



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 10:36 AM UTC

PDB ID : 8H6J / pdb_00008h6j
EMDB ID : EMD-34505
Title : Cryo-EM structure of human exon-defined spliceosome in the mature pre-B state.
Authors : Zhang, W.; Zhan, X.; Zhang, X.; Lei, J.; Yan, C.; Shi, Y.
Deposited on : 2022-10-18
Resolution : 3.25 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:

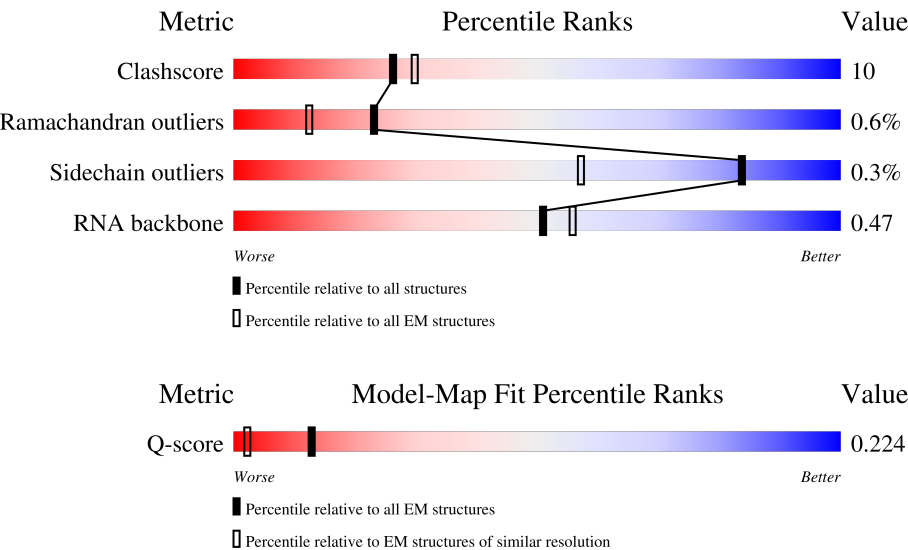
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.25 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	14599 (2.75 - 3.75)

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	29% 8% 15% . 71%
2	6A	107	21% 32% 10% 7% . 50%
3	6a	95	94% 87% 5% . 6%

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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	144	
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	81% 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 96473 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	42	Total	C	N	O	P	0	0
			864	387	124	311	42		

- Molecule 2 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	6A	54	Total	C	N	O	P	0	0
			1142	509	206	373	54		

- 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	2209	Total	C	N	O	S	0	0
			18244	11760	3170	3235	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	301	Total	C	N	O	0	0
			1481	879	301	301		

- 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	86	Total	C	N	O	0	0
			344	172	86	86		
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	74	Total	C	N	O	0	0
			363	215	74	74		
20	2f	66	Total	C	N	O	0	0
			264	132	66	66		

- 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
			2656	1188	468	876	124		

- 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
			953	567	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	270	Total	C	N	O	0	0
			1340	800	270	270		

- 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	784	Total	C	N	O	S	0	0
			4539	2745	884	901	9		

- 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	61	Total	C	N	O	S	0	0
			505	317	94	91	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	578	Total	C	N	O	S	1	0
			3414	2063	682	667	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	124	Total	C	N	O	0	0
			496	248	124	124		

- 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		

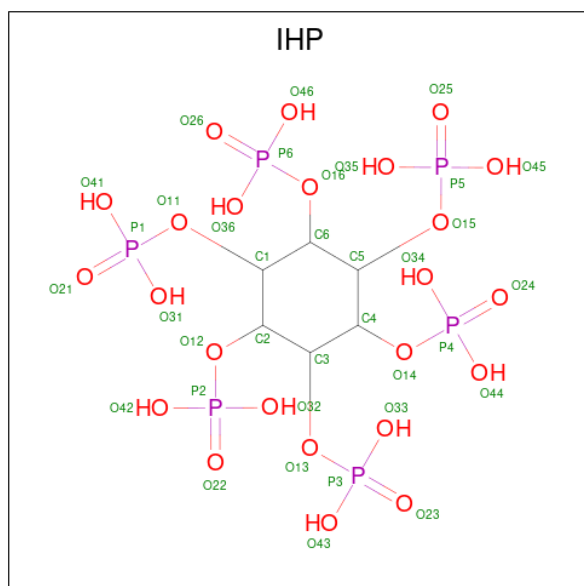
- Molecule 46 is a protein called PHD finger-like domain-containing protein 5A.

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: $C_6H_{18}O_{24}P_6$).

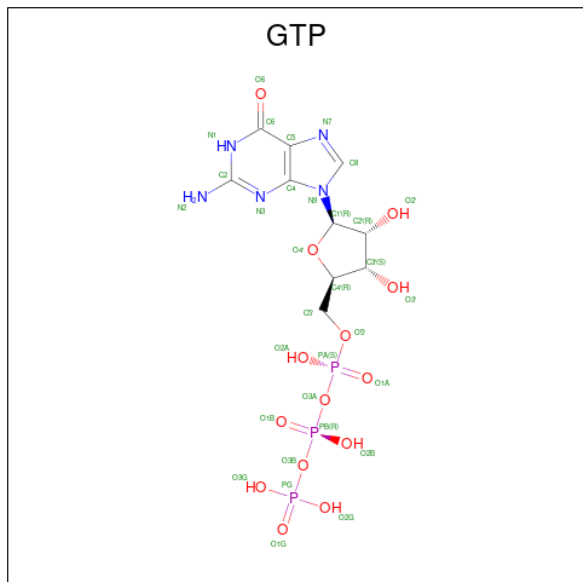


Mol	Chain	Residues	Atoms				AltConf
48	5B	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 49 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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	

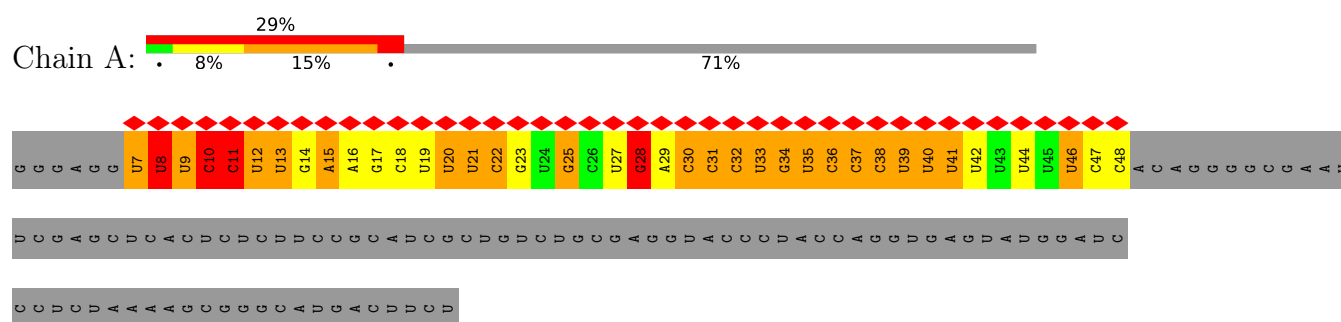
- Molecule 51 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

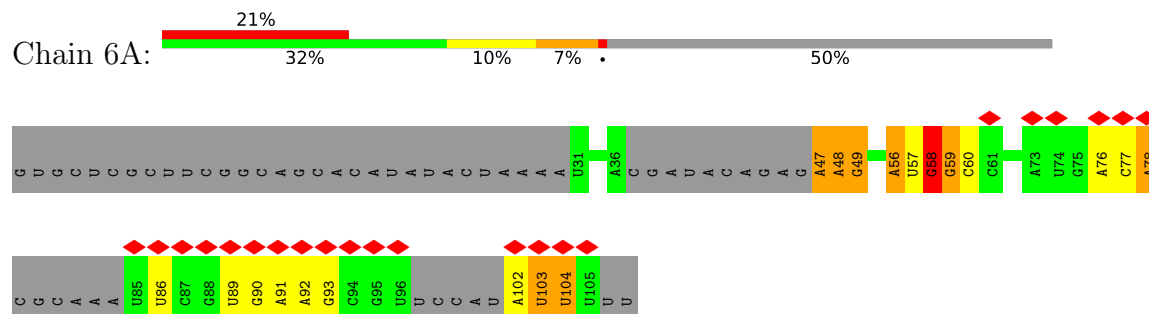
3 Residue-property plots [i](#)

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

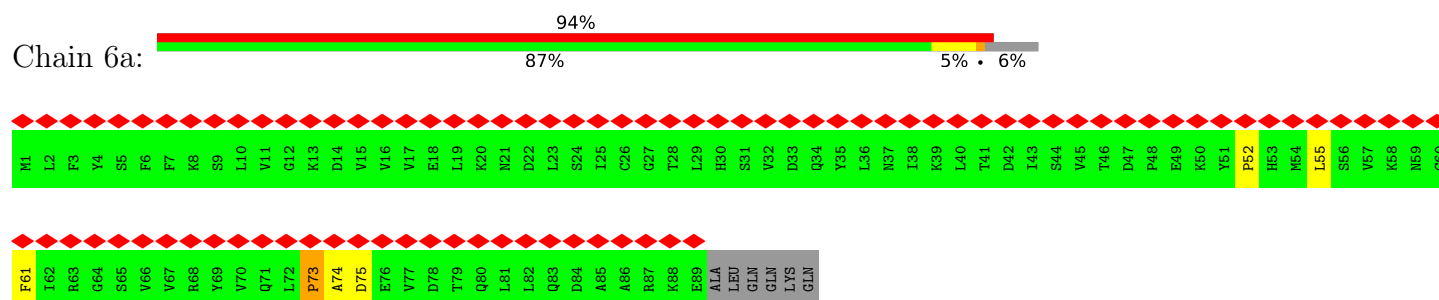
• Molecule 1: pre-mRNA



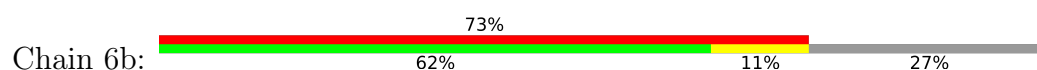
• Molecule 2: U6 snRNA



• Molecule 3: U6 snRNA-associated Sm-like protein LSm2

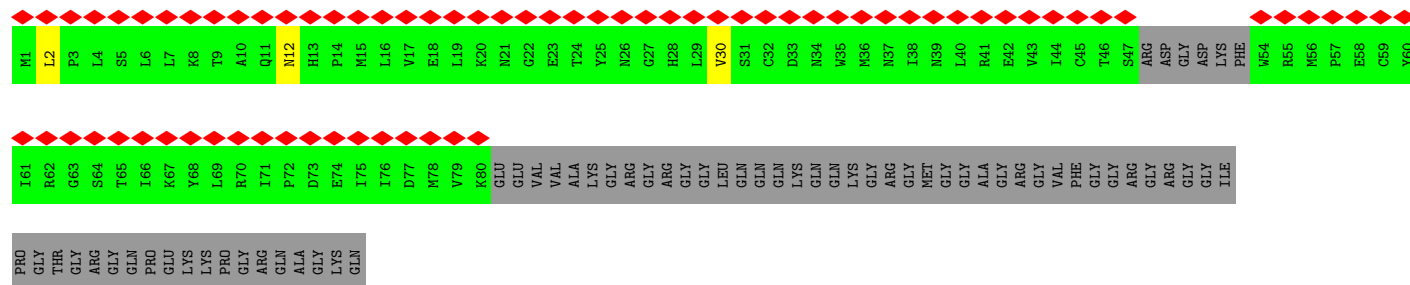


• Molecule 4: U6 snRNA-associated Sm-like protein LSm3

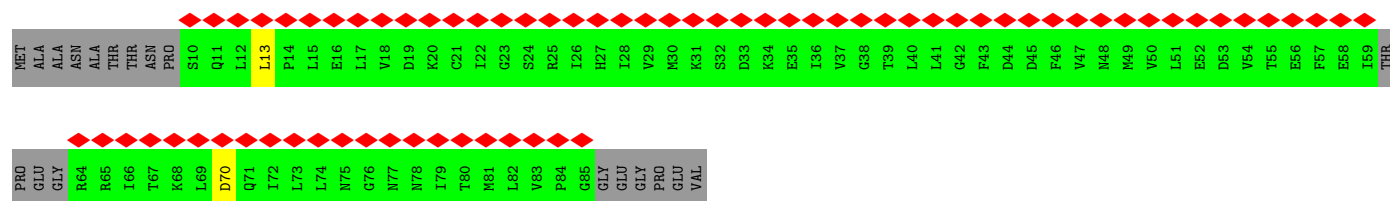
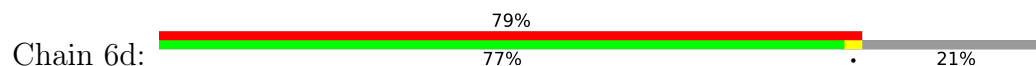




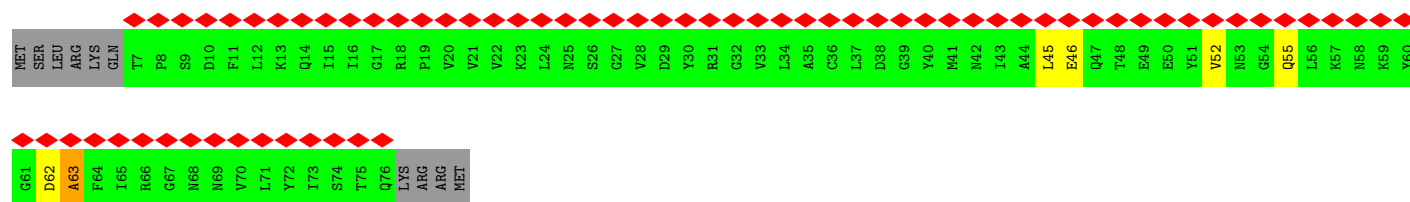
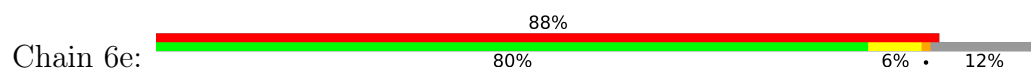
• Molecule 5: U6 snRNA-associated Sm-like protein LSm4



• Molecule 6: U6 snRNA-associated Sm-like protein LSm5



• Molecule 7: U6 snRNA-associated Sm-like protein LSm6

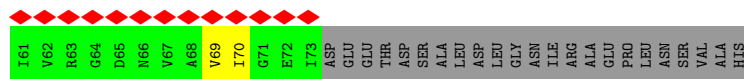


• Molecule 8: U6 snRNA-associated Sm-like protein LSm7

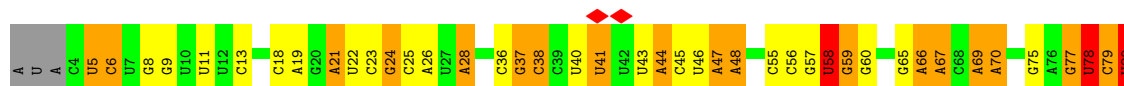




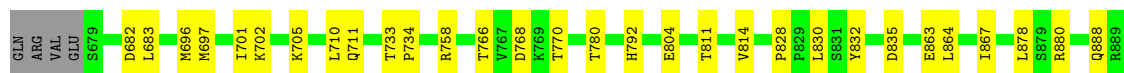
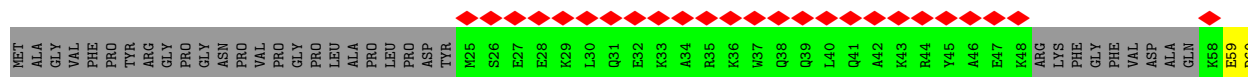
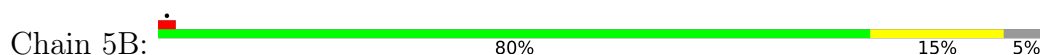
• Molecule 9: U6 snRNA-associated Sm-like protein LSm8

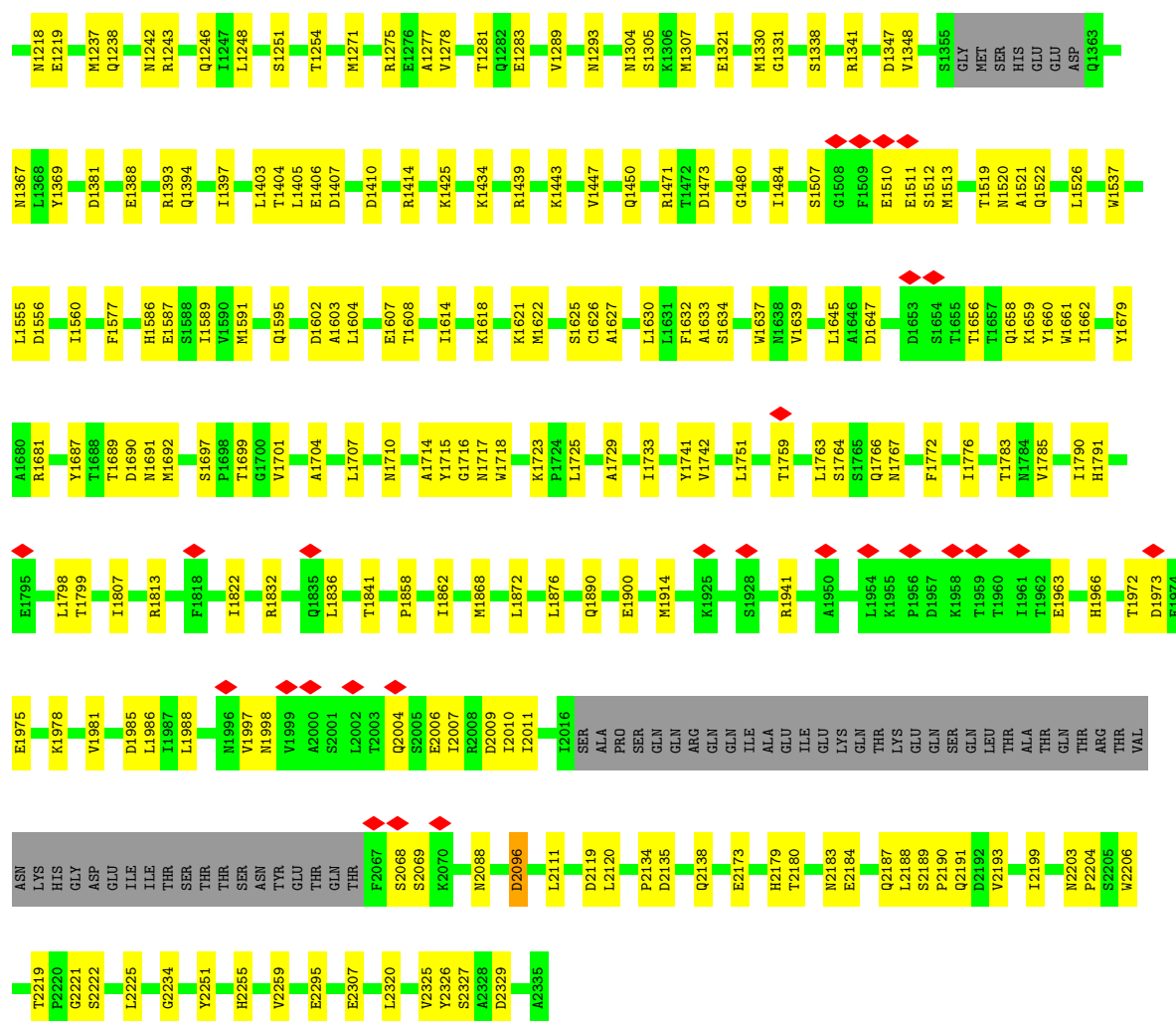


• Molecule 10: U5 snRNA

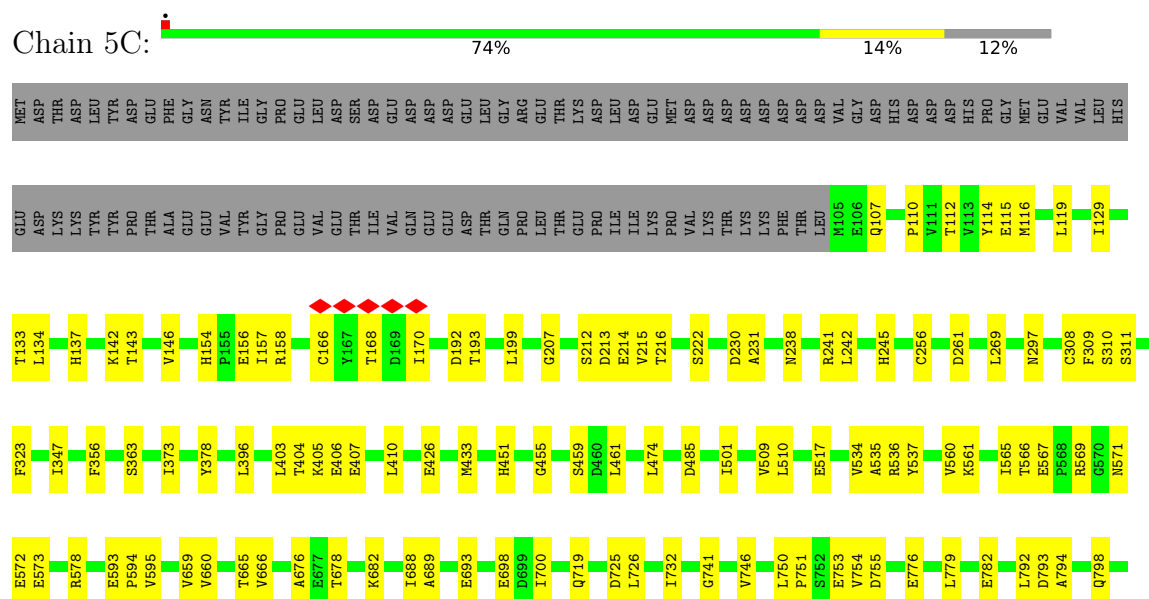


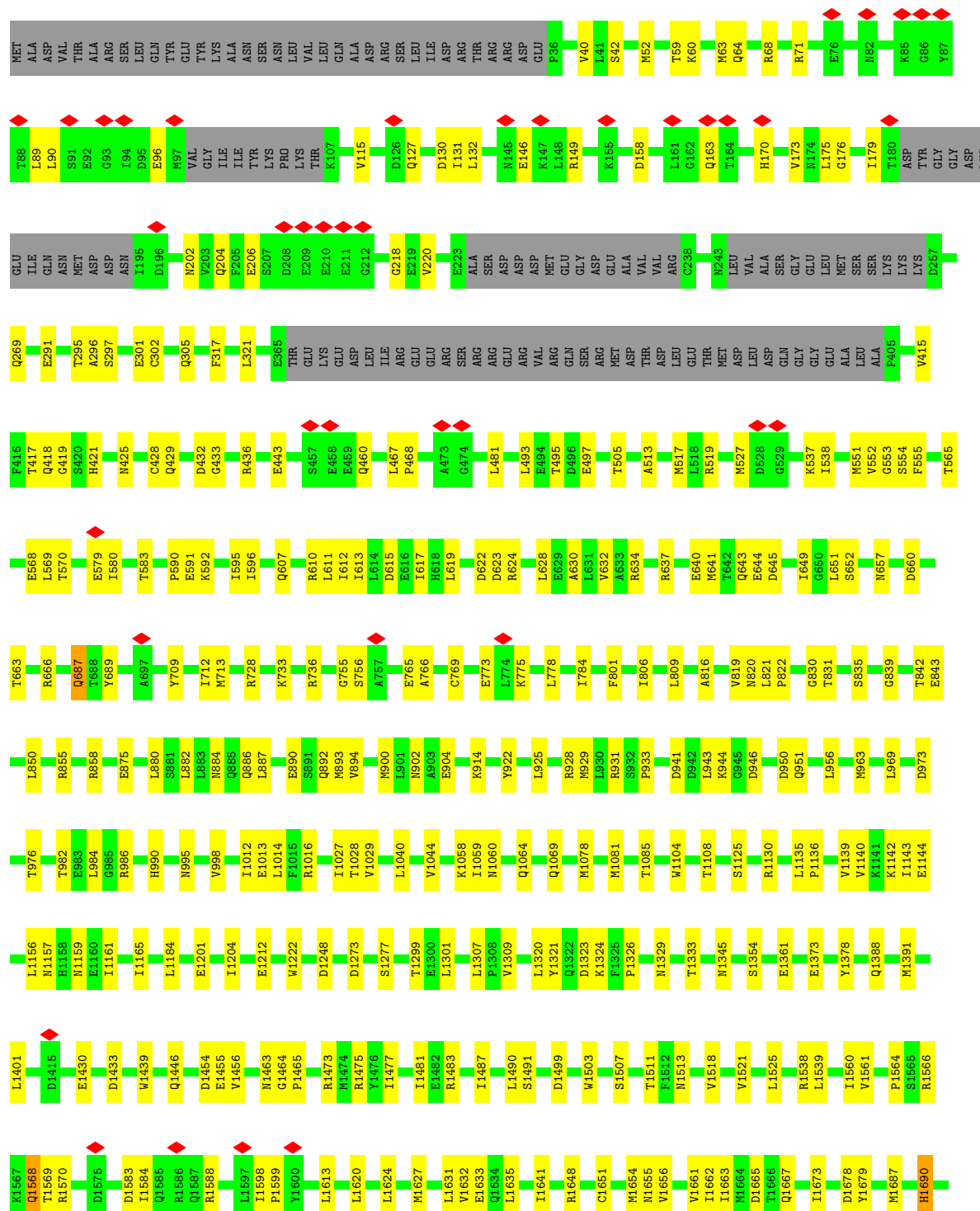
• Molecule 11: Pre-mRNA-processing-splicing factor 8

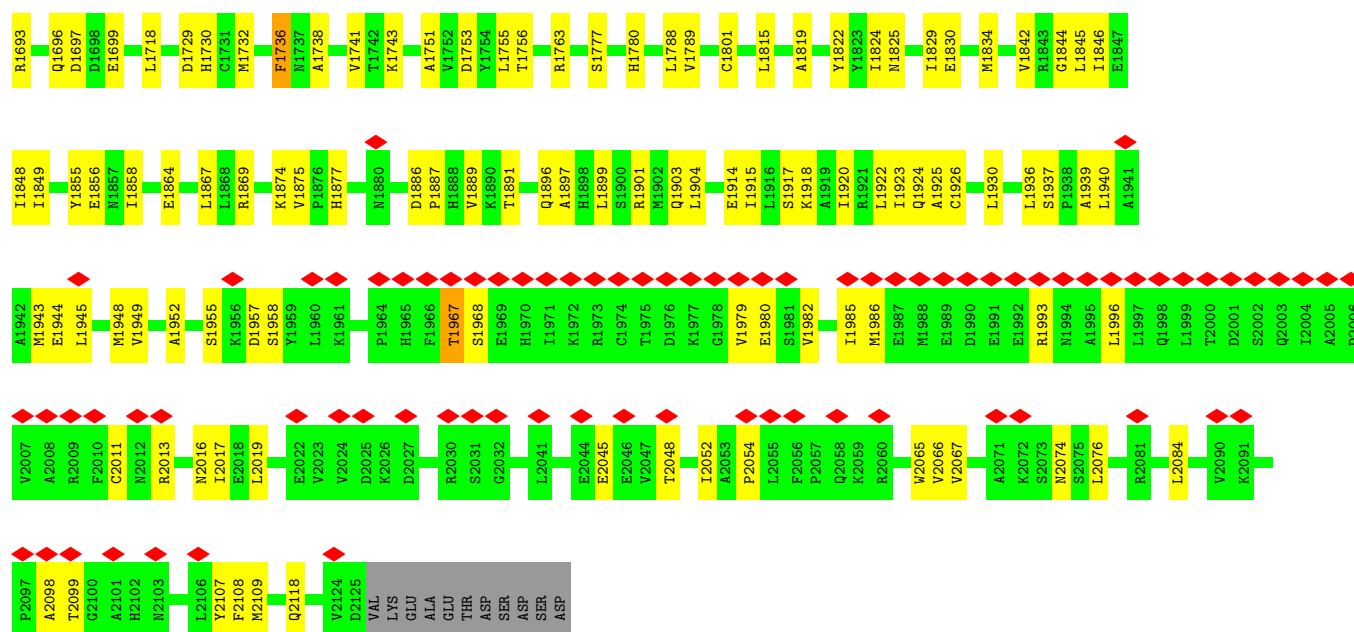




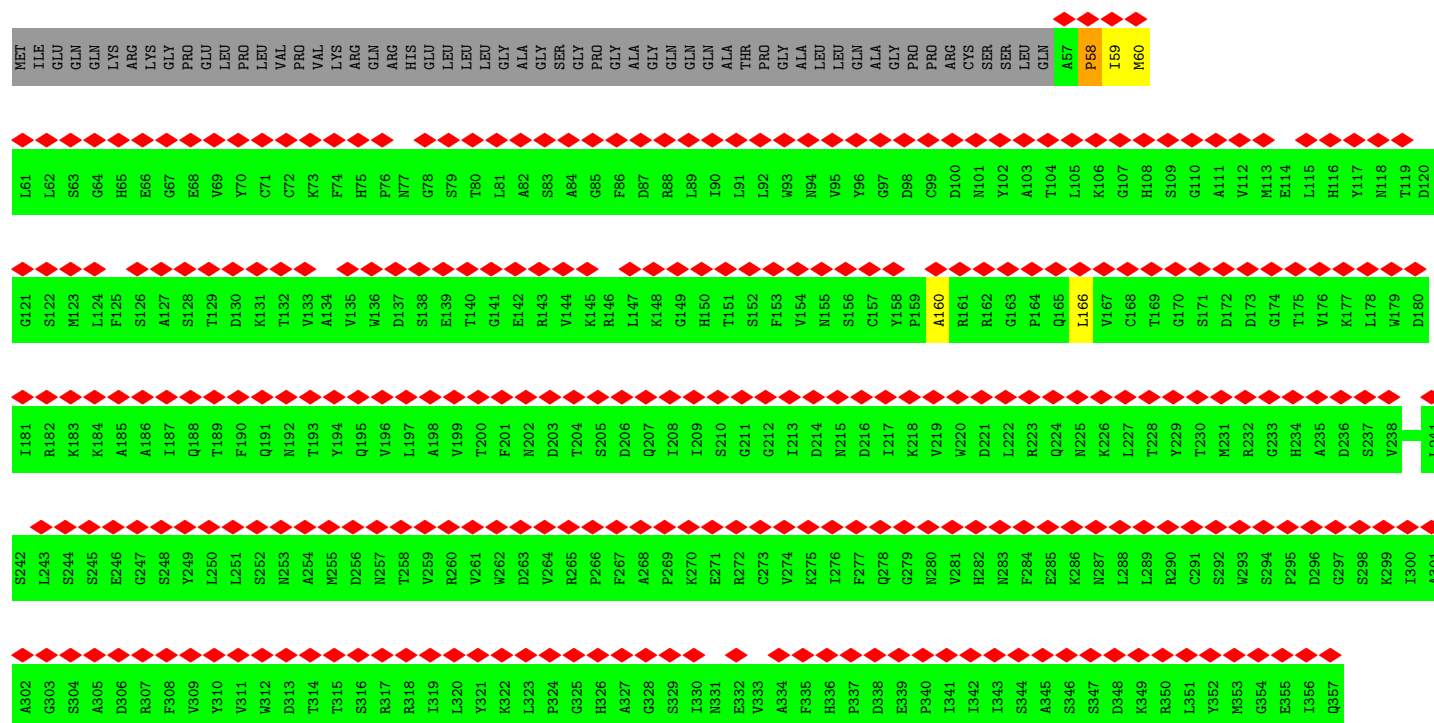
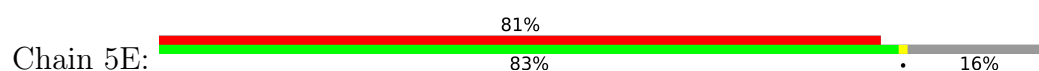
- Molecule 12: 116 kDa U5 small nuclear ribonucleoprotein component





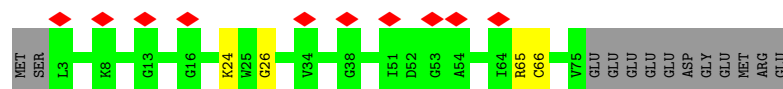
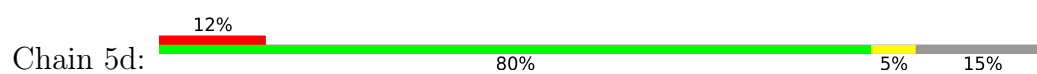


- Molecule 14: U5 small nuclear ribonucleoprotein 40 kDa protein

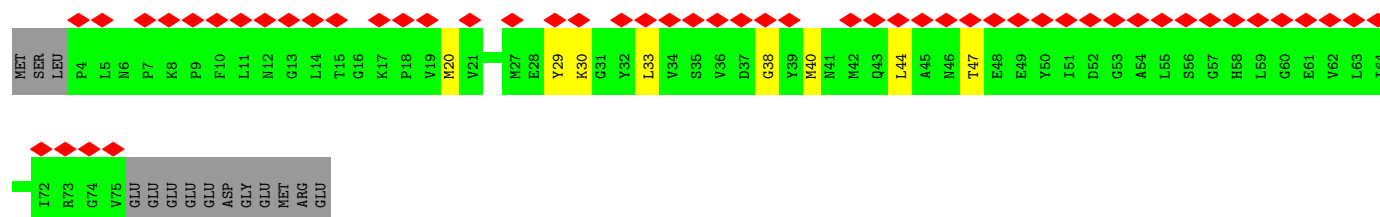
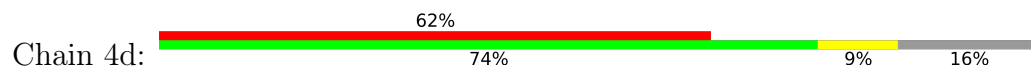


- Molecule 15: Isoform SM-B of Small nuclear ribonucleoprotein-associated proteins B and B'

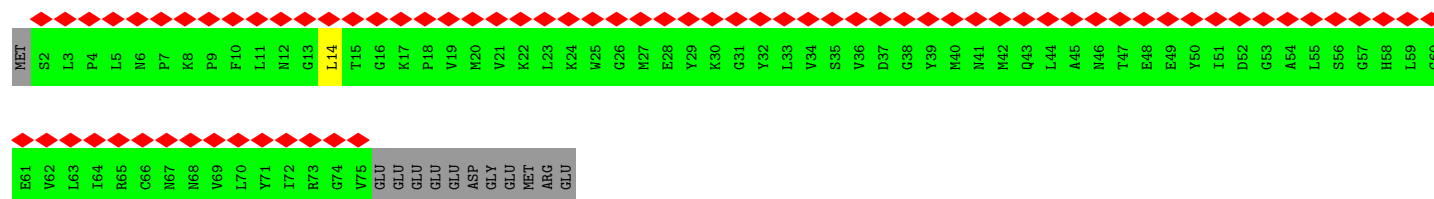
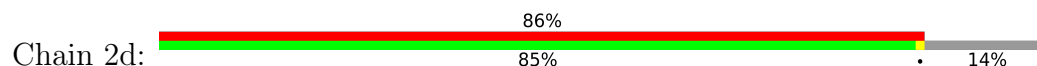




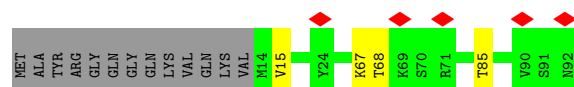
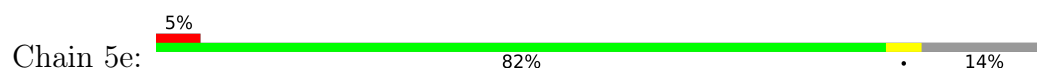
• Molecule 18: Small nuclear ribonucleoprotein F



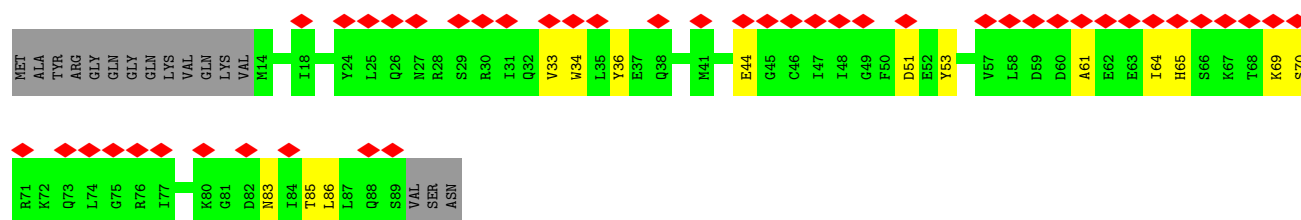
• Molecule 18: Small nuclear ribonucleoprotein F



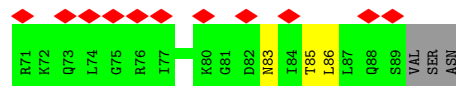
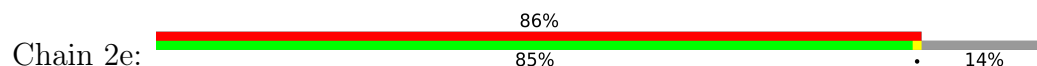
• Molecule 19: Small nuclear ribonucleoprotein E

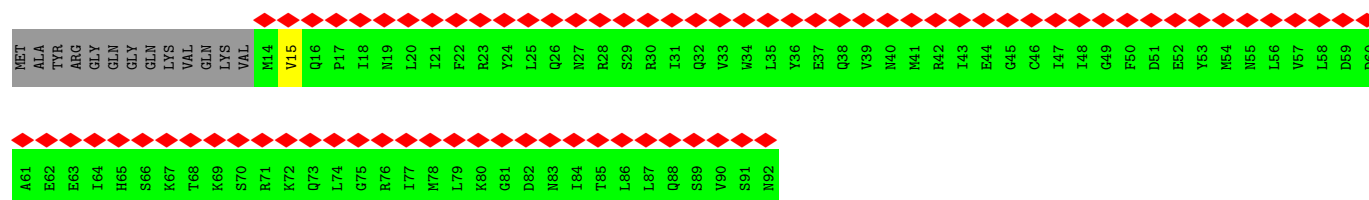


• Molecule 19: Small nuclear ribonucleoprotein E

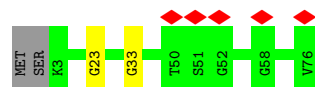


• Molecule 19: Small nuclear ribonucleoprotein E

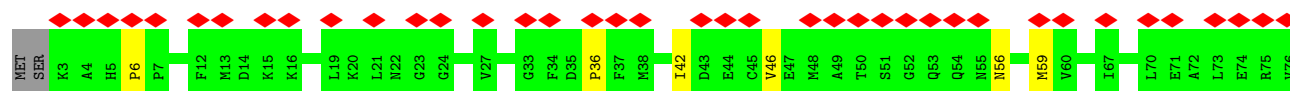
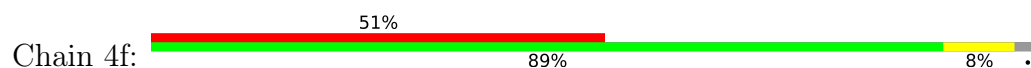




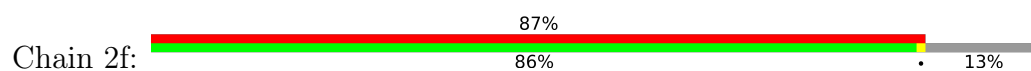
• Molecule 20: Small nuclear ribonucleoprotein G



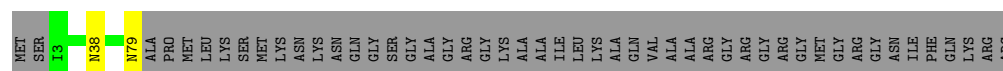
• Molecule 20: Small nuclear ribonucleoprotein G



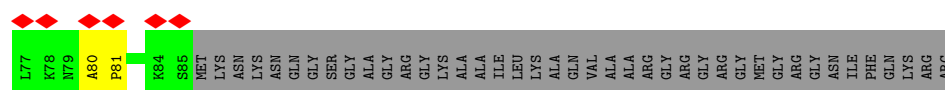
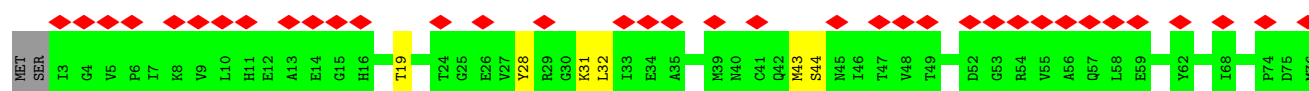
• Molecule 20: Small nuclear ribonucleoprotein G



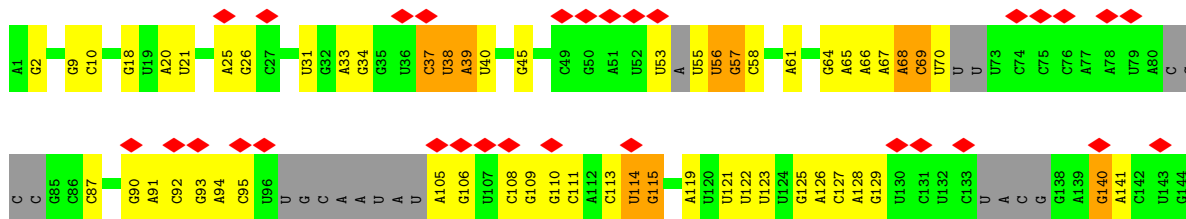
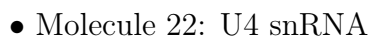
• Molecule 21: Small nuclear ribonucleoprotein Sm D3



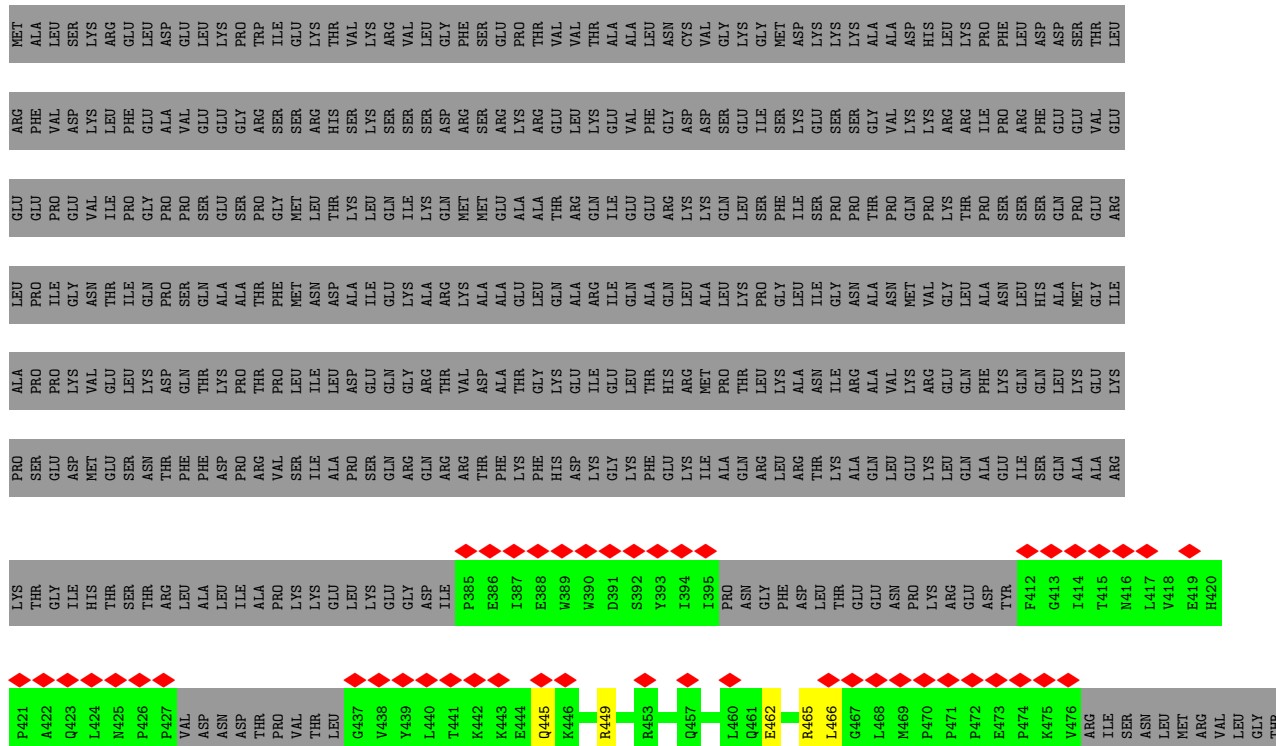
• Molecule 21: Small nuclear ribonucleoprotein Sm D3



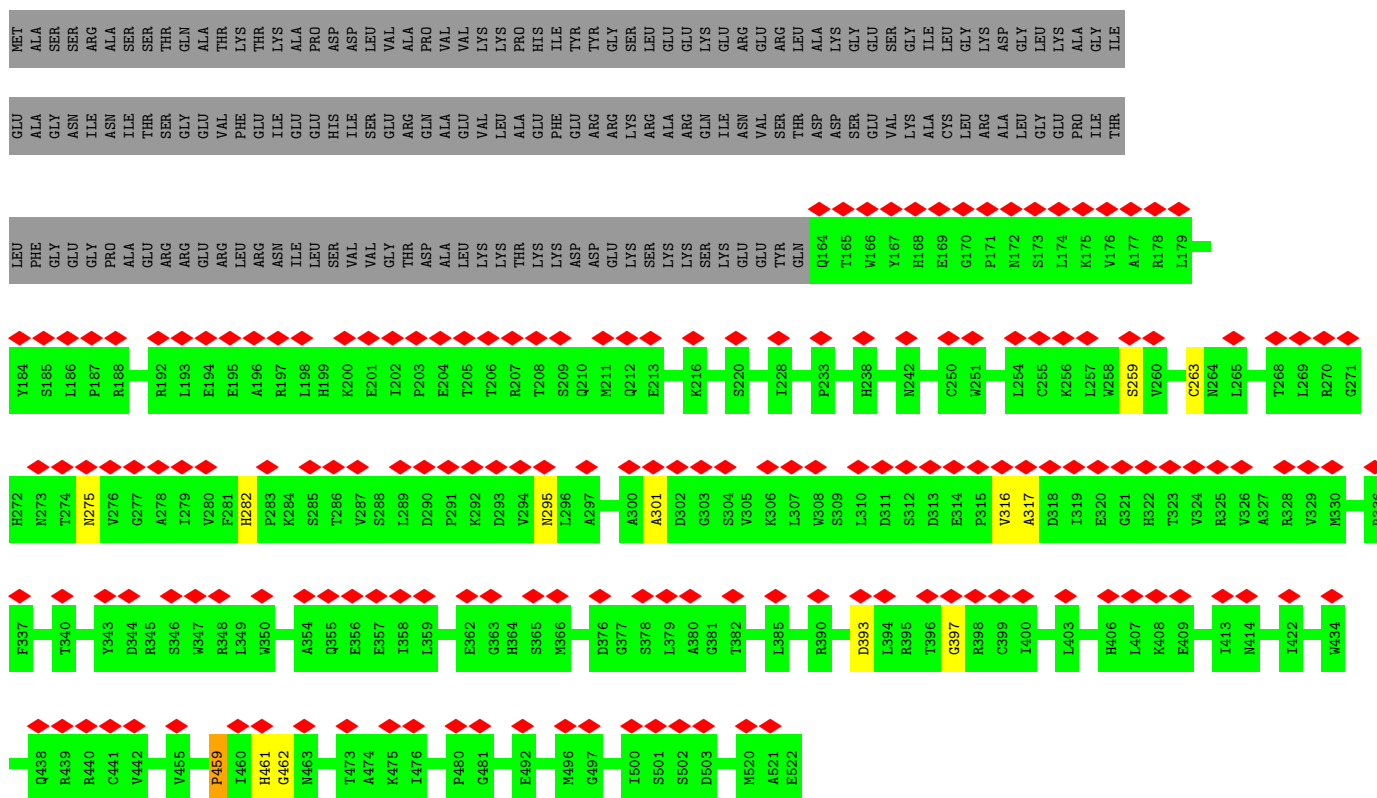
Chain 2g:



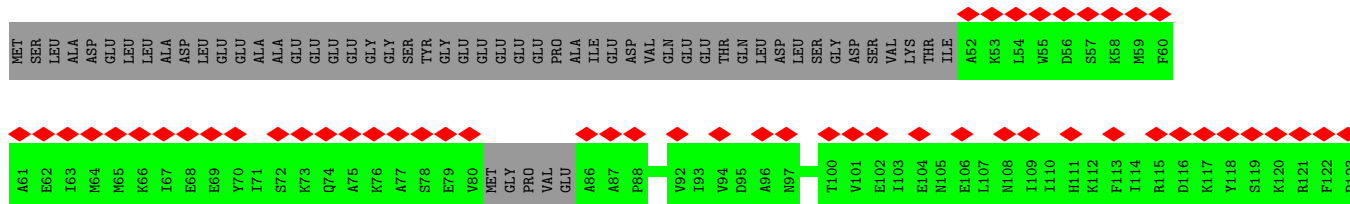
Chain 4B:

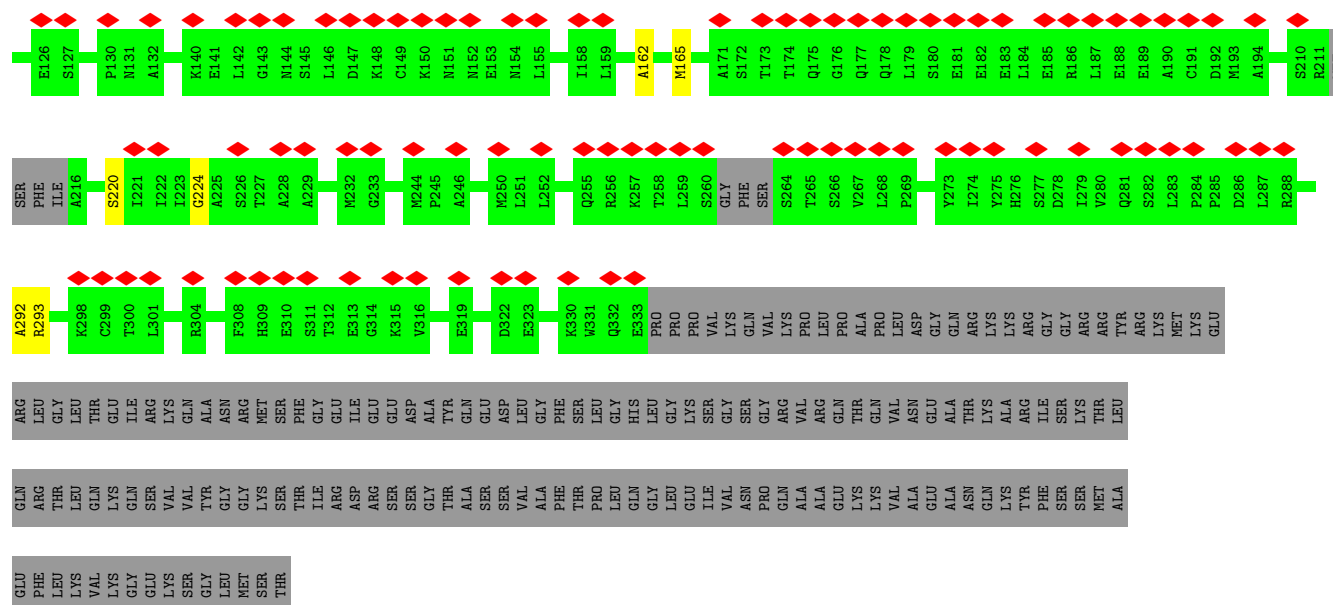


- Molecule 24: U4/U6 small nuclear ribonucleoprotein Prp4

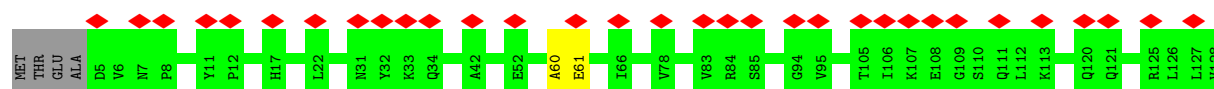


- Molecule 25: U4/U6 small nuclear ribonucleoprotein Prp31

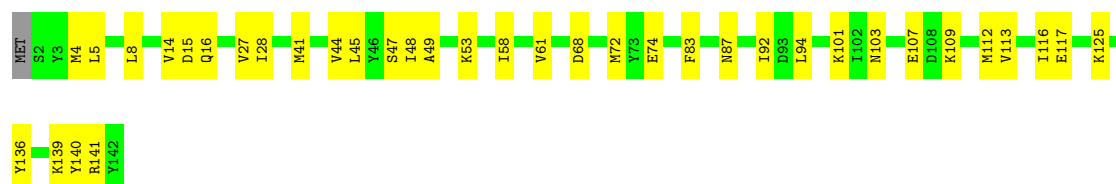
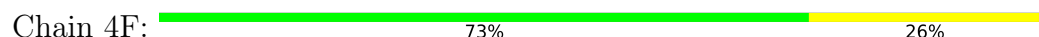




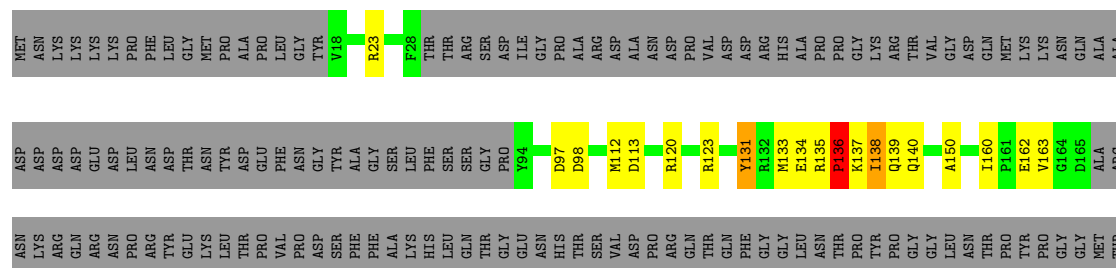
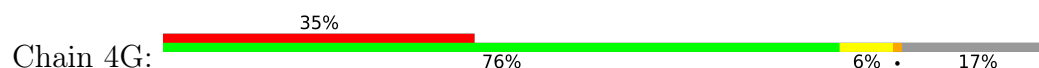
- Molecule 26: NHP2-like protein 1



- Molecule 27: Thioredoxin-like protein 4A

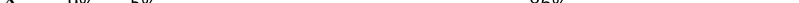


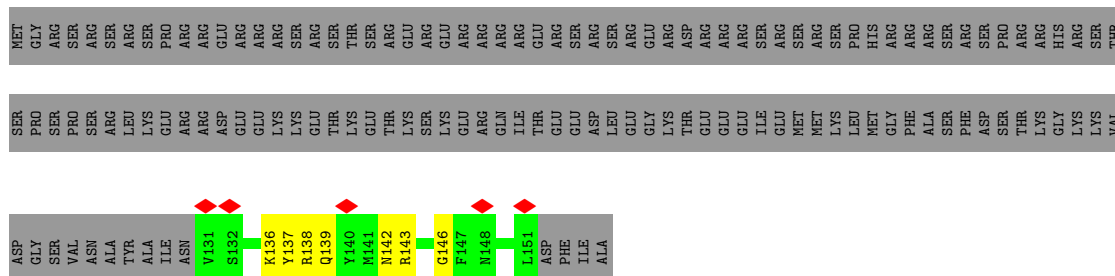
- Molecule 28: Pre-mRNA-processing factor 6

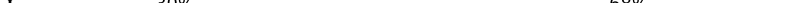


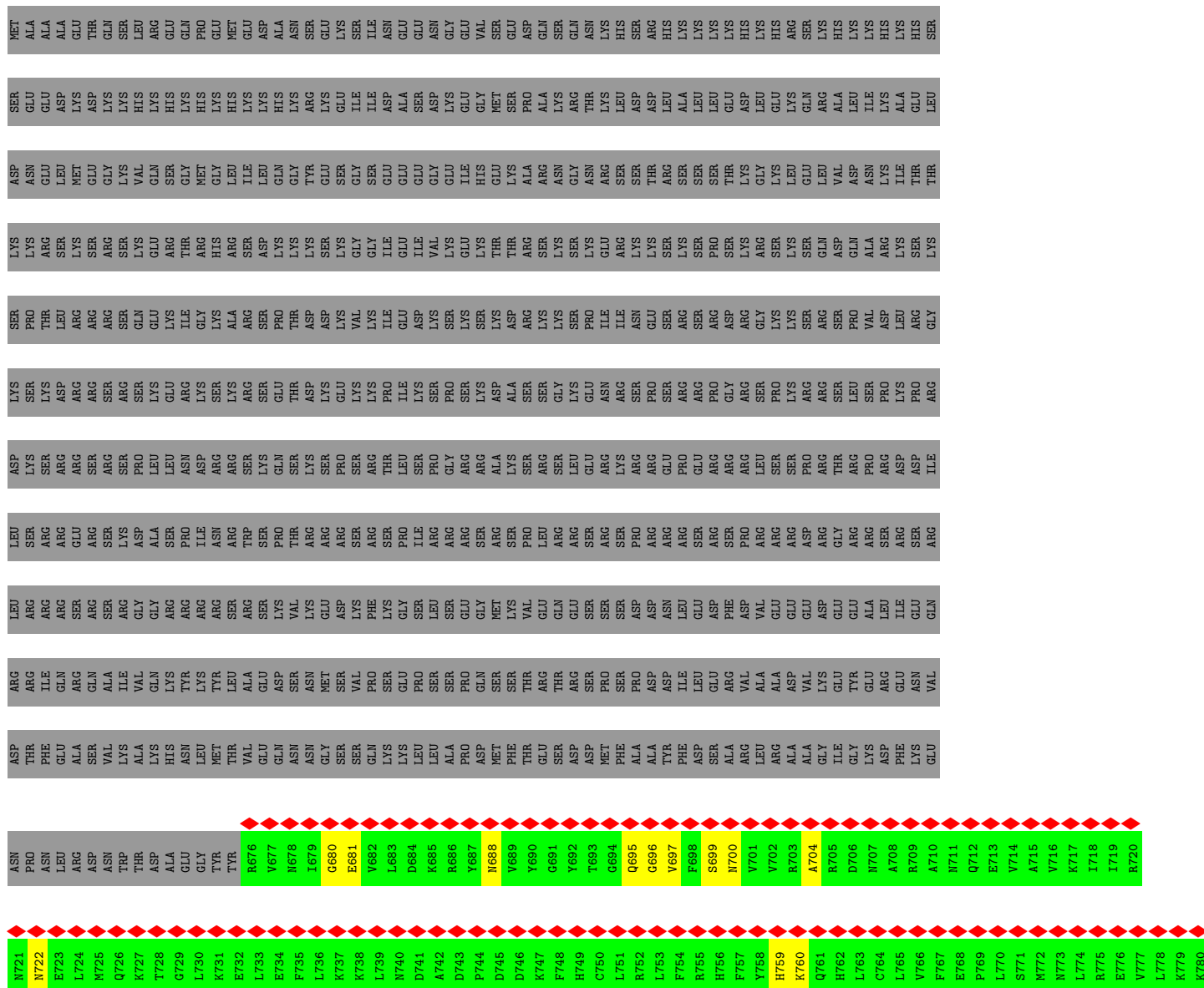


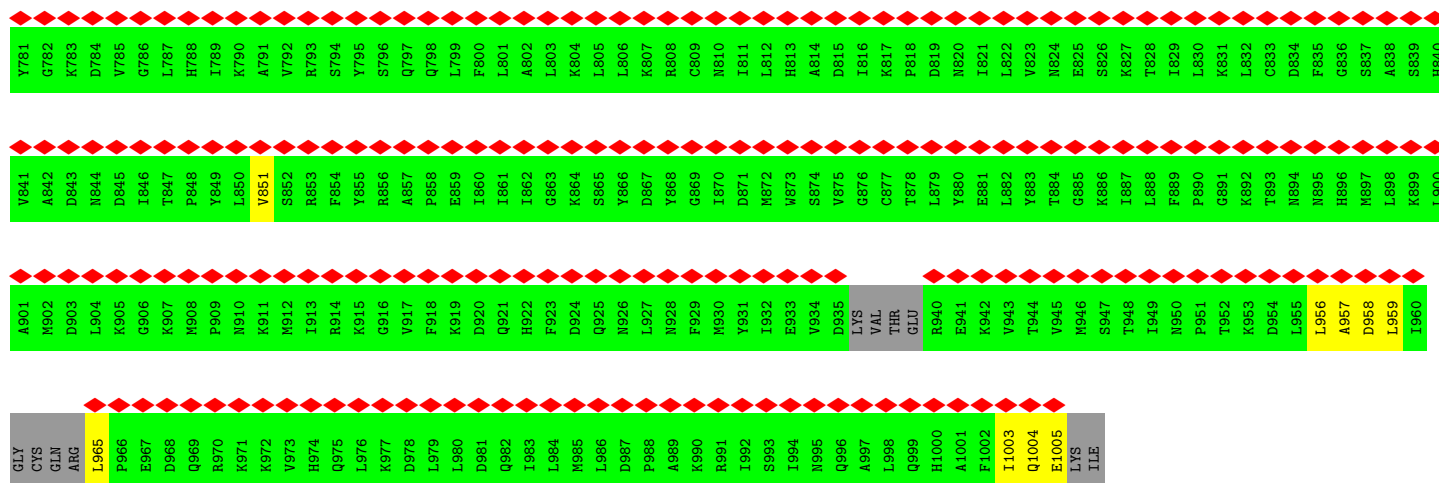


- Chain 4X: 

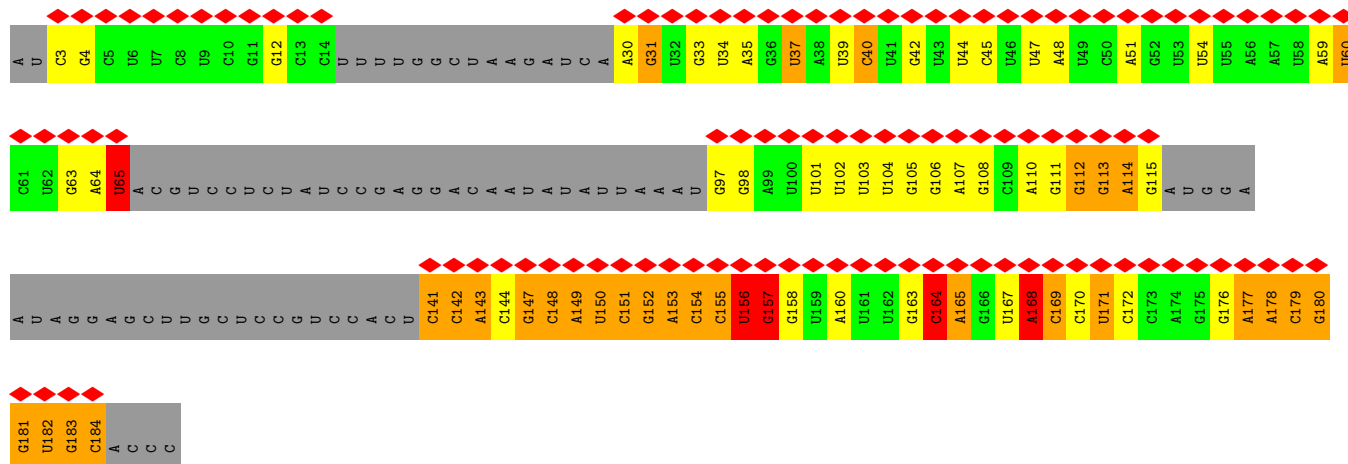
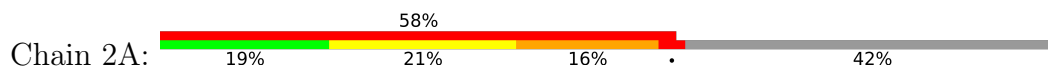


- Chain 4Y: 

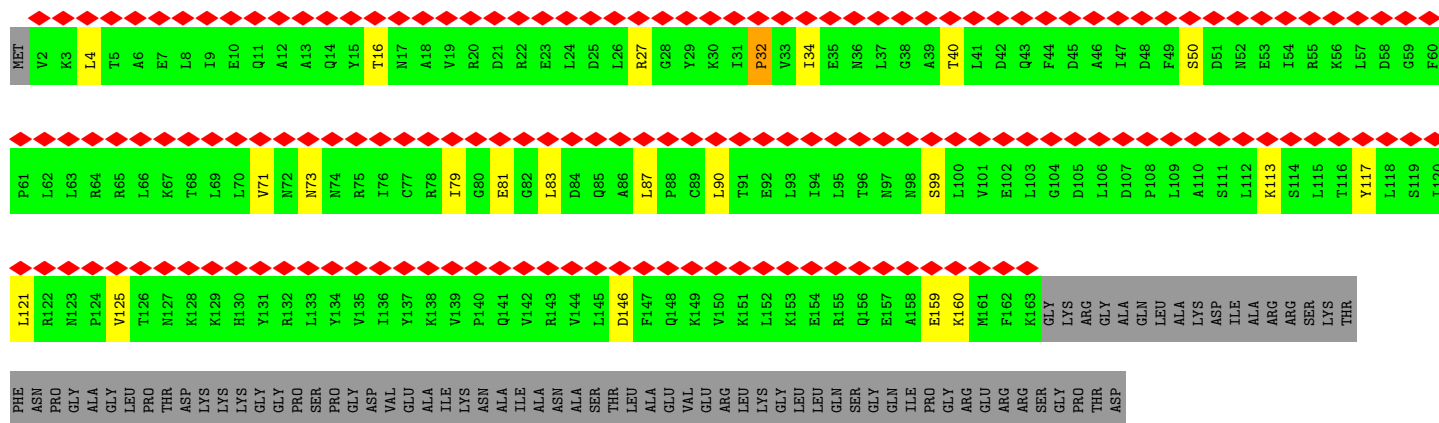




• Molecule 35: U2 snRNA



• Molecule 36: U2 small nuclear ribonucleoprotein A'



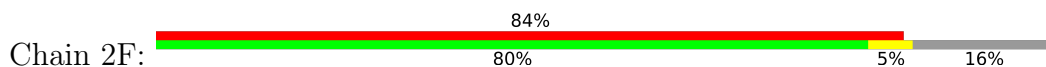


[illegible]

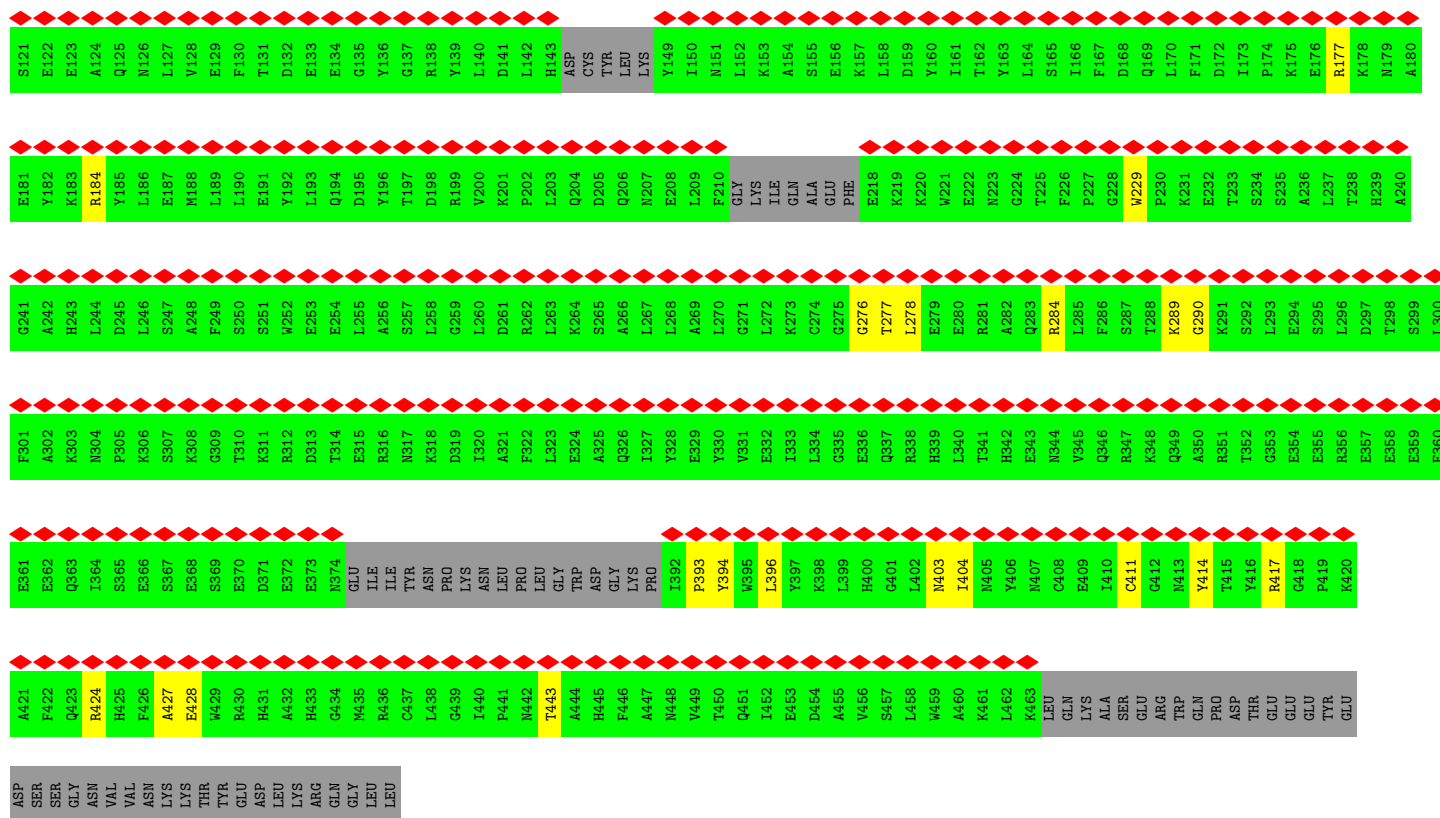
- Molecule 39: Splicing factor 3A subunit 2

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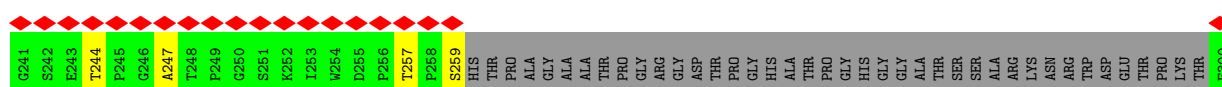
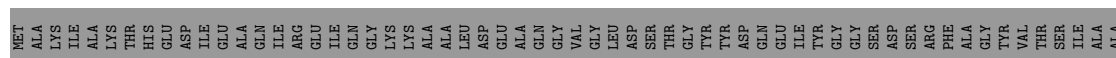
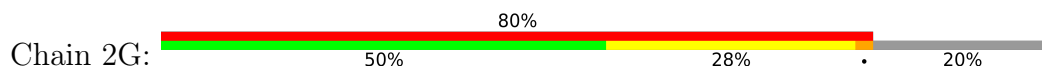
- Molecule 40: Splicing factor 3A subunit 3



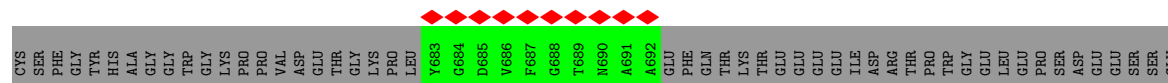
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Y61	D62	D63	K64	D65	G66	L67	R68	K69	E70	E71	L72	T73	A74	I75	S76	G77	P78	N79	E80	F81	A82	E83	F84	Y85	N86	R87	L88	K89	Q90	I91	K92	E93	F94	H95	R96	H98	PRO	ASN	GLU	ILE	CYS	VAL	PRO	MET	SER	VAL	GLU	F110	E111	E112	L113	L114	K115	A116	R117	E118	N119	P120	



• Molecule 41: Splicing factor 3B subunit 1

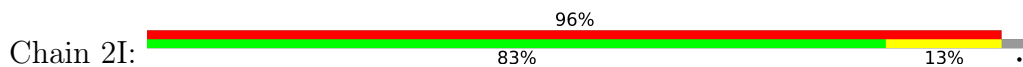


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G1082	P1022	M962	E902	N842	E782	E722	H662	K602	P542	V482	V422	THR
Y1083	I1023	K963	Q903	K843	E783	S723	T663	A603	T543	D483	P423	PRO
I1084	L1024	T964	T904	V844	M784	F724	G664	A604	L544	E484	I424	ALA
A1085	K1025	Q965	T905	G845	K785	D725	G665	G605	E545	S485	R425	ASN
K1086	N1026	C966	E906	G846	K786	S726	K666	L606	D546	THR	R426	MET
A1087	R1027	E967	D907	A847	I787	V727	I667	A607	Q547	LEU	T427	ALA
I1088	H1028	E968	S908	E848	V788	L728	V668	T608	E548	PRO	P427	THR
G1089	E1029	K969	V909	T849	L789	K729	Q669	M609	R549	THR	A428	PRO
P1090	K1030	L970	M910	T850	K790	P730	Q670	I610	H550	GLY	K430	PRO
H1091	V1031	M971	L911	S851	V791	L731	I671	S611	L551	GLY	R439	GLY
D1092	Q1032	G972	N912	R852	V792	V732	A672	T612	L552	ILE	K431	HIS
L1094	H1034	L974	F914	V854	Q794	K734	L674	M614	V553	MET	T432	MET
A1095	C1035	G975	G915	D855	C795	I735	M675	P615	K554	SER	A433	SER
T1096	I1036	V976	T916	D856	C796	R736	G676	D616	V555	THR	P435	THR
L1097	D1037	V977	V917	L857	G797	Q737	C677	I617	I556	PRO	T436	PRO
L1098	L1038	L978	V918	K858	T798	H738	A678	D618	D557	GLN	P437	GLN
M1099	V1039	Y979	N919	D859	D799	R739	I679	N619	R558	LEU	L438	LEU
N1100	G1040	E980	A920	E860	G800	G740	L680	M620	I559	GLN	G439	GLN
L1101	R1041	Y981	L921	A861	V801	K741	P681	D621	L560	ALA	G440	ALA
K1102	I1042	L982	G922	E862	E802	G742	H682	E622	Y561	TRP	M441	TRP
V1103	A1043	G983	K923	Q863	A903	L743	L683	Y623	K562	ARG	T442	ARG
T1104	D1044	E984	R924	Y864	N804	A744	G684	V624	L563	GLU	G443	GLU
E1105	R1045	E985	V925	R865	T805	A745	S685	R625	D564	GLU	F444	GLU
R1106	K1046	Y986	K926	K866	I806	F746	L686	N626	D565	ILE	H445	ILE
Q1107	A1047	P987	P927	K867	K807	L747	V687	T627	L566	ASP	M446	ASP
N1108	E1048	E988	Y928	V868	T808	K748	E688	T628	V567		Q447	
L1109	Y1049	V989	L929	H869	E809	A749	I689	A629	R568	THR	THR	
V1110	Y1050	G990	P930	E870	I810	I750	I690	R630	P569	GLU	ASP	
C1111	S1051	G991	Q931	T871	L811	G751	E691	A631	P510	ASP	ASP	
T1112	A1052	S992	I932	T872	P812	Y752	H692	R632	M511	THR	THR	
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V1114	E1054	L994	G934	K874	F814	I754	L694	V634	K513	THR	THR	
A1115	W1055	G995	T935	L875	F815	P755	V695	V635	A514	THR	THR	
I1116	M1056	A996	V936	H876	K816	L756	D696	A636	A515	THR	THR	
A1117	R1057	L997	L937	G877	H817	M757	E697	S637	L516	THR	THR	
I1118	I1058	K998	V938	N878	F818	D758	Q698	A638	R517	THR	THR	
V1119	C1059	A999	R939	L879	M819	A759	Q699	L639	T520	THR	THR	
A1120	F1060	I1000	L940	G880	Q820	E760	K700	G640	P580	THR	THR	
E1121	E1061	V1001	N941	A881	H821	Y761	V701	I641	L581	THR	THR	
T1122	L1062	N1002	N942	A882	R822	A762	R702	P642	R523	THR	THR	
C1123	L1063	V1003	K943	D883	M823	M763	T703	S643	R524	THR	THR	
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P1125	L1065	G1005	A945	D885	L825	V765	S705	L645	E585	THR	THR	
F1126	L1066	M1006	K946	H886	D826	T766	A706	P646	D586	THR	THR	
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V1128	A1068	K1008	R948	L888	R828	E768	A708	L648	Y588	THR	THR	
L1129	M1069	M1009	Q949	E889	N829	V769	I709	K649	G529	THR	THR	
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E1135	R1075	D1015	P955	G895	D835	R775	A715	K655	I535	THR	THR	
Y1136	A1076	L1016	S956	T896	T836	E776	A716	K656	L536	THR	THR	
V1137	T1077	L1017	R957	L897	T837	F777	T717	S657	P537	THR	THR	
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P1139	M1079	R1019	A959	A899	E839	S779	Y719	Q659	N539	THR	THR	
E1140	T1080	L1020	V960	F900	L840	P780	G720	A660	L600	THR	V480	



THR	GLN	LYS	TYR	GLU	GLU	HIS	VAL	ARG	GLU	GLN	GLN	ALA	ALA	GLN	VAL	GLU	LYS	ASP	PHE	SER	ASP	MET	VAL	ALA	ALA	GLU	HIS	ALA	ALA	LYS	GLN	LYS	GLN	LYS	LYS	LYS	LYS	LYS	ARG	LYS	ALA	ALA	GLN	GLN	PRO	PRO	GLY	GLY	GLY	SER	SER	LYS	LYS	LYS	TYR	LYS	LYS	PHE	PHE	LYS	PHE
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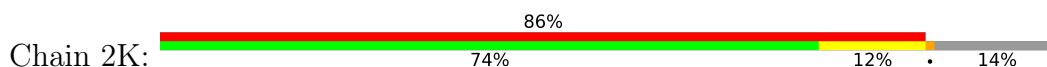
- Molecule 43: Splicing factor 3B subunit 3



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S602	K542	T482	Q422	A362	L302	S242	F182	A122	I62	F2
R603	L483	L483	L483	H363	A303	D243	A183	D243	R63	L3
F604	I544	V484	Y424	L364	Q304	G244	C184	D124	S64	Y4
L605	V545	L485	V425	G365	T305	S245	L185	P125	L65	N5
A606	K546	S486	A426	D366	E306	S246	E186	K126	H66	L6
G607	C547	I487	C427	D367	D307	G247	D187	G127	A67	T7
V608	A548	G488	G428	D368	G308	V248	D188	K128	F68	L8
L609	V549	E489	R429	E369	D309	L249	Y189	A129	R69	Q9
V610	N550	T490	G430	E370	I310	I250	E190	V130	L70	R10
D611	Q551	V491	P431	P371	F311	C251	E191	M131	T71	A11
N612	R552	E492	R432	E372	K312	S252	A192	I132	G72	T12
T613	Q553	E493	S433	F373	I313	E253	D193	I133	G73	G13
V614	V554	V494	S434	S374	T314	N254	N194	A134	T74	I14
R615	V555	T495	L435	S375	L315	Y255	D195	I135	K75	S15
L616	I556	D496	R436	A376	E316	I256	P196	E136	D76	F16
I617	A557	I497	V437	M377	T317	T257	T197	K137	Y77	A17
S618	L558	G498	L438	PR0	D318	Y258	G198	Q138	I78	I18
L619	T559	F499	R439	GLU	E319	K259	E199	K139	V79	H19
D620	G560	L500	HIS	GLU	D320	N260	A200	L140	V80	G20
P621	G561	G501	G441	GLY	M321	F261	A201	V141	G81	N21
S622	E562	T502	L442	V322	V322	G262	A202	Y142	S82	F22
G623	L563	T503	E443	T384	T323	D263	N203	I143	D83	S23
O624	V564	P504	V444	F385	E324	Q264	T204	L144	S84	G24
L625	Y565	T505	S445	F386	I325	P265	Q205	N145	G85	T25
Q626	F566	L506	E446	F387	R326	D266	Q206	R146	H86	K26
P627	E567	S507	M447	Q388	L327	I267	T207	D147	I87	Q27
L628	M568	C508	R448	P389	K328	R268	L208	A148	V88	Q28
S629	D569	S509	V449	R390	Y329	C269	T209	A149	I89	E29
M630	P570	L510	S450	P391	F330	P270	F210	A150	L90	I30
A632	S571	L511	E451	L392	D331	I271	Y211	R151	E91	V31
L633	G572	G512	L452	K393	T332	P272	E212	L152	Y92	V32
P634	Q573	D513	P453	N394	V333	R273	L213	T153	Q93	S33
L635	L574	D514	G454	L395	P334	R274	D214	T154	P94	R34
A635	N575	A515	M455	V396	V335	R275	L215	S155	S95	G35
Q636	E576	L516	P456	L397	A336	N276	G216	S156	K96	K36
P637	Y577	V517	M457	V398	A337	D277	L217	P157	N97	I37
E638	T578	Q518	A458	D399	A338	L278	N218	L158	V98	L38
S639	E579	V519	V459	E400	M339	D279	H219	E159	F99	E39
L640	R580	V520	V460	L401	C340	D280	V220	A160	E100	L40
O641	K581	P521	T461	D402	V341	P281	V221	H161	K101	L41
I642	E582	D522	V462	S403	L342	E282	R222	K162	I102	R42
V643	M583	I524	R464	A404	K343	G283	K223	A163	H103	P43
E644	S584	E524	S464	S405	T344	G284	Y224	N164	Q104	D44
M645	A585	R525	H465	P406	G345	N285	S225	T165	E105	P45
GLY	D586	H526	I466	T407	F346	I286	E226	L166	T106	N46
GLY	E587	I527	E467	L408	L347	F287	P227	Y167	F107	T47
THR	V588	R528	D468	F409	F348	V288	L228	Y168	G108	G48
GLY	C589	A529	E469	C410	V349	C289	E229	H169	K109	R49
GLN	M590	D530	F470	Q411	A350	S290	E230	V170	S110	V50
ASP	S591	K531	D471	I412	S351	A291	H231	V171	G111	H51
GLU	L592	R532	A413	A413	E352	T292	G232	G172	C112	T52
GLY	A593	V533	Y473	D414	F353	H293	N233	V173	R113	L53
GLU	N594	I474	I474	L415	G354	K294	F234	D174	R114	L54
ARG	V595	E534	I475	A416	N355	T295	L235	V175	I115	T55
GLY	E535	E535	I475	A416	N355	T295	L235	V175	I115	T55
SER	V596	V536	V476	M417	H556	K296	T236	G176	V116	V56
ILE	P597	K537	S477	E418	Y357	S297	T237	F177	P117	E57
	G598	T538	F478	D419	L358	M298	V238	E178	G118	V58
	E599	P539	V479		Y359	F299	P239	N179	Q119	F59
	Q600	G540	M480	T420	G360	F300	G240	P180	F120	G60

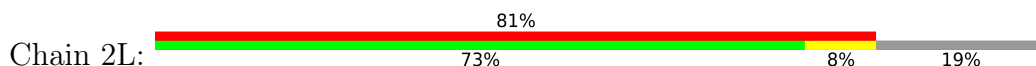
[illegible]

- Molecule 45: Splicing factor 3B subunit 6



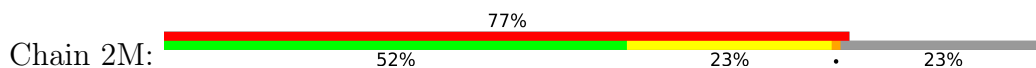
THR	ASP	PRO	LYS	MET	ALA	MET	GLN	ALA	LYS	ARG	ALA	ASN	ILE	R12	R13	P14	P15	E16	V17	M18	R19	I20	L21	Y22	I23	R24	M25	L26	P27	Y28	K29	I30	T31	A32	E33	E34	M35	Y36	D37	I38	F39	G40	K41	Y42	G43	P44	I45	R46	Q47	I48	R49	V50	G51	N52	T53	P54	E55	T56	R57	G58	T59	A60
	ASP													PRO	LYS	ALA	GLN	ALA	LYS	ARG	ALA	ASN	ILE	R12	R13	P14	P15	E16	V17	M18	R19	I20	L21	Y22	I23	R24	M25	L26	P27	Y28	K29	I30	T31	A32	E33	E34	M35	Y36	D37	I38	F39	G40	K41	Y42	G43	P44	I45	R46	Q47	I48	R49	V50
	V61	V62	V63	V64	E65	D66	I67	F68	D69	A70	K71	M72	A73	C74	D75	H76	L77	S78	G79	F80	M81	D82	C83	M84	R85	H86	L87	V88	H89	L90	Y91	Y92	N93	A94	N95	R96	A97	F98	D99	K100	M101	D102	T103	K104	K105	K106	E107	E108	Q109	L110	K111	L112	L113	K114	E115	K116	Y117	G118	I119	A120		

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



G61	G62	G63	G64	G65	G66	G67	G68	G69	G70	G71	G72	G73	G74	G75	G76	G77	G78	G79	G80	G81	G82	G83	G84	G85	G86	G87	G88	G89	G90	G91	G92	G93	G94	G95	THR	ASP	LEU	PHE	TYR	GLU	GLU	ARG	LYS	LYS	TYR	GLY	GLY	PHE	LYS	LYS	ARG							
ALA	LYS	HIS	HIS	PRO	D7	L8	I9	F10	C11	R12	K13	Q14	A15	G16	V17	A18	I19	G20	R21	L22	C23	E24	K25	C26	D27	G28	K29	C30	V31	I32	C33	D34	S35	V36	V37	R38	P39	C40	T41	L42	V43	R44	L45	C46	D47	E48	C49	N50	Y51	G52	S53	Y54	O55	G56	R57	C58	Y59	L60
MET	ALA	LYS	HIS	PRO	D7	L8	I9	F10	C11	R12	K13	Q14	A15	G16	V17	A18	I19	G20	R21	L22	C23	E24	K25	C26	D27	G28	K29	C30	V31	I32	C33	D34	S35	V36	V37	R38	P39	C40	T41	L42	V43	R44	L45	C46	D47	E48	C49	N50	Y51	G52	S53	Y54	O55	G56	R57	C58	Y59	L60

- Molecule 47: Splicing factor 3B subunit 5



K61	K62	K63	K64	K65	F66	F67	L68	M69	E70	K71	M72	L73	Q74	F75	F76	G77	F78	F79	A80	ASP	LYS	PRO	GLU	GLU	ASN	THR	ASP	ARG	TYR	THR	ILE	HIS	GLN	LEU	GLU	HIS	LEU	Q15	S16	K17	Y18	I19	G20	T21	G22	H23	A24	D25	T26	T27	K28	W29	E30	W31	L32	V33	N34	Q35	H36	R37	D38	S39	Y40	Q41	S42	Y43	M44	Q45	H46	F47	D48	L49	L50	N51	Y52	F53	A54	I55	E56	E57	N58	E59	E60
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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	116801	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	3.326	Depositor
Minimum map value	-0.959	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.062	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, IHP, MG, GTP

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	0.69	6/956 (0.6%)	0.75	2/1481 (0.1%)
2	6A	0.30	0/1274	0.48	2/1976 (0.1%)
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	0.22	0/2673	0.55	8/4156 (0.2%)
11	5B	0.13	0/18748	0.31	0/25452
12	5C	0.13	0/6879	0.32	0/9344
13	5D	0.12	0/16393	0.31	0/22174
14	5E	0.26	0/1480	0.67	0/2056
15	2a	0.86	0/339	1.19	2/422 (0.5%)
15	4a	0.30	0/404	0.71	0/561
15	5a	0.87	0/343	1.20	3/427 (0.7%)
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	1.23	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	0/262	1.04	0/324
20	4f	0.34	0/362	0.81	0/501
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	0.71	0/566
21	5g	0.78	0/307	1.01	0/382
22	4A	0.35	1/2963 (0.0%)	0.49	5/4603 (0.1%)
23	4B	0.17	0/948	0.40	0/1312
24	4C	0.13	0/1764	0.36	0/2450
25	4D	0.16	0/1336	0.33	0/1858
26	4E	0.11	0/614	0.29	0/855
27	4F	0.12	0/1198	0.31	0/1620
28	4G	0.29	4/4561 (0.1%)	0.51	11/6271 (0.2%)
29	4R	0.12	0/891	0.34	0/1188
30	4S	0.13	0/512	0.33	0/673
31	4T	0.12	0/3845	0.34	0/5208
32	4U	0.61	0/3422	0.89	5/4659 (0.1%)
33	4X	0.12	0/187	0.34	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	0.37	0/493	0.98	2/611 (0.3%)
39	2E	0.38	0/373	1.77	4/461 (0.9%)
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	1.15	0/355	1.10	0/442
47	2M	1.59	1/263 (0.4%)	1.24	0/327
All	All	0.61	88/98538 (0.1%)	0.73	174/133716 (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
28	4G	0	2
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	37

All (88) 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	9.19	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
28	4G	571	PRO	N-CA	6.99	1.56	1.47
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
43	2I	213	LEU	CA-C	-6.04	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	2G	678	ALA	N-CA	-6.04	1.38	1.46
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
28	4G	570	PHE	N-CA	5.96	1.54	1.46
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
41	2G	893	ILE	N-CA	-5.78	1.39	1.46
43	2I	115	ILE	N-CA	-5.77	1.40	1.46
28	4G	572	SER	N-CA	5.71	1.53	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

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	2G	672	ALA	CA-C	-5.26	1.46	1.52
41	2G	721	ILE	N-CA	-5.26	1.40	1.46
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	-5.06	1.46	1.52
41	2G	899	ALA	N-CA	-5.04	1.40	1.46
28	4G	570	PHE	CA-C	5.01	1.59	1.52

All (174) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	2E	146	MET	CA-C-N	21.08	146.19	119.84
39	2E	146	MET	C-N-CA	21.08	146.19	119.84
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'	-11.65	102.72	120.20
28	4G	571	PRO	N-CA-CB	-11.44	91.24	103.25
10	5A	58	U	P-O3'-C3'	-10.61	104.29	120.20
28	4G	569	VAL	O-C-N	-10.50	109.44	122.57
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
10	5A	57	G	P-O3'-C3'	-9.40	106.11	120.20
28	4G	572	SER	CA-C-O	-8.79	107.94	120.51
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

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
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
28	4G	571	PRO	N-CA-C	8.24	129.45	112.47
28	4G	707	ASP	CA-C-N	8.20	136.46	121.70
28	4G	707	ASP	C-N-CA	8.20	136.46	121.70
36	2B	16	THR	CA-C-O	-8.03	111.77	120.36
10	5A	80	U	P-O3'-C3'	-8.03	108.16	120.20
22	4A	56	U	P-O3'-C3'	-8.03	108.16	120.20
36	2B	99	SER	N-CA-C	8.03	122.85	112.26
22	4A	55	U	P-O3'-C3'	-7.96	108.27	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
35	2A	167	U	O3'-P-O5'	-7.30	93.05	104.00
28	4G	570	PHE	CA-C-N	7.22	128.86	119.84
28	4G	570	PHE	C-N-CA	7.22	128.86	119.84
41	2G	1100	ASN	N-CA-C	7.17	119.23	110.41
10	5A	78	U	C3'-C2'-C1'	-7.17	94.13	101.30
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
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

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	2B	87	LEU	C-N-CA	6.43	126.19	119.05
41	2G	406	ALA	O-C-N	6.42	130.57	122.23
35	2A	168	A	C5'-C4'-C3'	-6.34	106.50	116.00
10	5A	56	C	P-O3'-C3'	-6.30	110.75	120.20
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
41	2G	1180	ARG	N-CA-C	-6.16	103.28	111.96
28	4G	571	PRO	CB-CA-C	-6.15	101.41	111.56
36	2B	73	ASN	N-CA-C	6.15	119.84	111.17
22	4A	87	C	P-O3'-C3'	-6.11	111.03	120.20
42	2H	559	PRO	N-CA-C	6.10	120.05	111.33
28	4G	570	PHE	N-CA-C	6.08	123.26	109.81
41	2G	1275	GLY	N-CA-C	-6.08	104.94	111.93
10	5A	77	G	P-O3'-C3'	-6.04	111.13	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
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
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
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
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
32	4U	634	LYS	CA-C-N	5.71	125.83	119.32
32	4U	634	LYS	C-N-CA	5.71	125.83	119.32
28	4G	136	PRO	N-CA-CB	-5.69	97.27	103.25
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
32	4U	399	PRO	O-C-N	5.60	123.89	121.31
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
35	2A	168	A	O4'-C1'-C2'	-5.54	102.06	107.60
15	5a	52	LYS	CA-C-N	-5.54	114.22	119.76
15	5a	52	LYS	C-N-CA	-5.54	114.22	119.76
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
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
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
2	6A	58	G	P-O3'-C3'	-5.33	112.20	120.20
39	2E	199	TRP	N-CA-C	5.33	117.32	107.73
15	5a	5	LYS	N-CA-C	5.32	117.99	111.82
32	4U	461	ARG	N-CA-C	-5.31	106.75	113.18
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
2	6A	56	A	P-O3'-C3'	-5.25	112.33	120.20
32	4U	381	THR	N-CA-C	5.25	117.45	108.90
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

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	2C	20	LYS	N-CA-C	5.20	117.35	111.11
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	5.16	116.92	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	5e	85	THR	N-CA-C	-5.10	105.90	112.68
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
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
19	4e	53	TYR	CA-C-N	5.07	129.75	122.40
19	4e	53	TYR	C-N-CA	5.07	129.75	122.40
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
10	5A	78	U	C4'-C3'-C2'	-5.01	97.58	102.60
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 (37) 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

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Mol	Chain	Res	Type	Group
41	2G	941	ASN	Peptide
41	2G	944	SER	Peptide
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
28	4G	569	VAL	Mainchain
28	4G	572	SER	Mainchain
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 [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	864	0	443	142	0
2	6A	1142	0	575	39	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	98	0
11	5B	18244	0	18075	266	0
12	5C	6727	0	6735	93	0
13	5D	16077	0	16192	305	0
14	5E	1481	0	675	2	0
15	2a	340	0	90	4	0
15	4a	405	0	170	4	0
15	5a	344	0	93	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	6	0
18	2d	296	0	87	0	0
18	4d	351	0	155	4	0
18	5d	292	0	86	9	0
19	2e	316	0	85	1	0
19	4e	376	0	157	6	0
19	5e	316	0	85	4	0
20	2f	264	0	73	1	0
20	4f	363	0	160	3	0
20	5f	296	0	84	4	0
21	2g	320	0	88	0	0
21	4g	409	0	180	4	0
21	5g	308	0	86	5	0
22	4A	2656	0	1349	50	0
23	4B	953	0	411	17	0
24	4C	1765	0	801	7	0
25	4D	1340	0	616	5	0
26	4E	615	0	279	4	0
27	4F	1169	0	1141	42	0
28	4G	4539	0	3081	49	0
29	4R	874	0	883	23	0
30	4S	505	0	530	16	0
31	4T	3749	0	3767	46	0
32	4U	3414	0	2245	16	0
33	4X	184	0	192	8	0
34	4Y	1595	0	694	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	2A	2311	0	1170	143	0
36	2B	648	0	167	0	0
37	2C	376	0	102	0	0
38	2D	496	0	118	2	0
39	2E	376	0	85	0	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	2	0
49	5C	1	0	0	0	0
50	5C	32	0	12	0	0
51	4T	1	0	0	0	0
All	All	96473	0	67892	1662	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 10.

All (1662) 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)
23:4B:466:LEU:CA	29:4R:432:PRO:HG3	1.12	1.54
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	1.45
1:A:30:C:C2'	1:A:31:C:H5''	1.54	1.38
23:4B:466:LEU:CA	29:4R:432:PRO:CG	2.08	1.28
2:6A:76:A:N1	23:4B:562:ALA:CB	2.03	1.20
1:A:30:C:N4	1:A:31:C:C4	2.10	1.20
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	1.09
1:A:38:C:H4'	1:A:39:U:OP1	1.42	1.06
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)
10:5A:90:U:C5	21:5g:38:ASN:O	2.09	1.05
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	1.00
10:5A:95:G:H1'	18:5d:24:LYS:CA	1.91	1.00
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
1:A:30:C:C3'	1:A:31:C:C5'	2.40	0.98
35:2A:168:A:C8	35:2A:168:A:H5''	1.98	0.98
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
10:5A:59:G:H5''	10:5A:59:G:H8	1.31	0.96
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
23:4B:466:LEU:N	29:4R:432:PRO:HG3	1.81	0.95
10:5A:93:U:H1'	17:5c:104:ASP:CA	1.96	0.94
35:2A:156:U:H5''	35:2A:156:U:C6	2.02	0.94
1:A:31:C:O2	35:2A:33:G:C6	2.20	0.94
23:4B:465:ARG:O	29:4R:381:PHE:CD1	2.22	0.92
41:2G:86:ALA:O	41:2G:89:ALA:N	2.02	0.92
1:A:40:U:O2'	1:A:41:U:OP2	1.89	0.91
10:5A:95:G:H21	10:5A:96:A:H5''	1.36	0.90
25:4D:165:MET:CB	31:4T:540:GLN:HE22	1.85	0.90
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
10:5A:90:U:H5	21:5g:38:ASN:O	1.53	0.89
2:6A:76:A:C6	23:4B:562:ALA:HB3	2.07	0.89
35:2A:168:A:H5''	35:2A:168:A:H8	1.36	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
10:5A:93:U:O4	18:5d:66:CYS:N	2.06	0.88
10:5A:93:U:C1'	17:5c:104:ASP:CA	2.52	0.87
35:2A:154:C:O2	35:2A:176:G:N2	2.07	0.87
13:5D:1948:MET:SD	13:5D:1955:SER:OG	2.33	0.86
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:OP2	1:A:12:U:H2'	1.74	0.86
13:5D:537:LYS:NZ	13:5D:583:THR:O	2.09	0.85
35:2A:156:U:H6	35:2A:156:U:C5'	1.89	0.85
35:2A:40:C:H5''	35:2A:40:C:H6	1.39	0.85
1:A:11:C:H2'	1:A:11:C:O2	1.75	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:1388:GLN:NE2	13:5D:1655:ASN:OD1	2.10	0.84
22:4A:61:A:OP1	30:4S:749:LYS:NZ	2.10	0.84
11:5B:1589:ILE:HD11	11:5B:1733:ILE:HG21	1.59	0.84
11:5B:1271:MET:HE1	11:5B:1278:VAL:HG11	1.60	0.83
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
10:5A:59:G:H5''	10:5A:59:G:C8	2.13	0.83
1:A:36:C:H4'	1:A:37:C:H5	1.44	0.82
22:4A:68:A:O2'	22:4A:69:C:OP1	1.96	0.82
46:2L:56:GLY:O	46:2L:65:GLY:N	2.12	0.82
11:5B:1607:GLU:OE2	11:5B:1608:THR:OG1	1.97	0.82
13:5D:713:MET:HE3	13:5D:713:MET:HA	1.59	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
27:4F:87:ASN:OD1	28:4G:23:ARG:NH1	2.13	0.82
35:2A:105:G:C2'	35:2A:106:G:H5''	2.10	0.82
35:2A:152:G:H5''	35:2A:153:A:OP2	1.80	0.81
1:A:23:G:N2	35:2A:39:U:O2	2.14	0.81
23:4B:462:GLU:O	29:4R:432:PRO:HB2	1.79	0.81
31:4T:420:ALA:O	31:4T:423:ASN:ND2	2.13	0.81
41:2G:648:LEU:O	41:2G:651:VAL:N	2.13	0.81
1:A:28:G:H5'	1:A:28:G:H8	1.45	0.81
12:5C:137:HIS:O	12:5C:142:LYS:NZ	2.14	0.80
13:5D:1499:ASP:OD2	13:5D:1763:ARG:NH1	2.15	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
13:5D:1654:MET:SD	13:5D:1656:VAL:HG12	2.22	0.80
11:5B:110:TRP:O	11:5B:192:GLN:NE2	2.14	0.80
10:5A:92:U:H3	16:5b:36:MET:CA	1.93	0.80
11:5B:152:ARG:NH2	11:5B:618:THR:O	2.14	0.80
13:5D:769:CYS:O	13:5D:775:LYS:NZ	2.15	0.80
13:5D:1060:ASN:OD1	13:5D:1064:GLN:NE2	2.16	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
1:A:20:U:O2	35:2A:42:G:C2	2.35	0.79
11:5B:1434:LYS:O	11:5B:1439:ARG:NH2	2.16	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2G:669:GLN:O	41:2G:672:ALA:N	2.16	0.78
11:5B:2119:ASP:OD1	11:5B:2120:LEU:N	2.17	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
10:5A:94:U:H1'	10:5A:95:G:OP1	1.82	0.78
11:5B:292:ASP:OD2	11:5B:1130:ASN:ND2	2.16	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
11:5B:1321:GLU:OE2	11:5B:1471:ARG:NH2	2.17	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
13:5D:611:LEU:HD21	13:5D:613:ILE:HD11	1.65	0.77
22:4A:56:U:H2'	22:4A:57:G:C8	2.19	0.77
35:2A:153:A:H2'	35:2A:154:C:H5'	1.65	0.77
13:5D:1753:ASP:O	13:5D:1756:THR:OG1	2.01	0.77
41:2G:531:LEU:O	41:2G:534:GLN:N	2.18	0.77
1:A:31:C:H1'	35:2A:33:G:C2	2.20	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
13:5D:1538:ARG:NH1	13:5D:1665:ASP:OD1	2.19	0.76
13:5D:146:GLU:OE2	13:5D:149:ARG:NH2	2.18	0.76
11:5B:804:GLU:N	11:5B:804:GLU:OE1	2.17	0.76
13:5D:946:ASP:OD2	13:5D:951:GLN:N	2.19	0.76
15:4a:28:ILE:O	15:4a:45:CYS:HA	1.86	0.76
1:A:8:U:O2	1:A:8:U:H2'	1.84	0.76
11:5B:1783:THR:O	13:5D:202:ASN:ND2	2.20	0.75
11:5B:1914:MET:HE3	11:5B:1914:MET:N	2.00	0.75
28:4G:136:PRO:HB2	28:4G:140:GLN:CD	2.11	0.75
11:5B:1251:SER:O	11:5B:1254:THR:OG1	2.04	0.75
13:5D:1693:ARG:NH1	13:5D:1696:GLN:OE1	2.19	0.75
22:4A:114:U:H4'	22:4A:115:G:OP1	1.87	0.75
19:4e:64:ILE:HA	19:4e:70:SER:O	1.86	0.75
13:5D:619:LEU:HD22	13:5D:628:LEU:HD23	1.68	0.75
35:2A:143:A:H3'	35:2A:143:A:N3	2.01	0.75
31:4T:456:ARG:NH1	31:4T:469:THR:O	2.18	0.75
1:A:34:G:H2'	1:A:35:U:H6	1.52	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:5C:261:ASP:OD2	12:5C:311:SER:OG	2.05	0.75
13:5D:1678:ASP:OD1	13:5D:1679:TYR:N	2.20	0.75
1:A:34:G:H3'	1:A:35:U:H5''	1.67	0.74
10:5A:93:U:O4	18:5d:65:ARG:CA	2.35	0.74
10:5A:44:A:O2'	10:5A:46:U:OP2	2.05	0.74
41:2G:1016:LEU:O	41:2G:1019:ARG:N	2.19	0.74
11:5B:606:LYS:NZ	48:5B:2401:IHP:O41	2.19	0.74
13:5D:660:ASP:OD1	13:5D:931:ARG:NH1	2.21	0.74
41:2G:874:LYS:O	41:2G:877:GLY:N	2.20	0.74
12:5C:853:ARG:NH1	12:5C:879:ASP:O	2.21	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
13:5D:610:ARG:NH2	13:5D:645:ASP:O	2.21	0.74
11:5B:1304:ASN:OD1	11:5B:1305:SER:N	2.20	0.74
13:5D:1856:GLU:N	13:5D:1856:GLU:OE1	2.21	0.74
13:5D:1321:TYR:OH	13:5D:1361:GLU:OE1	2.04	0.74
2:6A:49:G:H2'	22:4A:68:A:N7	2.03	0.73
11:5B:2219:THR:OG1	11:5B:2222:SER:OG	2.05	0.73
43:2I:753:GLY:HA3	43:2I:765:LEU:O	1.88	0.73
10:5A:117:A:N1	18:5d:26:GLY:HA3	2.03	0.73
13:5D:297:SER:N	13:5D:301:GLU:OE2	2.21	0.73
1:A:31:C:O2	35:2A:33:G:C5	2.41	0.73
1:A:30:C:C4	1:A:31:C:C6	2.76	0.73
20:4f:42:ILE:O	20:4f:59:MET:HA	1.89	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
13:5D:1633:GLU:OE2	13:5D:1655:ASN:N	2.21	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
11:5B:1660:TYR:OH	11:5B:1717:ASN:O	2.05	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
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
31:4T:208:GLN:NE2	31:4T:210:LYS:O	2.22	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:19:U:H3	35:2A:42:G:H1	1.37	0.72
27:4F:28:ILE:HD11	27:4F:61:VAL:HG23	1.71	0.72
10:5A:47:A:O2'	10:5A:48:A:O5'	2.07	0.72
11:5B:476:PHE:O	11:5B:479:THR:OG1	2.06	0.72
35:2A:153:A:H2'	35:2A:154:C:C5'	2.19	0.72
11:5B:1637:TRP:O	11:5B:1656:THR:OG1	2.02	0.72
1:A:15:A:H2'	1:A:16:A:O4'	1.89	0.72
28:4G:136:PRO:HB2	28:4G:140:GLN:OE1	1.91	0.71
10:5A:92:U:N3	16:5b:36:MET:CA	2.53	0.71
1:A:21:U:H1'	1:A:22:C:OP1	1.90	0.71
27:4F:74:GLU:O	27:4F:101:LYS:NZ	2.23	0.71
1:A:38:C:OP1	1:A:39:U:OP2	2.09	0.71
13:5D:1741:VAL:O	13:5D:1743:LYS:NZ	2.22	0.71
41:2G:791:VAL:O	41:2G:794:GLN:N	2.23	0.71
11:5B:1338:SER:O	11:5B:1341:ARG:NH1	2.24	0.71
11:5B:1764:SER:OG	11:5B:1767:ASN:OD1	2.08	0.71
13:5D:1446:GLN:O	13:5D:1483:ARG:NH2	2.24	0.71
11:5B:579:GLN:NE2	11:5B:627:CYS:O	2.22	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
13:5D:1028:THR:O	13:5D:1058:LYS:NZ	2.24	0.71
43:2I:558:LEU:O	43:2I:561:GLY:N	2.24	0.70
10:5A:96:A:H4'	10:5A:97:G:H5''	1.72	0.70
11:5B:1661:TRP:NE1	11:5B:1697:SER:O	2.24	0.70
13:5D:1887:PRO:O	13:5D:1891:THR:HG23	1.91	0.70
13:5D:1903:GLN:N	13:5D:1903:GLN:OE1	2.24	0.70
46:2L:7:ASP:O	46:2L:91:LEU:N	2.25	0.70
11:5B:2199:ILE:O	11:5B:2203:ASN:ND2	2.24	0.70
2:6A:86:U:H3	35:2A:12:G:H1	1.39	0.70
41:2G:700:LYS:O	41:2G:703:THR:N	2.24	0.70
13:5D:1588:ARG:O	13:5D:1588:ARG:NH1	2.24	0.70
22:4A:56:U:H2'	22:4A:57:G:H8	1.55	0.70
10:5A:94:U:C1'	10:5A:95:G:OP1	2.39	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
10:5A:87:A:N6	10:5A:92:U:P	2.64	0.69
12:5C:192:ASP:OD1	12:5C:193:THR:N	2.24	0.69
11:5B:2187:GLN:N	11:5B:2187:GLN:OE1	2.24	0.69
35:2A:54:U:OP1	40:2F:427:ALA:O	2.10	0.69
12:5C:517:GLU:OE1	12:5C:517:GLU:N	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2A:40:C:H6	35:2A:40:C:C5'	2.05	0.69
12:5C:698:GLU:N	12:5C:698:GLU:OE1	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
11:5B:982:GLU:OE2	11:5B:1172:ASN:ND2	2.26	0.69
13:5D:1777:SER:OG	13:5D:1780:HIS:ND1	2.26	0.69
1:A:22:C:HO2'	1:A:23:G:H5'	1.54	0.69
10:5A:87:A:N6	10:5A:92:U:OP2	2.26	0.69
10:5A:93:U:O4	18:5d:65:ARG:C	2.36	0.69
10:5A:96:A:H61	20:5f:23:GLY:H	1.38	0.69
1:A:31:C:H5'	1:A:31:C:H6	1.58	0.69
42:2H:596:GLU:C	42:2H:598:GLU:H	2.00	0.69
13:5D:1561:VAL:HG22	13:5D:1662:ILE:HB	1.73	0.68
11:5B:1076:ASP:OD1	11:5B:1077:ILE:N	2.26	0.68
35:2A:30:A:N3	35:2A:30:A:H2'	2.06	0.68
2:6A:47:A:N6	22:4A:64:G:H21	1.90	0.68
10:5A:97:G:H1	10:5A:116:U:H3	1.41	0.68
11:5B:156:ARG:NH2	32:4U:354:ASP:OD2	2.27	0.68
13:5D:644:GLU:OE1	13:5D:644:GLU:N	2.27	0.68
28:4G:572:SER:O	28:4G:573:LYS:O	2.10	0.68
11:5B:1283:GLU:N	11:5B:1283:GLU:OE1	2.27	0.68
11:5B:1607:GLU:N	11:5B:1632:PHE:O	2.26	0.68
28:4G:133:MET:HE2	31:4T:433:TYR:HB3	1.74	0.68
13:5D:973:ASP:OD2	13:5D:976:THR:OG1	2.12	0.68
27:4F:15:ASP:OD1	27:4F:16:GLN:N	2.28	0.67
35:2A:151:C:H2'	35:2A:152:G:H8	1.60	0.67
28:4G:513:CYS:O	28:4G:517:GLY:N	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:798:GLN:O	12:5C:803:ARG:NH2	2.28	0.67
13:5D:816:ALA:O	13:5D:855:ARG:NH2	2.28	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
10:5A:93:U:O4'	17:5c:104:ASP:CA	2.42	0.67
28:4G:301:VAL:O	28:4G:305:ASN:ND2	2.28	0.67
27:4F:53:LYS:O	27:4F:53:LYS:NZ	2.23	0.67
22:4A:114:U:H6	22:4A:114:U:P	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
35:2A:153:A:C3'	35:2A:154:C:H5'	2.25	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:C:N4	1:A:31:C:C5	2.50	0.67
12:5C:779:LEU:O	12:5C:938:ARG:NH1	2.27	0.66
12:5C:116:MET:SD	12:5C:116:MET:N	2.67	0.66
13:5D:89:LEU:HD22	28:4G:363:ALA:CB	2.26	0.66
1:A:30:C:H41	1:A:31:C:N4	1.91	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
32:4U:282:THR:HG22	32:4U:283:SER:H	1.60	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
35:2A:151:C:C2	35:2A:152:G:C8	2.83	0.66
13:5D:630:ALA:HB2	13:5D:900:MET:SD	2.36	0.66
35:2A:54:U:OP1	40:2F:427:ALA:C	2.39	0.66
11:5B:1985:ASP:OD1	11:5B:1986:LEU:N	2.28	0.66
41:2G:400:SER:O	41:2G:404:LEU:N	2.28	0.66
23:4B:465:ARG:O	29:4R:381:PHE:CE1	2.48	0.66
1:A:8:U:O2	1:A:8:U:C2'	2.44	0.65
11:5B:2009:ASP:OD1	11:5B:2010:ILE:N	2.29	0.65
12:5C:573:GLU:OE2	12:5C:573:GLU:N	2.27	0.65
13:5D:660:ASP:OD2	13:5D:928:ARG:NH1	2.28	0.65
1:A:36:C:C4'	1:A:37:C:C5	2.79	0.65
43:2I:550:ASN:N	43:2I:553:GLN:O	2.27	0.65
11:5B:1331:GLY:O	11:5B:1367:ASN:ND2	2.28	0.65
22:4A:109:G:H2'	22:4A:110:G:C8	2.30	0.65
1:A:32:C:OP2	1:A:32:C:H3'	1.96	0.65
13:5D:1788:LEU:HD12	13:5D:1789:VAL:N	2.12	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:385:GLU:N	11:5B:385:GLU:OE1	2.30	0.65
13:5D:801:PHE:CG	13:5D:809:LEU:HD11	2.31	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
10:5A:89:U:H2'	10:5A:90:U:H5''	1.79	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
12:5C:207:GLY:O	12:5C:238:ASN:ND2	2.30	0.65
12:5C:256:CYS:SG	12:5C:310:SER:OG	2.53	0.65
13:5D:1566:ARG:O	13:5D:1569:THR:HG22	1.96	0.65
35:2A:114:A:H61	35:2A:142:C:H42	1.44	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:2204:PRO:O	32:4U:195:ARG:NH1	2.30	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
11:5B:422:LEU:O	11:5B:635:ARG:NE	2.29	0.65
11:5B:705:LYS:NZ	28:4G:160:ILE:O	2.28	0.65
11:5B:1604:LEU:HD11	11:5B:1725:LEU:HD22	1.78	0.65
41:2G:658:TRP:O	41:2G:661:ARG:N	2.30	0.65
12:5C:212:SER:O	12:5C:216:THR:HG23	1.97	0.64
41:2G:1018:PRO:O	41:2G:1021:THR:N	2.30	0.64
32:4U:357:TRP:CB	32:4U:369:ASP:CB	2.75	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
41:2G:886:HIS:O	41:2G:889:GLU:N	2.30	0.64
13:5D:417:THR:OG1	13:5D:418:GLN:OE1	2.15	0.64
13:5D:1507:SER:O	13:5D:1511:THR:HG23	1.97	0.64
2:6A:76:A:C2	23:4B:562:ALA:CB	2.64	0.64
29:4R:403:ARG:NH2	29:4R:441:GLU:OE2	2.31	0.64
1:A:35:U:OP1	46:2L:63:GLY:HA3	1.98	0.64
10:5A:95:G:H21	10:5A:96:A:C5'	2.06	0.64
13:5D:1201:GLU:N	13:5D:1201:GLU:OE1	2.31	0.64
28:4G:493:SER:O	28:4G:497:ASN:N	2.31	0.64
13:5D:429:GLN:N	13:5D:886:GLN:OE1	2.29	0.64
13:5D:607:GLN:OE1	13:5D:607:GLN:N	2.31	0.64
1:A:35:U:H4'	1:A:36:C:OP2	1.98	0.63
13:5D:568:GLU:OE2	13:5D:570:THR:OG1	2.16	0.63
13:5D:963:MET:HE3	13:5D:963:MET:HA	1.80	0.63
13:5D:1378:TYR:OH	13:5D:1454:ASP:OD2	2.16	0.63
13:5D:1539:LEU:HD21	13:5D:1568:GLN:HG3	1.80	0.63
10:5A:77:G:C8	10:5A:78:U:C5	2.87	0.63
10:5A:85:C:OP1	17:5c:20:GLU:CA	2.46	0.63
13:5D:1481:ILE:HG22	13:5D:1481:ILE:O	1.98	0.63
35:2A:164:C:H6	35:2A:164:C:H5'	1.63	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
12:5C:678:THR:OG1	12:5C:682:LYS:O	2.14	0.63
13:5D:89:LEU:HD22	28:4G:363:ALA:HB1	1.81	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
35:2A:152:G:C2	35:2A:153:A:C5	2.87	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:C:C2'	1:A:23:G:H5'	2.28	0.63
12:5C:426:GLU:N	12:5C:426:GLU:OE1	2.32	0.63
28:4G:572:SER:C	28:4G:573:LYS:O	2.42	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
1:A:31:C:N3	35:2A:33:G:C6	2.65	0.63
10:5A:88:A:H2'	10:5A:88:A:N3	2.14	0.63
31:4T:511:GLU:OE1	31:4T:511:GLU:O	2.17	0.63
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
10:5A:90:U:H5	21:5g:38:ASN:C	2.06	0.62
13:5D:1986:MET:HE3	13:5D:2011:CYS:SG	2.39	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
11:5B:2329:ASP:OD1	13:5D:728:ARG:NH2	2.32	0.62
11:5B:1405:LEU:HD23	11:5B:1405:LEU:O	2.00	0.62
12:5C:133:THR:OG1	12:5C:222:SER:OG	1.98	0.62
41:2G:1264:VAL:O	41:2G:1267:LYS:N	2.32	0.62
1:A:31:C:H2'	1:A:32:C:H6	1.65	0.62
10:5A:81:U:H2'	10:5A:81:U:O2	1.98	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
11:5B:1914:MET:HE3	11:5B:1914:MET:H	1.62	0.62
31:4T:362:HIS:O	31:4T:370:LYS:NZ	2.33	0.62
11:5B:1595:GLN:O	11:5B:1595:GLN:NE2	2.33	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
10:5A:80:U:H6	10:5A:80:U:H5'	1.65	0.61
11:5B:1248:LEU:O	11:5B:1251:SER:OG	2.12	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
12:5C:572:GLU:N	12:5C:572:GLU:OE1	2.33	0.61
41:2G:88:VAL:CA	41:2G:92:ASN:H	2.13	0.61
13:5D:429:GLN:O	13:5D:886:GLN:NE2	2.32	0.61
27:4F:4:MET:SD	27:4F:4:MET:N	2.66	0.61
1:A:40:U:H5''	1:A:41:U:H5''	1.82	0.61
13:5D:1222:TRP:NE1	13:5D:1273:ASP:OD2	2.32	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
12:5C:688:ILE:HD13	12:5C:792:LEU:HD22	1.82	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
11:5B:682:ASP:OD1	11:5B:683:LEU:N	2.34	0.61
11:5B:1237:MET:CE	11:5B:1281:THR:HG21	2.30	0.61
29:4R:374:LEU:H	29:4R:374:LEU:HD23	1.65	0.61
41:2G:784:MET:O	41:2G:787:ILE:N	2.33	0.61
11:5B:2295:GLU:N	11:5B:2295:GLU:OE1	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
10:5A:19:A:N3	10:5A:21:A:N6	2.49	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
13:5D:63:MET:O	13:5D:63:MET:HG3	2.00	0.61
41:2G:929:LEU:O	41:2G:932:ILE:N	2.34	0.61
11:5B:1406:GLU:OE1	13:5D:71:ARG:NH2	2.33	0.60
13:5D:206:GLU:N	13:5D:206:GLU:OE1	2.34	0.60
10:5A:95:G:N3	10:5A:95:G:H2'	2.15	0.60
41:2G:610:ILE:O	41:2G:613:MET:N	2.34	0.60
2:6A:48:A:C5	29:4R:450:ARG:HG2	2.35	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
29:4R:383:ILE:HD12	29:4R:455:ARG:O	2.01	0.60
32:4U:282:THR:O	32:4U:283:SER:OG	2.13	0.60
2:6A:103:U:C3'	2:6A:104:U:H5''	2.31	0.60
1:A:10:C:O2'	1:A:11:C:OP2	2.16	0.60
43:2I:638:GLU:N	43:2I:668:GLY:O	2.32	0.60
1:A:13:U:O5'	1:A:13:U:H6	1.84	0.60
13:5D:1345:ASN:OD1	13:5D:1487:ILE:N	2.32	0.60
13:5D:1945:LEU:O	13:5D:1949:VAL:HG13	2.02	0.60
28:4G:333:MET:HE3	28:4G:333:MET:O	2.01	0.60
43:2I:563:LEU:N	43:2I:581:LYS:O	2.27	0.60
11:5B:950:LEU:HD23	11:5B:950:LEU:O	2.02	0.59
13:5D:1143:ILE:HD13	13:5D:1165:ILE:HD13	1.83	0.59
13:5D:1699:GLU:N	13:5D:1699:GLU:OE1	2.35	0.59
41:2G:173:ALA:C	41:2G:176:ALA:H	2.09	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:6A:47:A:H2'	2:6A:49:G:N3	2.17	0.59
12:5C:474:LEU:HD21	12:5C:501:ILE:HD13	1.84	0.59
41:2G:1125:PRO:O	41:2G:1128:VAL:N	2.35	0.59
10:5A:87:A:N6	10:5A:91:U:O3'	2.36	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
13:5D:1693:ARG:NH2	13:5D:1697:ASP:OD1	2.35	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
11:5B:357:ASN:ND2	12:5C:866:SER:O	2.36	0.59
13:5D:89:LEU:HD21	13:5D:96:GLU:OE1	2.02	0.59
22:4A:68:A:OP1	30:4S:742:LYS:NZ	2.35	0.59
11:5B:1868:MET:HE3	11:5B:1872:LEU:HD21	1.85	0.59
13:5D:1212:GLU:N	13:5D:1212:GLU:OE1	2.34	0.59
13:5D:1433:ASP:OD1	13:5D:1473:ARG:NH2	2.33	0.59
41:2G:1182:LEU:O	41:2G:1185:ARG:N	2.35	0.59
10:5A:18:C:OP2	11:5B:468:LYS:NZ	2.35	0.59
31:4T:146:ARG:O	31:4T:150:SER:OG	2.21	0.59
11:5B:1963:GLU:OE1	11:5B:1966:HIS:ND1	2.36	0.59
13:5D:1864:GLU:OE2	13:5D:1867:LEU:HD21	2.03	0.59
13:5D:1957:ASP:OD1	13:5D:1958:SER:N	2.37	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
10:5A:95:G:O2'	18:5d:24:LYS:C	2.46	0.58
11:5B:2206:TRP:O	32:4U:195:ARG:NH1	2.36	0.58
13:5D:1277:SER:O	13:5D:1277:SER:OG	2.20	0.58
13:5D:1373:GLU:N	13:5D:1373:GLU:OE1	2.36	0.58
18:4d:20:MET:HA	18:4d:29:TYR:O	2.02	0.58
11:5B:211:GLN:OE1	11:5B:214:ARG:NE	2.25	0.58
11:5B:2188:LEU:O	11:5B:2251:TYR:OH	2.14	0.58
13:5D:1142:LYS:HB3	13:5D:1165:ILE:HD11	1.86	0.58
41:2G:745:ALA:O	41:2G:748:LYS:N	2.36	0.58
10:5A:96:A:N6	20:5f:23:GLY:H	2.02	0.58
27:4F:41:MET:O	27:4F:45:LEU:HD23	2.03	0.58
31:4T:107:TYR:O	31:4T:110:THR:HG22	2.04	0.58
32:4U:581:GLU:C	32:4U:583:GLU:H	2.10	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
11:5B:1406:GLU:OE2	13:5D:64:GLN:NE2	2.36	0.58
12:5C:156:GLU:OE2	12:5C:156:GLU:N	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:1651:CYS:O	13:5D:1690:HIS:NE2	2.32	0.58
47:2M:48:ASP:O	47:2M:51:ASN:N	2.37	0.58
10:5A:95:G:N2	10:5A:96:A:H5''	2.13	0.58
13:5D:612:ILE:C	13:5D:613:ILE:HD13	2.29	0.58
18:4d:33:LEU:HA	18:4d:44:LEU:HA	1.86	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
11:5B:1941:ARG:NE	11:5B:2011:ILE:O	2.35	0.58
11:5B:1972:THR:OG1	11:5B:1975:GLU:OE1	2.22	0.58
13:5D:1329:ASN:ND2	13:5D:1354:SER:O	2.37	0.58
13:5D:1936:LEU:HD11	13:5D:1940:LEU:HD11	1.86	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:1076:ASP:OD1	11:5B:1078:ALA:N	2.34	0.58
41:2G:1149:LYS:O	41:2G:1152:SER:N	2.36	0.58
11:5B:1890:GLN:OE1	11:5B:1890:GLN:N	2.37	0.57
13:5D:493:LEU:O	13:5D:519:ARG:NH1	2.37	0.57
13:5D:1732:MET:HE3	13:5D:1755:LEU:HD11	1.85	0.57
35:2A:154:C:O2'	35:2A:155:C:H5'	2.04	0.57
22:4A:37:C:H1'	22:4A:38:U:H2'	1.85	0.57
41:2G:929:LEU:O	41:2G:930:PRO:C	2.46	0.57
13:5D:1518:VAL:HG12	13:5D:1518:VAL:O	2.03	0.57
28:4G:97:ASP:OD1	28:4G:98:ASP:N	2.37	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
13:5D:657:ASN:ND2	13:5D:890:GLU:OE2	2.38	0.57
13:5D:1248:ASP:OD1	13:5D:1248:ASP:N	2.36	0.57
13:5D:1620:LEU:HD21	13:5D:1632:VAL:HB	1.86	0.57
41:2G:424:ILE:O	41:2G:428:ALA:N	2.36	0.57
13:5D:527:MET:HE3	13:5D:527:MET:H	1.70	0.57
12:5C:112:THR:OG1	12:5C:114:TYR:O	2.22	0.57
13:5D:538:ILE:HG23	13:5D:611:LEU:HD23	1.86	0.57
13:5D:1985:ILE:HD11	13:5D:1996:LEU:HD22	1.87	0.57
35:2A:152:G:N2	35:2A:153:A:C5	2.73	0.57
11:5B:1237:MET:HE2	11:5B:1281:THR:HG21	1.86	0.57
13:5D:1157:ASN:OD1	13:5D:1159:ASN:N	2.38	0.57
13:5D:1801:CYS:SG	13:5D:1829:ILE:HD11	2.44	0.57
11:5B:377:GLU:OE1	11:5B:377:GLU:N	2.36	0.57
11:5B:1289:VAL:HG11	13:5D:42:SER:HA	1.86	0.57
11:5B:1602:ASP:OD1	11:5B:1603:ALA:N	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:5C:922:GLU:O	12:5C:924:GLN:NE2	2.37	0.57
22:4A:31:U:O4	26:4E:60:ALA:CA	2.53	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
10:5A:80:U:H5'	10:5A:80:U:C6	2.40	0.57
10:5A:81:U:O2	10:5A:81:U:C2'	2.53	0.57
11:5B:950:LEU:HD23	11:5B:950:LEU:C	2.30	0.57
12:5C:822:MET:HE3	12:5C:822:MET:HA	1.87	0.57
13:5D:2098:ALA:O	13:5D:2099:THR:HG22	2.05	0.57
1:A:34:G:C2'	1:A:35:U:C6	2.88	0.56
11:5B:711:GLN:HB3	28:4G:163:VAL:HG11	1.87	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
11:5B:733:THR:HG23	11:5B:734:PRO:HD3	1.87	0.56
11:5B:2189:SER:OG	11:5B:2191:GLN:OE1	2.23	0.56
13:5D:1901:ARG:NH2	13:5D:1952:ALA:O	2.38	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
11:5B:710:LEU:HD12	11:5B:710:LEU:O	2.05	0.56
12:5C:753:GLU:N	12:5C:753:GLU:OE1	2.36	0.56
13:5D:835:SER:O	13:5D:839:GLY:N	2.38	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
11:5B:60:ASP:OD1	11:5B:61:MET:N	2.39	0.56
11:5B:1776:ILE:HG23	11:5B:1858:PRO:HA	1.87	0.56
1:A:36:C:C5'	1:A:37:C:H5	2.17	0.56
10:5A:78:U:H6	10:5A:78:U:O5'	1.89	0.56
1:A:36:C:O2'	1:A:37:C:OP1	2.24	0.56
13:5D:1307:LEU:HB2	13:5D:1333:THR:HG22	1.88	0.56
28:4G:358:ALA:O	28:4G:362:VAL:HG23	2.06	0.56
33:4X:143:ARG:NH2	33:4X:146:GLY:O	2.39	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:1013:GLU:OE1	13:5D:1016:ARG:NH2	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:4U:328:ARG:NE	32:4U:332:GLU:OE1	2.39	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
2:6A:56:A:H2'	2:6A:57:U:O4'	2.06	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:766:THR:O	27:4F:141:ARG:NH2	2.39	0.56
11:5B:1511:GLU:O	11:5B:1512:SER:OG	2.16	0.56
11:5B:1872:LEU:O	11:5B:1876:LEU:HD12	2.05	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
13:5D:637:ARG:HG2	13:5D:641:MET:HE1	1.88	0.56
13:5D:933:PRO:HG3	13:5D:943:LEU:HD12	1.88	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
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:58:U:C6	10:5A:58:U:H5''	2.40	0.55
10:5A:110:C:H2'	10:5A:111:A:C8	2.41	0.55
12:5C:725:ASP:N	12:5C:725:ASP:OD1	2.37	0.55
13:5D:2013:ARG:NE	13:5D:2048:THR:O	2.40	0.55
31:4T:456:ARG:NH2	31:4T:547:ALA:O	2.36	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:87:A:C6	10:5A:92:U:OP2	2.59	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
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
10:5A:117:A:C2	18:5d:26:GLY:HA3	2.41	0.55
12:5C:485:ASP:OD1	12:5C:485:ASP:N	2.38	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
13:5D:1869:ARG:O	13:5D:1869:ARG:NH1	2.34	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
10:5A:110:C:H2'	10:5A:111:A:H8	1.70	0.55
11:5B:265:THR:HG23	11:5B:327:VAL:HG23	1.88	0.55
11:5B:946:GLU:HB2	11:5B:950:LEU:HD22	1.89	0.55
13:5D:801:PHE:CD1	13:5D:809:LEU:HD11	2.42	0.55
30:4S:740:LYS:O	30:4S:743:THR:OG1	2.23	0.55
35:2A:181:G:H2'	35:2A:182:U:H6	1.71	0.55
30:4S:743:THR:HG22	30:4S:746:ARG:HH21	1.71	0.55
45:2K:98:PHE:O	45:2K:100:LYS:N	2.39	0.55
11:5B:1589:ILE:HD11	11:5B:1733:ILE:CG2	2.33	0.55
22:4A:9:G:OP1	23:4B:445:GLN:CB	2.55	0.55
1:A:31:C:N3	35:2A:33:G:O6	2.40	0.55
22:4A:114:U:H2'	22:4A:114:U:O2	2.06	0.55
35:2A:153:A:H3'	35:2A:154:C:C5'	2.37	0.55
10:5A:108:G:H3'	10:5A:109:G:H8	1.73	0.54
13:5D:986:ARG:O	13:5D:990:HIS:ND1	2.40	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:1133:CYS:HG	11:5B:1134:TRP:CD1	2.25	0.54
11:5B:1766:GLN:NE2	11:5B:1767:ASN:OD1	2.40	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
10:5A:69:A:H2'	10:5A:70:A:O4'	2.08	0.54
11:5B:893:GLU:N	11:5B:893:GLU:OE1	2.40	0.54
13:5D:640:GLU:OE1	13:5D:922:TYR:OH	2.17	0.54
13:5D:2016:ASN:N	13:5D:2045:GLU:OE2	2.39	0.54
11:5B:1763:LEU:HD22	11:5B:1862:ILE:CD1	2.37	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
13:5D:1135:LEU:HD23	13:5D:1140:VAL:HG12	1.88	0.54
43:2I:1195:GLU:C	43:2I:1198:ASP:H	2.14	0.54
13:5D:432:ASP:OD1	13:5D:433:GLY:N	2.39	0.54
13:5D:1464:GLY:N	13:5D:1465:PRO:HD2	2.22	0.54
13:5D:1525:LEU:HD21	13:5D:1718:LEU:HD23	1.89	0.54
31:4T:230:ILE:HG22	31:4T:231:LYS:H	1.73	0.54
7:6e:46:GLU:H	7:6e:63:ALA:CA	2.21	0.54
12:5C:455:GLY:O	12:5C:459:SER:OG	2.24	0.54
13:5D:640:GLU:O	13:5D:643:GLN:NE2	2.41	0.54
1:A:38:C:O2	1:A:38:C:H2'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:1815:LEU:HB3	13:5D:1829:ILE:HD12	1.90	0.54
27:4F:49:ALA:HB2	27:4F:58:ILE:HD11	1.90	0.54
41:2G:747:LEU:O	41:2G:748:LYS:C	2.48	0.54
13:5D:619:LEU:O	13:5D:619:LEU:HD23	2.07	0.54
13:5D:637:ARG:O	13:5D:641:MET:CE	2.56	0.54
29:4R:375:GLU:N	29:4R:375:GLU:OE1	2.41	0.54
35:2A:153:A:C3'	35:2A:154:C:C5'	2.85	0.54
43:2I:785:PRO:CA	43:2I:800:ILE:O	2.56	0.54
11:5B:118:VAL:N	11:5B:485:THR:O	2.34	0.53
11:5B:1807:ILE:HG13	11:5B:1822:ILE:HD11	1.89	0.53
10:5A:99:C:H2'	10:5A:100:C:C6	2.43	0.53
13:5D:130:ASP:OD1	13:5D:131:ILE:N	2.41	0.53
13:5D:1130:ARG:NH2	13:5D:1144:GLU:OE1	2.39	0.53
28:4G:651:LEU:O	28:4G:655:ASN:N	2.42	0.53
41:2G:978:LEU:O	41:2G:979:TYR:C	2.51	0.53
22:4A:31:U:O4	26:4E:60:ALA:C	2.49	0.53
35:2A:54:U:P	40:2F:424:ARG:O	2.67	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
31:4T:529:LEU:HD23	31:4T:534:VAL:HG22	1.90	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
11:5B:259:ASP:OD1	11:5B:259:ASP:N	2.42	0.53
11:5B:863:GLU:O	11:5B:867:ILE:HD12	2.09	0.53
11:5B:1586:HIS:O	11:5B:1589:ILE:HG22	2.09	0.53
27:4F:83:PHE:HD2	27:4F:92:ILE:HD11	1.74	0.53
27:4F:107:GLU:N	27:4F:107:GLU:OE1	2.41	0.53
1:A:15:A:O2'	1:A:16:A:H5'	2.09	0.53
13:5D:1986:MET:O	13:5D:1993:ARG:NH2	2.38	0.53
31:4T:242:ALA:HB2	31:4T:503:ILE:HD11	1.90	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
12:5C:157:ILE:O	12:5C:158:ARG:NH1	2.41	0.53
13:5D:941:ASP:OD1	13:5D:944:LYS:NZ	2.42	0.53
13:5D:1824:ILE:HD11	13:5D:1925:ALA:HB2	1.91	0.53
27:4F:45:LEU:HD12	27:4F:58:ILE:HG21	1.91	0.53
1:A:41:U:H2'	1:A:41:U:O2	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
2:6A:47:A:H61	22:4A:64:G:H21	1.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:912:GLU:OE1	11:5B:914:LEU:N	2.41	0.53
28:4G:707:ASP:HA	28:4G:708:PHE:C	2.33	0.53
41:2G:1280:LEU:O	41:2G:1281:ILE:C	2.51	0.53
11:5B:165:ARG:NH1	11:5B:168:PRO:O	2.42	0.52
11:5B:1347:ASP:OD1	11:5B:1348:VAL:N	2.43	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
11:5B:2068:SER:O	11:5B:2069:SER:OG	2.24	0.52
27:4F:28:ILE:HD11	27:4F:61:VAL:CG2	2.39	0.52
19:4e:33:VAL:HA	19:4e:86:LEU:O	2.09	0.52
11:5B:1645:LEU:N	11:5B:1714:ALA:O	2.39	0.52
11:5B:2088:ASN:C	11:5B:2088:ASN:OD1	2.52	0.52
13:5D:59:THR:OG1	13:5D:60:LYS:N	2.42	0.52
10:5A:77:G:C8	10:5A:78:U:C6	2.98	0.52
10:5A:78:U:C6	10:5A:78:U:H3'	2.44	0.52
10:5A:90:U:C5	21:5g:38:ASN:C	2.85	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:570:ASP:OD1	11:5B:571:ALA:N	2.39	0.52
11:5B:1307:MET:HA	11:5B:1307:MET:HE2	1.92	0.52
12:5C:891:THR:HG22	12:5C:891:THR:O	2.09	0.52
13:5D:830:GLY:O	13:5D:831:THR:OG1	2.15	0.52
13:5D:1920:ILE:O	13:5D:1923:ILE:HG22	2.10	0.52
11:5B:67:ARG:NE	11:5B:491:GLU:OE2	2.43	0.52
11:5B:1076:ASP:OD1	11:5B:1076:ASP:C	2.53	0.52
11:5B:1832:ARG:HG3	11:5B:1836:LEU:HD13	1.92	0.52
43:2I:546:LYS:O	43:2I:556:ILE:CA	2.58	0.52
10:5A:59:G:C8	10:5A:59:G:C5'	2.91	0.52
11:5B:1973:ASP:OD1	11:5B:1973:ASP:N	2.42	0.52
12:5C:566:THR:OG1	12:5C:567:GLU:N	2.43	0.52
28:4G:131:TYR:CD1	28:4G:131:TYR:C	2.88	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
10:5A:87:A:H61	10:5A:92:U:P	2.32	0.52
11:5B:1555:LEU:HD23	11:5B:1556:ASP:N	2.25	0.52
11:5B:1622:MET:HE2	11:5B:1622:MET:HA	1.92	0.52
11:5B:1690:ASP:OD1	11:5B:1691:ASN:N	2.43	0.52
13:5D:296:ALA:HB1	13:5D:302:CYS:HB2	1.90	0.52
13:5D:663:THR:O	13:5D:666:ARG:NH2	2.43	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:931:ASP:OD1	11:5B:931:ASP:C	2.53	0.52
12:5C:700:ILE:HG21	12:5C:741:GLY:O	2.10	0.52
13:5D:1184:LEU:HD12	13:5D:1204:ILE:HG22	1.92	0.52
28:4G:356:ASP:OD1	28:4G:356:ASP:N	2.39	0.52
13:5D:568:GLU:OE1	13:5D:568:GLU:N	2.42	0.52
13:5D:2066:VAL:HG22	13:5D:2108:PHE:CD1	2.45	0.52
23:4B:466:LEU:N	29:4R:432:PRO:CG	2.56	0.52
29:4R:383:ILE:HD11	29:4R:454:LEU:HB3	1.91	0.52
11:5B:511:LYS:NZ	11:5B:537:LYS:O	2.36	0.51
31:4T:443:LEU:O	31:4T:484:LEU:HD23	2.09	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:490:VAL:HG22	11:5B:562:VAL:HG12	1.92	0.51
13:5D:628:LEU:O	13:5D:632:VAL:HG23	2.10	0.51
22:4A:91:A:H2	22:4A:110:G:H22	1.58	0.51
28:4G:332:ILE:HG21	28:4G:349:ALA:HA	1.91	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
11:5B:95:MET:HA	11:5B:95:MET:HE3	1.93	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
13:5D:1627:MET:O	13:5D:1631:LEU:HG	2.11	0.51
13:5D:1967:THR:HG22	13:5D:1968:SER:H	1.74	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
10:5A:95:G:N3	10:5A:95:G:C2'	2.73	0.51
11:5B:528:LYS:NZ	11:5B:529:THR:O	2.37	0.51
22:4A:114:U:P	22:4A:114:U:C6	3.02	0.51
28:4G:162:GLU:OE1	28:4G:162:GLU:N	2.40	0.51
31:4T:362:HIS:HB3	31:4T:365:LEU:HD13	1.92	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:269:GLN:NE2	31:4T:106:PRO:O	2.39	0.51
14:5E:160:ALA:HB3	14:5E:166:LEU:H	1.74	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
12:5C:143:THR:HG23	12:5C:168:THR:OG1	2.11	0.51
12:5C:461:LEU:HD11	12:5C:571:ASN:ND2	2.26	0.51
12:5C:569:ARG:CZ	12:5C:569:ARG:HA	2.40	0.51
13:5D:527:MET:H	13:5D:527:MET:CE	2.24	0.51
41:2G:1207:SER:O	41:2G:1210:HIS:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:5A:85:C:OP1	17:5c:20:GLU:N	2.44	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
11:5B:559:ASP:HA	11:5B:562:VAL:HG22	1.93	0.51
11:5B:1772:PHE:O	11:5B:1813:ARG:NH1	2.44	0.51
22:4A:69:C:HO2'	29:4R:426:PHE:HE1	1.59	0.51
28:4G:559:ALA:CB	28:4G:587:HIS:CB	2.88	0.51
10:5A:96:A:N6	20:5f:23:GLY:N	2.58	0.50
17:4c:53:LEU:O	17:4c:70:VAL:HA	2.11	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:910:ASP:OD1	11:5B:910:ASP:O	2.29	0.50
12:5C:776:GLU:O	12:5C:782:GLU:N	2.45	0.50
13:5D:202:ASN:OD1	13:5D:204:GLN:NE2	2.44	0.50
13:5D:2084:LEU:HD23	13:5D:2084:LEU:H	1.75	0.50
21:4g:19:THR:HA	21:4g:28:TYR:O	2.11	0.50
45:2K:46:ARG:N	45:2K:63:VAL:O	2.44	0.50
11:5B:1614:ILE:O	33:4X:138:ARG:NH2	2.42	0.50
13:5D:527:MET:SD	13:5D:527:MET:N	2.85	0.50
28:4G:634:ALA:O	28:4G:638:ASN:N	2.40	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:758:ARG:O	11:5B:758:ARG:HD3	2.10	0.50
11:5B:1330:MET:HE1	11:5B:1369:TYR:HB3	1.94	0.50
27:4F:44:VAL:O	27:4F:48:ILE:HG13	2.12	0.50
34:4Y:956:LEU:O	34:4Y:958:ASP:O	2.30	0.50
41:2G:849:ILE:O	41:2G:850:ILE:C	2.54	0.50
10:5A:100:C:H2'	10:5A:101:U:C6	2.46	0.50
13:5D:68:ARG:O	13:5D:68:ARG:NH1	2.45	0.50
30:4S:739:GLY:O	30:4S:743:THR:HG23	2.11	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
11:5B:1520:ASN:OD1	11:5B:1521:ALA:N	2.44	0.50
11:5B:1661:TRP:C	11:5B:1662:ILE:HD12	2.37	0.50
13:5D:115:VAL:HG13	13:5D:175:LEU:HD11	1.93	0.50
13:5D:513:ALA:HB1	13:5D:517:MET:HE3	1.93	0.50
13:5D:902:ASN:OD1	13:5D:969:LEU:HD23	2.11	0.50
28:4G:336:THR:HG22	28:4G:345:VAL:HG12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
31:4T:177:ASP:N	31:4T:177:ASP:OD1	2.43	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
12:5C:134:LEU:HD12	12:5C:146:VAL:HG23	1.92	0.50
41:2G:708:ALA:O	41:2G:709:ILE:C	2.54	0.50
2:6A:58:G:H3'	2:6A:58:G:N3	2.27	0.50
12:5C:719:GLN:OE1	12:5C:726:LEU:N	2.44	0.50
25:4D:162:ALA:HB2	28:4G:242:LYS:HE3	1.94	0.50
27:4F:44:VAL:O	27:4F:47:SER:OG	2.24	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
15:4a:17:MET:O	15:4a:28:ILE:HA	2.12	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
10:5A:98:G:H2'	10:5A:99:C:H6	1.77	0.49
11:5B:1275:ARG:O	13:5D:52:MET:HE1	2.12	0.49
11:5B:2134:PRO:O	11:5B:2135:ASP:OD1	2.30	0.49
13:5D:1819:ALA:HB2	13:5D:1829:ILE:HD13	1.94	0.49
19:4e:36:TYR:N	19:4e:83:ASN:O	2.41	0.49
10:5A:92:U:H3'	10:5A:92:U:H6	1.77	0.49
10:5A:115:C:OP1	19:5e:67:LYS:O	2.30	0.49
13:5D:893:MET:HE3	13:5D:925:LEU:HD22	1.93	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:555:LYS:O	11:5B:559:ASP:OD1	2.30	0.49
11:5B:1522:GLN:O	11:5B:1526:LEU:HG	2.12	0.49
11:5B:2190:PRO:HA	11:5B:2193:VAL:HG12	1.93	0.49
13:5D:766:ALA:HA	13:5D:778:LEU:HD23	1.94	0.49
22:4A:109:G:H2'	22:4A:110:G:H8	1.77	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:5A:98:G:H2'	10:5A:99:C:C6	2.47	0.49
11:5B:1381:ASP:OD2	11:5B:1414:ARG:NH1	2.46	0.49
11:5B:1519:THR:HG21	27:4F:117:GLU:OE1	2.11	0.49
33:4X:139:GLN:NE2	33:4X:142:ASN:O	2.46	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
12:5C:297:ASN:OD1	12:5C:297:ASN:N	2.46	0.49
13:5D:425:ASN:ND2	13:5D:886:GLN:O	2.45	0.49
13:5D:538:ILE:HG23	13:5D:611:LEU:CD2	2.43	0.49
13:5D:565:THR:O	13:5D:583:THR:OG1	2.30	0.49
13:5D:1855:TYR:HB3	13:5D:1891:THR:HG21	1.94	0.49
13:5D:1897:ALA:HB1	13:5D:1904:LEU:HD21	1.94	0.49
13:5D:1899:LEU:HD21	13:5D:1949:VAL:HG12	1.94	0.49
19:5e:15:VAL:O	20:5f:33:GLY:HA3	2.12	0.49
22:4A:94:A:O2'	22:4A:95:C:H5'	2.12	0.49
28:4G:112:MET:HE2	28:4G:112:MET:HA	1.94	0.49
4:6b:48:GLN:C	4:6b:50:LEU:N	2.69	0.49
10:5A:77:G:N7	10:5A:78:U:C4	2.80	0.49
11:5B:2183:ASN:OD1	11:5B:2184:GLU:N	2.45	0.49
19:4e:65:HIS:O	19:4e:69:LYS:N	2.45	0.49
41:2G:803:ALA:O	41:2G:804:ASN:C	2.54	0.49
13:5D:619:LEU:HD22	13:5D:628:LEU:CD2	2.42	0.49
13:5D:619:LEU:HD21	13:5D:624:ARG:HB2	1.95	0.49
31:4T:188:ASP:OD1	31:4T:188:ASP:N	2.44	0.49
41:2G:553:VAL:O	41:2G:556:ILE:N	2.46	0.49
13:5D:1329:ASN:O	13:5D:1333:THR:HG23	2.13	0.49
43:2I:930:LEU:C	43:2I:934:GLY:HA2	2.38	0.49
12:5C:688:ILE:CD1	12:5C:792:LEU:HD22	2.43	0.49
12:5C:693:GLU:OE1	12:5C:693:GLU:N	2.45	0.49
13:5D:1320:LEU:HA	13:5D:1324:LYS:HZ3	1.78	0.49
27:4F:48:ILE:HD13	27:4F:113:VAL:HG23	1.93	0.49
41:2G:625:ARG:O	41:2G:628:THR:N	2.46	0.49
11:5B:354:PRO:O	32:4U:327:ARG:NH1	2.46	0.48
11:5B:1633:ALA:O	11:5B:1634:SER:OG	2.15	0.48
12:5C:954:ASP:OD1	12:5C:955:ASP:N	2.46	0.48
13:5D:1439:TRP:CG	13:5D:1477:ILE:HD11	2.48	0.48
22:4A:10:C:OP1	23:4B:449:ARG:HA	2.13	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
11:5B:59:GLU:OE1	11:5B:59:GLU:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:864:LEU:HD12	11:5B:864:LEU:O	2.13	0.48
12:5C:170:ILE:HG22	12:5C:536:ARG:HE	1.78	0.48
13:5D:497:GLU:OE2	13:5D:497:GLU:HA	2.11	0.48
13:5D:969:LEU:HD11	13:5D:998:VAL:CG2	2.42	0.48
32:4U:353:ASP:OD1	32:4U:353:ASP:C	2.55	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:81:U:C2	10:5A:82:A:C5	3.02	0.48
11:5B:300:ASN:O	12:5C:939:ARG:NH1	2.46	0.48
13:5D:1069:GLN:CG	13:5D:1069:GLN:O	2.61	0.48
13:5D:1081:MET:O	13:5D:1085:THR:HG23	2.14	0.48
13:5D:1940:LEU:HD21	13:5D:2107:TYR:CD2	2.48	0.48
13:5D:1945:LEU:HD23	13:5D:1949:VAL:HG13	1.95	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
11:5B:519:ASP:OD1	11:5B:523:ASN:N	2.45	0.48
11:5B:1591:MET:HE3	33:4X:136:LYS:N	2.29	0.48
12:5C:363:SER:O	12:5C:363:SER:OG	2.26	0.48
13:5D:1920:ILE:O	13:5D:1924:GLN:HG3	2.13	0.48
27:4F:68:ASP:O	27:4F:72:MET:HE3	2.13	0.48
28:4G:241:ARG:O	28:4G:245:GLN:HG3	2.13	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
4:6b:47:ASP:O	4:6b:50:LEU:N	2.39	0.48
11:5B:184:ASP:OD1	11:5B:184:ASP:O	2.31	0.48
12:5C:406:GLU:OE1	12:5C:406:GLU:N	2.43	0.48
28:4G:113:ASP:OD1	28:4G:120:ARG:NH2	2.41	0.48
28:4G:668:ALA:O	28:4G:672:ALA:N	2.46	0.48
31:4T:230:ILE:O	31:4T:231:LYS:C	2.56	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
11:5B:110:TRP:HB3	11:5B:147:MET:CE	2.44	0.48
12:5C:509:VAL:HG22	12:5C:565:ILE:HD12	1.95	0.48
22:4A:70:U:C6	29:4R:413:ILE:HD13	2.49	0.48
31:4T:511:GLU:O	31:4T:511:GLU:CD	2.56	0.48
11:5B:1519:THR:HG21	27:4F:117:GLU:OE2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:1625:SER:OG	11:5B:1626:CYS:N	2.46	0.48
41:2G:1227:ILE:O	41:2G:1230:VAL:N	2.46	0.48
2:6A:76:A:H61	23:4B:563:ASN:N	2.12	0.48
11:5B:835:ASP:HB3	11:5B:878:LEU:HD21	1.96	0.48
11:5B:1614:ILE:O	33:4X:138:ARG:NH1	2.45	0.48
11:5B:2320:LEU:N	13:5D:1069:GLN:OE1	2.47	0.48
13:5D:1309:VAL:HG23	13:5D:1326:PRO:O	2.14	0.48
22:4A:108:C:H2'	22:4A:109:G:C8	2.49	0.48
24:4C:259:SER:O	24:4C:263:CYS:N	2.43	0.48
32:4U:581:GLU:C	32:4U:583:GLU:N	2.72	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:67:ARG:NH2	11:5B:491:GLU:OE1	2.46	0.48
11:5B:341:LYS:O	32:4U:301:ARG:NH1	2.42	0.48
13:5D:637:ARG:O	13:5D:641:MET:HE2	2.14	0.48
29:4R:392:VAL:HG22	29:4R:393:ASN:H	1.79	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:78:A:N3	2:6A:78:A:H2'	2.29	0.48
13:5D:1104:TRP:O	13:5D:1108:THR:HG22	2.14	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
10:5A:81:U:H1'	10:5A:82:A:C2	2.49	0.47
10:5A:111:A:H2'	10:5A:112:A:C8	2.49	0.47
11:5B:1410:ASP:OD1	11:5B:1410:ASP:N	2.46	0.47
35:2A:151:C:C2	35:2A:152:G:N7	2.82	0.47
13:5D:1040:LEU:O	13:5D:1044:VAL:HG13	2.14	0.47
13:5D:1391:MET:C	13:5D:1391:MET:SD	2.97	0.47
22:4A:20:A:H2'	22:4A:21:U:C6	2.48	0.47
27:4F:27:VAL:HG22	27:4F:83:PHE:CE1	2.50	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
11:5B:1507:SER:O	11:5B:1512:SER:N	2.47	0.47
11:5B:2307:GLU:OE2	13:5D:1125:SER:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:5C:230:ASP:OD1	12:5C:231:ALA:N	2.48	0.47
13:5D:90:LEU:HD23	13:5D:90:LEU:O	2.14	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
11:5B:555:LYS:O	11:5B:556:LEU:C	2.58	0.47
11:5B:1729:ALA:O	11:5B:1733:ILE:HG12	2.15	0.47
12:5C:404:THR:HG22	12:5C:405:LYS:N	2.30	0.47
13:5D:1631:LEU:O	13:5D:1635:LEU:HD23	2.13	0.47
28:4G:138:ILE:HG22	28:4G:139:GLN:N	2.29	0.47
1:A:7:U:H4'	1:A:8:U:OP1	2.15	0.47
13:5D:551:MET:HE3	13:5D:551:MET:HA	1.97	0.47
13:5D:622:ASP:OD1	13:5D:623:ASP:N	2.47	0.47
22:4A:140:G:H2'	22:4A:141:A:H8	1.79	0.47
29:4R:426:PHE:O	29:4R:427:VAL:HG23	2.14	0.47
11:5B:584:HIS:NE2	48:5B:2401:IHP:O36	2.43	0.47
11:5B:1587:GLU:CD	33:4X:137:TYR:CE1	2.92	0.47
11:5B:2173:GLU:N	11:5B:2173:GLU:OE1	2.48	0.47
13:5D:415:VAL:HG12	13:5D:894:VAL:HB	1.96	0.47
22:4A:92:C:O2'	22:4A:93:G:H5'	2.14	0.47
22:4A:110:G:O2'	22:4A:111:C:H5'	2.14	0.47
24:4C:316:VAL:O	24:4C:317:ALA:C	2.58	0.47
30:4S:725:ALA:O	30:4S:729:LEU:HG	2.15	0.47
31:4T:362:HIS:CD2	31:4T:365:LEU:HD13	2.50	0.47
31:4T:453:CYS:O	31:4T:453:CYS:SG	2.72	0.47
20:4f:6:PRO:HA	20:4f:36:PRO:HA	1.96	0.47
41:2G:210:ALA:O	41:2G:213:LYS:N	2.48	0.47
30:4S:726:PHE:CD1	30:4S:726:PHE:C	2.93	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
11:5B:1716:GLY:O	11:5B:1718:TRP:NE1	2.48	0.47
13:5D:551:MET:HE2	13:5D:555:PHE:CE2	2.50	0.47
21:4g:31:LYS:O	21:4g:44:SER:N	2.47	0.47
40:2F:411:CYS:O	40:2F:414:TYR:N	2.37	0.47
27:4F:103:ASN:OD1	27:4F:103:ASN:C	2.58	0.47
28:4G:239:ASP:O	28:4G:242:LYS:HG2	2.14	0.47
11:5B:1218:ASN:OD1	11:5B:1219:GLU:N	2.48	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:99:C:H2'	10:5A:100:C:H6	1.79	0.46
11:5B:1645:LEU:O	11:5B:1645:LEU:HD23	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:1791:HIS:O	11:5B:1798:LEU:HD12	2.14	0.46
13:5D:893:MET:O	13:5D:893:MET:SD	2.73	0.46
13:5D:1830:GLU:O	13:5D:1834:MET:HG2	2.16	0.46
31:4T:409:ILE:HG23	31:4T:410:ILE:HD13	1.97	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:216:THR:HG22	12:5C:245:HIS:HE2	1.80	0.46
13:5D:1307:LEU:CB	13:5D:1333:THR:HG22	2.45	0.46
29:4R:383:ILE:HD13	29:4R:435:TYR:CE2	2.51	0.46
31:4T:530:GLN:O	31:4T:531:ASP:C	2.57	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
10:5A:58:U:H2'	10:5A:58:U:O2	2.15	0.46
10:5A:117:A:C2	18:5d:26:GLY:O	2.68	0.46
13:5D:1521:VAL:HG23	13:5D:1521:VAL:O	2.15	0.46
13:5D:1819:ALA:HB2	13:5D:1829:ILE:HG21	1.97	0.46
29:4R:458:MET:SD	29:4R:458:MET:N	2.88	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
2:6A:47:A:H4'	2:6A:48:A:OP1	2.14	0.46
10:5A:41:U:OP1	27:4F:141:ARG:NE	2.49	0.46
10:5A:79:C:H4'	10:5A:80:U:OP2	2.08	0.46
13:5D:421:HIS:NE2	13:5D:875:GLU:OE2	2.43	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
11:5B:414:ARG:NH1	12:5C:410:LEU:O	2.40	0.46
11:5B:1626:CYS:SG	11:5B:1627:ALA:N	2.88	0.46
11:5B:1985:ASP:OD1	11:5B:1985:ASP:C	2.58	0.46
12:5C:129:ILE:HD12	12:5C:199:LEU:HD23	1.98	0.46
22:4A:64:G:N2	22:4A:67:A:OP2	2.49	0.46
28:4G:133:MET:HE1	31:4T:432:THR:OG1	2.16	0.46
32:4U:277:ASP:N	32:4U:277:ASP:OD1	2.48	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
12:5C:573:GLU:O	12:5C:573:GLU:HG2	2.15	0.46
13:5D:819:VAL:O	13:5D:855:ARG:NH2	2.48	0.46
24:4C:282:HIS:N	24:4C:295:ASN:O	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:4S:748:LYS:HA	30:4S:751:ASP:OD1	2.16	0.46
41:2G:1256:HIS:O	41:2G:1257:PRO:C	2.58	0.46
11:5B:1407:ASP:N	11:5B:1407:ASP:OD1	2.41	0.46
13:5D:127:GLN:O	13:5D:132:LEU:HD13	2.16	0.46
27:4F:27:VAL:HG13	27:4F:83:PHE:CE1	2.50	0.46
1:A:34:G:N3	1:A:35:U:H5''	2.31	0.46
13:5D:687:GLN:OE1	13:5D:689:TYR:OH	2.28	0.46
24:4C:459:PRO:O	24:4C:462:GLY:N	2.48	0.46
27:4F:112:MET:O	27:4F:116:ILE:HG12	2.16	0.46
28:4G:316:ALA:HB2	28:4G:332:ILE:HG12	1.98	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
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
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:880:ARG:HH11	11:5B:914:LEU:HD21	1.81	0.46
13:5D:880:LEU:O	13:5D:884:ASN:ND2	2.39	0.46
22:4A:31:U:O4	26:4E:60:ALA:HA	2.16	0.46
32:4U:176:ARG:NH1	32:4U:179:GLN:OE1	2.49	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
10:5A:38:C:O2	10:5A:38:C:O4'	2.33	0.45
11:5B:1763:LEU:HD22	11:5B:1862:ILE:HD13	1.98	0.45
11:5B:1785:VAL:HG22	11:5B:1807:ILE:HG13	1.96	0.45
13:5D:1560:ILE:HD11	13:5D:1654:MET:HE3	1.97	0.45
29:4R:383:ILE:HG22	29:4R:427:VAL:O	2.16	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:92:U:N3	16:5b:36:MET:N	2.64	0.45
11:5B:323:LEU:HD21	12:5C:595:VAL:HG21	1.97	0.45
11:5B:1404:THR:OG1	11:5B:1407:ASP:OD1	2.21	0.45
11:5B:1841:THR:HG23	11:5B:1868:MET:HE1	1.97	0.45
12:5C:451:HIS:O	12:5C:578:ARG:NH1	2.50	0.45
12:5C:593:GLU:HG3	12:5C:594:PRO:HD2	1.98	0.45
13:5D:1858:ILE:HG22	13:5D:1887:PRO:HB3	1.97	0.45
28:4G:334:LYS:HG3	28:4G:338:MET:SD	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4T:242:ALA:CB	31:4T:503:ILE:HD11	2.45	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
12:5C:676:ALA:HB3	12:5C:815:VAL:CG2	2.46	0.45
13:5D:1822:TYR:HB2	13:5D:1824:ILE:CD1	2.46	0.45
19:4e:34:TRP:O	19:4e:85:THR:N	2.41	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
11:5B:832:TYR:HB3	11:5B:835:ASP:OD1	2.16	0.45
11:5B:1647:ASP:O	11:5B:1723:LYS:NZ	2.50	0.45
13:5D:637:ARG:C	13:5D:641:MET:HE1	2.42	0.45
13:5D:1136:PRO:O	13:5D:1140:VAL:HG13	2.16	0.45
27:4F:48:ILE:HD11	27:4F:109:LYS:HB2	1.98	0.45
28:4G:280:MET:O	28:4G:280:MET:HG2	2.16	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:123:THR:HG22	11:5B:123:THR:O	2.16	0.45
13:5D:842:THR:HG22	13:5D:843:GLU:H	1.82	0.45
24:4C:275:ASN:O	24:4C:301:ALA:N	2.50	0.45
47:2M:46:HIS:O	47:2M:47:PHE:C	2.59	0.45
11:5B:963:GLN:O	11:5B:964:ASP:OD1	2.35	0.45
11:5B:1519:THR:HG21	27:4F:117:GLU:CD	2.41	0.45
13:5D:551:MET:HE3	13:5D:554:SER:OG	2.17	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
11:5B:900:ASP:O	11:5B:1246:GLN:NE2	2.50	0.45
11:5B:1900:GLU:OE1	11:5B:1900:GLU:N	2.44	0.45
13:5D:1136:PRO:O	13:5D:1139:VAL:HG12	2.17	0.45
13:5D:1886:ASP:HB3	13:5D:1889:VAL:HG22	1.98	0.45
25:4D:162:ALA:H	28:4G:242:LYS:NZ	2.15	0.45
1:A:20:U:C2	35:2A:42:G:C2	3.04	0.45
10:5A:81:U:C2'	10:5A:82:A:O5'	2.65	0.45
11:5B:768:ASP:OD1	11:5B:770:THR:HG22	2.17	0.45
11:5B:828:PRO:O	28:4G:273:TYR:OH	2.17	0.45
11:5B:1070:ASP:OD1	11:5B:1070:ASP:N	2.47	0.45
12:5C:166:CYS:C	12:5C:168:THR:H	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:4C:459:PRO:O	24:4C:461:HIS:N	2.50	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
11:5B:288:LEU:HD23	11:5B:288:LEU:H	1.82	0.45
13:5D:1299:THR:N	13:5D:1513:ASN:O	2.50	0.45
22:4A:66:A:OP1	30:4S:727:ARG:NH1	2.50	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
11:5B:1555:LEU:HD13	11:5B:1560:ILE:HD12	1.98	0.45
12:5C:560:VAL:HG23	12:5C:561:LYS:N	2.32	0.45
13:5D:96:GLU:O	28:4G:367:ARG:NH2	2.50	0.45
13:5D:1944:GLU:HG3	13:5D:2109:MET:HE1	1.98	0.45
28:4G:242:LYS:HG3	28:4G:243:ILE:N	2.32	0.45
28:4G:316:ALA:HB2	28:4G:332:ILE:CG1	2.47	0.45
31:4T:506:ASP:OD2	31:4T:515:ARG:NE	2.49	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
11:5B:150:MET:HE2	11:5B:192:GLN:C	2.41	0.44
11:5B:1293:ASN:OD1	13:5D:40:VAL:HG12	2.16	0.44
11:5B:1618:LYS:HA	11:5B:1621:LYS:HB2	1.99	0.44
22:4A:114:U:C6	22:4A:114:U:O5'	2.70	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
10:5A:92:U:C4	16:5b:36:MET:N	2.85	0.44
12:5C:216:THR:HG22	12:5C:245:HIS:NE2	2.32	0.44
13:5D:1323:ASP:OD1	13:5D:1324:LYS:NZ	2.50	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:45:C:O2	11:5B:603:ARG:NH2	2.51	0.44
11:5B:247:THR:HG22	11:5B:247:THR:O	2.16	0.44
11:5B:302:ILE:O	12:5C:936:LYS:NZ	2.36	0.44
11:5B:592:TYR:HA	11:5B:595:LYS:O	2.17	0.44
11:5B:1622:MET:O	11:5B:1687:TYR:OH	2.34	0.44
12:5C:569:ARG:HA	12:5C:569:ARG:NE	2.32	0.44
13:5D:914:LYS:HD3	13:5D:914:LYS:N	2.32	0.44
13:5D:995:ASN:O	13:5D:998:VAL:HG22	2.17	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:91:A:H2'	2:6A:92:A:C8	2.53	0.44
11:5B:1126:VAL:HG23	11:5B:1127:GLY:N	2.33	0.44
11:5B:1997:VAL:HG12	11:5B:1998:ASN:N	2.33	0.44
13:5D:613:ILE:HD12	13:5D:649:ILE:HB	1.99	0.44
22:4A:65:A:H2'	22:4A:66:A:O4'	2.17	0.44
28:4G:334:LYS:O	28:4G:338:MET:HG3	2.18	0.44
31:4T:415:LEU:HD22	31:4T:473:PHE:HB3	1.99	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
2:6A:48:A:N3	2:6A:48:A:H2'	2.31	0.44
11:5B:697:MET:HG3	11:5B:702:LYS:HB3	1.99	0.44
11:5B:1512:SER:O	11:5B:1513:MET:C	2.60	0.44
13:5D:460:GLN:OE1	13:5D:460:GLN:N	2.50	0.44
13:5D:1301:LEU:HD23	13:5D:1301:LEU:O	2.18	0.44
22:4A:119:A:N6	18:4d:38:GLY:O	2.43	0.44
33:4X:143:ARG:NH1	33:4X:146:GLY:O	2.49	0.44
15:4a:42:LEU:O	15:4a:69:LEU:HA	2.18	0.44
21:4g:80:ALA:HA	21:4g:81:PRO:HA	1.83	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
10:5A:89:U:C2'	10:5A:90:U:H5''	2.47	0.44
11:5B:758:ARG:HH12	11:5B:905:LEU:HD21	1.82	0.44
11:5B:910:ASP:OD1	11:5B:910:ASP:C	2.61	0.44
11:5B:1692:MET:HE3	11:5B:1692:MET:HA	2.00	0.44
12:5C:119:LEU:HD23	12:5C:119:LEU:O	2.17	0.44
12:5C:323:PHE:CG	12:5C:373:ILE:HD12	2.53	0.44
13:5D:63:MET:O	13:5D:63:MET:CG	2.64	0.44
31:4T:274:VAL:HG21	31:4T:334:LEU:HD21	1.98	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:1707:LEU:O	11:5B:1710:ASN:ND2	2.48	0.44
12:5C:510:LEU:N	12:5C:510:LEU:HD12	2.33	0.44
13:5D:176:GLY:O	13:5D:179:ILE:HG22	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
10:5A:117:A:C6	18:5d:26:GLY:HA3	2.52	0.44
11:5B:581:ILE:O	11:5B:585:VAL:HG23	2.18	0.44
11:5B:1658:GLN:OE1	11:5B:1658:GLN:N	2.51	0.44
12:5C:215:VAL:HG11	12:5C:242:LEU:HD22	1.99	0.44
13:5D:64:GLN:NE2	13:5D:64:GLN:O	2.51	0.44
13:5D:1980:GLU:N	13:5D:1980:GLU:OE1	2.51	0.44
22:4A:93:G:H2'	22:4A:94:A:H8	1.82	0.44
22:4A:113:C:O3'	22:4A:114:U:C5	2.71	0.44
27:4F:27:VAL:HG13	27:4F:83:PHE:HE1	1.82	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:1519:THR:HG22	11:5B:1520:ASN:H	1.83	0.44
12:5C:793:ASP:OD1	12:5C:794:ALA:N	2.50	0.44
12:5C:811:THR:O	12:5C:815:VAL:HG23	2.17	0.44
13:5D:537:LYS:NZ	13:5D:580:ILE:O	2.47	0.44
13:5D:773:GLU:OE2	13:5D:784:ILE:HD13	2.16	0.44
13:5D:1430:GLU:OE2	13:5D:1463:ASN:ND2	2.50	0.44
28:4G:297:LEU:O	28:4G:301:VAL:HG23	2.18	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:150:MET:HE2	11:5B:192:GLN:O	2.18	0.43
11:5B:1125:ILE:HG22	11:5B:1125:ILE:O	2.16	0.43
12:5C:308:CYS:HB3	12:5C:433:MET:HE2	2.00	0.43
12:5C:907:VAL:HG13	12:5C:930:ALA:HB2	1.99	0.43
22:4A:113:C:O3'	22:4A:114:U:C6	2.71	0.43
27:4F:68:ASP:OD1	27:4F:68:ASP:N	2.51	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
2:6A:48:A:C4	29:4R:450:ARG:HG2	2.53	0.43
11:5B:1405:LEU:N	13:5D:218:GLY:O	2.51	0.43
13:5D:2052:ILE:HG22	13:5D:2054:PRO:HD3	2.01	0.43
14:5E:58:PRO:O	14:5E:60:MET:N	2.45	0.43
22:4A:57:G:C6	22:4A:58:C:C4	3.06	0.43
30:4S:756:LEU:HD23	30:4S:756:LEU:O	2.18	0.43
35:2A:178:A:N3	35:2A:178:A:H2'	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
12:5C:659:VAL:HG22	12:5C:660:VAL:H	1.83	0.43
13:5D:969:LEU:HD12	13:5D:969:LEU:N	2.34	0.43
13:5D:1918:LYS:O	13:5D:1922:LEU:HD23	2.18	0.43
31:4T:393:LEU:HD11	31:4T:419:LEU:HD23	2.00	0.43
31:4T:422:PHE:HA	31:4T:441:PHE:HB2	2.00	0.43
43:2I:430:GLY:O	43:2I:431:PRO:C	2.61	0.43
13:5D:505:THR:HG21	13:5D:850:LEU:HB3	1.99	0.43
13:5D:613:ILE:HD13	13:5D:613:ILE:N	2.34	0.43
13:5D:1855:TYR:CE2	13:5D:1915:ILE:HG23	2.54	0.43
22:4A:105:A:H2'	22:4A:106:G:H8	1.83	0.43
28:4G:295:ARG:HD3	28:4G:295:ARG:O	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
10:5A:58:U:C6	10:5A:58:U:C5'	3.01	0.43
11:5B:151:MET:SD	11:5B:628:GLY:O	2.77	0.43
11:5B:273:ILE:O	11:5B:274:PRO:C	2.61	0.43
11:5B:2138:GLN:OE1	11:5B:2138:GLN:N	2.40	0.43
27:4F:48:ILE:O	27:4F:48:ILE:HG22	2.19	0.43
30:4S:743:THR:HG22	30:4S:746:ARG:NH2	2.33	0.43
31:4T:376:ASN:O	31:4T:377:ASP:CG	2.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:1403:LEU:N	11:5B:1403:LEU:HD22	2.33	0.43
13:5D:842:THR:HG22	13:5D:843:GLU:N	2.33	0.43
13:5D:1846:ILE:HD11	13:5D:1896:GLN:HG3	2.00	0.43
27:4F:48:ILE:HD11	27:4F:109:LYS:HA	2.00	0.43
31:4T:421:LYS:O	31:4T:422:PHE:HB2	2.18	0.43
34:4Y:759:HIS:O	34:4Y:760:LYS:C	2.61	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:1165:VAL:O	11:5B:1166:THR:OG1	2.33	0.43
11:5B:1798:LEU:HD12	11:5B:1799:THR:H	1.84	0.43
11:5B:2096:ASP:CG	11:5B:2096:ASP:O	2.62	0.43
13:5D:428:CYS:O	13:5D:428:CYS:SG	2.77	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
10:5A:92:U:O4	16:5b:34:VAL:O	2.37	0.43
11:5B:2004:GLN:O	11:5B:2007:ILE:HG22	2.19	0.43
11:5B:2327:SER:HA	13:5D:1078:MET:SD	2.59	0.43
12:5C:107:GLN:OE1	12:5C:107:GLN:N	2.41	0.43
12:5C:110:PRO:HD2	12:5C:537:TYR:CE2	2.54	0.43
13:5D:552:VAL:HG13	13:5D:553:GLY:N	2.34	0.43
13:5D:1014:LEU:HD23	13:5D:1014:LEU:O	2.19	0.43
13:5D:1320:LEU:HD23	13:5D:1401:LEU:HD23	2.00	0.43
27:4F:28:ILE:CD1	27:4F:61:VAL:HG23	2.46	0.43
31:4T:227:LEU:HD23	31:4T:294:VAL:HG13	2.01	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
2:6A:47:A:O2'	2:6A:48:A:P	2.77	0.43
11:5B:811:THR:HA	11:5B:814:VAL:HG22	1.99	0.43
11:5B:919:ASP:OD2	11:5B:1012:LYS:NZ	2.43	0.43
11:5B:1388:GLU:OE1	11:5B:2221:GLY:N	2.52	0.43
11:5B:1639:VAL:HG11	11:5B:1699:THR:HG21	2.00	0.43
13:5D:2066:VAL:HG22	13:5D:2108:PHE:HD1	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:2098:ALA:C	13:5D:2099:THR:HG22	2.44	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
2:6A:48:A:O2'	27:4F:125:LYS:O	2.36	0.43
13:5D:1475:ARG:NH1	13:5D:1503:TRP:O	2.52	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
11:5B:1645:LEU:HB2	11:5B:1714:ALA:H	1.83	0.42
12:5C:396:LEU:HD13	12:5C:403:LEU:HD22	2.01	0.42
13:5D:1569:THR:HG23	13:5D:1570:ARG:N	2.33	0.42
13:5D:1891:THR:HG22	13:5D:1915:ILE:HD11	2.01	0.42
27:4F:139:LYS:C	27:4F:140:TYR:CG	2.97	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
11:5B:1393:ARG:O	11:5B:1397:ILE:HG22	2.19	0.42
11:5B:1988:LEU:HD11	11:5B:2007:ILE:CG1	2.48	0.42
11:5B:2184:GLU:C	11:5B:2184:GLU:OE1	2.62	0.42
13:5D:291:GLU:O	13:5D:295:THR:HG22	2.19	0.42
13:5D:467:LEU:HB3	13:5D:468:PRO:HD2	2.01	0.42
13:5D:645:ASP:N	13:5D:645:ASP:OD1	2.52	0.42
27:4F:5:LEU:HD22	27:4F:5:LEU:H	1.83	0.42
20:4f:46:VAL:HA	20:4f:56:ASN:HA	2.01	0.42
21:4g:32:LEU:HA	21:4g:43:MET:HA	2.00	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
12:5C:215:VAL:HG11	12:5C:242:LEU:CD2	2.50	0.42
13:5D:1663:ILE:HD13	13:5D:1687:MET:HE2	2.01	0.42
13:5D:1939:ALA:O	13:5D:1943:MET:HG2	2.19	0.42
28:4G:123:ARG:O	28:4G:123:ARG:HD3	2.19	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:57:U:H6	2:6A:57:U:O5'	2.02	0.42
2:6A:89:U:H2'	2:6A:90:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:1165:VAL:HG23	11:5B:1166:THR:N	2.35	0.42
13:5D:495:THR:O	13:5D:519:ARG:NE	2.52	0.42
13:5D:1732:MET:CE	13:5D:1755:LEU:HD11	2.48	0.42
22:4A:127:C:H2'	22:4A:128:A:C8	2.55	0.42
29:4R:392:VAL:HG13	29:4R:393:ASN:N	2.34	0.42
31:4T:425:ILE:N	31:4T:425:ILE:HD12	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
12:5C:115:GLU:OE2	21:5g:79:ASN:C	2.61	0.42
12:5C:213:ASP:OD1	12:5C:214:GLU:N	2.52	0.42
12:5C:726:LEU:C	12:5C:726:LEU:HD23	2.45	0.42
13:5D:1583:ASP:OD1	13:5D:1584:ILE:N	2.52	0.42
31:4T:384:VAL:O	31:4T:385:GLU:C	2.61	0.42
17:4c:58:ALA:O	17:4c:65:MET:HA	2.19	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:H5''	1:A:20:U:H6	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:24:G:N3	10:5A:26:A:C2	2.88	0.42
11:5B:1537:TRP:CE3	11:5B:1751:LEU:HD13	2.55	0.42
11:5B:1914:MET:O	11:5B:1914:MET:HG2	2.20	0.42
11:5B:2325:VAL:HG23	11:5B:2326:TYR:N	2.34	0.42
12:5C:119:LEU:HD23	12:5C:119:LEU:C	2.44	0.42
13:5D:579:GLU:O	13:5D:583:THR:HG22	2.19	0.42
13:5D:822:PRO:O	13:5D:858:ARG:NH1	2.53	0.42
13:5D:1665:ASP:O	13:5D:1667:GLN:N	2.44	0.42
13:5D:1943:MET:HB2	13:5D:2065:TRP:CZ3	2.54	0.42
28:4G:354:PRO:O	28:4G:358:ALA:N	2.43	0.42
34:4Y:1004:GLN:O	34:4Y:1005:GLU:CB	2.67	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:13:C:N4	10:5A:65:G:O6	2.53	0.42
10:5A:47:A:HO2'	10:5A:48:A:P	2.41	0.42
10:5A:115:C:OP1	19:5e:67:LYS:CA	2.67	0.42
11:5B:298:ASP:OD1	11:5B:300:ASN:N	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:1701:VAL:HA	11:5B:1716:GLY:HA3	2.02	0.42
11:5B:2009:ASP:OD1	11:5B:2009:ASP:C	2.62	0.42
11:5B:2096:ASP:O	11:5B:2096:ASP:OD1	2.37	0.42
12:5C:407:GLU:O	12:5C:410:LEU:HD12	2.20	0.42
13:5D:158:ASP:O	13:5D:163:GLN:N	2.39	0.42
13:5D:1142:LYS:CB	13:5D:1165:ILE:HD11	2.48	0.42
13:5D:1455:GLU:N	13:5D:1490:LEU:O	2.52	0.42
13:5D:2017:ILE:HG21	13:5D:2108:PHE:HE2	1.84	0.42
22:4A:108:C:H2'	22:4A:109:G:H8	1.85	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
10:5A:28:A:O2'	11:5B:643:GLY:HA3	2.20	0.42
11:5B:1090:ARG:HG2	11:5B:1091:TYR:O	2.20	0.42
11:5B:1443:LYS:O	11:5B:1447:VAL:HG22	2.20	0.42
13:5D:766:ALA:CA	13:5D:778:LEU:HD23	2.50	0.42
13:5D:925:LEU:HD11	13:5D:929:MET:HE3	2.01	0.42
13:5D:1027:ILE:HG21	13:5D:1059:ILE:HD11	2.02	0.42
13:5D:1945:LEU:HD23	13:5D:1949:VAL:CG1	2.50	0.42
27:4F:8:LEU:HD13	27:4F:14:VAL:HA	2.02	0.42
17:4c:76:GLU:O	17:4c:89:PRO:HA	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:1876:LEU:HD12	11:5B:1876:LEU:H	1.85	0.42
12:5C:308:CYS:CB	12:5C:433:MET:HE2	2.50	0.42
13:5D:220:VAL:HG12	13:5D:220:VAL:O	2.20	0.42
13:5D:689:TYR:CE2	13:5D:880:LEU:HD11	2.55	0.42
13:5D:765:GLU:HB3	13:5D:778:LEU:HD21	2.02	0.42
13:5D:820:ASN:O	13:5D:821:LEU:HD22	2.20	0.42
13:5D:1560:ILE:HG22	13:5D:1661:VAL:HG22	2.00	0.42
13:5D:1620:LEU:HA	13:5D:1624:LEU:HD12	2.02	0.42
13:5D:1729:ASP:OD1	13:5D:1730:HIS:N	2.53	0.42
22:4A:33:A:H2'	22:4A:34:G:O4'	2.20	0.42
22:4A:128:A:H2'	22:4A:129:G:H8	1.85	0.42
31:4T:488:VAL:O	31:4T:488:VAL:HG12	2.18	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:9:G:C6	10:5A:69:A:C2	3.07	0.42
11:5B:1790:ILE:HG22	11:5B:1798:LEU:HD11	2.02	0.42
12:5C:154:HIS:NE2	12:5C:537:TYR:OH	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:5C:732:ILE:HD13	12:5C:746:VAL:HG12	2.02	0.42
12:5C:750:LEU:HD22	12:5C:751:PRO:HD2	2.02	0.42
12:5C:754:VAL:HG12	12:5C:755:ASP:N	2.34	0.42
13:5D:929:MET:HE1	13:5D:956:LEU:HD11	2.01	0.42
13:5D:1875:VAL:HG23	13:5D:1877:HIS:O	2.20	0.42
27:4F:27:VAL:HB	27:4F:58:ILE:HG22	2.02	0.42
27:4F:94:LEU:HD22	27:4F:136:TYR:CE1	2.55	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:1001:VAL:HG22	11:5B:1002:ASP:H	1.85	0.41
11:5B:1589:ILE:HD12	11:5B:1733:ILE:HD12	2.02	0.41
11:5B:1630:LEU:HD21	11:5B:1659:LYS:HB3	2.01	0.41
11:5B:2179:HIS:ND1	11:5B:2180:THR:O	2.52	0.41
13:5D:1979:VAL:HG11	13:5D:1985:ILE:HD13	2.01	0.41
16:4b:16:THR:HA	16:4b:25:VAL:O	2.20	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
2:6A:56:A:N1	22:4A:57:G:C6	2.88	0.41
10:5A:23:C:H2'	10:5A:23:C:O2	2.20	0.41
10:5A:116:U:OP2	19:5e:68:THR:CA	2.67	0.41
11:5B:888:GLN:NE2	11:5B:890:ALA:O	2.53	0.41
11:5B:2111:LEU:HD11	11:5B:2225:LEU:HD11	2.02	0.41
12:5C:534:VAL:O	12:5C:535:ALA:C	2.62	0.41
13:5D:611:LEU:CD2	13:5D:613:ILE:HD11	2.44	0.41
13:5D:1844:GLY:O	13:5D:1848:ILE:HG12	2.20	0.41
13:5D:1937:SER:N	13:5D:2074:ASN:OD1	2.49	0.41
13:5D:1948:MET:SD	13:5D:1955:SER:HA	2.60	0.41
31:4T:138:VAL:HG11	31:4T:161:HIS:CD2	2.54	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
10:5A:8:G:H2'	10:5A:9:G:H5'	2.03	0.41
10:5A:11:U:C2	10:5A:67:A:C2	3.08	0.41
11:5B:1741:TYR:CD1	11:5B:1741:TYR:C	2.98	0.41
12:5C:659:VAL:HG22	12:5C:660:VAL:N	2.36	0.41
13:5D:592:LYS:O	13:5D:595:ILE:HG22	2.20	0.41
13:5D:1564:PRO:O	13:5D:1648:ARG:NH2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:4D:292:ALA:O	25:4D:293:ARG:C	2.62	0.41
31:4T:419:LEU:HB3	31:4T:483:TYR:CE2	2.56	0.41
31:4T:425:ILE:HD12	31:4T:425:ILE:H	1.85	0.41
32:4U:197:GLN:O	32:4U:200:ASP:OD1	2.38	0.41
19:4e:44:GLU:O	19:4e:61:ALA:HA	2.20	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
11:5B:95:MET:N	11:5B:96:PRO:HD2	2.35	0.41
11:5B:1689:THR:O	11:5B:1689:THR:HG22	2.21	0.41
11:5B:1742:VAL:HG21	30:4S:726:PHE:CD2	2.55	0.41
12:5C:241:ARG:CZ	12:5C:900:VAL:HG21	2.50	0.41
13:5D:301:GLU:OE1	13:5D:305:GLN:NE2	2.53	0.41
13:5D:619:LEU:HD23	13:5D:619:LEU:C	2.45	0.41
13:5D:806:ILE:HG21	13:5D:809:LEU:HD23	2.02	0.41
13:5D:1738:ALA:O	13:5D:1741:VAL:HG22	2.19	0.41
34:4Y:695:GLN:HA	34:4Y:700:ASN:HA	2.02	0.41
2:6A:103:U:H3'	2:6A:104:U:C5'	2.47	0.41
10:5A:66:A:C2	10:5A:67:A:C5	3.08	0.41
10:5A:93:U:C4'	17:5c:104:ASP:CA	2.97	0.41
11:5B:780:THR:HG23	11:5B:898:PHE:CD1	2.56	0.41
13:5D:1456:VAL:HG22	13:5D:1491:SER:OG	2.20	0.41
13:5D:1982:VAL:HA	13:5D:1985:ILE:HG22	2.02	0.41
31:4T:271:PHE:O	31:4T:274:VAL:HG12	2.20	0.41
43:2I:1210:ASP:O	43:2I:1211:ILE:C	2.64	0.41
10:5A:5:U:C2	10:5A:77:G:N2	2.88	0.41
11:5B:201:ALA:N	11:5B:202:PRO:HD2	2.36	0.41
11:5B:697:MET:SD	11:5B:701:ILE:HG23	2.60	0.41
11:5B:792:HIS:CD2	31:4T:409:ILE:HG22	2.55	0.41
11:5B:880:ARG:HH11	11:5B:880:ARG:HG2	1.86	0.41
11:5B:923:ASP:OD1	11:5B:927:TRP:HD1	2.04	0.41
11:5B:1425:LYS:H	11:5B:1425:LYS:HG2	1.70	0.41
11:5B:1679:TYR:HE2	11:5B:1704:ALA:HB1	1.85	0.41
11:5B:1729:ALA:HA	30:4S:708:VAL:HG11	2.02	0.41
12:5C:269:LEU:O	12:5C:378:TYR:OH	2.20	0.41
13:5D:590:PRO:HG2	13:5D:628:LEU:HD21	2.02	0.41
13:5D:2098:ALA:O	13:5D:2099:THR:CG2	2.68	0.41
22:4A:38:U:H4'	22:4A:39:A:OP1	2.21	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:C2	1:A:10:C:OP2	2.73	0.41
11:5B:696:MET:HE1	28:4G:150:ALA:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:5B:1473:ASP:OD1	11:5B:1473:ASP:N	2.52	0.41
13:5D:946:ASP:OD2	13:5D:950:ASP:N	2.54	0.41
13:5D:1029:VAL:HG13	13:5D:1029:VAL:O	2.20	0.41
13:5D:1324:LYS:H	13:5D:1324:LYS:HD2	1.84	0.41
13:5D:1598:ILE:N	13:5D:1599:PRO:CD	2.84	0.41
41:2G:997:LEU:O	41:2G:998:LYS:C	2.62	0.41
11:5B:1607:GLU:O	11:5B:1608:THR:HG23	2.21	0.41
12:5C:665:THR:OG1	12:5C:666:VAL:N	2.54	0.41
13:5D:882:LEU:HD12	13:5D:887:LEU:HD23	2.02	0.41
31:4T:406:GLU:O	31:4T:408:LEU:N	2.54	0.41
41:2G:1146:GLY:O	41:2G:1147:VAL:C	2.63	0.41
10:5A:5:U:C2'	10:5A:6:C:O5'	2.69	0.41
11:5B:539:ARG:O	11:5B:539:ARG:NE	2.54	0.41
11:5B:598:LEU:HD21	11:5B:640:PHE:CZ	2.56	0.41
11:5B:1238:GLN:OE1	11:5B:1242:ASN:ND2	2.50	0.41
11:5B:1394:GLN:OE1	11:5B:1394:GLN:HA	2.20	0.41
11:5B:1978:LYS:O	11:5B:1981:VAL:HG12	2.21	0.41
12:5C:347:ILE:HG23	12:5C:356:PHE:HB3	2.02	0.41
13:5D:569:LEU:HD22	13:5D:596:ILE:CD1	2.51	0.41
13:5D:709:TYR:HA	13:5D:712:ILE:HG22	2.03	0.41
13:5D:1156:LEU:HB2	13:5D:1161:ILE:HG23	2.01	0.41
13:5D:1663:ILE:HG23	13:5D:1687:MET:HE1	2.03	0.41
13:5D:1842:VAL:O	13:5D:1846:ILE:HG22	2.21	0.41
22:4A:113:C:O2'	22:4A:114:U:P	2.79	0.41
27:4F:27:VAL:HG22	27:4F:83:PHE:CD1	2.56	0.41
27:4F:44:VAL:HG11	27:4F:112:MET:HE2	2.03	0.41
27:4F:44:VAL:HG11	27:4F:112:MET:CE	2.51	0.41
28:4G:332:ILE:CG2	28:4G:349:ALA:HB2	2.51	0.41
31:4T:516:ILE:HG12	31:4T:518:VAL:HG13	2.02	0.41
32:4U:195:ARG:O	32:4U:199:GLN:HG2	2.21	0.41
34:4Y:1003:ILE:C	34:4Y:1005:GLU:N	2.78	0.41
18:4d:30:LYS:O	18:4d:47:THR:HA	2.20	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
2:6A:58:G:N3	2:6A:58:G:H5'	2.36	0.41
11:5B:488:ASP:OD1	11:5B:489:TRP:N	2.53	0.41
11:5B:830:LEU:HD21	28:4G:276:ASP:HB3	2.02	0.41
13:5D:170:HIS:HA	13:5D:173:VAL:HG22	2.03	0.41
13:5D:436:ARG:NE	13:5D:443:GLU:OE2	2.35	0.41
13:5D:615:ASP:OD1	13:5D:651:LEU:HD12	2.20	0.41
13:5D:733:LYS:O	13:5D:736:ARG:NH2	2.54	0.41
35:2A:153:A:C8	35:2A:154:C:O4'	2.74	0.41
41:2G:303:THR:O	41:2G:304:PRO:C	2.63	0.41
11:5B:1480:GLY:O	11:5B:1484:ILE:HG13	2.20	0.40
11:5B:1587:GLU:OE2	33:4X:137:TYR:CD1	2.73	0.40
11:5B:1681:ARG:NH1	11:5B:1715:TYR:OH	2.54	0.40
11:5B:1785:VAL:HG22	11:5B:1807:ILE:CG1	2.51	0.40
11:5B:2234:GLY:HA2	11:5B:2255:HIS:CG	2.56	0.40
13:5D:1012:ILE:N	13:5D:1012:ILE:HD12	2.36	0.40
13:5D:1736:PHE:HZ	13:5D:1751:ALA:HB1	1.86	0.40
13:5D:1824:ILE:HG22	13:5D:1825:ASN:N	2.36	0.40
22:4A:69:C:OP2	30:4S:740:LYS:NZ	2.35	0.40
23:4B:466:LEU:N	29:4R:432:PRO:CB	2.84	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
11:5B:640:PHE:CZ	11:5B:644:ILE:HG13	2.56	0.40
11:5B:1277:ALA:O	11:5B:1281:THR:OG1	2.32	0.40
13:5D:467:LEU:HD21	13:5D:481:LEU:HD11	2.03	0.40
13:5D:634:ARG:NH2	13:5D:904:GLU:OE2	2.50	0.40
13:5D:1914:GLU:O	13:5D:1917:SER:OG	2.29	0.40
13:5D:1926:CYS:O	13:5D:1930:LEU:HG	2.21	0.40
22:4A:68:A:HO2'	22:4A:69:C:P	2.31	0.40
27:4F:48:ILE:HD11	27:4F:109:LYS:CA	2.51	0.40
31:4T:456:ARG:HD2	31:4T:467:ASN:O	2.22	0.40
35:2A:63:G:H2'	35:2A:64:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:78:U:C6	10:5A:78:U:C3'	3.03	0.40
10:5A:101:U:H2'	10:5A:102:U:C6	2.57	0.40
11:5B:1587:GLU:OE2	30:4S:733:PHE:CD1	2.74	0.40
12:5C:308:CYS:SG	12:5C:309:PHE:N	2.94	0.40
12:5C:688:ILE:HG22	12:5C:689:ALA:N	2.36	0.40
13:5D:317:PHE:O	13:5D:321:LEU:HG	2.21	0.40
13:5D:709:TYR:O	13:5D:713:MET:HG2	2.22	0.40
13:5D:1673:ILE:HG13	13:5D:1673:ILE:O	2.21	0.40
13:5D:1845:LEU:O	13:5D:1849:ILE:HG13	2.21	0.40
13:5D:1940:LEU:HD21	13:5D:2107:TYR:HD2	1.85	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
2:6A:59:G:C6	2:6A:60:C:C4	3.10	0.40
10:5A:37:G:N2	10:5A:38:C:H41	2.19	0.40
11:5B:1243:ARG:NH1	11:5B:1450:GLN:OE1	2.55	0.40
11:5B:1510:GLU:OE1	11:5B:1510:GLU:N	2.54	0.40
11:5B:1587:GLU:OE2	30:4S:733:PHE:HD1	2.04	0.40
11:5B:2006:GLU:O	11:5B:2009:ASP:OD1	2.39	0.40
13:5D:755:GLY:O	13:5D:756:SER:C	2.64	0.40
13:5D:1012:ILE:HD12	13:5D:1012:ILE:H	1.87	0.40
13:5D:1324:LYS:HD2	13:5D:1324:LYS:N	2.37	0.40
13:5D:2013:ARG:HB3	13:5D:2052:ILE:HD11	2.04	0.40
13:5D:2019:LEU:HD11	13:5D:2118:GLN:HB3	2.04	0.40
13:5D:2067:VAL:CG2	13:5D:2076:LEU:HD11	2.51	0.40
22:4A:127:C:H2'	22:4A:128:A:H8	1.87	0.40
27:4F:48:ILE:HD11	27:4F:109:LYS:CB	2.51	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
11:5B:1560:ILE:HD11	11:5B:1577:PHE:CD2	2.57	0.40
13:5D:419:GLY:O	13:5D:892:GLN:NE2	2.54	0.40
13:5D:591:GLU:OE1	13:5D:591:GLU:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:5D:617:ILE:HG22	13:5D:652:SER:HB2	2.03	0.40
13:5D:982:THR:HG22	13:5D:984:LEU:H	1.85	0.40
13:5D:1613:LEU:CD1	13:5D:1641:ILE:HG21	2.51	0.40
25:4D:220:SER:O	25:4D:224:GLY:O	2.40	0.40
31:4T:250:ARG:NH2	31:4T:251:ASN:OD1	2.53	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 [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	6a	87/95 (92%)	76 (87%)	7 (8%)	4 (5%)	2	11
4	6b	70/102 (69%)	64 (91%)	3 (4%)	3 (4%)	2	13
5	6c	70/139 (50%)	64 (91%)	5 (7%)	1 (1%)	9	33
6	6d	68/91 (75%)	63 (93%)	4 (6%)	1 (2%)	8	32
7	6e	68/80 (85%)	64 (94%)	2 (3%)	2 (3%)	3	20
8	6f	61/103 (59%)	56 (92%)	5 (8%)	0	100	100
9	6g	57/96 (59%)	52 (91%)	4 (7%)	1 (2%)	6	29
11	5B	2195/2335 (94%)	2099 (96%)	96 (4%)	0	100	100
12	5C	850/972 (87%)	823 (97%)	27 (3%)	0	100	100
13	5D	1989/2136 (93%)	1912 (96%)	77 (4%)	0	100	100
14	5E	299/357 (84%)	280 (94%)	17 (6%)	2 (1%)	18	48
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	84/231 (36%)	82 (98%)	2 (2%)	0	100	100
16	2b	80/119 (67%)	77 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	4b	79/119 (66%)	75 (95%)	4 (5%)	0	100	100
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	62/76 (82%)	60 (97%)	2 (3%)	0	100	100
20	4f	72/76 (95%)	66 (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%)	333 (93%)	24 (7%)	0	100	100
25	4D	262/499 (52%)	252 (96%)	10 (4%)	0	100	100
26	4E	122/128 (95%)	114 (93%)	8 (7%)	0	100	100
27	4F	139/142 (98%)	136 (98%)	3 (2%)	0	100	100
28	4G	776/941 (82%)	739 (95%)	33 (4%)	4 (0%)	24	55
29	4R	104/480 (22%)	93 (89%)	11 (11%)	0	100	100
30	4S	59/800 (7%)	57 (97%)	2 (3%)	0	100	100
31	4T	454/565 (80%)	425 (94%)	29 (6%)	0	100	100
32	4U	559/820 (68%)	541 (97%)	17 (3%)	1 (0%)	43	70
33	4X	19/155 (12%)	19 (100%)	0	0	100	100
34	4Y	316/1007 (31%)	294 (93%)	18 (6%)	4 (1%)	9	34
36	2B	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	9	34
37	2C	92/225 (41%)	90 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	2D	118/793 (15%)	106 (90%)	6 (5%)	6 (5%)	1	10
39	2E	88/464 (19%)	63 (72%)	16 (18%)	9 (10%)	0	2
40	2F	413/501 (82%)	367 (89%)	41 (10%)	5 (1%)	10	36
41	2G	1032/1304 (79%)	845 (82%)	165 (16%)	22 (2%)	5	25
42	2H	170/895 (19%)	151 (89%)	15 (9%)	4 (2%)	4	23
43	2I	1152/1217 (95%)	1053 (91%)	89 (8%)	10 (1%)	14	42
44	2J	76/424 (18%)	75 (99%)	1 (1%)	0	100	100
45	2K	106/125 (85%)	85 (80%)	18 (17%)	3 (3%)	4	20
46	2L	87/110 (79%)	75 (86%)	12 (14%)	0	100	100
47	2M	64/86 (74%)	55 (86%)	8 (12%)	1 (2%)	7	30
All	All	14353/22191 (65%)	13407 (93%)	861 (6%)	85 (1%)	23	51

All (85) 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
14	5E	59	ILE
28	4G	136	PRO
28	4G	571	PRO
28	4G	573	LYS
34	4Y	697	VAL
38	2D	301	PRO
39	2E	139	PRO
39	2E	141	ILE
39	2E	146	MET
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

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Mol	Chain	Res	Type
41	2G	941	ASN
41	2G	1107	GLN
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
34	4Y	851	VAL
36	2B	160	LYS
38	2D	223	LYS
38	2D	280	VAL
40	2F	277	THR
41	2G	113	ALA
41	2G	1110	VAL
42	2H	597	PHE
43	2I	917	PRO
32	4U	582	ALA
40	2F	177	ARG
40	2F	393	PRO
41	2G	437	PRO
42	2H	510	TYR
4	6b	96	ALA
14	5E	58	PRO
34	4Y	699	SER
36	2B	32	PRO
38	2D	300	THR
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
28	4G	569	VAL
34	4Y	722	ASN
39	2E	147	PRO
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
39	2E	220	PRO
41	2G	326	THR
41	2G	932	ILE
43	2I	918	ARG
43	2I	1138	HIS
41	2G	417	PRO
38	2D	221	PRO
41	2G	223	THR
43	2I	1204	VAL
40	2F	229	TRP
38	2D	298	PRO
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	1978/2108 (94%)	1975 (100%)	3 (0%)	87	87
12	5C	754/866 (87%)	754 (100%)	0	100	100
13	5D	1779/1908 (93%)	1773 (100%)	6 (0%)	86	86
27	4F	129/130 (99%)	129 (100%)	0	100	100
28	4G	185/792 (23%)	179 (97%)	6 (3%)	34	58
29	4R	94/369 (26%)	94 (100%)	0	100	100
30	4S	54/681 (8%)	54 (100%)	0	100	100
31	4T	418/511 (82%)	418 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	4U	133/721 (18%)	133 (100%)	0	100	100
33	4X	19/144 (13%)	19 (100%)	0	100	100
All	All	5543/8230 (67%)	5528 (100%)	15 (0%)	84	86

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	5B	1759	THR
11	5B	2096	ASP
11	5B	2259	VAL
13	5D	687	GLN
13	5D	1568	GLN
13	5D	1690	HIS
13	5D	1736	PHE
13	5D	1874	LYS
13	5D	1967	THR
28	4G	131	TYR
28	4G	134	GLU
28	4G	135	ARG
28	4G	137	LYS
28	4G	138	ILE
28	4G	242	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (53) such sidechains are listed below:

Mol	Chain	Res	Type
11	5B	210	HIS
11	5B	321	ASN
11	5B	429	ASN
11	5B	434	HIS
11	5B	884	HIS
11	5B	1117	HIS
11	5B	1296	GLN
11	5B	1554	GLN
11	5B	1623	ASN
11	5B	1766	GLN
11	5B	1784	ASN
11	5B	1823	HIS
11	5B	1946	ASN
11	5B	2084	HIS

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Mol	Chain	Res	Type
11	5B	2089	HIS
11	5B	2165	GLN
11	5B	2203	ASN
12	5C	140	HIS
12	5C	768	GLN
12	5C	802	HIS
12	5C	807	GLN
12	5C	903	HIS
13	5D	121	GLN
13	5D	174	ASN
13	5D	271	GLN
13	5D	305	GLN
13	5D	362	GLN
13	5D	472	GLN
13	5D	726	HIS
13	5D	785	HIS
13	5D	824	HIS
13	5D	958	HIS
13	5D	1101	ASN
13	5D	1158	HIS
13	5D	1159	ASN
13	5D	1341	ASN
13	5D	1388	GLN
13	5D	1441	GLN
13	5D	1463	ASN
13	5D	1727	HIS
13	5D	1784	HIS
13	5D	2086	GLN
13	5D	2102	HIS
27	4F	7	HIS
27	4F	32	HIS
27	4F	100	ASN
28	4G	139	GLN
28	4G	305	ASN
28	4G	307	HIS
31	4T	293	HIS
31	4T	350	GLN
31	4T	520	HIS
31	4T	540	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	41/144 (28%)	27 (65%)	9 (21%)
10	5A	113/117 (96%)	39 (34%)	6 (5%)
2	6A	50/107 (46%)	8 (16%)	3 (6%)
22	4A	119/144 (82%)	21 (17%)	2 (1%)
35	2A	105/188 (55%)	22 (20%)	3 (2%)
All	All	428/700 (61%)	117 (27%)	23 (5%)

All (117) 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
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
2	6A	48	A
2	6A	49	G
2	6A	58	G
2	6A	59	G
2	6A	77	C
2	6A	78	A

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Mol	Chain	Res	Type
2	6A	103	U
2	6A	104	U
10	5A	5	U
10	5A	6	C
10	5A	21	A
10	5A	22	U
10	5A	24	G
10	5A	25	C
10	5A	28	A
10	5A	36	C
10	5A	37	G
10	5A	38	C
10	5A	40	U
10	5A	41	U
10	5A	43	U
10	5A	44	A
10	5A	47	A
10	5A	48	A
10	5A	55	C
10	5A	58	U
10	5A	59	G
10	5A	60	G
10	5A	66	A
10	5A	67	A
10	5A	69	A
10	5A	70	A
10	5A	75	G
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	2	G

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Mol	Chain	Res	Type
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	53	U
22	4A	57	G
22	4A	68	A
22	4A	69	C
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 (23) 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
1	A	38	C
1	A	40	U
1	A	41	U
2	6A	47	A
2	6A	48	A
2	6A	77	C
10	5A	58	U
10	5A	59	G
10	5A	78	U
10	5A	79	C
10	5A	94	U
10	5A	96	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	$\# Z > 2$
48	IHP	5B	2401	-	36,36,36	0.74	0	60,60,60	1.22	3 (5%)
50	GTP	5C	1002	49	33,34,34	0.94	1 (3%)	50,54,54	1.54	8 (16%)

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
48	IHP	5B	2401	-	-	2/30/54/54	0/1/1/1
50	GTP	5C	1002	49	-	4/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	5C	1002	GTP	C2-N3	2.07	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	-4.91	120.58	128.39
50	5C	1002	GTP	C2-N3-C4	4.67	120.35	112.30
48	5B	2401	IHP	C5-C4-C3	3.34	117.76	110.43
50	5C	1002	GTP	N9-C4-N3	3.14	132.22	125.95
50	5C	1002	GTP	C2-N1-C6	-3.02	119.64	125.11
50	5C	1002	GTP	C5-C6-N1	2.66	120.02	113.25
48	5B	2401	IHP	C6-C5-C4	2.61	116.16	110.43
50	5C	1002	GTP	N9-C8-N7	-2.57	108.64	113.40
50	5C	1002	GTP	O6-C6-C5	-2.44	120.10	126.53
50	5C	1002	GTP	C8-N7-C5	2.32	108.40	104.26
48	5B	2401	IHP	C4-C3-C2	2.30	115.46	110.43

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
50	5C	1002	GTP	C5'-O5'-PA-O3A

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Mol	Chain	Res	Type	Atoms
50	5C	1002	GTP	C5'-O5'-PA-O2A
50	5C	1002	GTP	O4'-C4'-C5'-O5'
50	5C	1002	GTP	C3'-C4'-C5'-O5'
48	5B	2401	IHP	C1-O11-P1-O41
48	5B	2401	IHP	C4-O14-P4-O44

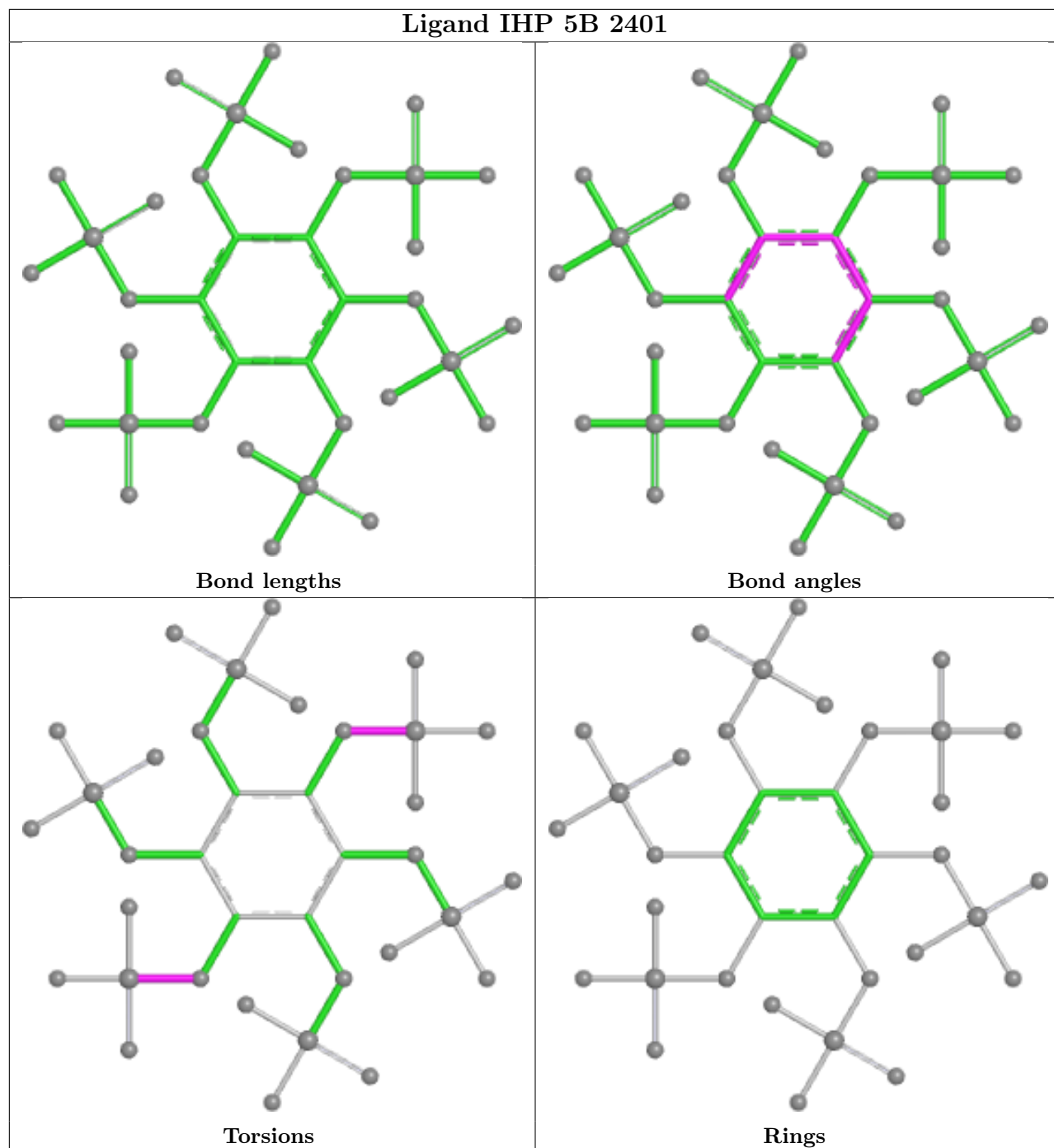
There are no ring outliers.

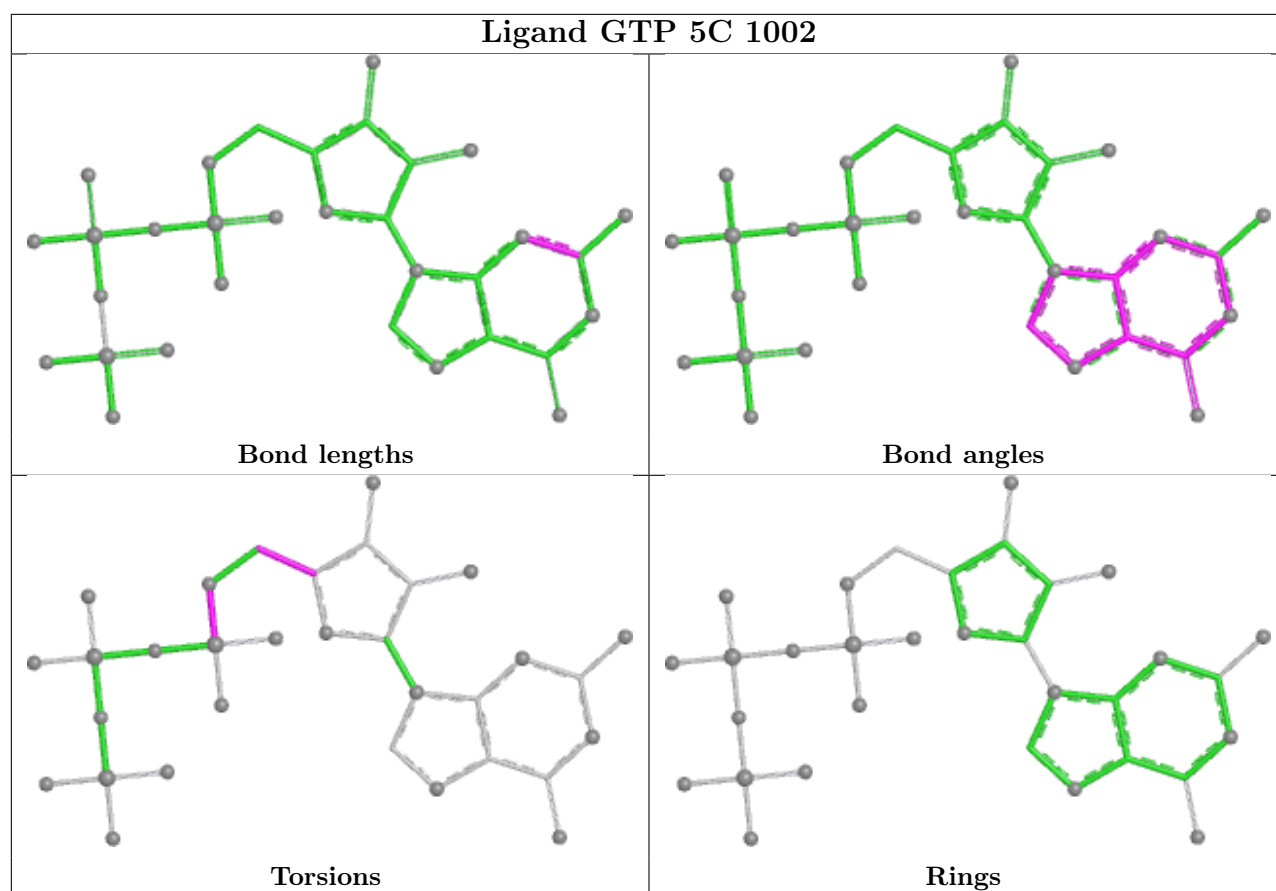
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
48	5B	2401	IHP	2	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.

Ligand IHP 5B 2401





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.

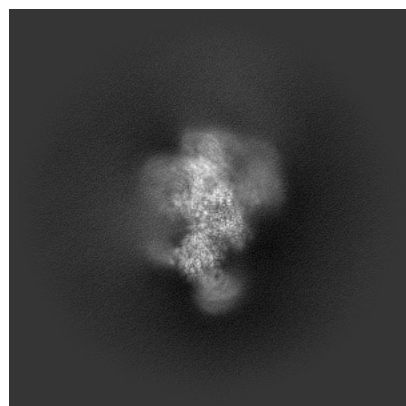
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34505. These allow visual inspection of the internal detail of the map and identification of artifacts.

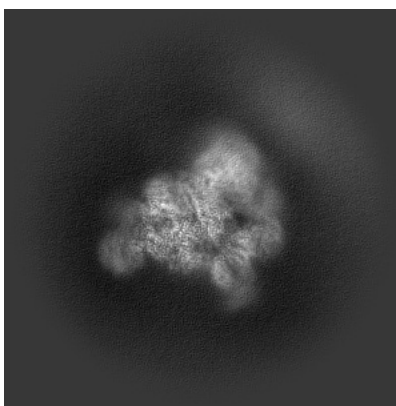
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

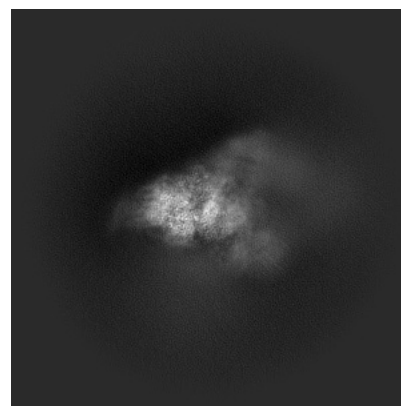
6.1.1 Primary map



X

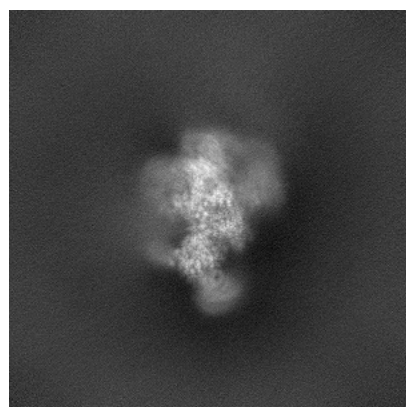


Y

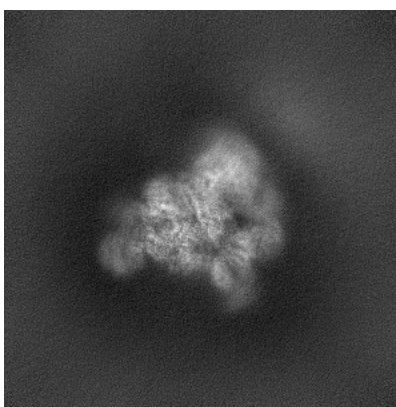


Z

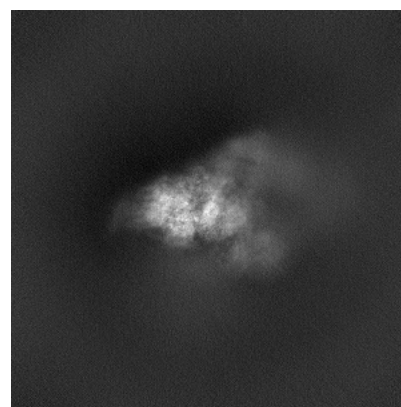
6.1.2 Raw map



X



Y

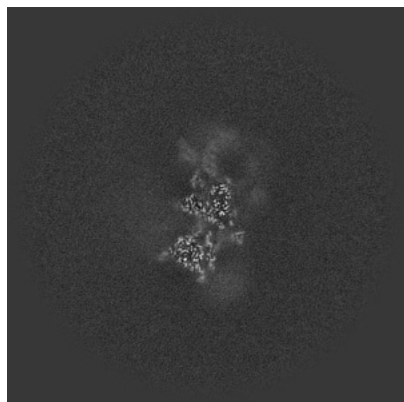


Z

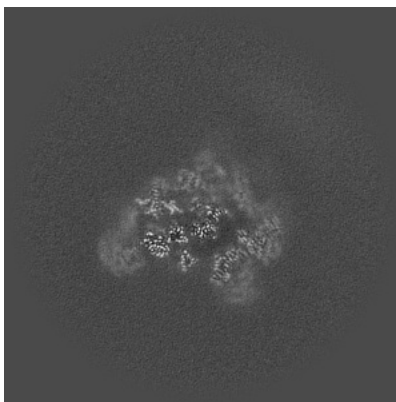
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

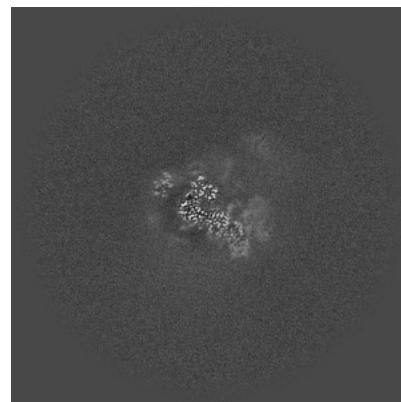
6.2.1 Primary map



X Index: 256

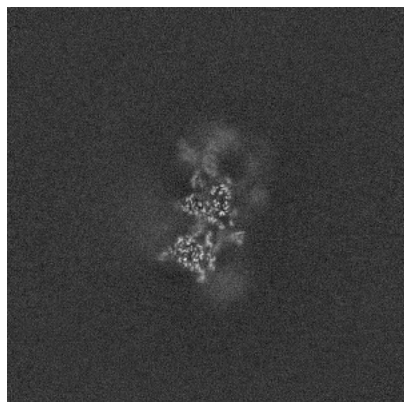


Y Index: 256

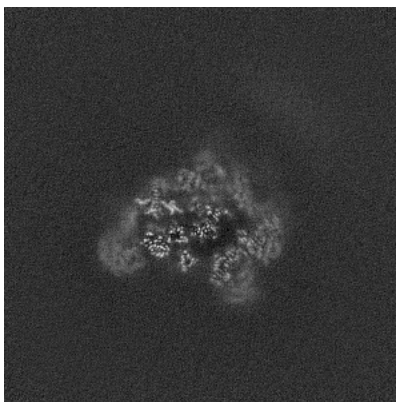


Z Index: 256

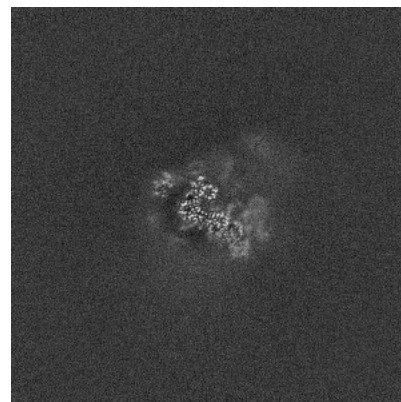
6.2.2 Raw map



X Index: 256



Y Index: 256

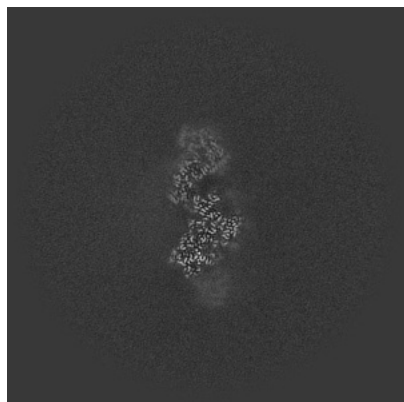


Z Index: 256

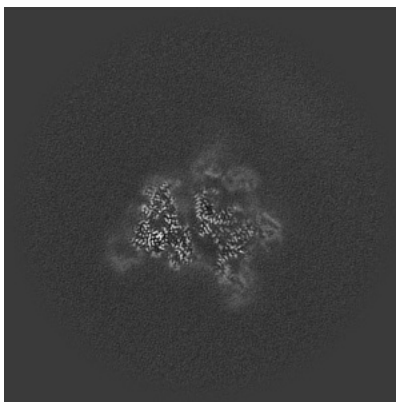
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

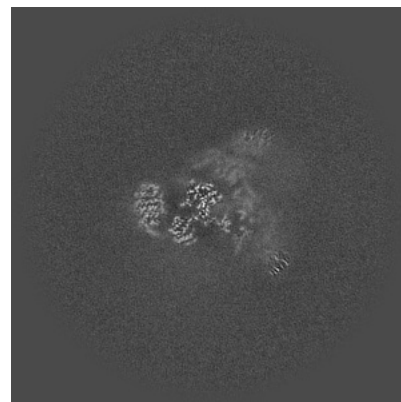
6.3.1 Primary map



X Index: 222

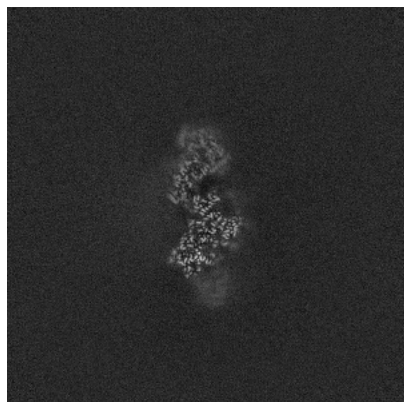


Y Index: 242

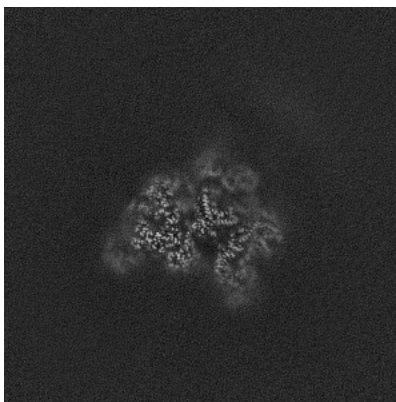


Z Index: 272

6.3.2 Raw map



X Index: 222



Y Index: 245

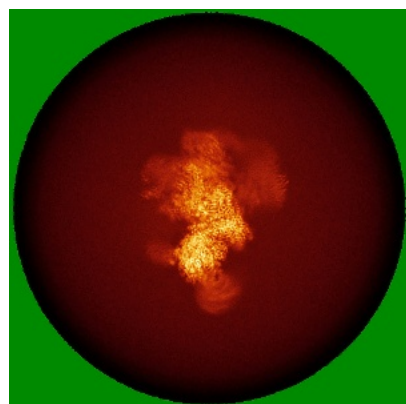


Z Index: 272

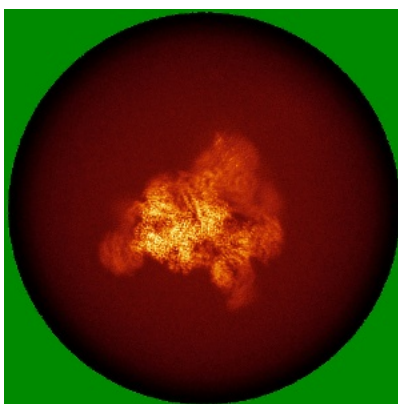
The images above show the largest variance slices of the map in three orthogonal directions.

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

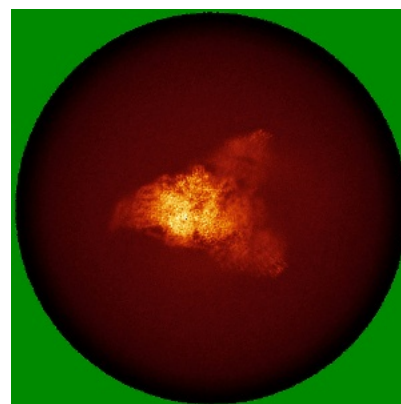
6.4.1 Primary map



X

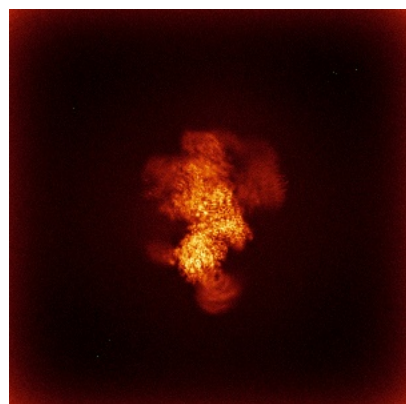


Y

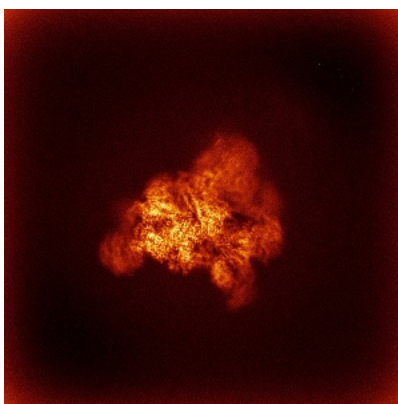


Z

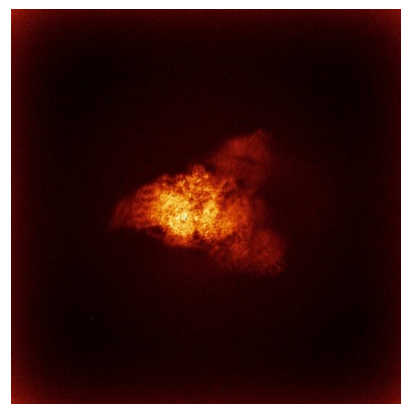
6.4.2 Raw map



X



Y

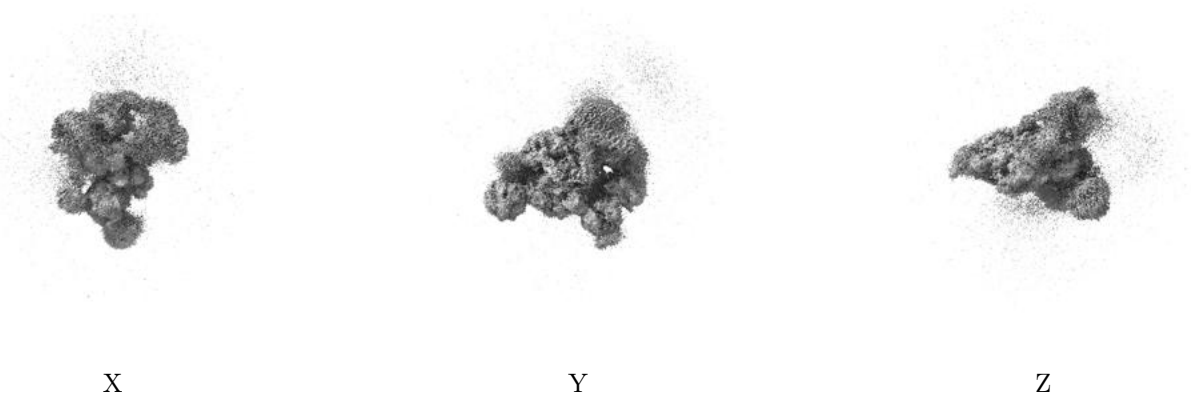


Z

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.

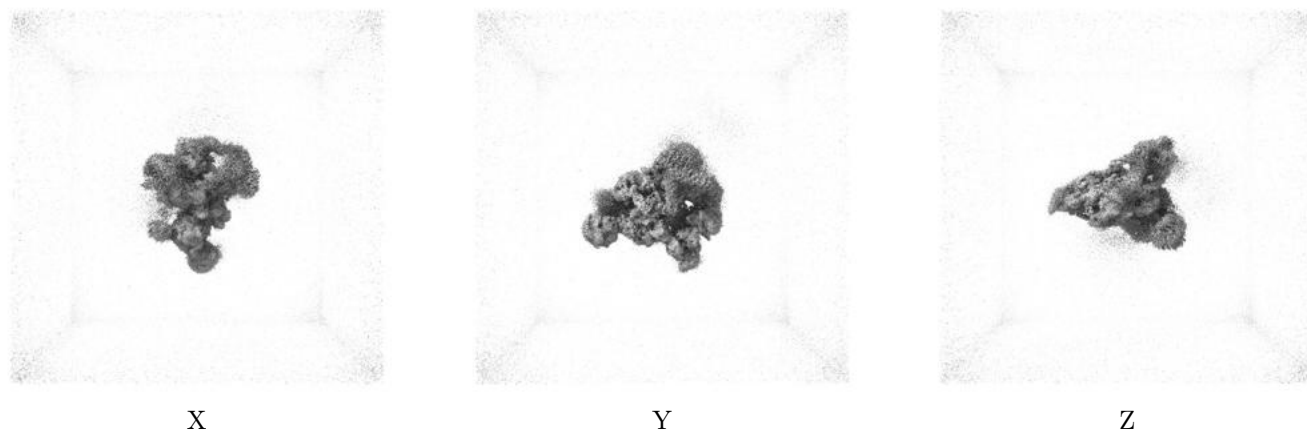
6.5 Orthogonal surface views [i](#)

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.

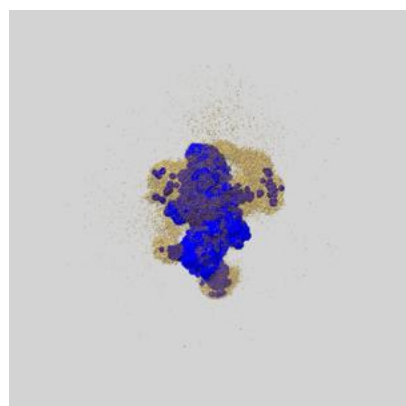
6.6 Mask visualisation [i](#)

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

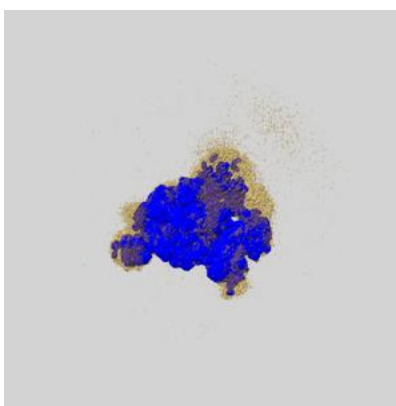
A mask typically either:

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

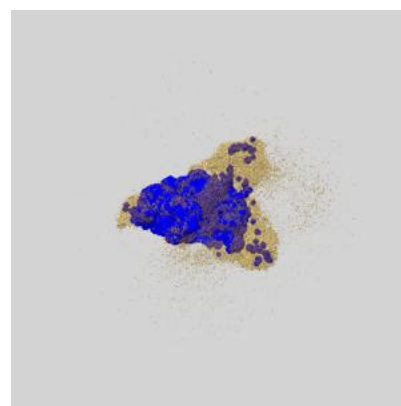
6.6.1 emd_34505_msk_1.map [i](#)



X



Y

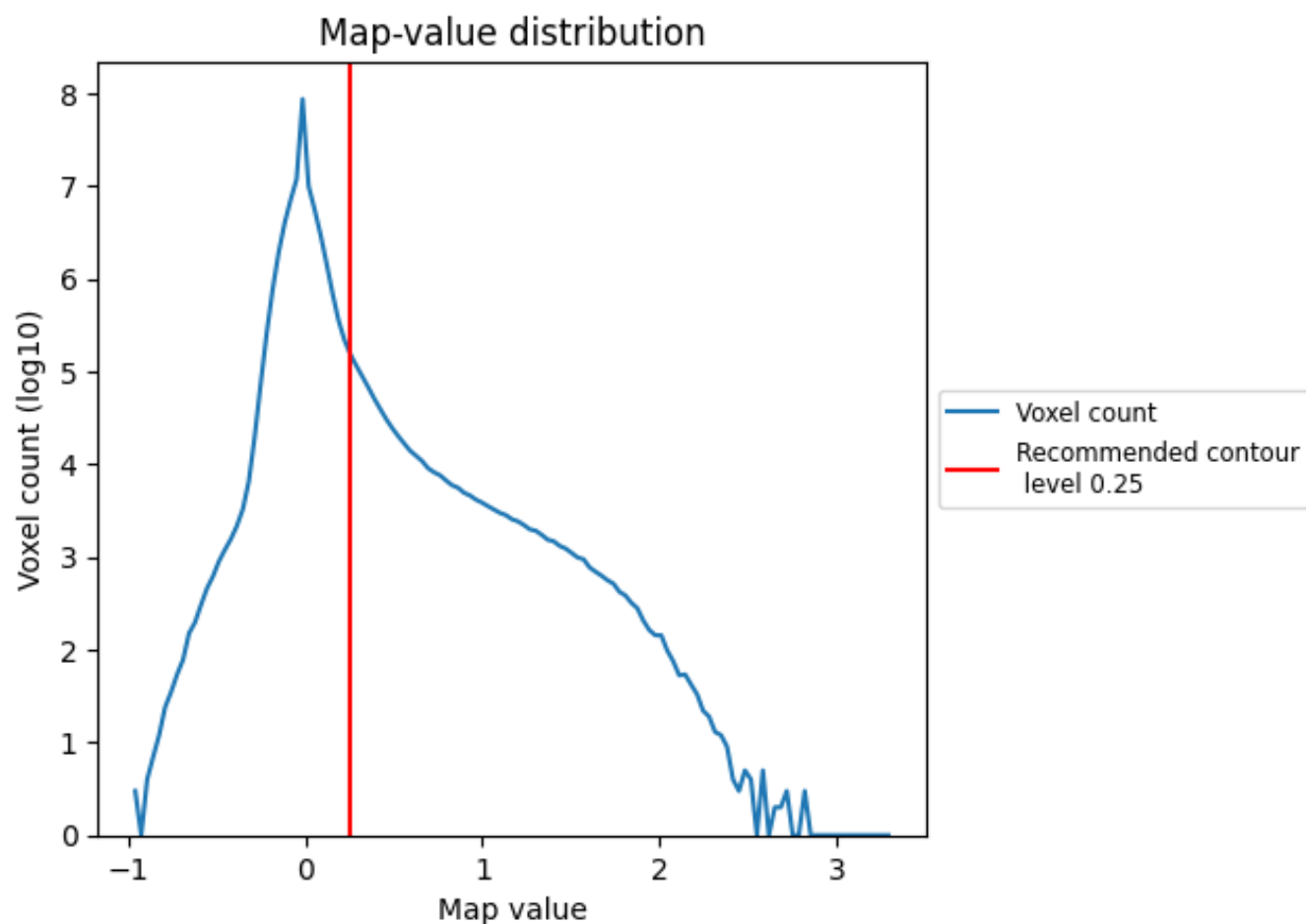


Z

7 Map analysis [i](#)

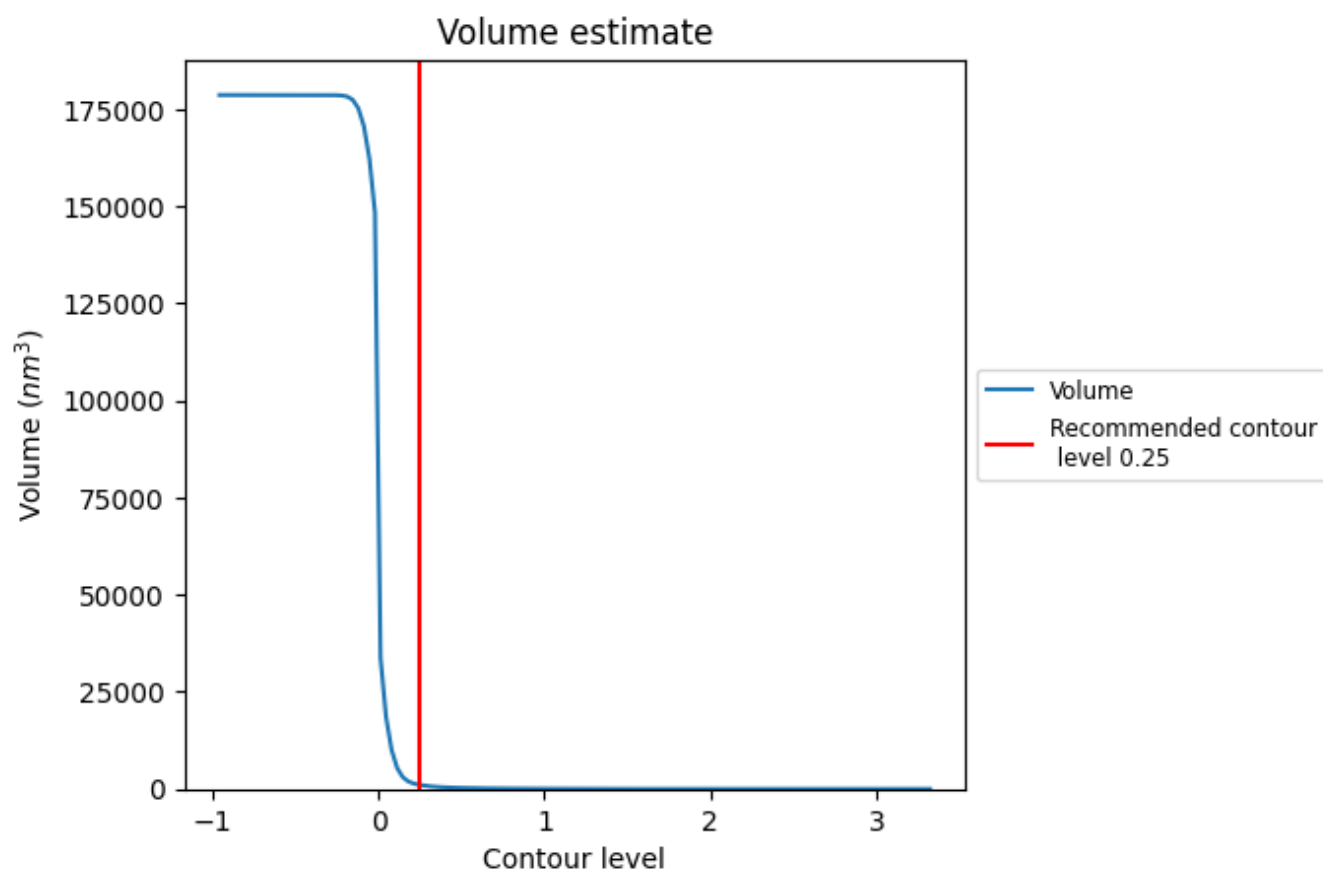
This section contains the results of statistical analysis of the map.

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.

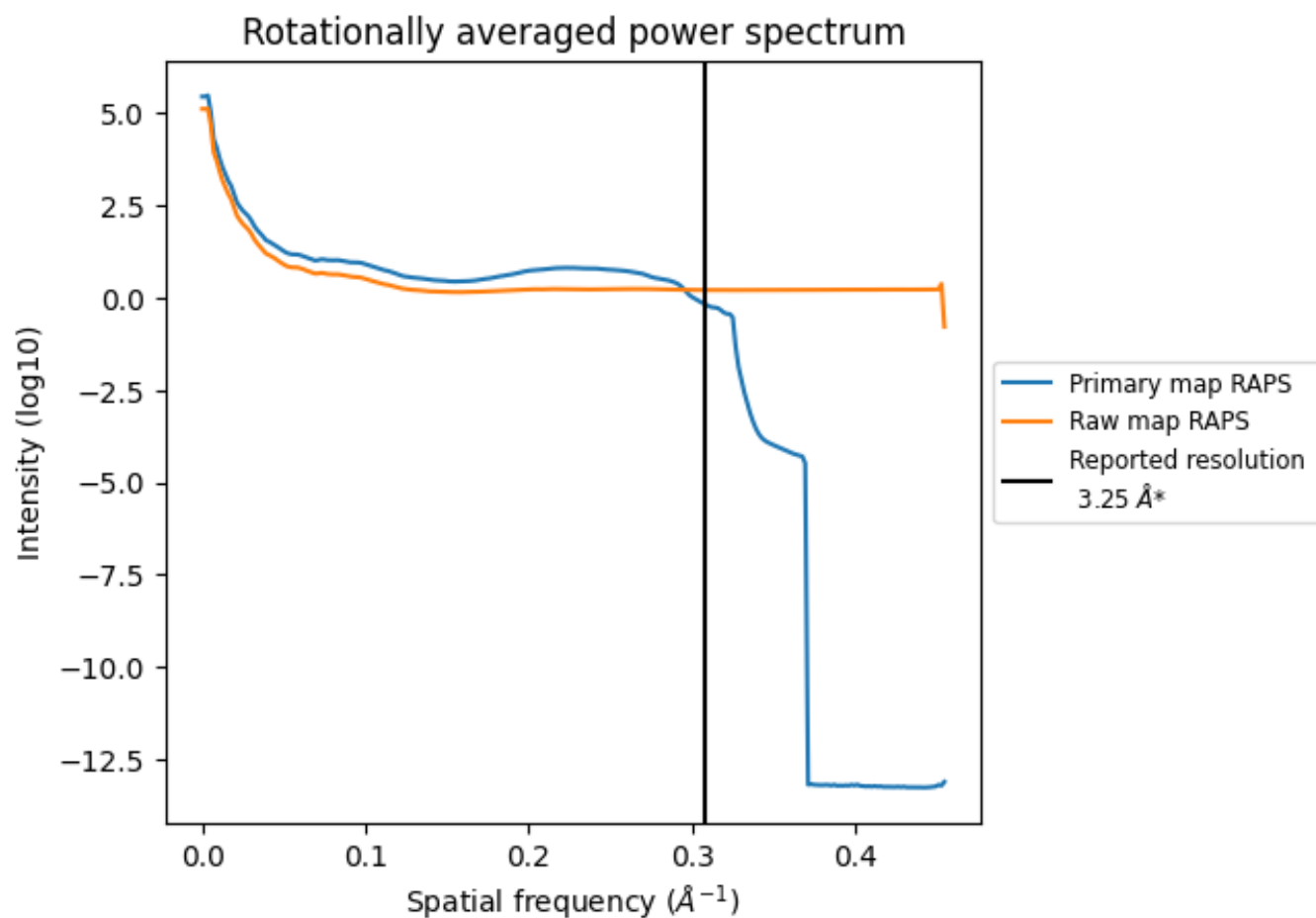
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1031 nm^3 ; this corresponds to an approximate mass of 932 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 ⓘ

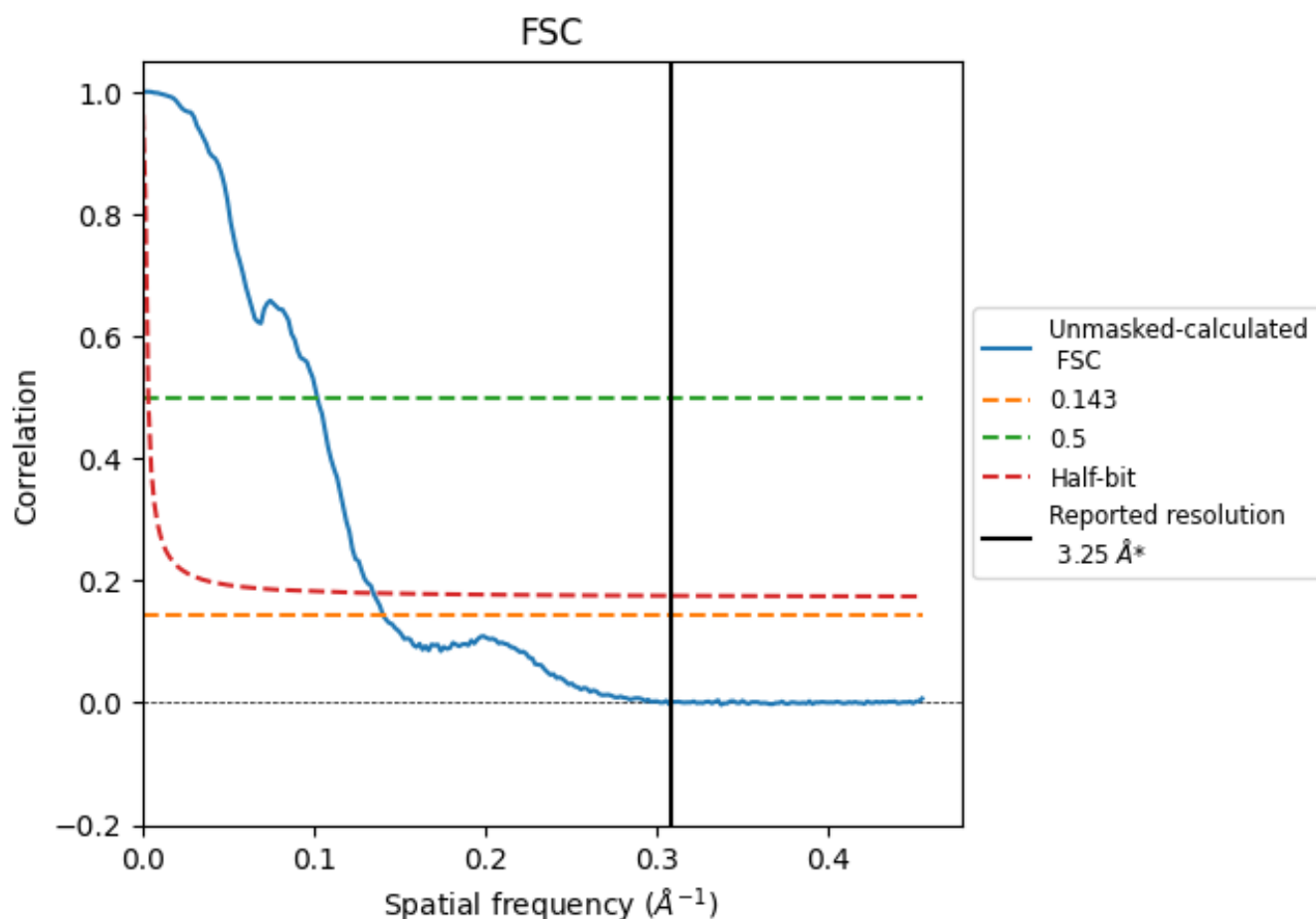


*Reported resolution corresponds to spatial frequency of 0.308 $\text{\AA}^{-1}$

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 $0.308 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

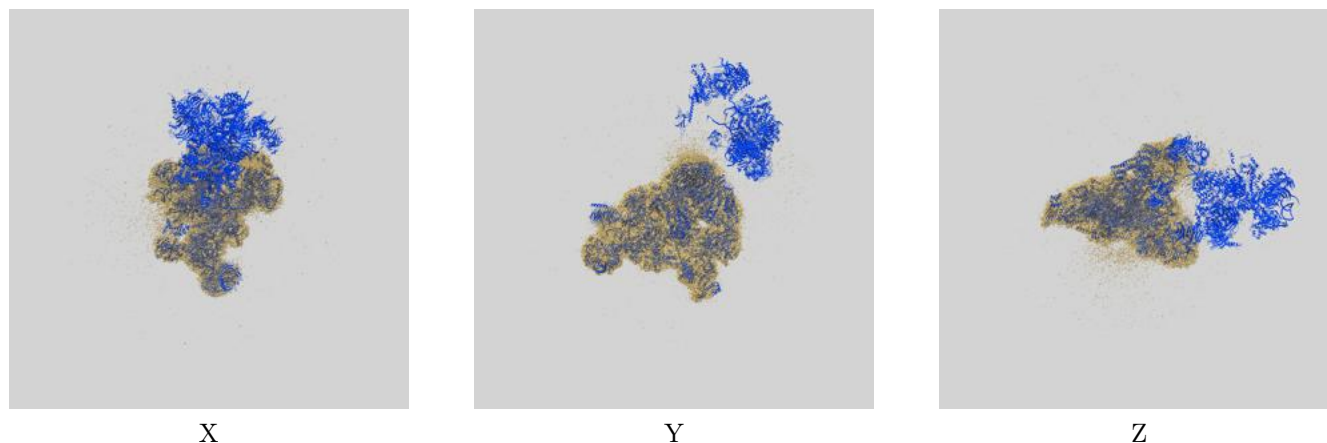
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.25	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.13	9.80	7.42

*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 7.13 differs from the reported value 3.25 by more than 10 %

9 Map-model fit [i](#)

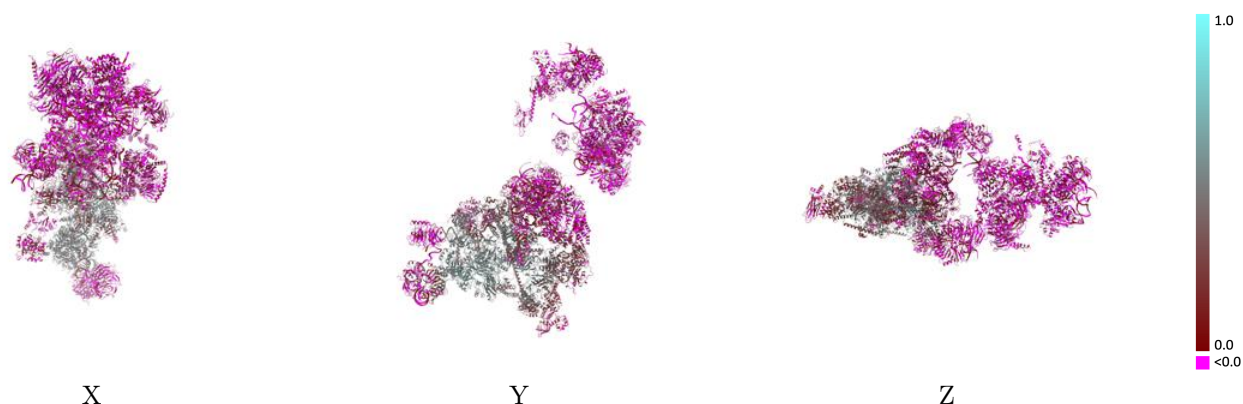
This section contains information regarding the fit between EMDB map EMD-34505 and PDB model 8H6J. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



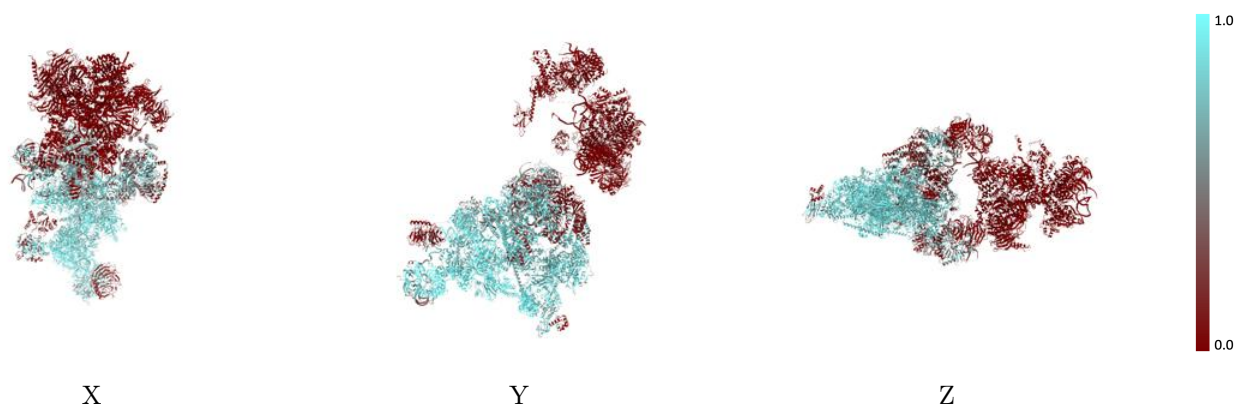
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



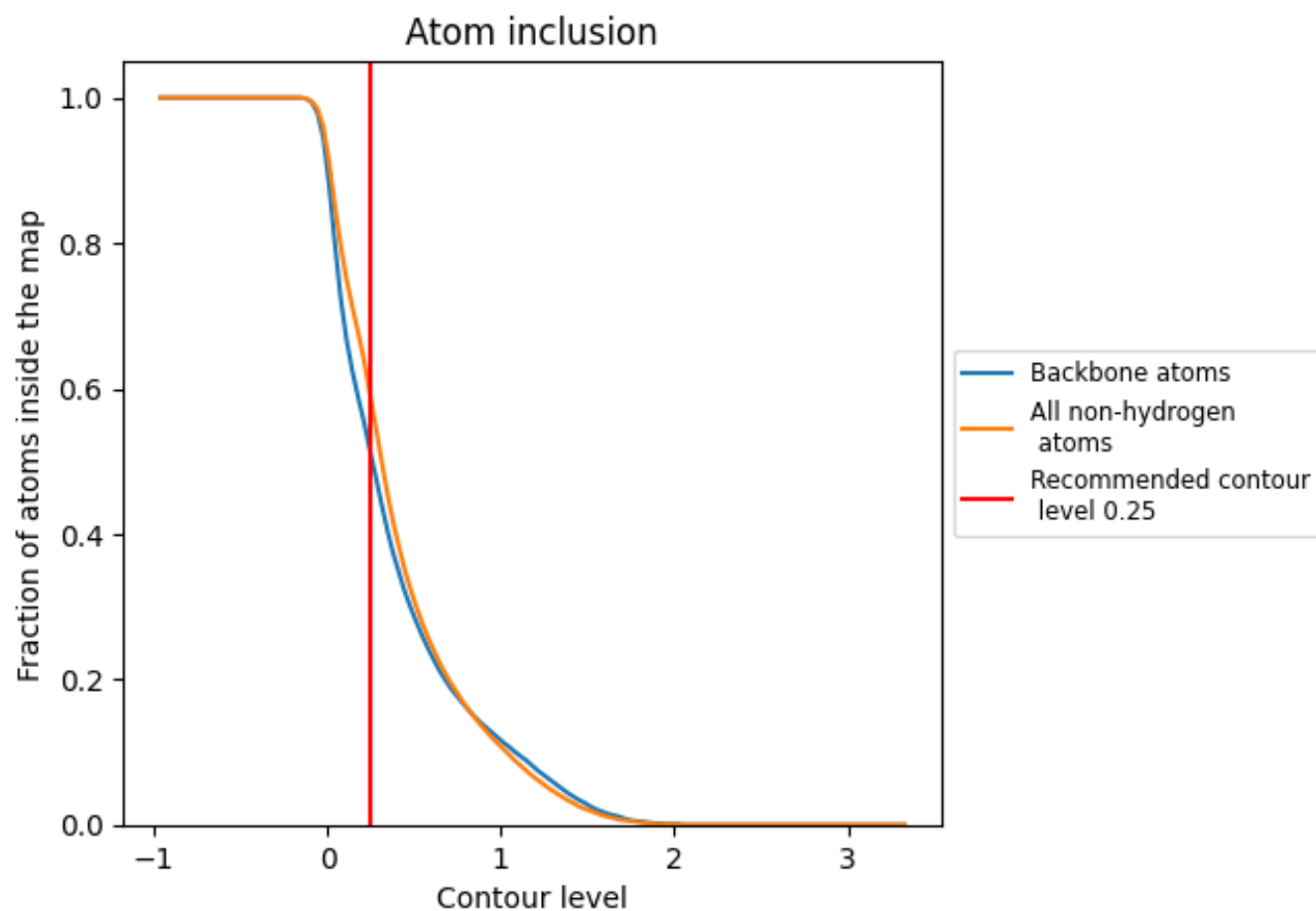
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 51% of all backbone atoms, 59% 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	 0.5890	 0.2240
2A	 0.0010	 -0.0090
2B	 0.0000	 0.0020
2C	 0.0000	 -0.0250
2D	 0.0000	 -0.0050
2E	 0.0000	 -0.0070
2F	 0.0000	 -0.0040
2G	 0.0000	 -0.0130
2H	 0.0000	 -0.0150
2I	 0.0000	 -0.0050
2J	 0.0000	 0.0460
2K	 0.0000	 0.0320
2L	 0.0030	 0.0220
2M	 0.0040	 0.0130
2a	 0.0000	 -0.0400
2b	 0.0000	 0.0190
2c	 0.0000	 0.0430
2d	 0.0000	 -0.0030
2e	 0.0000	 0.0050
2f	 0.0040	 0.0320
2g	 0.0000	 -0.0340
4A	 0.6140	 0.0630
4B	 0.3690	 0.0180
4C	 0.4930	 0.0170
4D	 0.4580	 0.1080
4E	 0.6550	 0.1050
4F	 0.9280	 0.3440
4G	 0.6020	 0.1260
4R	 0.6290	 0.1390
4S	 0.7320	 0.2420
4T	 0.9740	 0.4940
4U	 0.5510	 0.1870
4X	 0.6610	 0.0650
4Y	 0.0040	 0.0250
4a	 0.5210	 0.0460



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Chain	Atom inclusion	Q-score
4b	 0.5810	 0.0520
4c	 0.3080	 0.0180
4d	 0.3190	 0.0190
4e	 0.4070	 0.0180
4f	 0.4790	 0.0320
4g	 0.4910	 0.0270
5A	 0.8090	 0.2300
5B	 0.9200	 0.4330
5C	 0.9680	 0.5180
5D	 0.8510	 0.3060
5E	 0.0920	 -0.0080
5a	 0.7880	 0.1740
5b	 0.8840	 0.1430
5c	 0.7550	 0.0820
5d	 0.7940	 0.0890
5e	 0.8700	 0.1520
5f	 0.8580	 0.2450
5g	 0.9770	 0.3590
6A	 0.5270	 0.0800
6a	 0.0000	 -0.0160
6b	 0.0000	 0.0040
6c	 0.0000	 0.0300
6d	 0.0000	 0.0130
6e	 0.0000	 0.0170
6f	 0.0000	 0.0310
6g	 0.0000	 0.0220
A	 0.0000	 -0.0130