0.47
22:4A:56:U:H2'	22:4A:57:G:C8	2.49	0.47
22:4A:78:A:H3'	22:4A:79:U:H6	1.79	0.47
28:4G:137:LYS:HE3	38:2D:479:VAL:HG13	1.94	0.47
29:4R:383:ILE:HD11	29:4R:454:LEU:HB3	1.96	0.47
35:2A:151:C:C2	35:2A:152:G:N7	2.82	0.47
10:5A:65:G:O6	10:5A:66:A:N6	2.47	0.47
10:5A:111:A:H2'	10:5A:112:A:C8	2.49	0.47
11:5B:1759:THR:O	11:5B:1760:GLU:HB2	2.14	0.47
13:5D:540:TYR:HD2	13:5D:587:VAL:HG13	1.79	0.47
13:5D:714:GLU:O	13:5D:718:LYS:NZ	2.42	0.47
13:5D:933:PRO:HG3	13:5D:943:LEU:HD12	1.95	0.47
43:2I:147:ASP:N	43:2I:151:ARG:O	2.42	0.47
47:2M:42:SER:O	47:2M:45:GLY:N	2.48	0.47
1:A:38:C:H4'	1:A:38:C:OP1	2.14	0.47
10:5A:96:A:H61	20:5f:23:GLY:N	2.07	0.47
11:5B:147:MET:HE1	11:5B:191:ILE:CG2	2.44	0.47
13:5D:1468:GLU:OE2	13:5D:1759:PHE:N	2.43	0.47
35:2A:143:A:N3	35:2A:143:A:C3'	2.73	0.47
43:2I:923:GLY:HA3	43:2I:947:GLU:O	2.14	0.47
1:A:34:G:H3'	1:A:34:G:N3	2.28	0.47
13:5D:1473:ARG:NH1	13:5D:1739:GLU:OE2	2.48	0.47
1:A:7:U:H4'	1:A:8:U:OP1	2.15	0.47
11:5B:1701:VAL:HA	11:5B:1716:GLY:HA3	1.96	0.47
13:5D:1455:GLU:HB3	13:5D:1457:HIS:CE1	2.49	0.47
22:4A:79:U:C4	22:4A:80:A:C5	3.02	0.47
22:4A:109:G:H2'	22:4A:110:G:H8	1.77	0.47
2:6A:37:C:O2	28:4G:29:THR:HG23	2.15	0.47
11:5B:853:LYS:O	11:5B:854:SER:OG	2.27	0.47
13:5D:565:THR:CG2	13:5D:583:THR:HG22	2.44	0.47
13:5D:1189:HIS:ND1	13:5D:1201:GLU:OE2	2.48	0.47
13:5D:1329:ASN:OD1	13:5D:1329:ASN:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:2036:VAL:HG23	13:5D:2093:ASP:OD1	2.15	0.47
22:4A:140:G:H2'	22:4A:141:A:H8	1.79	0.47
41:2G:210:ALA:O	41:2G:213:LYS:N	2.48	0.47
11:5B:1511:GLU:O	11:5B:1512:SER:OG	2.25	0.47
13:5D:734:THR:CG2	13:5D:810:VAL:HG11	2.44	0.47
13:5D:785:HIS:CD2	13:5D:815:LEU:HD13	2.50	0.47
22:4A:68:A:HO2'	22:4A:69:C:P	2.30	0.47
41:2G:955:ILE:O	41:2G:956:SER:C	2.57	0.47
43:2I:44:ASP:O	43:2I:48:GLY:HA2	2.15	0.47
13:5D:146:GLU:OE2	13:5D:149:ARG:NH2	2.48	0.47
40:2F:411:CYS:O	40:2F:414:TYR:N	2.37	0.47
11:5B:176:LEU:HD12	11:5B:181:ASN:HD22	1.79	0.47
11:5B:738:MET:HE3	28:4G:145:LEU:HB3	1.97	0.47
11:5B:1002:ASP:OD1	11:5B:1004:ASN:ND2	2.44	0.47
11:5B:1807:ILE:HG13	11:5B:1822:ILE:HD11	1.97	0.47
13:5D:1164:LEU:HD12	13:5D:1164:LEU:O	2.15	0.47
13:5D:1439:TRP:CE3	13:5D:1477:ILE:HG12	2.50	0.47
10:5A:24:G:C5	10:5A:57:G:C2	3.02	0.46
11:5B:559:ASP:HA	11:5B:562:VAL:HG22	1.97	0.46
13:5D:709:TYR:HB2	13:5D:741:MET:SD	2.56	0.46
13:5D:1822:TYR:OH	13:5D:1928:ASP:OD2	2.20	0.46
24:4C:459:PRO:O	24:4C:462:GLY:N	2.48	0.46
28:4G:354:PRO:O	28:4G:358:ALA:N	2.40	0.46
41:2G:82:PRO:O	41:2G:86:ALA:N	2.42	0.46
41:2G:914:PHE:O	41:2G:915:GLY:C	2.58	0.46
10:5A:117:A:C2	18:5d:26:GLY:O	2.68	0.46
13:5D:592:LYS:O	13:5D:595:ILE:HG22	2.14	0.46
41:2G:631:ALA:O	41:2G:632:PHE:C	2.58	0.46
41:2G:994:LEU:O	41:2G:995:GLY:C	2.56	0.46
12:5C:566:THR:OG1	12:5C:567:GLU:N	2.48	0.46
12:5C:572:GLU:N	12:5C:572:GLU:OE1	2.47	0.46
12:5C:584:THR:OG1	12:5C:585:THR:N	2.48	0.46
13:5D:1409:THR:OG1	13:5D:1411:GLU:OE1	2.16	0.46
13:5D:1650:LEU:O	13:5D:1654:MET:HG2	2.15	0.46
22:4A:74:C:H3'	22:4A:75:C:C6	2.50	0.46
33:4X:143:ARG:NH1	33:4X:146:GLY:O	2.48	0.46
35:2A:114:A:H2'	35:2A:115:G:H8	1.81	0.46
35:2A:181:G:H2'	35:2A:182:U:C6	2.50	0.46
43:2I:558:LEU:O	43:2I:561:GLY:CA	2.63	0.46
11:5B:587:GLN:OE1	11:5B:587:GLN:N	2.49	0.46
12:5C:645:ARG:NH1	12:5C:653:ILE:O	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:447:VAL:HB	13:5D:687:GLN:HG3	1.96	0.46
13:5D:891:SER:N	13:5D:936:TYR:OH	2.49	0.46
35:2A:107:A:C6	35:2A:108:G:C6	3.04	0.46
41:2G:831:ARG:O	41:2G:832:GLN:C	2.58	0.46
43:2I:1148:LEU:O	43:2I:1149:ARG:C	2.57	0.46
1:A:28:G:H22	35:2A:34:U:H3	1.62	0.46
11:5B:490:VAL:CG2	11:5B:562:VAL:HG12	2.46	0.46
11:5B:710:LEU:HD23	11:5B:710:LEU:O	2.16	0.46
11:5B:1126:VAL:HG23	11:5B:1127:GLY:N	2.31	0.46
11:5B:1658:GLN:OE1	11:5B:1658:GLN:N	2.48	0.46
11:5B:1832:ARG:HG3	11:5B:1836:LEU:HD13	1.98	0.46
13:5D:1664:MET:HG2	13:5D:1705:MET:HE1	1.97	0.46
22:4A:119:A:N6	18:4d:38:GLY:O	2.43	0.46
28:4G:280:MET:C	28:4G:280:MET:SD	2.98	0.46
28:4G:355:GLY:HA2	28:4G:382:LEU:HD22	1.97	0.46
35:2A:141:C:H2'	35:2A:142:C:C6	2.50	0.46
41:2G:693:GLY:O	41:2G:695:VAL:N	2.49	0.46
41:2G:952:ALA:O	41:2G:953:ASP:C	2.57	0.46
2:6A:56:A:C2	2:6A:57:U:C2	3.04	0.46
11:5B:1368:LEU:O	11:5B:1372:ILE:HG12	2.15	0.46
35:2A:180:G:H2'	35:2A:181:G:H8	1.81	0.46
41:2G:1119:VAL:O	41:2G:1122:THR:N	2.49	0.46
11:5B:733:THR:N	11:5B:734:PRO:HD2	2.31	0.46
11:5B:1692:MET:HE2	11:5B:1692:MET:HA	1.98	0.46
11:5B:1763:LEU:HD11	11:5B:1768:TYR:HA	1.97	0.46
28:4G:339:CYS:O	28:4G:342:SER:OG	2.28	0.46
41:2G:1256:HIS:O	41:2G:1257:PRO:C	2.58	0.46
11:5B:2242:THR:O	11:5B:2242:THR:HG22	2.16	0.46
12:5C:418:LEU:C	12:5C:418:LEU:HD23	2.41	0.46
22:4A:77:A:H2'	22:4A:78:A:H8	1.78	0.46
24:4C:316:VAL:O	24:4C:317:ALA:C	2.58	0.46
29:4R:388:LEU:HD12	29:4R:423:GLY:O	2.15	0.46
1:A:34:G:N3	1:A:35:U:H5''	2.31	0.46
11:5B:1625:SER:OG	11:5B:1626:CYS:N	2.46	0.46
13:5D:2066:VAL:HG22	13:5D:2108:PHE:CD1	2.51	0.46
28:4G:21:LEU:HD12	38:2D:509:MET:CG	2.45	0.46
35:2A:3:C:H2'	35:2A:4:G:C8	2.51	0.46
35:2A:183:G:H2'	35:2A:184:C:C6	2.50	0.46
38:2D:514:GLN:O	38:2D:518:ALA:N	2.39	0.46
41:2G:708:ALA:O	41:2G:711:ALA:N	2.49	0.46
41:2G:889:GLU:O	41:2G:890:GLU:C	2.57	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2M:64:VAL:O	47:2M:65:ARG:C	2.59	0.46
1:A:28:G:C2	35:2A:35:A:C2	3.05	0.46
3:6a:73:PRO:O	3:6a:75:ASP:N	2.49	0.46
11:5B:682:ASP:OD1	11:5B:682:ASP:C	2.58	0.46
13:5D:2017:ILE:HG21	13:5D:2108:PHE:CE2	2.51	0.46
24:4C:459:PRO:O	24:4C:461:HIS:N	2.50	0.46
35:2A:142:C:H2'	35:2A:143:A:H5'	1.98	0.46
40:2F:394:TYR:C	40:2F:396:LEU:H	2.24	0.46
41:2G:953:ASP:O	41:2G:954:LEU:C	2.56	0.46
1:A:105:C:O2'	1:A:106:A:OP2	2.27	0.45
2:6A:37:C:N4	38:2D:504:GLY:HA3	2.30	0.45
10:5A:92:U:N3	16:5b:36:MET:N	2.64	0.45
11:5B:1405:LEU:N	13:5D:218:GLY:O	2.49	0.45
13:5D:89:LEU:HD13	13:5D:95:ASP:HB3	1.97	0.45
13:5D:1808:MET:SD	13:5D:1808:MET:O	2.73	0.45
22:4A:70:U:O3'	29:4R:370:ASP:OD2	2.19	0.45
25:4D:387:ALA:CB	25:4D:388:TYR:CD1	2.99	0.45
41:2G:257:THR:O	41:2G:259:SER:N	2.49	0.45
41:2G:567:VAL:O	41:2G:568:ARG:C	2.58	0.45
41:2G:1062:LEU:O	41:2G:1065:LEU:N	2.39	0.45
41:2G:1246:MET:O	41:2G:1247:LEU:C	2.59	0.45
10:5A:79:C:P	10:5A:80:U:H5	2.33	0.45
11:5B:1346:THR:CG2	11:5B:1348:VAL:HG12	2.46	0.45
13:5D:586:ILE:HD13	13:5D:586:ILE:N	2.30	0.45
13:5D:1324:LYS:N	13:5D:1324:LYS:HD2	2.30	0.45
13:5D:2017:ILE:HG21	13:5D:2108:PHE:HE2	1.79	0.45
25:4D:349:GLY:HA3	25:4D:351:ARG:NH2	2.31	0.45
28:4G:362:VAL:HG11	28:4G:379:ALA:HB2	1.98	0.45
29:4R:439:MET:SD	29:4R:439:MET:C	2.98	0.45
35:2A:153:A:C8	35:2A:154:C:H5'	2.50	0.45
41:2G:830:TYR:O	41:2G:831:ARG:C	2.57	0.45
44:2J:70:ALA:O	44:2J:74:MET:N	2.41	0.45
1:A:116:G:H1	2:6A:38:G:H22	1.64	0.45
13:5D:712:ILE:HD13	13:5D:721:VAL:HG11	1.97	0.45
32:4U:304:ILE:H	32:4U:304:ILE:HD12	1.82	0.45
41:2G:792:VAL:O	41:2G:793:LYS:C	2.59	0.45
41:2G:935:THR:O	41:2G:936:VAL:C	2.58	0.45
10:5A:58:U:H4'	10:5A:59:G:OP1	2.16	0.45
11:5B:1364:LEU:HD23	11:5B:1364:LEU:H	1.81	0.45
11:5B:1660:TYR:OH	11:5B:1717:ASN:O	2.33	0.45
12:5C:684:LYS:C	12:5C:685:ILE:HD13	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:66:GLU:OE1	13:5D:66:GLU:N	2.49	0.45
13:5D:1397:PHE:O	13:5D:1401:LEU:N	2.48	0.45
41:2G:663:THR:O	41:2G:664:GLY:C	2.56	0.45
43:2I:672:GLY:O	43:2I:691:THR:N	2.49	0.45
43:2I:1141:PHE:O	43:2I:1144:VAL:N	2.49	0.45
47:2M:62:ALA:O	47:2M:65:ARG:N	2.50	0.45
4:6b:19:ASP:C	4:6b:21:ILE:H	2.23	0.45
11:5B:1609:VAL:HG12	11:5B:1631:LEU:HD22	1.99	0.45
12:5C:763:LYS:O	12:5C:767:VAL:HG23	2.17	0.45
13:5D:673:LEU:HD23	13:5D:673:LEU:C	2.42	0.45
13:5D:824:HIS:ND1	13:5D:862:ASP:OD1	2.42	0.45
47:2M:46:HIS:O	47:2M:47:PHE:C	2.59	0.45
11:5B:2136:ASN:OD1	11:5B:2138:GLN:NE2	2.50	0.45
11:5B:2329:ASP:OD1	13:5D:728:ARG:NE	2.46	0.45
12:5C:357:THR:OG1	12:5C:359:LYS:O	2.35	0.45
13:5D:812:THR:OG1	13:5D:813:ALA:N	2.48	0.45
13:5D:912:ASN:OD1	13:5D:912:ASN:N	2.50	0.45
13:5D:1344:ASP:C	13:5D:1344:ASP:OD1	2.60	0.45
22:4A:74:C:H3'	22:4A:75:C:C5	2.52	0.45
22:4A:76:C:H2'	22:4A:77:A:H8	1.81	0.45
43:2I:215:LEU:O	43:2I:218:ASN:N	2.50	0.45
43:2I:672:GLY:C	43:2I:691:THR:H	2.25	0.45
1:A:33:U:O3'	1:A:34:G:O4'	2.35	0.45
13:5D:1055:PRO:O	13:5D:1059:ILE:HG12	2.16	0.45
1:A:20:U:C2	35:2A:42:G:C2	3.04	0.45
11:5B:292:ASP:OD1	11:5B:1139:ARG:NE	2.47	0.45
11:5B:1399:GLN:OE1	11:5B:1399:GLN:HA	2.17	0.45
11:5B:2166:HIS:ND1	11:5B:2272:MET:HE1	2.32	0.45
13:5D:726:HIS:HB2	13:5D:833:VAL:HG12	1.97	0.45
13:5D:766:ALA:HB2	13:5D:778:LEU:HB2	1.99	0.45
13:5D:831:THR:HG21	13:5D:869:LEU:HD11	1.99	0.45
41:2G:749:ALA:O	41:2G:750:ILE:C	2.60	0.45
41:2G:1223:SER:O	41:2G:1224:PRO:C	2.60	0.45
43:2I:1191:LYS:O	43:2I:1192:ASN:C	2.59	0.45
10:5A:92:U:C4	16:5b:36:MET:N	2.85	0.45
12:5C:560:VAL:HG23	12:5C:561:LYS:H	1.81	0.45
13:5D:1808:MET:SD	13:5D:1808:MET:C	3.00	0.45
35:2A:113:G:H2'	35:2A:114:A:H8	1.82	0.45
35:2A:149:A:H2'	35:2A:150:U:C6	2.50	0.45
41:2G:429:ARG:O	41:2G:432:THR:N	2.46	0.45
43:2I:663:LEU:O	43:2I:678:VAL:CA	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:5A:89:U:C2'	10:5A:90:U:H5''	2.47	0.45
11:5B:1690:ASP:OD1	11:5B:1691:ASN:N	2.49	0.45
11:5B:2207:ASP:O	11:5B:2211:THR:HG23	2.17	0.45
12:5C:119:LEU:HD23	12:5C:119:LEU:C	2.42	0.45
22:4A:78:A:C5	22:4A:79:U:C4	3.05	0.45
32:4U:319:PHE:CD1	32:4U:319:PHE:C	2.95	0.45
35:2A:54:U:H5'	40:2F:424:ARG:CA	2.47	0.45
35:2A:148:C:H2'	35:2A:149:A:H8	1.82	0.45
41:2G:1110:VAL:O	41:2G:1111:CYS:C	2.57	0.45
41:2G:1128:VAL:O	41:2G:1129:LEU:C	2.60	0.45
43:2I:406:PRO:CA	43:2I:1122:LEU:O	2.65	0.45
1:A:30:C:C3'	1:A:31:C:H5'	2.42	0.44
1:A:34:G:C5	1:A:35:U:C4	3.05	0.44
2:6A:38:G:C2'	2:6A:39:A:O5'	2.64	0.44
12:5C:745:LEU:HD11	12:5C:791:ILE:HG13	1.99	0.44
13:5D:116:LEU:HB2	13:5D:175:LEU:HD12	1.99	0.44
13:5D:488:LEU:CD2	13:5D:501:LEU:HD13	2.47	0.44
13:5D:673:LEU:HD23	13:5D:674:PHE:N	2.32	0.44
13:5D:1661:VAL:CG2	13:5D:1691:ALA:HB2	2.47	0.44
22:4A:78:A:C2	22:4A:79:U:C2	3.06	0.44
25:4D:383:ILE:O	25:4D:385:GLU:N	2.50	0.44
40:2F:403:ASN:N	40:2F:417:ARG:O	2.49	0.44
41:2G:810:ILE:O	41:2G:811:LEU:C	2.58	0.44
41:2G:937:LEU:O	41:2G:938:TRP:C	2.59	0.44
1:A:33:U:O2'	1:A:34:G:C8	2.70	0.44
2:6A:89:U:H2'	2:6A:90:G:C8	2.53	0.44
11:5B:1441:ASP:OD1	11:5B:1441:ASP:C	2.60	0.44
11:5B:1759:THR:O	11:5B:1760:GLU:CB	2.65	0.44
13:5D:1345:ASN:OD1	13:5D:1487:ILE:N	2.44	0.44
13:5D:1661:VAL:C	13:5D:1662:ILE:HD13	2.43	0.44
22:4A:31:U:O4	26:4E:60:ALA:HA	2.16	0.44
22:4A:61:A:OP1	30:4S:749:LYS:NZ	2.46	0.44
35:2A:153:A:C2'	35:2A:154:C:C5'	2.86	0.44
35:2A:182:U:H2'	35:2A:183:G:H8	1.81	0.44
38:2D:482:THR:O	38:2D:483:ALA:HB3	2.17	0.44
41:2G:687:VAL:O	41:2G:690:ILE:N	2.50	0.44
41:2G:841:ALA:C	41:2G:843:LYS:N	2.73	0.44
41:2G:867:MET:O	41:2G:868:VAL:C	2.57	0.44
41:2G:948:ARG:O	41:2G:949:GLN:C	2.60	0.44
1:A:32:C:N3	35:2A:31:G:O6	2.50	0.44
10:5A:11:U:C2	10:5A:67:A:C2	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:5A:58:U:C6	10:5A:58:U:H5''	2.52	0.44
11:5B:246:LEU:HD11	11:5B:411:PHE:CE2	2.52	0.44
11:5B:710:LEU:CD1	27:4F:4:MET:HE2	2.47	0.44
13:5D:313:ASN:O	13:5D:314:THR:OG1	2.31	0.44
13:5D:830:GLY:O	13:5D:831:THR:OG1	2.25	0.44
22:4A:56:U:C4	25:4D:354:ARG:NE	2.85	0.44
22:4A:93:G:H2'	22:4A:94:A:H8	1.83	0.44
41:2G:471:ASP:O	41:2G:472:ILE:C	2.57	0.44
41:2G:645:LEU:O	41:2G:646:PRO:C	2.56	0.44
41:2G:1078:VAL:O	41:2G:1081:PHE:N	2.50	0.44
2:6A:46:G:HO2'	2:6A:47:A:C5'	2.29	0.44
2:6A:91:A:H2'	2:6A:92:A:C8	2.53	0.44
10:5A:117:A:C6	18:5d:26:GLY:HA3	2.52	0.44
12:5C:215:VAL:HG11	12:5C:242:LEU:HD22	1.99	0.44
12:5C:481:MET:HE1	12:5C:556:ASP:HB2	2.00	0.44
13:5D:929:MET:HE3	13:5D:949:LEU:CD2	2.48	0.44
13:5D:1100:LEU:HD21	13:5D:1222:TRP:CZ3	2.52	0.44
13:5D:1636:PHE:CD2	13:5D:1656:VAL:HG21	2.53	0.44
22:4A:113:C:O3'	22:4A:114:U:C5	2.71	0.44
28:4G:668:ALA:O	28:4G:672:ALA:N	2.46	0.44
41:2G:429:ARG:C	41:2G:432:THR:H	2.26	0.44
41:2G:834:VAL:O	41:2G:835:ASP:C	2.60	0.44
41:2G:1031:VAL:O	41:2G:1032:GLN:C	2.60	0.44
11:5B:1676:ILE:HD11	11:5B:1704:ALA:HB1	1.99	0.44
13:5D:176:GLY:O	13:5D:179:ILE:HG22	2.17	0.44
24:4C:259:SER:O	24:4C:263:CYS:N	2.43	0.44
25:4D:383:ILE:HG12	25:4D:385:GLU:O	2.17	0.44
28:4G:362:VAL:HG13	28:4G:375:ILE:HG23	2.00	0.44
31:4T:174:CYS:CB	31:4T:181:ILE:HD11	2.47	0.44
35:2A:59:A:H2'	35:2A:60:U:O4'	2.17	0.44
35:2A:143:A:OP2	35:2A:143:A:C2	2.71	0.44
41:2G:710:ALA:O	41:2G:711:ALA:C	2.61	0.44
41:2G:723:SER:C	41:2G:725:ASP:H	2.26	0.44
41:2G:745:ALA:O	41:2G:746:PHE:C	2.59	0.44
41:2G:916:THR:O	41:2G:917:VAL:C	2.61	0.44
41:2G:1129:LEU:O	41:2G:1130:PRO:C	2.59	0.44
41:2G:1165:TYR:O	41:2G:1166:ILE:C	2.59	0.44
43:2I:676:ARG:O	43:2I:686:LEU:CA	2.65	0.44
1:A:35:U:O2'	1:A:36:C:C5	2.71	0.44
12:5C:216:THR:HG22	12:5C:245:HIS:NE2	2.33	0.44
12:5C:798:GLN:O	12:5C:803:ARG:NH2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:1493:SER:HG	13:5D:1514:PHE:C	2.24	0.44
22:4A:76:C:C4	22:4A:77:A:C5	3.05	0.44
31:4T:339:LYS:O	31:4T:339:LYS:NZ	2.46	0.44
31:4T:384:VAL:O	31:4T:384:VAL:HG13	2.18	0.44
35:2A:152:G:O2'	35:2A:153:A:H1'	2.16	0.44
41:2G:872:ILE:O	41:2G:873:GLU:C	2.57	0.44
2:6A:92:A:H2'	2:6A:93:G:H8	1.83	0.44
11:5B:1330:MET:HG3	11:5B:1330:MET:O	2.17	0.44
11:5B:2009:ASP:OD1	11:5B:2009:ASP:C	2.60	0.44
13:5D:843:GLU:OE1	13:5D:875:GLU:OE2	2.35	0.44
13:5D:1165:ILE:O	13:5D:1165:ILE:HG22	2.18	0.44
22:4A:55:U:H2'	22:4A:56:U:C6	2.53	0.44
32:4U:246:GLU:O	32:4U:250:ILE:HG13	2.18	0.44
35:2A:142:C:O2'	35:2A:143:A:H5'	2.18	0.44
41:2G:658:TRP:O	41:2G:659:GLN:C	2.60	0.44
2:6A:90:G:H2'	2:6A:91:A:H8	1.82	0.44
11:5B:2278:SER:OG	11:5B:2309:HIS:NE2	2.31	0.44
13:5D:541:ILE:HD12	13:5D:614:LEU:HD23	2.00	0.44
35:2A:150:U:H2'	35:2A:151:C:C6	2.50	0.44
41:2G:606:LEU:O	41:2G:609:MET:N	2.51	0.44
41:2G:706:ALA:O	41:2G:707:LEU:C	2.61	0.44
41:2G:998:LYS:O	41:2G:1001:VAL:N	2.51	0.44
11:5B:1125:ILE:O	11:5B:1125:ILE:HG22	2.18	0.44
11:5B:1463:LYS:HE3	25:4D:389:GLN:HE22	1.82	0.44
12:5C:403:LEU:HD23	12:5C:403:LEU:H	1.82	0.44
13:5D:817:TRP:CD2	13:5D:851:GLN:HG2	2.53	0.44
22:4A:113:C:O3'	22:4A:114:U:C6	2.71	0.44
35:2A:112:G:H2'	35:2A:113:G:C8	2.50	0.44
41:2G:1090:PRO:O	41:2G:1091:HIS:C	2.61	0.44
10:5A:81:U:C6	10:5A:81:U:O5'	2.70	0.43
10:5A:99:C:H2'	10:5A:100:C:H6	1.79	0.43
12:5C:164:ASP:OD1	12:5C:164:ASP:N	2.49	0.43
12:5C:715:GLY:HA2	12:5C:729:ALA:HB1	1.99	0.43
13:5D:596:ILE:HG13	13:5D:597:THR:N	2.32	0.43
41:2G:874:LYS:O	41:2G:875:ILE:C	2.60	0.43
41:2G:1082:GLY:O	41:2G:1083:TYR:C	2.61	0.43
41:2G:1262:ARG:O	41:2G:1263:ASP:C	2.61	0.43
11:5B:274:PRO:O	32:4U:283:SER:N	2.51	0.43
11:5B:1403:LEU:HD22	11:5B:1403:LEU:H	1.83	0.43
13:5D:726:HIS:CB	13:5D:833:VAL:HG12	2.48	0.43
13:5D:1367:MET:HE2	13:5D:1376:CYS:SG	2.58	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:4U:177:ARG:HA	32:4U:180:GLU:HG3	2.00	0.43
35:2A:178:A:H2'	35:2A:178:A:N3	2.34	0.43
41:2G:86:ALA:O	41:2G:89:ALA:CA	2.66	0.43
41:2G:1029:GLU:O	41:2G:1032:GLN:N	2.51	0.43
41:2G:1115:ALA:O	41:2G:1116:ILE:C	2.61	0.43
11:5B:770:THR:HG23	11:5B:771:VAL:N	2.33	0.43
11:5B:1507:SER:OG	11:5B:1752:GLN:NE2	2.50	0.43
11:5B:1519:THR:HG22	11:5B:1520:ASN:H	1.83	0.43
11:5B:1790:ILE:HG22	11:5B:1798:LEU:HD11	1.99	0.43
12:5C:510:LEU:N	12:5C:510:LEU:HD12	2.33	0.43
13:5D:275:PHE:CG	13:5D:314:THR:HG22	2.54	0.43
13:5D:1738:ALA:O	13:5D:1741:VAL:HG22	2.19	0.43
13:5D:1844:GLY:O	13:5D:1848:ILE:HG12	2.18	0.43
22:4A:105:A:H2'	22:4A:106:G:H8	1.83	0.43
22:4A:114:U:C6	22:4A:114:U:O5'	2.70	0.43
28:4G:280:MET:O	28:4G:281:ILE:C	2.61	0.43
29:4R:392:VAL:HG13	29:4R:393:ASN:N	2.32	0.43
32:4U:322:ASP:O	32:4U:325:GLU:HG2	2.17	0.43
43:2I:430:GLY:O	43:2I:431:PRO:C	2.61	0.43
11:5B:122:ILE:HG23	11:5B:481:PHE:O	2.19	0.43
11:5B:1394:GLN:C	11:5B:1394:GLN:CD	2.86	0.43
11:5B:2190:PRO:O	11:5B:2194:THR:HG22	2.19	0.43
12:5C:363:SER:O	12:5C:363:SER:OG	2.30	0.43
12:5C:764:ASP:N	12:5C:764:ASP:OD1	2.51	0.43
13:5D:542:ALA:HB1	13:5D:547:LEU:HD23	2.01	0.43
27:4F:4:MET:O	38:2D:457:ALA:N	2.42	0.43
28:4G:363:ALA:O	28:4G:366:VAL:HG22	2.18	0.43
15:4a:42:LEU:O	15:4a:69:LEU:HA	2.18	0.43
35:2A:98:G:H5'	35:2A:104:U:OP2	2.19	0.43
41:2G:594:ARG:O	41:2G:595:GLU:C	2.61	0.43
41:2G:791:VAL:O	41:2G:792:VAL:C	2.60	0.43
41:2G:1230:VAL:O	41:2G:1233:ALA:N	2.51	0.43
2:6A:46:G:H1'	2:6A:47:A:O5'	2.18	0.43
11:5B:694:LEU:CD2	11:5B:709:ILE:HD11	2.48	0.43
11:5B:861:ARG:NH1	11:5B:861:ARG:O	2.52	0.43
13:5D:1813:LEU:O	13:5D:1817:MET:HG3	2.19	0.43
13:5D:2037:VAL:HG13	13:5D:2092:LEU:HG	2.01	0.43
35:2A:157:G:H2'	35:2A:158:G:O4'	2.19	0.43
41:2G:1013:ILE:O	41:2G:1014:LYS:C	2.60	0.43
11:5B:1644:LEU:HD23	11:5B:1715:TYR:CD1	2.53	0.43
11:5B:2329:ASP:OD1	13:5D:728:ARG:NH2	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:725:VAL:HG11	13:5D:734:THR:HG21	2.00	0.43
13:5D:785:HIS:CE1	13:5D:815:LEU:HD13	2.54	0.43
13:5D:1037:LEU:HD21	13:5D:1077:LEU:HD11	1.99	0.43
22:4A:77:A:C2'	22:4A:78:A:C8	3.01	0.43
31:4T:352:SER:C	31:4T:444:THR:HG1	2.25	0.43
34:4Y:759:HIS:O	34:4Y:760:LYS:C	2.61	0.43
19:4e:34:TRP:O	19:4e:85:THR:N	2.41	0.43
35:2A:64:A:H2'	35:2A:65:U:C6	2.54	0.43
40:2F:404:ILE:N	40:2F:417:ARG:O	2.44	0.43
43:2I:5:ASN:O	43:2I:1176:GLY:HA3	2.19	0.43
43:2I:1148:LEU:O	43:2I:1151:GLU:N	2.51	0.43
1:A:37:C:C2'	1:A:38:C:O5'	2.67	0.43
2:6A:91:A:H2'	2:6A:92:A:H8	1.82	0.43
11:5B:1175:VAL:O	11:5B:1175:VAL:HG13	2.18	0.43
11:5B:1978:LYS:O	11:5B:1981:VAL:HG12	2.18	0.43
13:5D:1662:ILE:HG22	13:5D:1705:MET:HE2	2.01	0.43
13:5D:1945:LEU:HA	13:5D:1948:MET:CG	2.48	0.43
25:4D:380:PHE:CD1	25:4D:381:GLY:N	2.86	0.43
28:4G:297:LEU:O	28:4G:301:VAL:HG23	2.19	0.43
28:4G:316:ALA:HB2	28:4G:332:ILE:HG12	2.00	0.43
31:4T:233:ASN:OD1	31:4T:237:ASN:OD1	2.37	0.43
35:2A:3:C:H2'	35:2A:4:G:H8	1.84	0.43
41:2G:665:ILE:O	41:2G:668:VAL:N	2.52	0.43
41:2G:889:GLU:O	41:2G:892:LEU:N	2.51	0.43
42:2H:504:TRP:C	42:2H:506:PHE:H	2.27	0.43
11:5B:923:ASP:OD2	11:5B:1439:ARG:NH1	2.51	0.43
12:5C:129:ILE:HD12	12:5C:199:LEU:HD23	2.01	0.43
13:5D:158:ASP:O	13:5D:163:GLN:N	2.38	0.43
20:4f:46:VAL:HA	20:4f:56:ASN:HA	2.00	0.43
41:2G:310:TRP:O	41:2G:311:ALA:C	2.62	0.43
41:2G:951:ALA:O	41:2G:952:ALA:C	2.62	0.43
43:2I:1141:PHE:O	43:2I:1142:GLN:C	2.60	0.43
11:5B:1335:ILE:O	11:5B:1335:ILE:HG23	2.18	0.43
13:5D:1081:MET:O	13:5D:1085:THR:HG23	2.19	0.43
13:5D:1832:PHE:CE1	13:5D:1926:CYS:SG	3.12	0.43
22:4A:57:G:O6	25:4D:354:ARG:HG2	2.18	0.43
24:4C:275:ASN:O	24:4C:301:ALA:N	2.50	0.43
40:2F:34:ARG:O	40:2F:35:ASP:C	2.62	0.43
41:2G:669:GLN:O	41:2G:670:GLN:C	2.60	0.43
41:2G:1279:ALA:O	41:2G:1280:LEU:C	2.61	0.43
10:5A:115:C:OP1	19:5e:67:LYS:CA	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:710:LEU:HD12	27:4F:4:MET:HE2	2.01	0.43
11:5B:1676:ILE:HD11	11:5B:1704:ALA:CB	2.49	0.43
12:5C:688:ILE:HG22	12:5C:689:ALA:N	2.33	0.43
13:5D:632:VAL:HB	13:5D:664:PHE:CZ	2.54	0.43
13:5D:1685:LEU:HA	13:5D:1688:VAL:HG12	2.01	0.43
15:4a:18:ARG:N	15:4a:81:THR:O	2.44	0.43
35:2A:154:C:O2'	35:2A:155:C:C5'	2.66	0.43
43:2I:1211:ILE:O	43:2I:1212:ARG:C	2.62	0.43
1:A:31:C:C4	1:A:32:C:N4	2.73	0.42
10:5A:19:A:O2'	10:5A:21:A:N7	2.48	0.42
10:5A:58:U:O2'	10:5A:59:G:P	2.77	0.42
10:5A:93:U:C4'	17:5c:104:ASP:CA	2.97	0.42
11:5B:691:HIS:HB3	38:2D:477:PHE:HE2	1.84	0.42
12:5C:440:SER:N	12:5C:441:PRO:HA	2.34	0.42
12:5C:891:THR:O	12:5C:891:THR:CG2	2.66	0.42
13:5D:1092:MET:HE3	13:5D:1092:MET:O	2.19	0.42
13:5D:1419:LEU:HD12	13:5D:1425:ILE:HG13	1.99	0.42
13:5D:1747:ASN:HB2	13:5D:1808:MET:SD	2.59	0.42
13:5D:1940:LEU:HA	13:5D:1943:MET:HE3	2.01	0.42
13:5D:1957:ASP:OD1	13:5D:1958:SER:N	2.52	0.42
28:4G:305:ASN:HD22	28:4G:308:HIS:CB	2.32	0.42
32:4U:335:GLN:OE1	32:4U:335:GLN:HA	2.19	0.42
40:2F:394:TYR:C	40:2F:396:LEU:N	2.75	0.42
45:2K:51:GLY:HA3	45:2K:56:THR:O	2.19	0.42
13:5D:269:GLN:NE2	31:4T:106:PRO:O	2.45	0.42
13:5D:1345:ASN:C	13:5D:1506:CYS:HG	2.27	0.42
13:5D:1454:ASP:O	13:5D:1455:GLU:C	2.62	0.42
13:5D:1636:PHE:HD2	13:5D:1656:VAL:HG21	1.83	0.42
22:4A:77:A:C3'	22:4A:78:A:H8	2.32	0.42
35:2A:153:A:H2'	35:2A:154:C:H5''	1.99	0.42
41:2G:682:HIS:O	41:2G:683:LEU:C	2.61	0.42
46:2L:30:CYS:N	46:2L:35:SER:O	2.38	0.42
1:A:30:C:C5	1:A:31:C:H5	2.32	0.42
4:6b:19:ASP:C	4:6b:21:ILE:N	2.77	0.42
10:5A:92:U:O4	16:5b:34:VAL:O	2.37	0.42
11:5B:422:LEU:HD21	11:5B:638:LEU:HD13	2.01	0.42
11:5B:1310:ARG:NH1	11:5B:1310:ARG:O	2.52	0.42
12:5C:793:ASP:OD1	12:5C:794:ALA:N	2.53	0.42
13:5D:430:LEU:HB3	13:5D:431:PRO:HD2	2.00	0.42
13:5D:471:ALA:HA	13:5D:518:LEU:HD22	2.00	0.42
25:4D:357:ARG:CG	25:4D:358:ARG:HG3	2.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4T:174:CYS:HB2	31:4T:181:ILE:HD11	2.01	0.42
31:4T:502:ASN:C	31:4T:502:ASN:OD1	2.62	0.42
35:2A:54:U:H5'	40:2F:424:ARG:C	2.45	0.42
41:2G:301:ARG:O	41:2G:302:ASP:C	2.63	0.42
41:2G:1016:LEU:O	41:2G:1017:LEU:C	2.62	0.42
1:A:22:C:H2'	1:A:23:G:C5'	2.49	0.42
2:6A:89:U:H2'	2:6A:90:G:H8	1.84	0.42
10:5A:77:G:N7	10:5A:78:U:C6	2.88	0.42
11:5B:89:LEU:HD21	11:5B:506:LEU:HD21	2.00	0.42
12:5C:166:CYS:C	12:5C:168:THR:H	2.27	0.42
12:5C:705:VAL:HG21	12:5C:717:PHE:CE2	2.54	0.42
13:5D:201:VAL:HG11	28:4G:301:VAL:HG22	2.01	0.42
13:5D:1760:LEU:O	13:5D:1764:MET:HG3	2.19	0.42
22:4A:78:A:C3'	22:4A:79:U:C6	3.03	0.42
31:4T:294:VAL:HG12	31:4T:295:SER:N	2.34	0.42
41:2G:625:ARG:O	41:2G:626:ASN:C	2.61	0.42
41:2G:950:GLN:O	41:2G:951:ALA:C	2.61	0.42
11:5B:211:GLN:OE1	11:5B:214:ARG:NE	2.35	0.42
11:5B:440:PRO:O	11:5B:443:VAL:HG12	2.20	0.42
11:5B:598:LEU:HD22	11:5B:637:TRP:HZ3	1.84	0.42
13:5D:350:MET:O	13:5D:356:LEU:HB2	2.19	0.42
13:5D:1301:LEU:HD22	13:5D:1518:VAL:CG1	2.49	0.42
13:5D:1352:THR:O	13:5D:1519:ARG:NE	2.53	0.42
22:4A:77:A:C4	22:4A:78:A:C8	3.07	0.42
41:2G:627:THR:O	41:2G:630:ARG:N	2.52	0.42
41:2G:806:ILE:O	41:2G:807:LYS:C	2.62	0.42
43:2I:886:GLU:CA	43:2I:910:ALA:O	2.67	0.42
43:2I:1189:LYS:O	43:2I:1190:GLN:C	2.62	0.42
1:A:17:G:H2'	1:A:18:C:C6	2.53	0.42
1:A:20:U:H6	1:A:20:U:H5''	1.85	0.42
1:A:40:U:O4'	1:A:41:U:C5	2.72	0.42
7:6e:46:GLU:CA	7:6e:63:ALA:H	2.21	0.42
10:5A:79:C:C3'	10:5A:80:U:C5	2.87	0.42
11:5B:153:ARG:NH2	11:5B:194:GLU:OE2	2.52	0.42
11:5B:1308:PRO:HB3	11:5B:1548:TYR:CE1	2.54	0.42
13:5D:461:LEU:HD22	13:5D:481:LEU:O	2.20	0.42
13:5D:1343:ASP:OD1	13:5D:1486:ARG:NH1	2.53	0.42
13:5D:1560:ILE:HG22	13:5D:1661:VAL:HG22	2.01	0.42
13:5D:1693:ARG:NH2	13:5D:1697:ASP:OD1	2.49	0.42
22:4A:56:U:OP2	25:4D:354:ARG:NH2	2.52	0.42
34:4Y:1004:GLN:O	34:4Y:1005:GLU:CB	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:4c:58:ALA:O	17:4c:65:MET:HA	2.19	0.42
35:2A:155:C:H2'	35:2A:156:U:H5''	2.02	0.42
41:2G:1205:GLU:O	41:2G:1206:ASP:C	2.62	0.42
47:2M:62:ALA:O	47:2M:63:ARG:C	2.62	0.42
1:A:34:G:C8	1:A:35:U:O4	2.71	0.42
10:5A:79:C:H4'	10:5A:80:U:H6	1.80	0.42
11:5B:598:LEU:HD21	11:5B:640:PHE:CE1	2.54	0.42
12:5C:215:VAL:HG11	12:5C:242:LEU:CD2	2.50	0.42
13:5D:942:ASP:O	13:5D:946:ASP:OD1	2.37	0.42
22:4A:33:A:H2'	22:4A:34:G:O4'	2.20	0.42
27:4F:10:ASN:OD1	27:4F:10:ASN:N	2.51	0.42
28:4G:385:ASP:OD1	28:4G:388:ALA:HB3	2.20	0.42
31:4T:511:GLU:O	31:4T:511:GLU:CD	2.63	0.42
41:2G:1078:VAL:O	41:2G:1079:ASN:C	2.63	0.42
1:A:37:C:O2'	1:A:38:C:O4'	2.38	0.42
11:5B:151:MET:SD	11:5B:628:GLY:O	2.77	0.42
11:5B:247:THR:HG22	11:5B:247:THR:O	2.20	0.42
11:5B:553:LEU:HD13	11:5B:585:VAL:HG22	2.00	0.42
11:5B:1202:THR:O	11:5B:1202:THR:HG22	2.20	0.42
13:5D:547:LEU:O	13:5D:551:MET:HG2	2.20	0.42
22:4A:127:C:H2'	22:4A:128:A:C8	2.55	0.42
16:4b:16:THR:HA	16:4b:25:VAL:O	2.20	0.42
41:2G:318:ARG:O	41:2G:321:ASP:N	2.52	0.42
41:2G:704:ILE:O	41:2G:705:SER:C	2.61	0.42
41:2G:854:VAL:O	41:2G:856:ASP:N	2.52	0.42
44:2J:77:ILE:O	44:2J:84:ILE:CA	2.68	0.42
11:5B:428:LYS:HA	11:5B:431:TYR:CE2	2.55	0.42
12:5C:269:LEU:O	12:5C:378:TYR:OH	2.28	0.42
12:5C:475:MET:HE1	12:5C:574:ALA:HB1	2.00	0.42
13:5D:815:LEU:HD11	13:5D:821:LEU:HD21	2.01	0.42
13:5D:1828:THR:OG1	13:5D:1853:ALA:N	2.48	0.42
25:4D:292:ALA:O	25:4D:293:ARG:C	2.62	0.42
27:4F:106:MET:SD	27:4F:112:MET:HE2	2.60	0.42
28:4G:286:GLY:O	28:4G:287:ASP:C	2.62	0.42
28:4G:316:ALA:HB2	28:4G:332:ILE:CG1	2.50	0.42
28:4G:383:GLU:HB3	28:4G:385:ASP:OD1	2.19	0.42
41:2G:981:TYR:C	41:2G:983:GLY:N	2.76	0.42
41:2G:1038:LEU:O	41:2G:1039:VAL:C	2.62	0.42
10:5A:26:A:H2'	10:5A:27:U:O4'	2.19	0.42
11:5B:1512:SER:O	11:5B:1513:MET:C	2.62	0.42
11:5B:1662:ILE:HG23	11:5B:1701:VAL:HG13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:5C:593:GLU:HG3	12:5C:594:PRO:HD2	2.00	0.42
13:5D:1521:VAL:O	13:5D:1521:VAL:HG23	2.19	0.42
28:4G:244:GLY:O	28:4G:248:ASN:OD1	2.38	0.42
21:4g:32:LEU:HA	21:4g:43:MET:HA	2.00	0.42
35:2A:40:C:H5''	35:2A:40:C:C6	2.32	0.42
35:2A:107:A:N1	35:2A:108:G:C5	2.88	0.42
41:2G:981:TYR:O	41:2G:983:GLY:N	2.53	0.42
1:A:12:U:O2	1:A:12:U:O2'	2.36	0.41
2:6A:92:A:H2'	2:6A:93:G:C8	2.54	0.41
11:5B:1070:ASP:OD1	11:5B:1070:ASP:N	2.53	0.41
13:5D:112:THR:O	13:5D:115:VAL:HG12	2.20	0.41
13:5D:130:ASP:OD1	13:5D:131:ILE:N	2.52	0.41
13:5D:654:THR:O	13:5D:655:LEU:HD23	2.19	0.41
13:5D:828:ILE:HG23	13:5D:852:MET:HE2	2.01	0.41
13:5D:929:MET:HB2	13:5D:949:LEU:HD21	2.01	0.41
24:4C:282:HIS:N	24:4C:295:ASN:O	2.46	0.41
29:4R:439:MET:SD	29:4R:440:ARG:N	2.93	0.41
35:2A:103:U:C3'	35:2A:104:U:H5'	2.50	0.41
35:2A:157:G:H5''	35:2A:157:G:C8	2.50	0.41
41:2G:944:SER:O	41:2G:946:LYS:N	2.38	0.41
11:5B:2193:VAL:HG23	11:5B:2230:LEU:HD11	2.02	0.41
13:5D:528:ASP:N	13:5D:528:ASP:OD1	2.54	0.41
13:5D:1270:VAL:O	13:5D:1270:VAL:HG23	2.19	0.41
13:5D:1577:LEU:HD21	13:5D:1617:VAL:HG23	2.02	0.41
22:4A:113:C:HO2'	22:4A:114:U:P	2.43	0.41
32:4U:197:GLN:O	32:4U:200:ASP:OD1	2.37	0.41
34:4Y:688:ASN:O	34:4Y:704:ALA:HA	2.20	0.41
40:2F:184:ARG:CA	15:2a:85:PRO:C	2.94	0.41
41:2G:963:LYS:O	41:2G:966:GLN:N	2.30	0.41
13:5D:969:LEU:HD12	13:5D:969:LEU:N	2.35	0.41
13:5D:1157:ASN:OD1	13:5D:1159:ASN:N	2.52	0.41
13:5D:1870:GLN:C	13:5D:1870:GLN:OE1	2.63	0.41
27:4F:48:ILE:HG22	27:4F:109:LYS:HB2	2.02	0.41
28:4G:316:ALA:HB1	28:4G:352:LEU:HD11	2.02	0.41
31:4T:132:ASN:O	31:4T:145:GLY:N	2.54	0.41
41:2G:574:ILE:O	41:2G:575:LEU:C	2.63	0.41
41:2G:750:ILE:O	41:2G:753:LEU:N	2.54	0.41
10:5A:37:G:H3'	10:5A:38:C:O4'	2.20	0.41
10:5A:116:U:OP2	19:5e:68:THR:CA	2.67	0.41
11:5B:163:ARG:NH1	11:5B:576:ASP:OD1	2.54	0.41
11:5B:1811:ASN:OD1	11:5B:1811:ASN:C	2.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:1890:GLN:OE1	11:5B:1890:GLN:N	2.53	0.41
12:5C:732:ILE:HD12	12:5C:744:ILE:HD11	2.02	0.41
13:5D:296:ALA:HB1	13:5D:302:CYS:HB2	2.02	0.41
13:5D:488:LEU:HD12	13:5D:488:LEU:O	2.20	0.41
13:5D:617:ILE:HG22	13:5D:652:SER:CB	2.50	0.41
13:5D:2098:ALA:C	13:5D:2099:THR:HG22	2.45	0.41
34:4Y:695:GLN:HA	34:4Y:700:ASN:HA	2.02	0.41
2:6A:46:G:O2'	2:6A:47:A:O5'	2.36	0.41
2:6A:103:U:H3'	2:6A:104:U:C5'	2.47	0.41
11:5B:657:ALA:HB3	11:5B:659:GLN:O	2.20	0.41
11:5B:852:VAL:O	11:5B:852:VAL:HG13	2.20	0.41
13:5D:722:LEU:HD23	13:5D:724:PHE:CZ	2.56	0.41
22:4A:113:C:O2'	22:4A:114:U:P	2.79	0.41
27:4F:12:TRP:O	27:4F:15:ASP:OD1	2.38	0.41
28:4G:111:ARG:HG2	28:4G:112:MET:HE2	2.01	0.41
31:4T:230:ILE:HG22	31:4T:231:LYS:N	2.34	0.41
19:4e:44:GLU:O	19:4e:61:ALA:HA	2.20	0.41
38:2D:506:SER:HA	38:2D:509:MET:SD	2.59	0.41
43:2I:1210:ASP:O	43:2I:1211:ILE:C	2.64	0.41
11:5B:811:THR:HA	11:5B:814:VAL:HG22	2.01	0.41
11:5B:1633:ALA:HB2	11:5B:1637:TRP:CH2	2.55	0.41
11:5B:1941:ARG:NH2	11:5B:2012:LEU:O	2.53	0.41
11:5B:2190:PRO:HA	11:5B:2193:VAL:CG1	2.50	0.41
12:5C:408:LEU:HD12	12:5C:408:LEU:O	2.20	0.41
12:5C:687:MET:SD	12:5C:791:ILE:HG12	2.60	0.41
13:5D:722:LEU:HD23	13:5D:724:PHE:HZ	1.85	0.41
13:5D:946:ASP:OD1	13:5D:946:ASP:O	2.38	0.41
13:5D:1456:VAL:HG22	13:5D:1491:SER:OG	2.20	0.41
13:5D:1892:ASN:OD1	13:5D:1896:GLN:NE2	2.51	0.41
25:4D:382:GLU:H	25:4D:382:GLU:HG3	1.69	0.41
31:4T:230:ILE:O	31:4T:231:LYS:C	2.63	0.41
41:2G:862:GLU:O	41:2G:864:TYR:N	2.53	0.41
43:2I:811:THR:C	43:2I:813:ALA:N	2.78	0.41
1:A:10:C:OP2	1:A:10:C:C2	2.73	0.41
11:5B:1766:GLN:NE2	11:5B:1767:ASN:OD1	2.53	0.41
11:5B:2004:GLN:O	11:5B:2007:ILE:HG22	2.20	0.41
12:5C:308:CYS:SG	12:5C:309:PHE:N	2.94	0.41
13:5D:593:TRP:CE3	13:5D:631:LEU:HD22	2.55	0.41
13:5D:1459:ILE:HD11	13:5D:1468:GLU:HG2	2.03	0.41
13:5D:1496:ASN:OD1	13:5D:1496:ASN:C	2.63	0.41
27:4F:103:ASN:OD1	27:4F:103:ASN:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:4G:21:LEU:HD23	28:4G:22:GLY:H	1.81	0.41
41:2G:997:LEU:O	41:2G:998:LYS:C	2.62	0.41
1:A:105:C:H1'	1:A:106:A:OP2	2.20	0.41
10:5A:43:U:H2'	10:5A:44:A:O4'	2.21	0.41
12:5C:401:ILE:HD11	12:5C:423:PHE:HA	2.02	0.41
13:5D:347:MET:HE2	13:5D:347:MET:HB2	1.96	0.41
13:5D:430:LEU:CD2	13:5D:880:LEU:HD12	2.50	0.41
13:5D:737:ALA:HB1	13:5D:741:MET:HE3	2.03	0.41
13:5D:785:HIS:CG	13:5D:815:LEU:HD13	2.56	0.41
13:5D:1088:ALA:O	13:5D:1089:GLY:C	2.64	0.41
13:5D:1891:THR:CG2	13:5D:1915:ILE:HD11	2.40	0.41
28:4G:383:GLU:OE2	28:4G:392:VAL:HG21	2.21	0.41
17:4c:76:GLU:O	17:4c:89:PRO:HA	2.20	0.41
41:2G:1146:GLY:O	41:2G:1147:VAL:C	2.63	0.41
10:5A:47:A:C2	10:5A:48:A:C5	3.08	0.41
11:5B:164:MET:HG3	11:5B:569:VAL:HG11	2.02	0.41
11:5B:273:ILE:O	11:5B:274:PRO:C	2.61	0.41
11:5B:660:PHE:CG	28:4G:35:GLY:HA2	2.55	0.41
11:5B:696:MET:HE3	28:4G:150:ALA:HB2	2.03	0.41
11:5B:1047:VAL:C	11:5B:1048:MET:HE2	2.45	0.41
11:5B:1251:SER:O	11:5B:1254:THR:HG22	2.21	0.41
11:5B:1393:ARG:HA	11:5B:1403:LEU:HD21	2.02	0.41
11:5B:1516:LYS:HB3	11:5B:1518:LEU:HG	2.02	0.41
11:5B:1722:SER:O	11:5B:1726:ILE:HG12	2.21	0.41
12:5C:347:ILE:CG2	12:5C:356:PHE:HB3	2.50	0.41
12:5C:390:THR:OG1	12:5C:391:SER:N	2.54	0.41
13:5D:488:LEU:HD21	13:5D:501:LEU:CD2	2.43	0.41
13:5D:1317:PHE:HB3	13:5D:1365:LEU:HD13	2.03	0.41
13:5D:1331:ILE:HD13	13:5D:1350:ALA:HB1	2.03	0.41
13:5D:1474:MET:HA	13:5D:1477:ILE:HD12	2.02	0.41
22:4A:128:A:H2'	22:4A:129:G:H8	1.85	0.41
34:4Y:1003:ILE:C	34:4Y:1005:GLU:N	2.78	0.41
35:2A:152:G:N3	35:2A:152:G:H2'	2.36	0.41
35:2A:171:U:H2'	35:2A:172:C:O4'	2.21	0.41
35:2A:183:G:C6	35:2A:184:C:N4	2.89	0.41
41:2G:301:ARG:O	41:2G:304:PRO:N	2.54	0.41
41:2G:407:MET:CA	41:2G:407:MET:H	2.07	0.41
41:2G:549:ARG:O	41:2G:550:HIS:C	2.64	0.41
41:2G:671:ILE:O	41:2G:672:ALA:C	2.62	0.41
41:2G:685:SER:O	41:2G:686:LEU:C	2.63	0.41
41:2G:782:GLU:O	41:2G:783:GLU:C	2.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2G:928:TYR:O	41:2G:929:LEU:C	2.61	0.41
41:2G:1169:VAL:O	41:2G:1172:LEU:N	2.54	0.41
43:2I:437:VAL:O	43:2I:776:GLN:CA	2.69	0.41
43:2I:1193:VAL:O	43:2I:1196:GLU:N	2.54	0.41
47:2M:52:TYR:O	47:2M:53:PHE:C	2.62	0.41
11:5B:1309:SER:O	11:5B:1310:ARG:HG3	2.20	0.41
11:5B:1703:ILE:HG21	11:5B:1730:MET:SD	2.60	0.41
11:5B:1785:VAL:HG22	11:5B:1807:ILE:CG1	2.51	0.41
11:5B:1982:GLN:O	11:5B:1985:ASP:OD1	2.38	0.41
11:5B:2104:TYR:OH	11:5B:2210:LYS:O	2.35	0.41
11:5B:2334:TYR:CD1	11:5B:2334:TYR:N	2.89	0.41
12:5C:829:GLU:N	12:5C:905:GLN:O	2.48	0.41
13:5D:1466:VAL:O	13:5D:1469:VAL:HG12	2.21	0.41
22:4A:77:A:C5	22:4A:78:A:C5	3.08	0.41
28:4G:34:ILE:HD12	28:4G:34:ILE:N	2.36	0.41
35:2A:153:A:C8	35:2A:154:C:O4'	2.74	0.41
38:2D:522:LEU:HD23	38:2D:523:GLN:OE1	2.21	0.41
41:2G:303:THR:O	41:2G:304:PRO:C	2.63	0.41
11:5B:118:VAL:N	11:5B:485:THR:O	2.45	0.40
11:5B:232:LEU:HD12	12:5C:388:VAL:HG12	2.04	0.40
11:5B:242:ALA:O	11:5B:243:ASN:C	2.64	0.40
11:5B:591:MET:HB3	11:5B:598:LEU:CD1	2.51	0.40
12:5C:129:ILE:O	12:5C:440:SER:O	2.39	0.40
13:5D:1307:LEU:HD21	13:5D:1311:ALA:HB3	2.03	0.40
13:5D:2098:ALA:O	13:5D:2099:THR:CG2	2.69	0.40
22:4A:108:C:H2'	22:4A:109:G:H8	1.85	0.40
31:4T:362:HIS:CD2	31:4T:365:LEU:HD13	2.56	0.40
31:4T:422:PHE:HA	31:4T:441:PHE:HB2	2.03	0.40
34:4Y:1003:ILE:C	34:4Y:1005:GLU:H	2.30	0.40
35:2A:152:G:H2'	35:2A:153:A:C1'	2.51	0.40
41:2G:871:THR:O	41:2G:872:ILE:C	2.62	0.40
41:2G:887:LYS:O	41:2G:888:LEU:C	2.63	0.40
41:2G:1112:THR:O	41:2G:1113:THR:C	2.63	0.40
41:2G:1188:ALA:O	41:2G:1189:SER:C	2.63	0.40
43:2I:672:GLY:N	43:2I:697:ARG:O	2.54	0.40
2:6A:37:C:O2	28:4G:29:THR:OG1	2.31	0.40
11:5B:785:LYS:O	11:5B:789:GLU:HG2	2.21	0.40
11:5B:827:PHE:CD2	11:5B:828:PRO:HD2	2.56	0.40
11:5B:1723:LYS:HB3	11:5B:1724:PRO:HD3	2.02	0.40
13:5D:1074:GLY:O	13:5D:1078:MET:HG3	2.21	0.40
13:5D:2067:VAL:HG13	13:5D:2107:TYR:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:4C:398:ARG:O	24:4C:399:CYS:C	2.64	0.40
25:4D:383:ILE:HD11	25:4D:387:ALA:HA	2.02	0.40
28:4G:401:PRO:O	28:4G:407:TRP:CE2	2.74	0.40
29:4R:388:LEU:CD2	29:4R:452:ILE:HG22	2.51	0.40
35:2A:63:G:H2'	35:2A:64:A:C8	2.56	0.40
41:2G:183:VAL:O	41:2G:184:VAL:C	2.65	0.40
41:2G:1040:GLY:O	41:2G:1041:ARG:C	2.63	0.40
41:2G:1097:LEU:O	41:2G:1098:LEU:C	2.61	0.40
43:2I:1143:HIS:O	43:2I:1144:VAL:C	2.64	0.40
1:A:37:C:C3'	1:A:37:C:C6	3.04	0.40
2:6A:90:G:H2'	2:6A:91:A:C8	2.57	0.40
10:5A:45:C:H4'	11:5B:596:TYR:HB3	2.03	0.40
11:5B:510:ARG:NH1	11:5B:655:LEU:HD21	2.36	0.40
11:5B:2189:SER:HB3	11:5B:2192:ASP:OD2	2.21	0.40
13:5D:526:ASN:O	13:5D:527:MET:C	2.64	0.40
13:5D:929:MET:HE3	13:5D:949:LEU:HD21	2.03	0.40
13:5D:1598:ILE:N	13:5D:1599:PRO:CD	2.84	0.40
13:5D:1945:LEU:HA	13:5D:1948:MET:HG3	2.03	0.40
22:4A:77:A:H3'	22:4A:78:A:H8	1.86	0.40
25:4D:357:ARG:O	25:4D:360:ARG:HG2	2.21	0.40
41:2G:758:ASP:O	41:2G:761:TYR:N	2.54	0.40
41:2G:1211:LEU:O	41:2G:1212:LEU:C	2.64	0.40
47:2M:55:ILE:O	47:2M:56:ALA:C	2.63	0.40
10:5A:23:C:O2	10:5A:23:C:H2'	2.21	0.40
13:5D:174:ASN:O	13:5D:178:LYS:HG3	2.21	0.40
13:5D:298:ASP:OD1	13:5D:298:ASP:C	2.64	0.40
13:5D:995:ASN:HA	13:5D:998:VAL:HG22	2.03	0.40
13:5D:1477:ILE:O	13:5D:1478:SER:C	2.62	0.40
13:5D:1569:THR:HG23	13:5D:1570:ARG:N	2.36	0.40
13:5D:1832:PHE:CE1	13:5D:1848:ILE:HG22	2.56	0.40
25:4D:220:SER:O	25:4D:224:GLY:O	2.40	0.40
34:4Y:958:ASP:O	34:4Y:959:LEU:CB	2.70	0.40
41:2G:647:PHE:O	41:2G:648:LEU:C	2.63	0.40
41:2G:897:LEU:O	41:2G:898:TYR:C	2.64	0.40
41:2G:1189:SER:O	41:2G:1190:ALA:C	2.65	0.40
17:2c:62:HIS:O	17:2c:103:GLY:HA3	2.21	0.40
10:5A:101:U:H2'	10:5A:102:U:C6	2.57	0.40
11:5B:137:GLU:OE2	11:5B:419:ARG:NH1	2.52	0.40
11:5B:844:GLU:OE1	11:5B:1459:ARG:NH2	2.54	0.40
12:5C:446:LYS:HB3	12:5C:447:PRO:HD3	2.04	0.40
13:5D:640:GLU:HB2	13:5D:641:MET:HE2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:1337:ASN:O	13:5D:1341:ASN:HB2	2.21	0.40
17:5c:62:HIS:O	17:5c:103:GLY:HA3	2.21	0.40
22:4A:77:A:C2'	22:4A:78:A:H8	2.33	0.40
41:2G:854:VAL:C	41:2G:856:ASP:H	2.28	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	6a	87/95 (92%)	76 (87%)	7 (8%)	4 (5%)	2	15
4	6b	70/102 (69%)	64 (91%)	3 (4%)	3 (4%)	2	16
5	6c	70/139 (50%)	64 (91%)	5 (7%)	1 (1%)	9	39
6	6d	68/91 (75%)	63 (93%)	4 (6%)	1 (2%)	8	37
7	6e	68/80 (85%)	64 (94%)	2 (3%)	2 (3%)	3	24
8	6f	61/103 (59%)	56 (92%)	5 (8%)	0	100	100
9	6g	57/96 (59%)	52 (91%)	4 (7%)	1 (2%)	6	34
11	5B	2200/2335 (94%)	2105 (96%)	92 (4%)	3 (0%)	48	79
12	5C	850/972 (87%)	819 (96%)	31 (4%)	0	100	100
13	5D	1989/2136 (93%)	1906 (96%)	83 (4%)	0	100	100
14	5E	300/357 (84%)	282 (94%)	18 (6%)	0	100	100
15	2a	83/231 (36%)	81 (98%)	2 (2%)	0	100	100
15	4a	80/231 (35%)	71 (89%)	9 (11%)	0	100	100
15	5a	83/231 (36%)	81 (98%)	2 (2%)	0	100	100
16	2b	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
16	4b	79/119 (66%)	75 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	5b	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
17	2c	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
17	4c	90/118 (76%)	84 (93%)	6 (7%)	0	100	100
17	5c	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
18	2d	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
18	4d	70/86 (81%)	69 (99%)	1 (1%)	0	100	100
18	5d	71/86 (83%)	68 (96%)	3 (4%)	0	100	100
19	2e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
19	4e	74/92 (80%)	71 (96%)	3 (4%)	0	100	100
19	5e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
20	2f	63/76 (83%)	61 (97%)	2 (3%)	0	100	100
20	4f	71/76 (93%)	65 (92%)	6 (8%)	0	100	100
20	5f	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
21	2g	76/126 (60%)	74 (97%)	2 (3%)	0	100	100
21	4g	81/126 (64%)	76 (94%)	5 (6%)	0	100	100
21	5g	75/126 (60%)	73 (97%)	2 (3%)	0	100	100
23	4B	183/683 (27%)	177 (97%)	6 (3%)	0	100	100
24	4C	357/522 (68%)	332 (93%)	25 (7%)	0	100	100
25	4D	321/499 (64%)	297 (92%)	19 (6%)	5 (2%)	7	36
26	4E	122/128 (95%)	114 (93%)	8 (7%)	0	100	100
27	4F	139/142 (98%)	134 (96%)	5 (4%)	0	100	100
28	4G	786/941 (84%)	744 (95%)	39 (5%)	3 (0%)	30	62
29	4R	104/480 (22%)	95 (91%)	9 (9%)	0	100	100
30	4S	66/800 (8%)	64 (97%)	2 (3%)	0	100	100
31	4T	454/565 (80%)	419 (92%)	35 (8%)	0	100	100
32	4U	147/820 (18%)	143 (97%)	4 (3%)	0	100	100
33	4X	19/155 (12%)	19 (100%)	0	0	100	100
34	4Y	316/1007 (31%)	294 (93%)	18 (6%)	4 (1%)	9	40
36	2B	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	9	40
37	2C	92/225 (41%)	90 (98%)	2 (2%)	0	100	100
38	2D	173/793 (22%)	157 (91%)	12 (7%)	4 (2%)	5	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	2E	88/464 (19%)	61 (69%)	17 (19%)	10 (11%)	0	2
40	2F	413/501 (82%)	367 (89%)	41 (10%)	5 (1%)	10	42
41	2G	1032/1304 (79%)	845 (82%)	165 (16%)	22 (2%)	5	31
42	2H	170/895 (19%)	151 (89%)	15 (9%)	4 (2%)	4	28
43	2I	1152/1217 (95%)	1053 (91%)	89 (8%)	10 (1%)	14	47
44	2J	76/424 (18%)	75 (99%)	1 (1%)	0	100	100
45	2K	106/125 (85%)	85 (80%)	18 (17%)	3 (3%)	4	25
46	2L	87/110 (79%)	74 (85%)	13 (15%)	0	100	100
47	2M	64/86 (74%)	55 (86%)	8 (12%)	1 (2%)	7	36
All	All	14077/22191 (63%)	13104 (93%)	885 (6%)	88 (1%)	23	56

All (88) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	6a	55	LEU
4	6b	84	MET
6	6d	70	ASP
7	6e	52	VAL
7	6e	55	GLN
11	5B	1549	VAL
11	5B	1760	GLU
25	4D	351	ARG
28	4G	36	PRO
34	4Y	697	VAL
39	2E	139	PRO
39	2E	141	ILE
39	2E	146	MET
39	2E	147	PRO
39	2E	162	PRO
39	2E	165	ARG
39	2E	218	PRO
40	2F	284	ARG
41	2G	208	PRO
41	2G	416	PRO
41	2G	418	PRO
41	2G	456	VAL
41	2G	717	THR
41	2G	941	ASN
41	2G	1107	GLN

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Mol	Chain	Res	Type
43	2I	405	SER
43	2I	919	SER
45	2K	99	GLN
45	2K	105	LYS
3	6a	74	ALA
4	6b	97	PRO
5	6c	12	ASN
25	4D	384	GLU
34	4Y	851	VAL
36	2B	160	LYS
38	2D	223	LYS
38	2D	280	VAL
38	2D	483	ALA
40	2F	277	THR
41	2G	113	ALA
41	2G	1110	VAL
42	2H	597	PHE
43	2I	917	PRO
25	4D	352	LYS
28	4G	31	ARG
40	2F	177	ARG
40	2F	393	PRO
41	2G	437	PRO
42	2H	510	TYR
4	6b	96	ALA
25	4D	385	GLU
34	4Y	699	SER
36	2B	32	PRO
41	2G	112	ILE
41	2G	523	ALA
41	2G	909	VAL
41	2G	1006	MET
42	2H	463	ALA
42	2H	574	ALA
43	2I	529	ALA
43	2I	578	THR
3	6a	73	PRO
25	4D	387	ALA
28	4G	287	ASP
34	4Y	722	ASN
39	2E	217	PRO
41	2G	1047	ALA

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Mol	Chain	Res	Type
41	2G	1075	ARG
41	2G	1186	GLN
43	2I	95	SER
43	2I	229	GLU
45	2K	75	ASP
9	6g	34	ILE
11	5B	1758	PRO
39	2E	220	PRO
41	2G	326	THR
41	2G	932	ILE
43	2I	918	ARG
43	2I	1138	HIS
39	2E	145	ILE
41	2G	417	PRO
38	2D	221	PRO
41	2G	223	THR
43	2I	1204	VAL
40	2F	229	TRP
41	2G	1031	VAL
47	2M	64	VAL
3	6a	52	PRO

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	
11	5B	1980/2108 (94%)	1977 (100%)	3 (0%)	87	89
12	5C	754/866 (87%)	752 (100%)	2 (0%)	86	88
13	5D	1779/1908 (93%)	1775 (100%)	4 (0%)	87	89
25	4D	35/424 (8%)	29 (83%)	6 (17%)	2	11
27	4F	129/130 (99%)	129 (100%)	0	100	100
28	4G	246/792 (31%)	243 (99%)	3 (1%)	63	79
29	4R	94/369 (26%)	93 (99%)	1 (1%)	65	79
30	4S	54/681 (8%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	4T	418/511 (82%)	417 (100%)	1 (0%)	87	89
32	4U	139/721 (19%)	139 (100%)	0	100	100
33	4X	19/144 (13%)	19 (100%)	0	100	100
38	2D	53/709 (8%)	49 (92%)	4 (8%)	12	42
All	All	5700/9363 (61%)	5676 (100%)	24 (0%)	81	86

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	5B	533	LYS
11	5B	680	HIS
11	5B	2315	LEU
12	5C	298	LEU
12	5C	433	MET
13	5D	89	LEU
13	5D	170	HIS
13	5D	992	TYR
13	5D	1117	MET
25	4D	351	ARG
25	4D	380	PHE
25	4D	382	GLU
25	4D	383	ILE
25	4D	384	GLU
25	4D	389	GLN
28	4G	21	LEU
28	4G	133	MET
28	4G	284	HIS
29	4R	435	TYR
31	4T	377	ASP
38	2D	506	SER
38	2D	508	SER
38	2D	521	THR
38	2D	522	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (60) such sidechains are listed below:

Mol	Chain	Res	Type
11	5B	65	HIS
11	5B	181	ASN
11	5B	270	ASN

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Mol	Chain	Res	Type
11	5B	439	GLN
11	5B	457	ASN
11	5B	545	HIS
11	5B	691	HIS
11	5B	712	HIS
11	5B	752	ASN
11	5B	815	HIS
11	5B	994	ASN
11	5B	1117	HIS
11	5B	1345	GLN
11	5B	1446	GLN
11	5B	1583	GLN
11	5B	1737	ASN
11	5B	1752	GLN
11	5B	1766	GLN
11	5B	1823	HIS
11	5B	1946	ASN
11	5B	1947	ASN
12	5C	280	HIS
12	5C	436	GLN
12	5C	802	HIS
13	5D	719	ASN
13	5D	720	GLN
13	5D	785	HIS
13	5D	902	ASN
13	5D	967	ASN
13	5D	1158	HIS
13	5D	1159	ASN
13	5D	1341	ASN
13	5D	1526	HIS
13	5D	1670	ASN
13	5D	1735	HIS
13	5D	1862	HIS
13	5D	1877	HIS
13	5D	1885	ASN
13	5D	1965	HIS
13	5D	1994	ASN
13	5D	2016	ASN
13	5D	2040	GLN
13	5D	2086	GLN
25	4D	389	GLN
27	4F	89	HIS

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Mol	Chain	Res	Type
27	4F	100	ASN
28	4G	257	GLN
28	4G	265	GLN
28	4G	284	HIS
30	4S	731	HIS
30	4S	734	HIS
31	4T	155	HIS
31	4T	228	ASN
31	4T	350	GLN
31	4T	362	HIS
31	4T	412	GLN
31	4T	494	ASN
31	4T	517	HIS
31	4T	533	GLN
31	4T	540	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	57/144 (39%)	33 (57%)	10 (17%)
10	5A	113/117 (96%)	36 (31%)	5 (4%)
2	6A	56/107 (52%)	13 (23%)	5 (8%)
22	4A	119/146 (81%)	24 (20%)	3 (2%)
35	2A	105/188 (55%)	22 (20%)	3 (2%)
All	All	450/702 (64%)	128 (28%)	26 (5%)

All (128) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	U
1	A	9	U
1	A	10	C
1	A	11	C
1	A	12	U
1	A	13	U
1	A	15	A
1	A	20	U
1	A	21	U
1	A	22	C
1	A	25	G
1	A	29	A

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Mol	Chain	Res	Type
1	A	30	C
1	A	31	C
1	A	32	C
1	A	33	U
1	A	34	G
1	A	35	U
1	A	36	C
1	A	37	C
1	A	39	U
1	A	41	U
1	A	42	U
1	A	44	U
1	A	46	U
1	A	47	C
1	A	48	C
1	A	104	C
1	A	105	C
1	A	106	A
1	A	108	G
1	A	116	G
1	A	118	A
2	6A	37	C
2	6A	38	G
2	6A	39	A
2	6A	46	G
2	6A	47	A
2	6A	49	G
2	6A	56	A
2	6A	58	G
2	6A	59	G
2	6A	77	C
2	6A	78	A
2	6A	103	U
2	6A	104	U
10	5A	5	U
10	5A	6	C
10	5A	9	G
10	5A	21	A
10	5A	22	U
10	5A	24	G
10	5A	25	C
10	5A	26	A

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Mol	Chain	Res	Type
10	5A	28	A
10	5A	38	C
10	5A	39	C
10	5A	40	U
10	5A	45	C
10	5A	55	C
10	5A	57	G
10	5A	59	G
10	5A	66	A
10	5A	67	A
10	5A	69	A
10	5A	70	A
10	5A	75	G
10	5A	78	U
10	5A	79	C
10	5A	80	U
10	5A	81	U
10	5A	83	A
10	5A	88	A
10	5A	89	U
10	5A	90	U
10	5A	92	U
10	5A	93	U
10	5A	94	U
10	5A	95	G
10	5A	96	A
10	5A	97	G
10	5A	109	G
22	4A	18	G
22	4A	25	A
22	4A	26	G
22	4A	37	C
22	4A	38	U
22	4A	39	A
22	4A	40	U
22	4A	45	G
22	4A	56	U
22	4A	67	A
22	4A	68	A
22	4A	69	C
22	4A	74	C
22	4A	75	C

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Mol	Chain	Res	Type
22	4A	76	C
22	4A	78	A
22	4A	114	U
22	4A	115	G
22	4A	121	U
22	4A	122	U
22	4A	123	U
22	4A	125	G
22	4A	126	A
22	4A	140	G
35	2A	31	G
35	2A	37	U
35	2A	40	C
35	2A	45	C
35	2A	47	U
35	2A	51	A
35	2A	65	U
35	2A	112	G
35	2A	143	A
35	2A	147	G
35	2A	152	G
35	2A	153	A
35	2A	154	C
35	2A	156	U
35	2A	157	G
35	2A	164	C
35	2A	165	A
35	2A	168	A
35	2A	169	C
35	2A	177	A
35	2A	178	A
35	2A	179	C

All (26) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	9	U
1	A	21	U
1	A	28	G
1	A	33	U
1	A	35	U
1	A	36	C

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Mol	Chain	Res	Type
1	A	38	C
1	A	40	U
1	A	41	U
1	A	105	C
2	6A	36	A
2	6A	37	C
2	6A	46	G
2	6A	59	G
2	6A	77	C
10	5A	58	U
10	5A	79	C
10	5A	80	U
10	5A	94	U
10	5A	96	A
22	4A	1	A
22	4A	68	A
22	4A	114	U
35	2A	156	U
35	2A	164	C
35	2A	168	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
50	GTP	5C	1002	49	33,34,34	0.90	1 (3%)	50,54,54	1.61	8 (16%)
48	IHP	5B	2401	-	36,36,36	0.75	0	60,60,60	1.18	3 (5%)

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
50	GTP	5C	1002	49	-	2/22/38/38	0/3/3/3
48	IHP	5B	2401	-	-	3/30/54/54	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	5C	1002	GTP	C2-N3	2.06	1.38	1.33

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	5C	1002	GTP	C5-C4-N3	-5.07	120.33	128.39
50	5C	1002	GTP	C2-N3-C4	4.67	120.34	112.30
48	5B	2401	IHP	C5-C4-C3	3.22	117.50	110.43
50	5C	1002	GTP	N9-C4-N3	3.13	132.22	125.95
50	5C	1002	GTP	C2-N1-C6	-3.02	119.64	125.11
50	5C	1002	GTP	N9-C8-N7	-2.77	108.26	113.40
50	5C	1002	GTP	C8-N7-C5	2.60	108.89	104.26
50	5C	1002	GTP	C5-C6-N1	2.59	119.86	113.25
48	5B	2401	IHP	C4-C3-C2	2.47	115.84	110.43
50	5C	1002	GTP	O6-C6-C5	-2.44	120.10	126.53
48	5B	2401	IHP	C6-C5-C4	2.34	115.56	110.43

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
50	5C	1002	GTP	O4'-C4'-C5'-O5'
50	5C	1002	GTP	C3'-C4'-C5'-O5'
48	5B	2401	IHP	C2-O12-P2-O32
48	5B	2401	IHP	C3-O13-P3-O43

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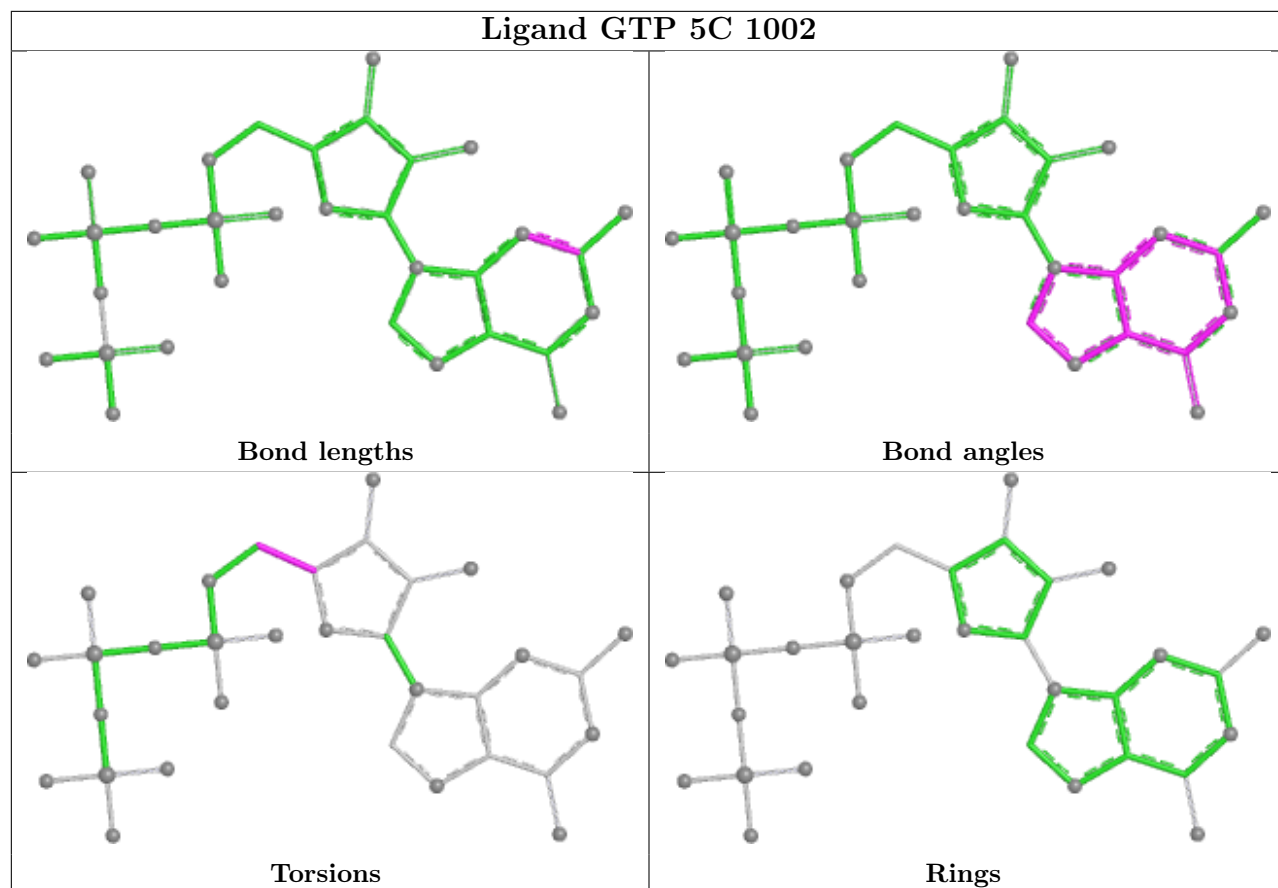
Mol	Chain	Res	Type	Atoms
48	5B	2401	IHP	C5-O15-P5-O45

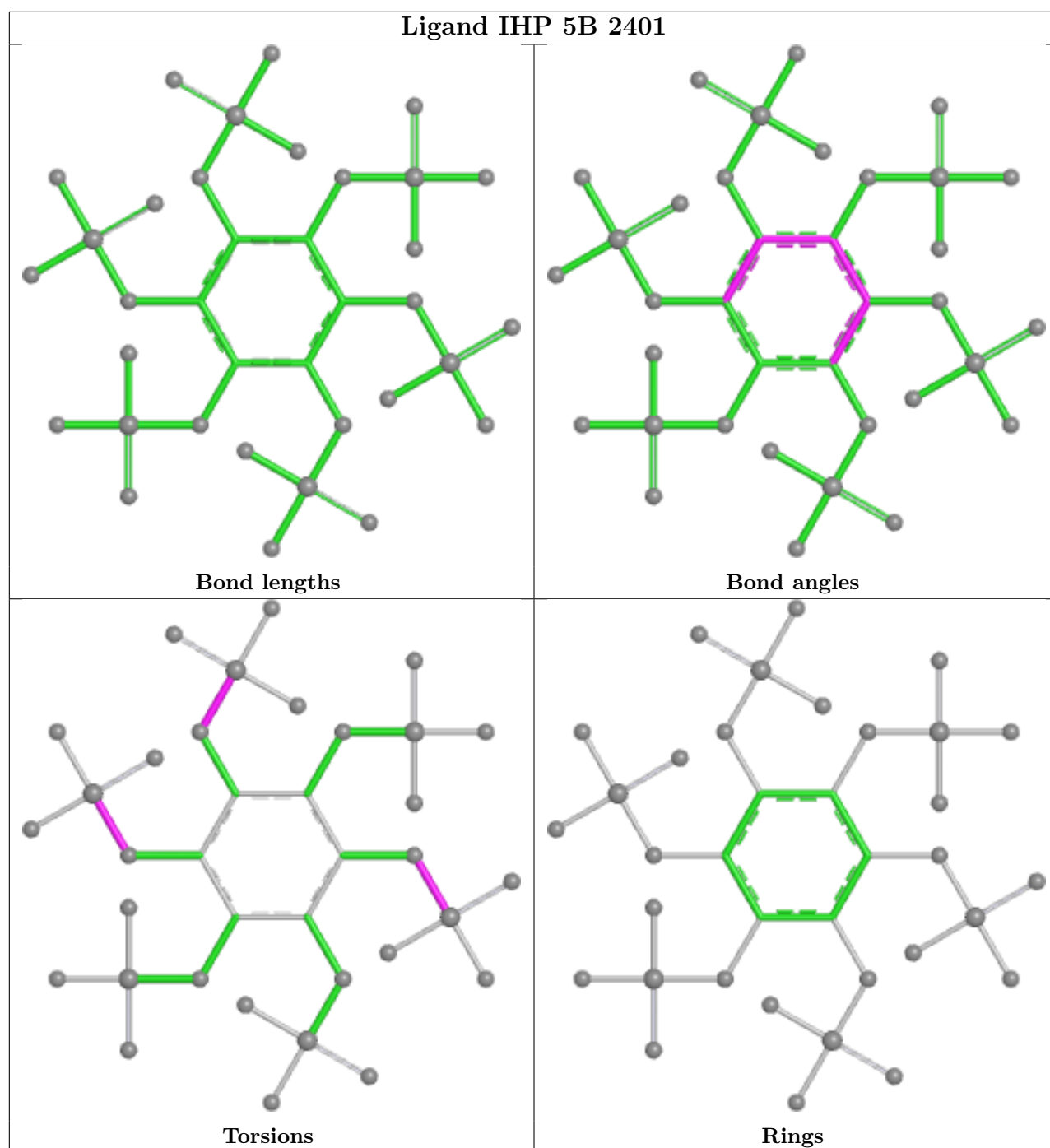
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
50	5C	1002	GTP	1	0
48	5B	2401	IHP	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

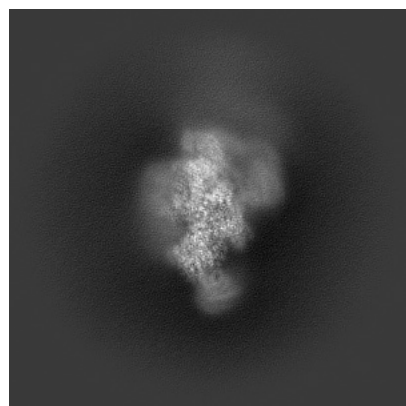
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34500. These allow visual inspection of the internal detail of the map and identification of artifacts.

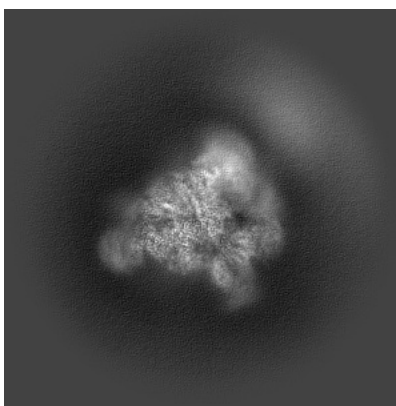
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

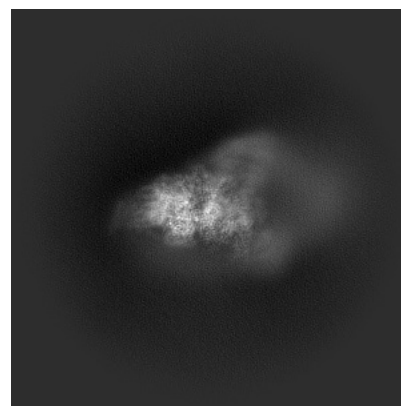
6.1.1 Primary map



X

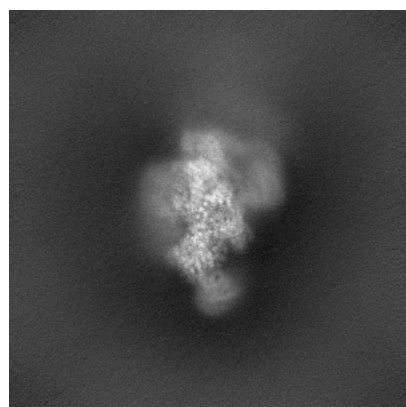


Y

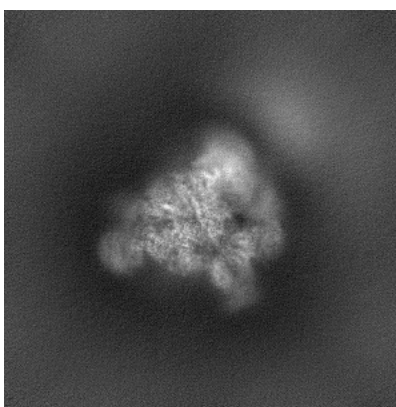


Z

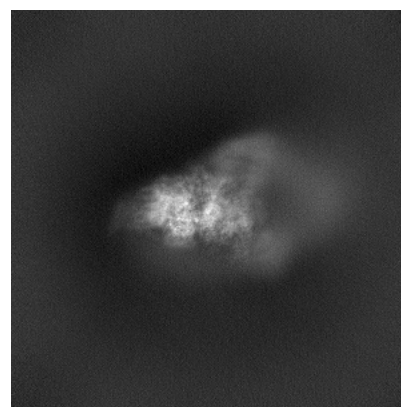
6.1.2 Raw map



X



Y

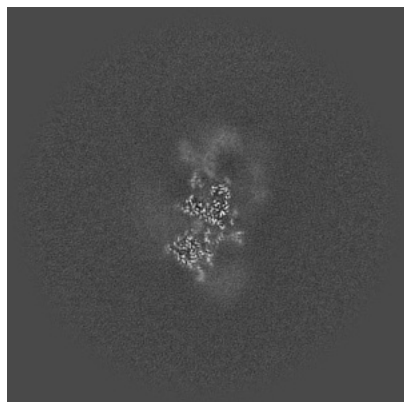


Z

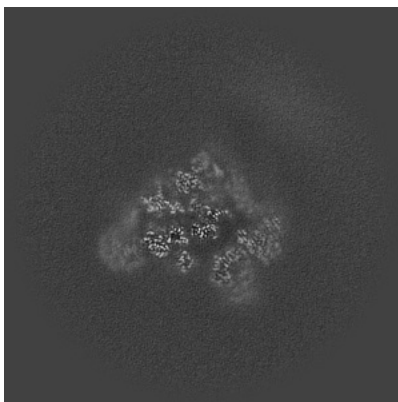
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

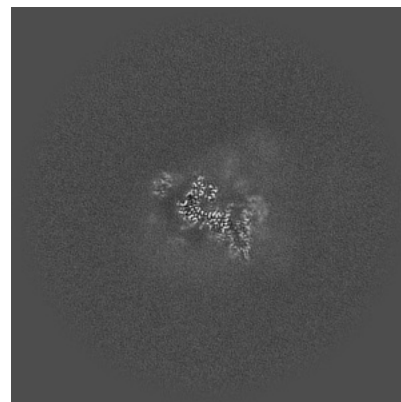
6.2.1 Primary map



X Index: 256

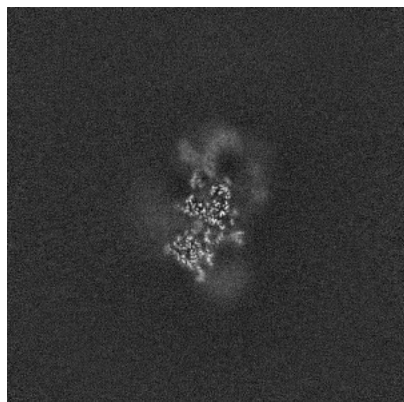


Y Index: 256

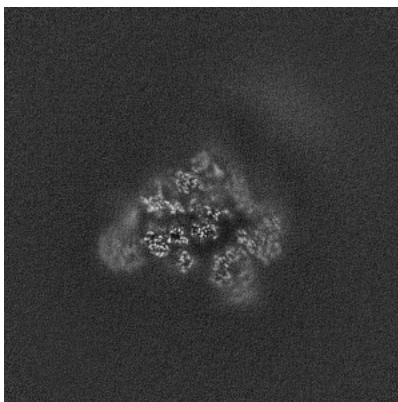


Z Index: 256

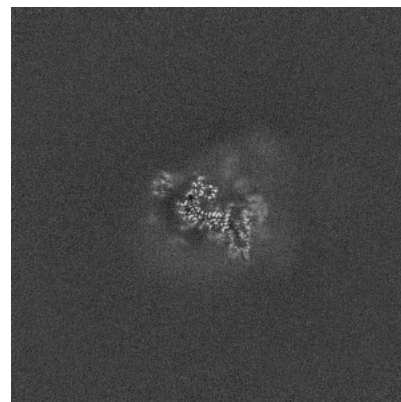
6.2.2 Raw map



X Index: 256



Y Index: 256

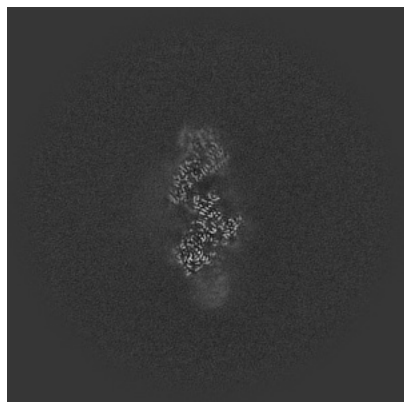


Z Index: 256

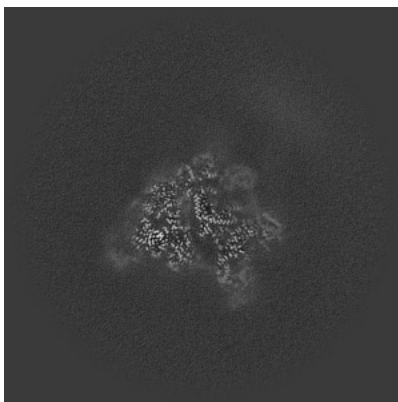
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

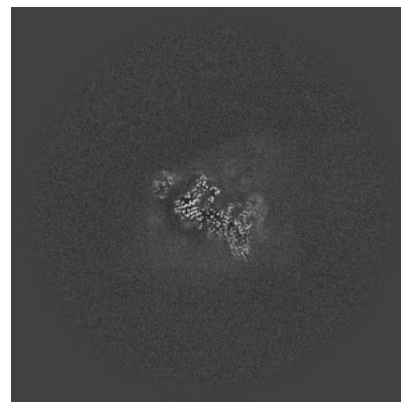
6.3.1 Primary map



X Index: 222

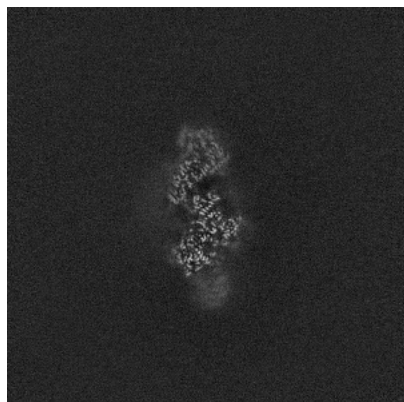


Y Index: 242

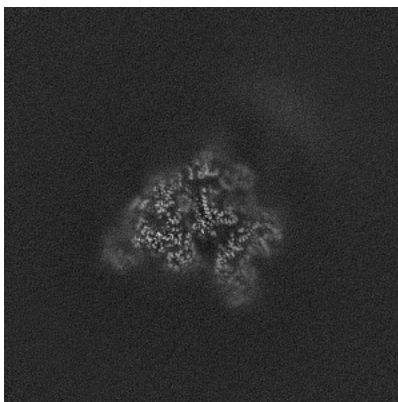


Z Index: 253

6.3.2 Raw map



X Index: 222



Y Index: 245

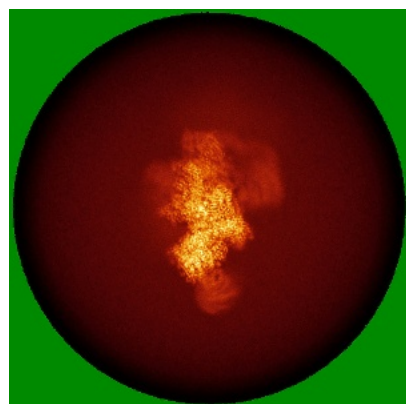


Z Index: 271

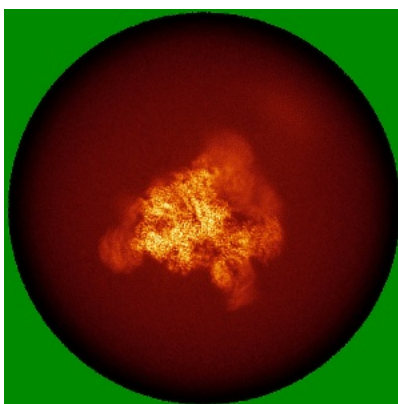
The images above show the largest variance slices of the map in three orthogonal directions.

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

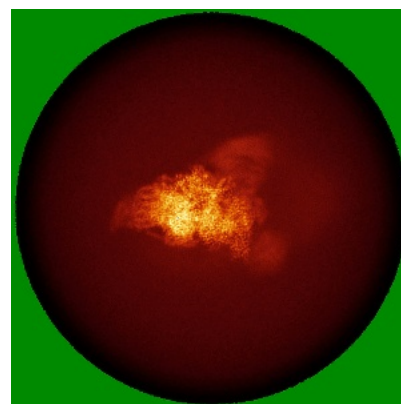
6.4.1 Primary map



X

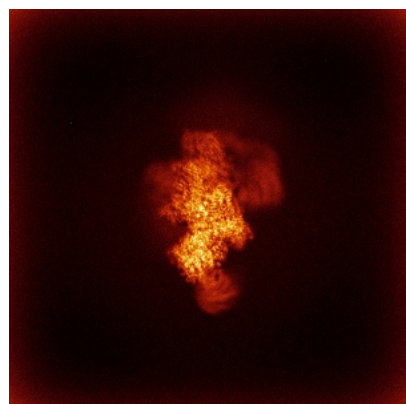


Y

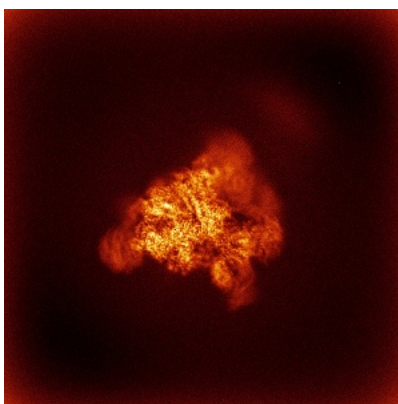


Z

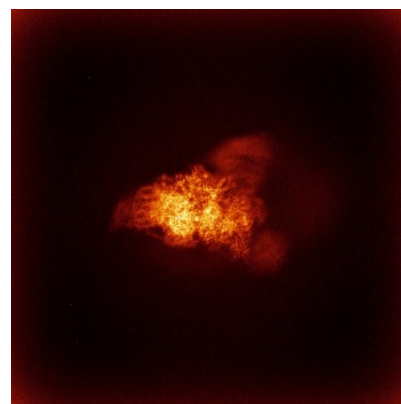
6.4.2 Raw map



X



Y

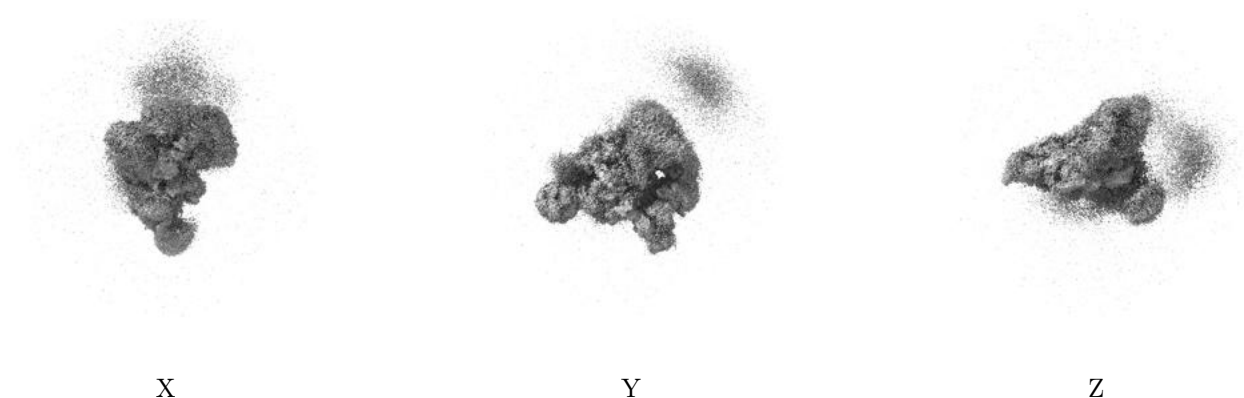


Z

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

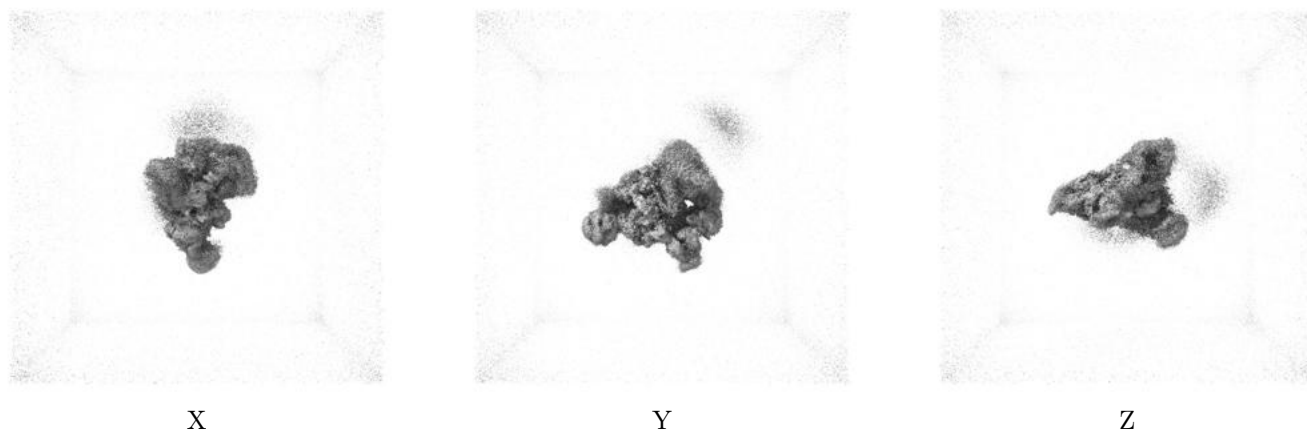
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

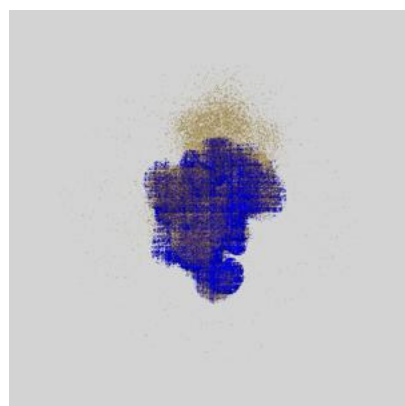
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

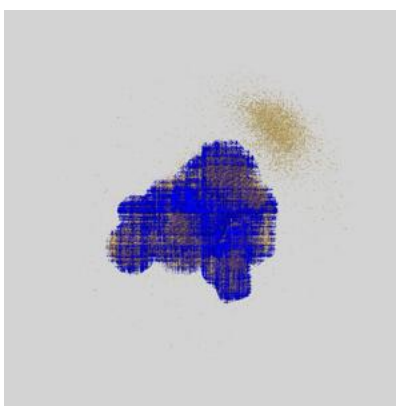
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

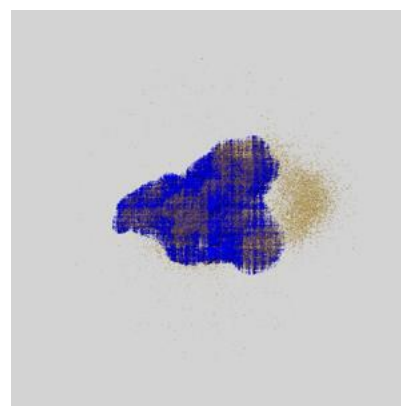
6.6.1 emd_34500_msk_1.map [i](#)



X



Y

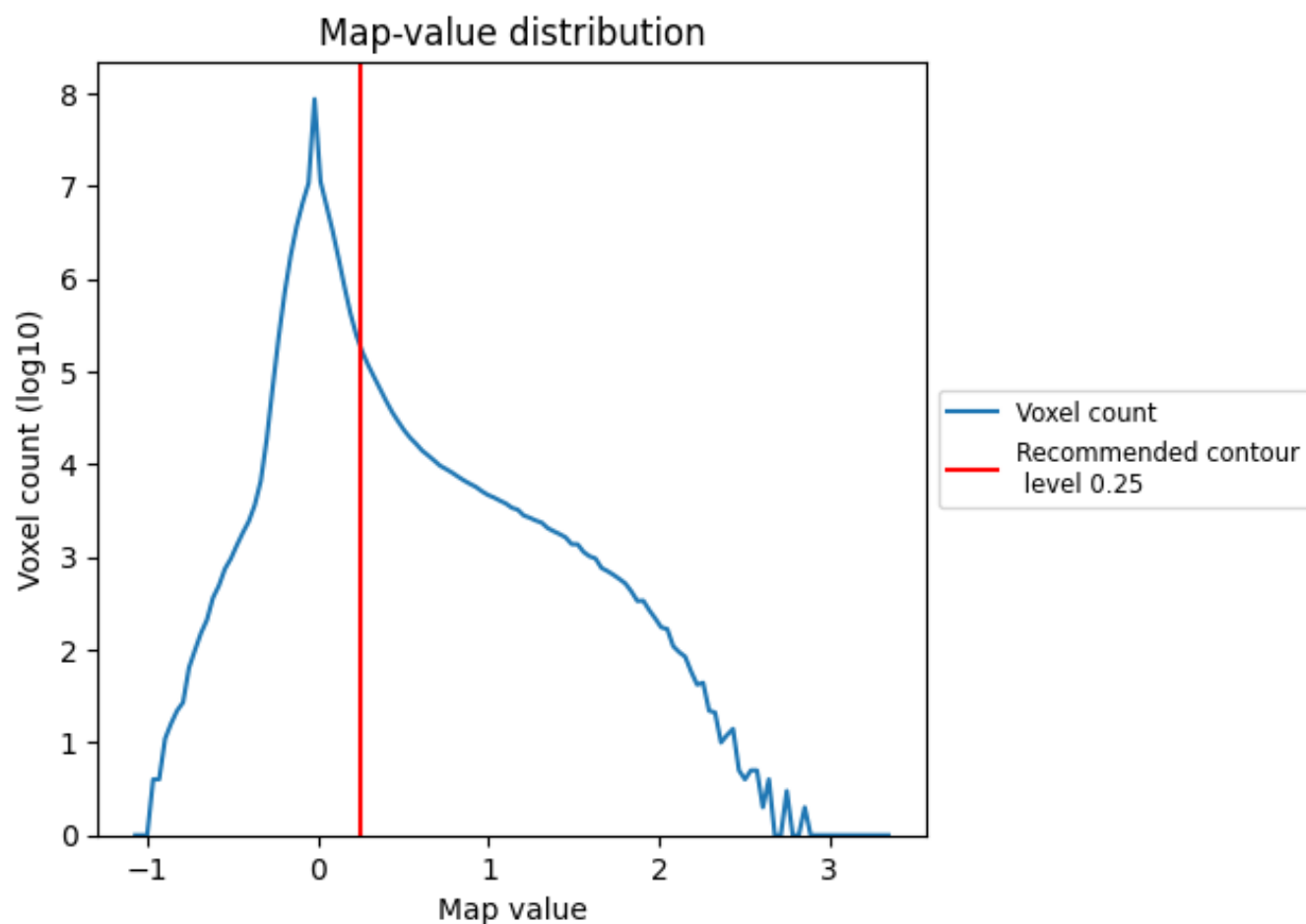


Z

7 Map analysis [i](#)

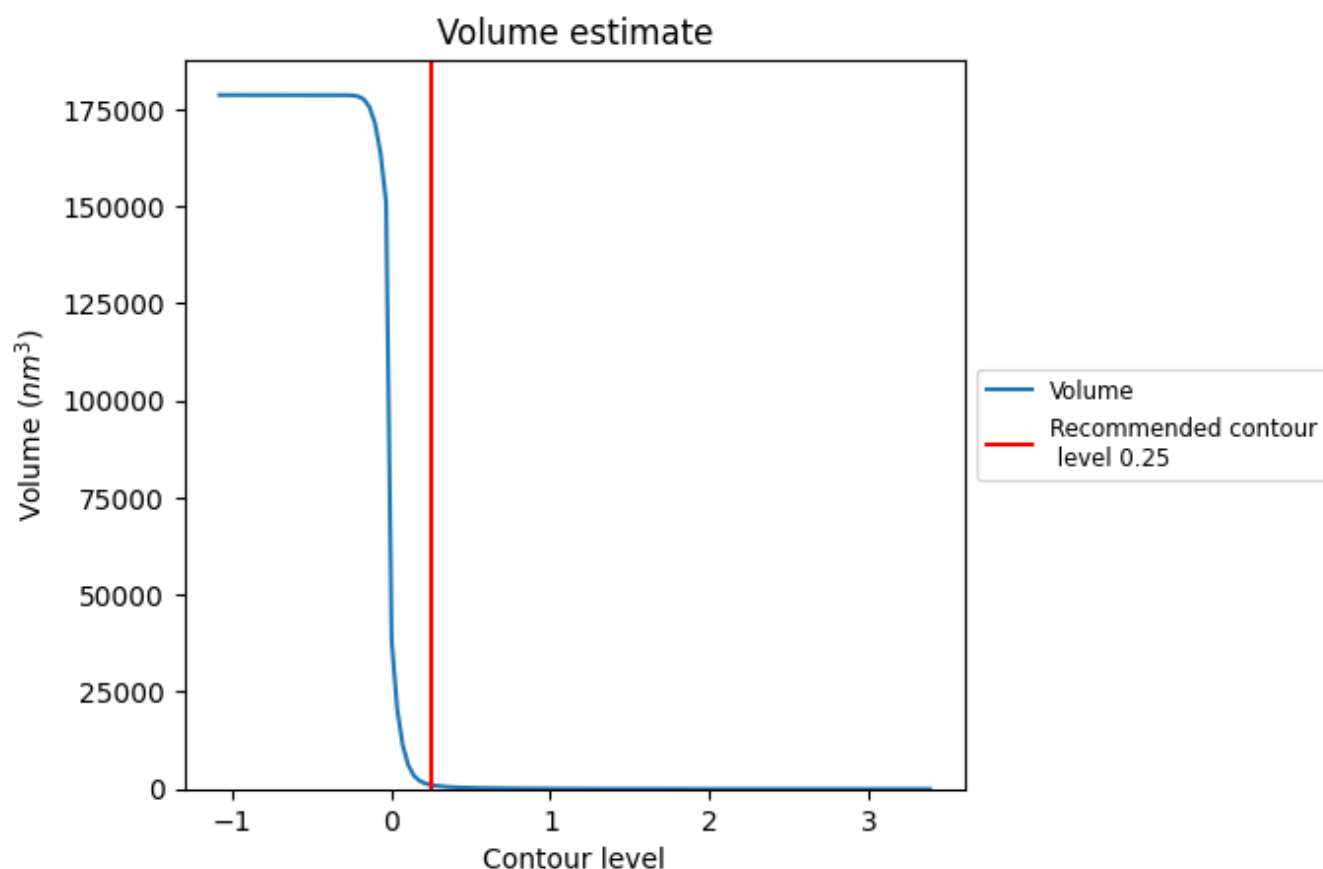
This section contains the results of statistical analysis of the map.

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.

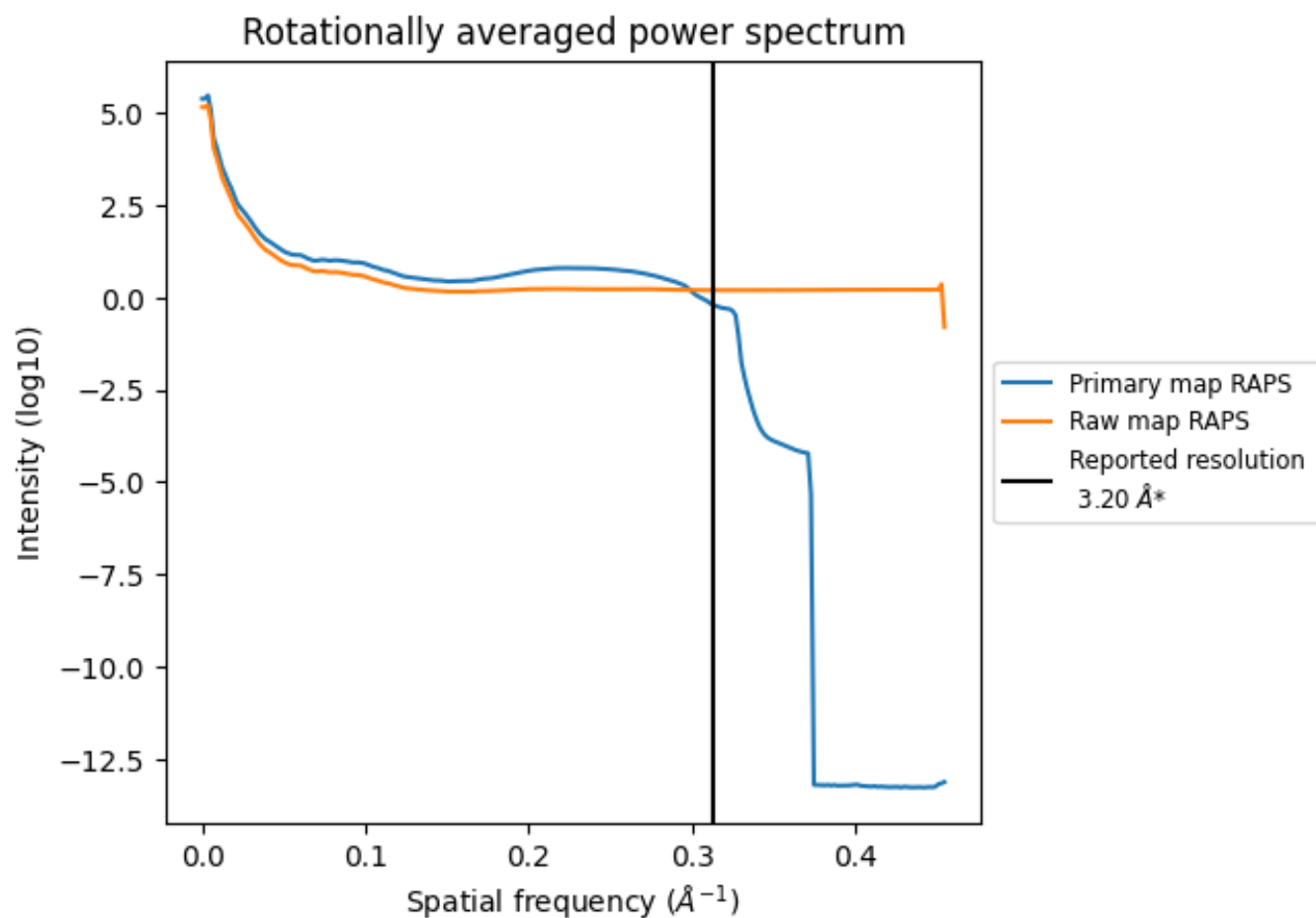
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1064 nm^3 ; this corresponds to an approximate mass of 961 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 ⓘ

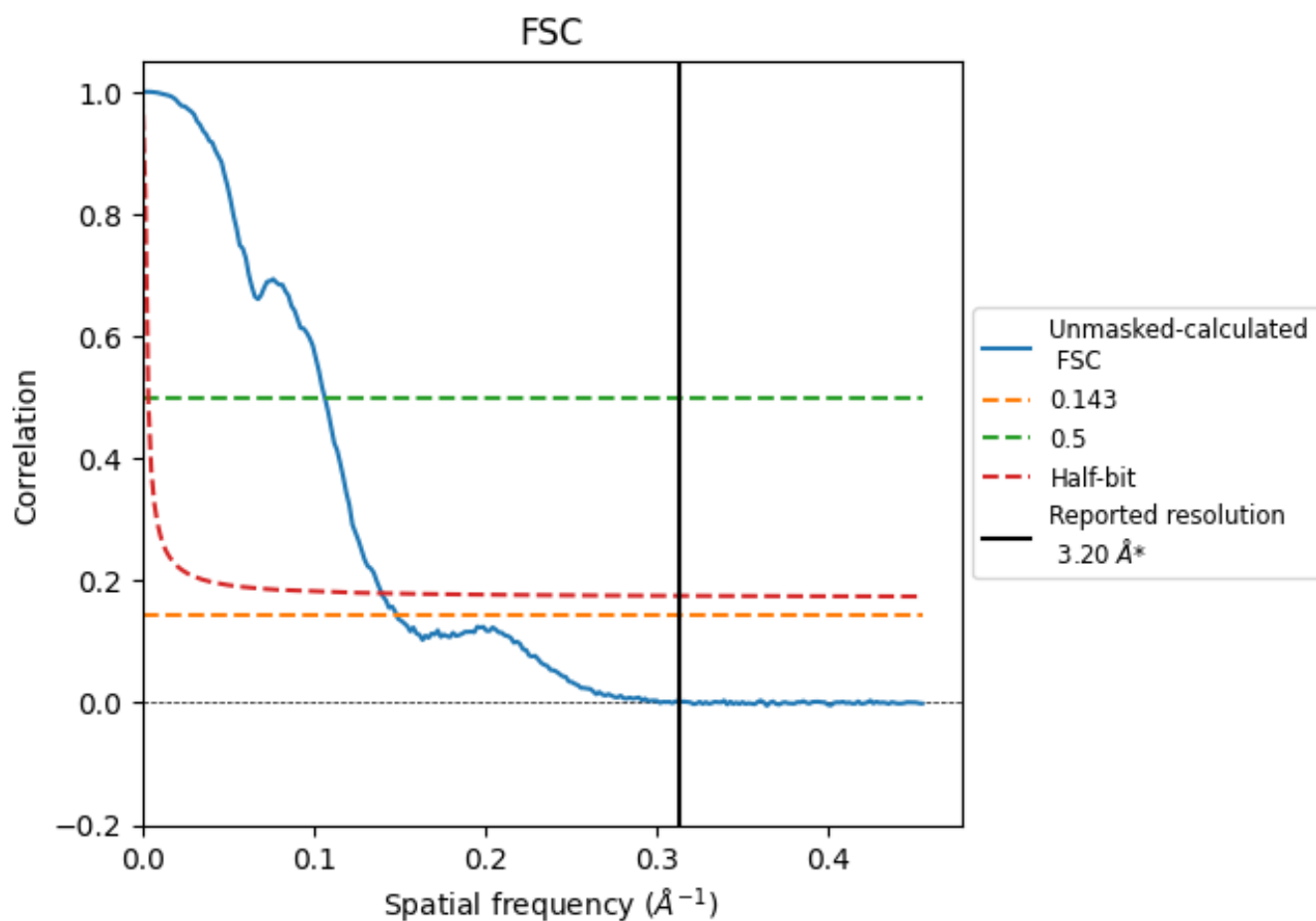


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

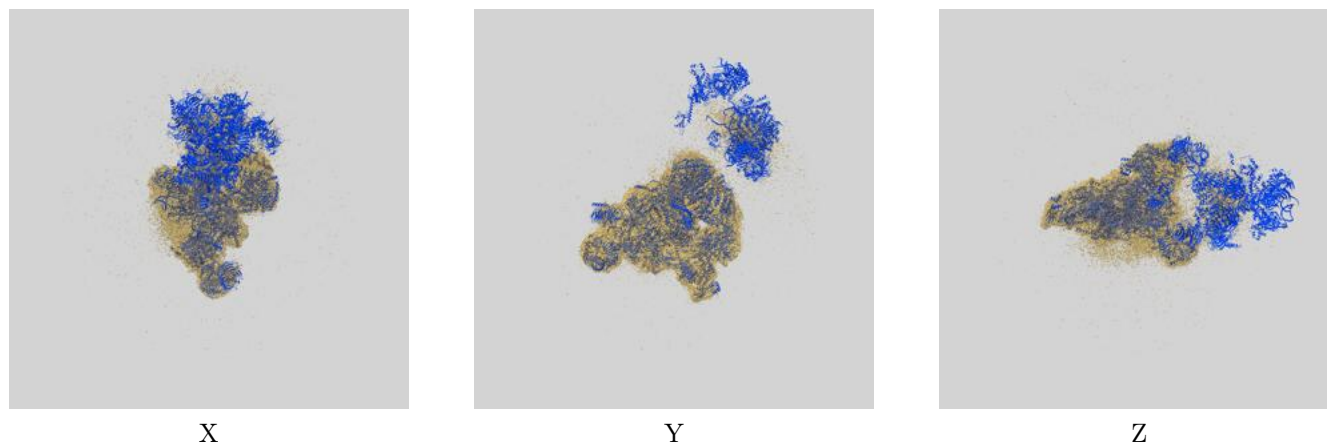
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.74	9.40	7.17

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.74 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

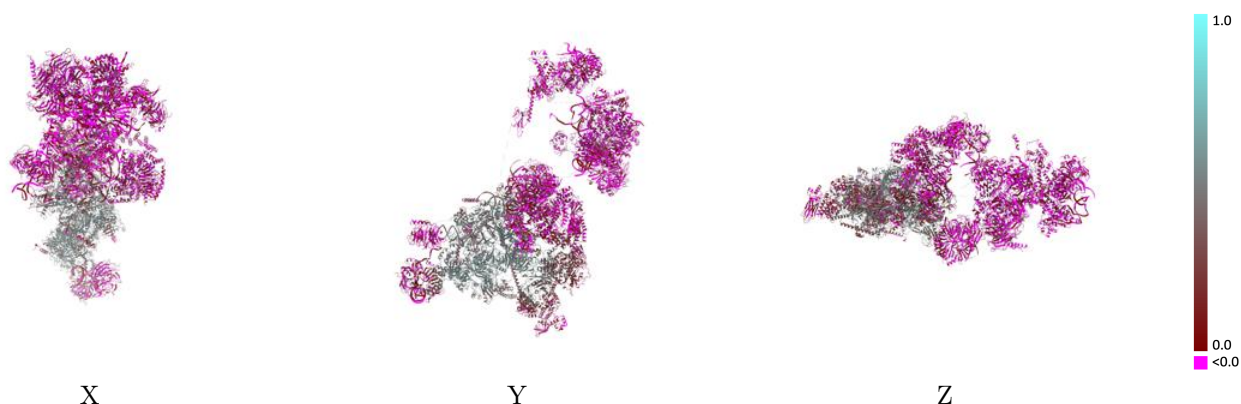
This section contains information regarding the fit between EMDB map EMD-34500 and PDB model 8H6E. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



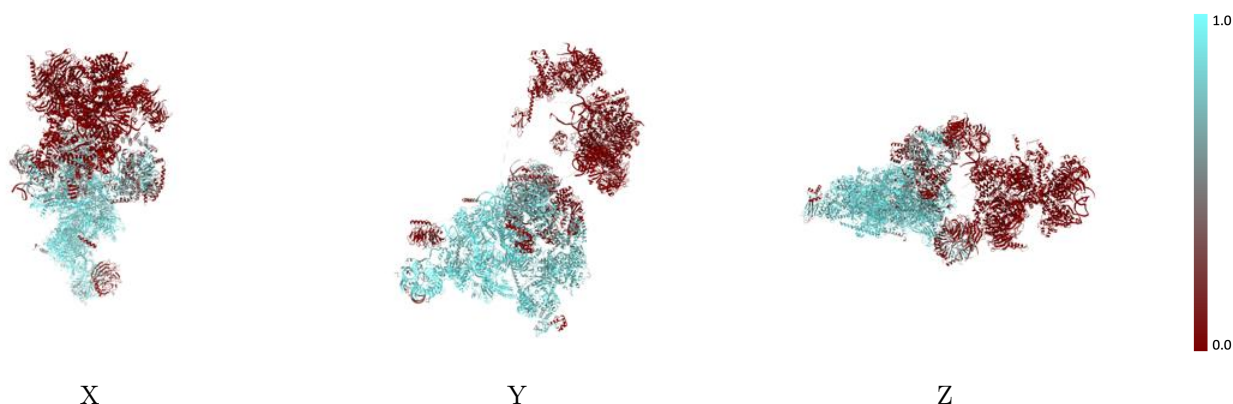
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



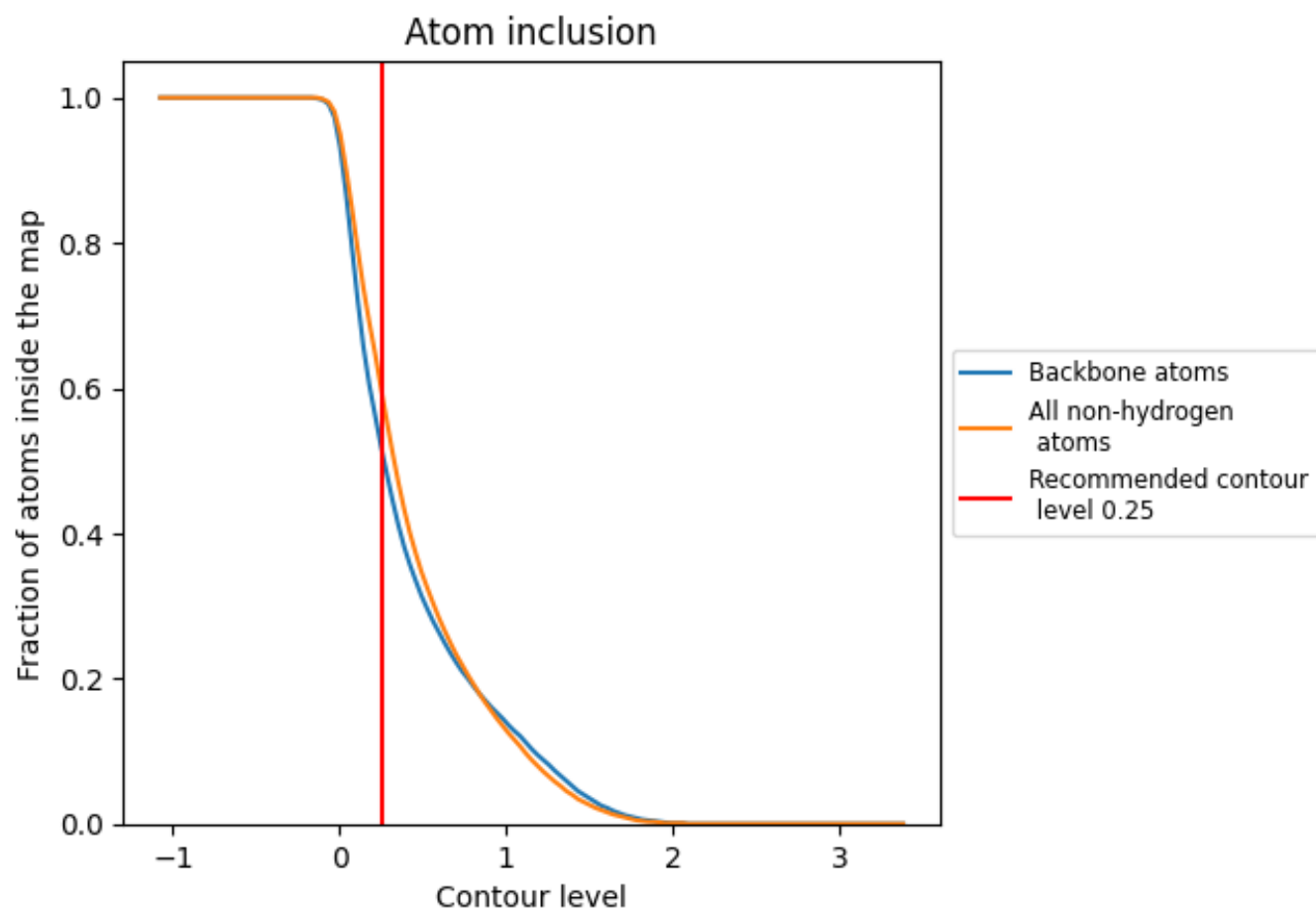
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.25).

9.4 Atom inclusion ⓘ



At the recommended contour level, 52% of all backbone atoms, 60% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5990	 0.2360
2A	 0.0050	 -0.0080
2B	 0.0000	 -0.0110
2C	 0.0000	 -0.0400
2D	 0.3370	 0.2070
2E	 0.0000	 0.0010
2F	 0.0010	 0.0060
2G	 0.0080	 0.0050
2H	 0.0040	 0.0140
2I	 0.0040	 -0.0000
2J	 0.0000	 0.0150
2K	 0.0000	 -0.0320
2L	 0.0170	 -0.0300
2M	 0.0080	 0.0260
2a	 0.0000	 0.0180
2b	 0.0000	 0.0160
2c	 0.0000	 -0.0750
2d	 0.0000	 0.0100
2e	 0.0000	 0.0210
2f	 0.0000	 0.0070
2g	 0.0000	 0.0390
4A	 0.6490	 0.0900
4B	 0.3900	 0.0270
4C	 0.5380	 0.0200
4D	 0.3980	 0.1020
4E	 0.6080	 0.0780
4F	 0.9680	 0.5220
4G	 0.6630	 0.1510
4R	 0.8340	 0.2830
4S	 0.7650	 0.3010
4T	 0.9700	 0.4950
4U	 0.7840	 0.3270
4X	 0.7990	 0.3030
4Y	 0.0340	 -0.0070
4a	 0.4320	 0.0060



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Chain	Atom inclusion	Q-score
4b	 0.4860	 0.0410
4c	 0.2770	 0.0130
4d	 0.2740	 0.0420
4e	 0.3060	 -0.0230
4f	 0.4580	 0.0350
4g	 0.4940	 -0.0130
5A	 0.8410	 0.2620
5B	 0.9230	 0.4610
5C	 0.9620	 0.5050
5D	 0.8300	 0.2890
5E	 0.0730	 -0.0100
5a	 0.8030	 0.1790
5b	 0.8870	 0.1170
5c	 0.7220	 0.0460
5d	 0.8150	 0.0990
5e	 0.9050	 0.1350
5f	 0.8580	 0.2370
5g	 0.9420	 0.3440
6A	 0.6380	 0.1840
6a	 0.0060	 -0.0090
6b	 0.0030	 -0.0680
6c	 0.0030	 -0.0030
6d	 0.0040	 -0.0000
6e	 0.0040	 0.0190
6f	 0.0000	 0.0500
6g	 0.0000	 0.0380
A	 0.2620	 0.1110