



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 01:37 AM UTC

PDB ID : 8H6K / pdb_00008h6k
EMDB ID : EMD-34507
Title : Cryo-EM structure of human exon-defined spliceosome in the mature B state.
Authors : Zhang, W.; Zhan, X.; Zhang, X.; Bai, R.; Lei, J.; Yan, C.; Shi, Y.
Deposited on : 2022-10-18
Resolution : 2.70 Å(reported)

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A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

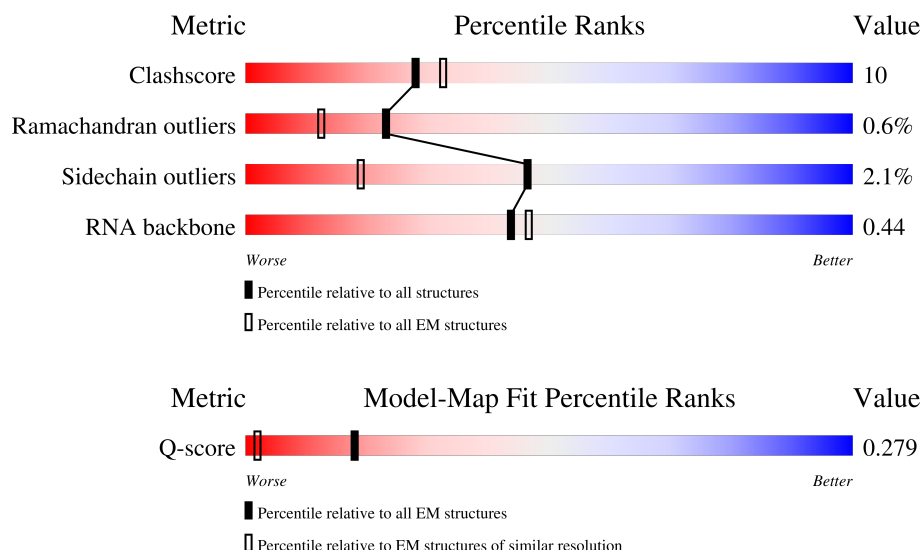
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.70 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.



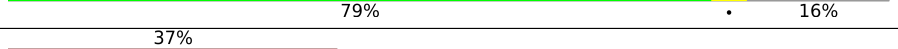
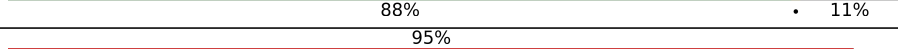
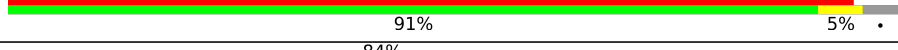
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10327 (2.20 - 3.20)

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

Mol	Chain	Length	Quality of chain
1	A	144	
2	5A	117	
3	5B	2335	

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Mol	Chain	Length	Quality of chain
4	5C	972	
5	5D	2136	
6	5E	357	
7	2a	231	
7	4a	231	
7	5a	231	
8	2b	119	
8	4b	119	
8	5b	119	
9	2c	118	
9	4c	118	
9	5c	118	
10	2d	86	
10	4d	86	
10	5d	86	
11	2e	92	
11	4e	92	
11	5e	92	
12	2f	76	
12	4f	76	
12	5f	76	
13	2g	126	
13	4g	126	
13	5g	126	
14	6A	107	

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Mol	Chain	Length	Quality of chain
15	6a	95	
16	6b	102	
17	6c	139	
18	6d	91	
19	6e	80	
20	6f	103	
21	6g	96	
22	4A	145	
23	4B	683	
24	4C	522	
25	4D	499	
26	4E	128	
27	4F	142	
28	4G	941	
29	4H	177	
30	4I	376	
31	4J	800	
32	4K	439	
33	4L	312	
34	4M	73	
35	4N	199	
36	4Z	513	
37	2A	188	
38	2B	255	
39	2C	225	

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Mol	Chain	Length	Quality of chain
40	2D	793	
41	2E	464	
42	2F	501	
43	2G	1304	
44	2H	895	
45	2I	1217	
46	2J	424	
47	2K	125	
48	2L	110	
49	2M	86	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 98459 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	64	Total	C	N	O	P	0	0
			1334	597	209	464	64		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5A	115	Total	C	N	O	P	0	0
			2420	1084	403	818	115		

- Molecule 3 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5B	2253	Total	C	N	O	S	0	0
			18639	11991	3249	3318	81		

- Molecule 4 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5C	818	Total	C	N	O	S	0	0
			6430	4108	1085	1205	32		

- Molecule 5 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5D	1696	Total	C	N	O	S	0	0
			13633	8715	2329	2519	70		

- Molecule 6 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	5E	299	Total	C	N	O	0	0
			1196	598	299	299		

- Molecule 7 is a protein called Isoform SM-B of Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	5a	84	Total	C	N	O	0	0
			336	168	84	84		
7	4a	64	Total	C	N	O	0	0
			256	128	64	64		
7	2a	86	Total	C	N	O	0	0
			344	172	86	86		

- Molecule 8 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	5b	82	Total	C	N	O	0	0
			328	164	82	82		
8	4b	82	Total	C	N	O	0	0
			334	170	82	82		
8	2b	82	Total	C	N	O	0	0
			328	164	82	82		

- Molecule 9 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	5c	97	Total	C	N	O	0	0
			388	194	97	97		
9	4c	74	Total	C	N	O	0	0
			300	152	74	74		
9	2c	85	Total	C	N	O	0	0
			340	170	85	85		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	5d	74	Total	C	N	O	0	0
			296	148	74	74		
10	4d	71	Total	C	N	O	0	0
			292	150	71	71		
10	2d	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	5e	79	Total	C	N	O	0	0
			316	158	79	79		
11	4e	78	Total	C	N	O	0	0
			314	158	78	78		
11	2e	79	Total	C	N	O	0	0
			316	158	79	79		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	5f	72	Total	C	N	O	0	0
			288	144	72	72		
12	4f	73	Total	C	N	O	0	0
			298	152	73	73		
12	2f	68	Total	C	N	O	0	0
			272	136	68	68		

- Molecule 13 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	5g	77	Total	C	N	O	0	0
			308	154	77	77		
13	4g	71	Total	C	N	O	0	0
			288	146	71	71		
13	2g	80	Total	C	N	O	0	0
			320	160	80	80		

- Molecule 14 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	6A	60	Total	C	N	O	P	0	0
			1273	568	235	410	60		

- Molecule 15 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	6a	90	Total	C	N	O	0	0
			360	180	90	90		

- Molecule 16 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	6b	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 17 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	6c	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 18 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	6d	72	Total	C	N	O	0	0
			288	144	72	72		

- Molecule 19 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	6e	70	Total	C	N	O	0	0
			280	140	70	70		

- Molecule 20 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	6f	65	Total	C	N	O	0	0
			260	130	65	65		

- Molecule 21 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	6g	61	Total	C	N	O	0	0
			244	122	61	61		

- Molecule 22 is a RNA chain called U4 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	4A	129	Total	C	N	O	P	0	0
			2744	1225	472	917	130		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	4B	256	Total	C	N	O	S	0	0
			2076	1316	385	367	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	4C	426	Total	C	N	O	S	0	0
			3370	2118	612	620	20		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	4D	376	Total	C	N	O	S	0	0
			2874	1788	524	550	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4E	124	Total	C	N	O	S	0	0
			962	608	171	178	5		

- 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	801	Total	C	N	O	S	0	0
			5504	3419	1043	1026	16		

- Molecule 29 is a protein called Peptidyl-prolyl cis-trans isomerase H.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	4H	169	Total	C	N	O	0	0
			844	506	169	169		

- Molecule 30 is a protein called WW domain-binding protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4I	75	Total	C	N	O	S	0	0
			494	304	96	91	3		

- Molecule 31 is a protein called U4/U6.U5 tri-snRNP-associated protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4J	152	Total	C	N	O	S	0	0
			1144	709	204	229	2		

- Molecule 32 is a protein called Microfibrillar-associated protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	4K	188	Total	C	N	O	S	0	0
			1192	741	219	230	2		

- Molecule 33 is a protein called Pre-mRNA-splicing factor 38A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	4L	175	Total	C	N	O	S	0	0
			1452	934	244	265	9		

- Molecule 34 is a protein called Ubiquitin-like protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	4M	73	Total	C	N	O	S	0	0
			599	383	103	109	4		

- Molecule 35 is a protein called Zinc finger matrin-type protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	4N	80	Total	C	N	O	S	0	0
			640	397	116	120	7		

- Molecule 36 is a protein called WD40 repeat-containing protein SMU1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	4Z	420	Total	C	N	O		0	0
			2092	1252	420	420			

- Molecule 37 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	2A	109	Total	C	N	O	P	0	0
			2311	1032	396	774	109		

- Molecule 38 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	2B	162	Total	C	N	O	0	0
			648	324	162	162		

- Molecule 39 is a protein called U2 small nuclear ribonucleoprotein B'.

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

- Molecule 40 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	2D	204	Total	C	N	O	S	0	0
			1134	644	238	250	2		

- Molecule 41 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	2E	94	Total	C	N	O	0	0
			376	188	94	94		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
42	2F	423	Total	C	N	O	0	0
			1693	847	423	423		

- Molecule 43 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	2G	1048	Total	C	N	O	0	0
			4192	2096	1048	1048		

- Molecule 44 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	2H	213	Total	C	N	O	S	0	0
			959	510	220	226	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2I	1168	Total	C	N	O		0	0
			4672	2336	1168	1168			

- Molecule 46 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	2J	78	Total	C	N	O		0	0
			312	156	78	78			

- Molecule 47 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2K	108	Total	C	N	O		0	0
			432	216	108	108			

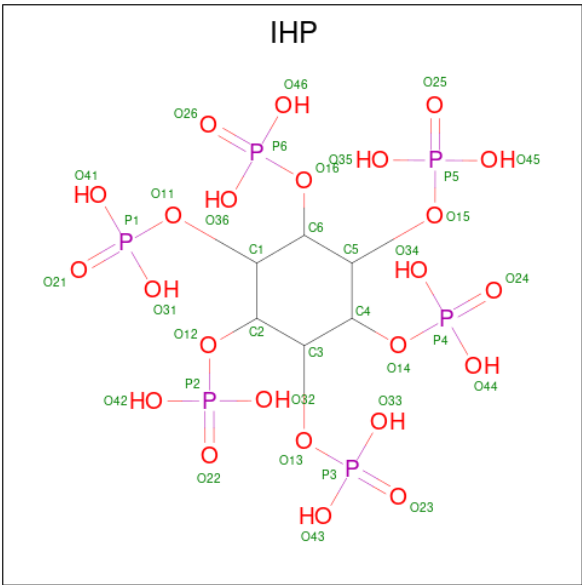
- Molecule 48 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	2L	89	Total	C	N	O		0	0
			356	178	89	89			

- Molecule 49 is a protein called Splicing factor 3B subunit 5.

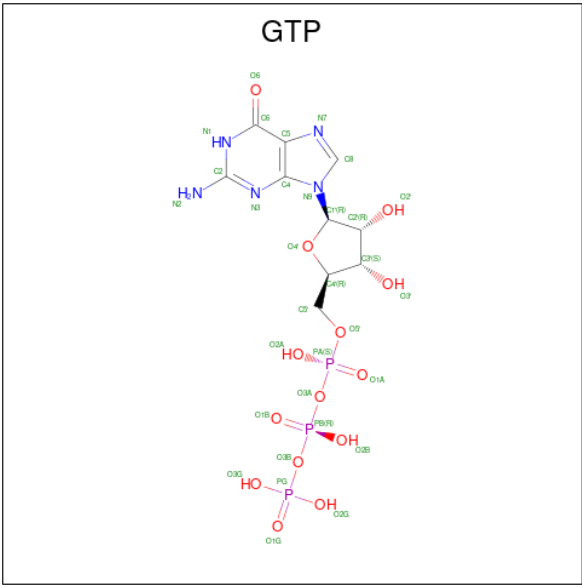
Mol	Chain	Residues	Atoms					AltConf	Trace
49	2M	66	Total	C	N	O		0	0
			264	132	66	66			

- Molecule 50 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: C₆H₁₈O₂₄P₆).



Mol	Chain	Residues	Atoms				AltConf
50	5B	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 51 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
51	5C	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 52 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
52	5C	1	Total	Mg	0
			1	1	

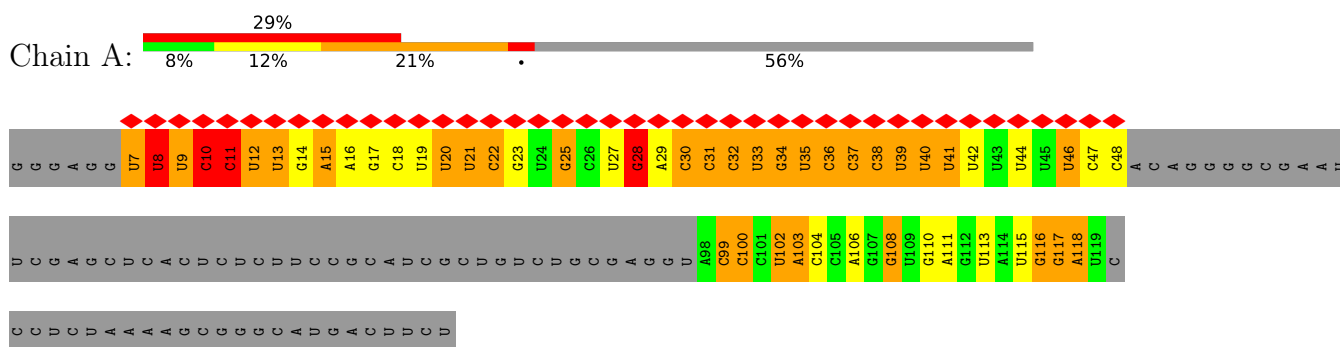
- Molecule 53 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
53	4I	1	Total	Zn	0
			1	1	
53	4N	1	Total	Zn	0
			1	1	

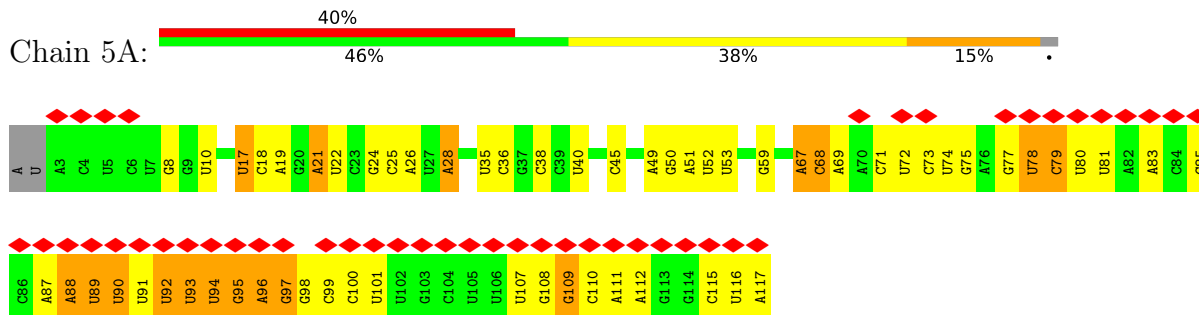
3 Residue-property plots

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

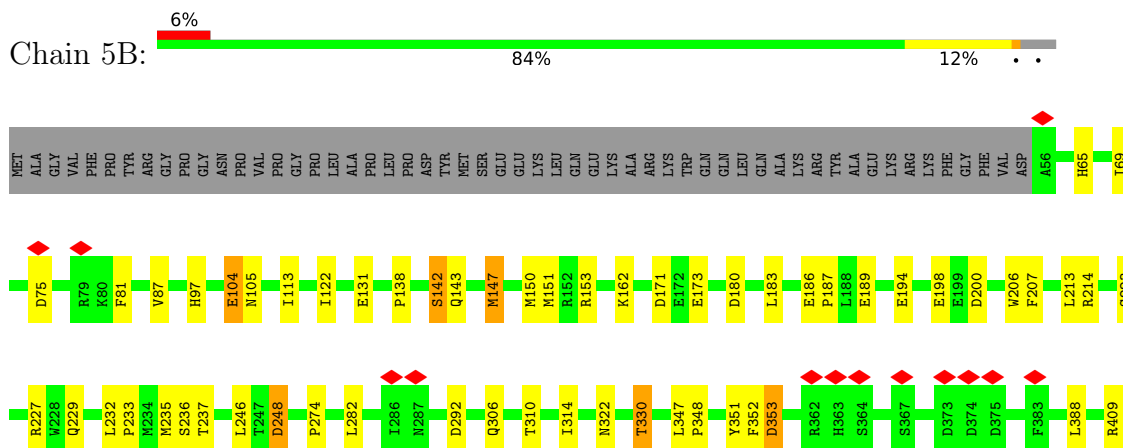
• Molecule 1: pre-mRNA

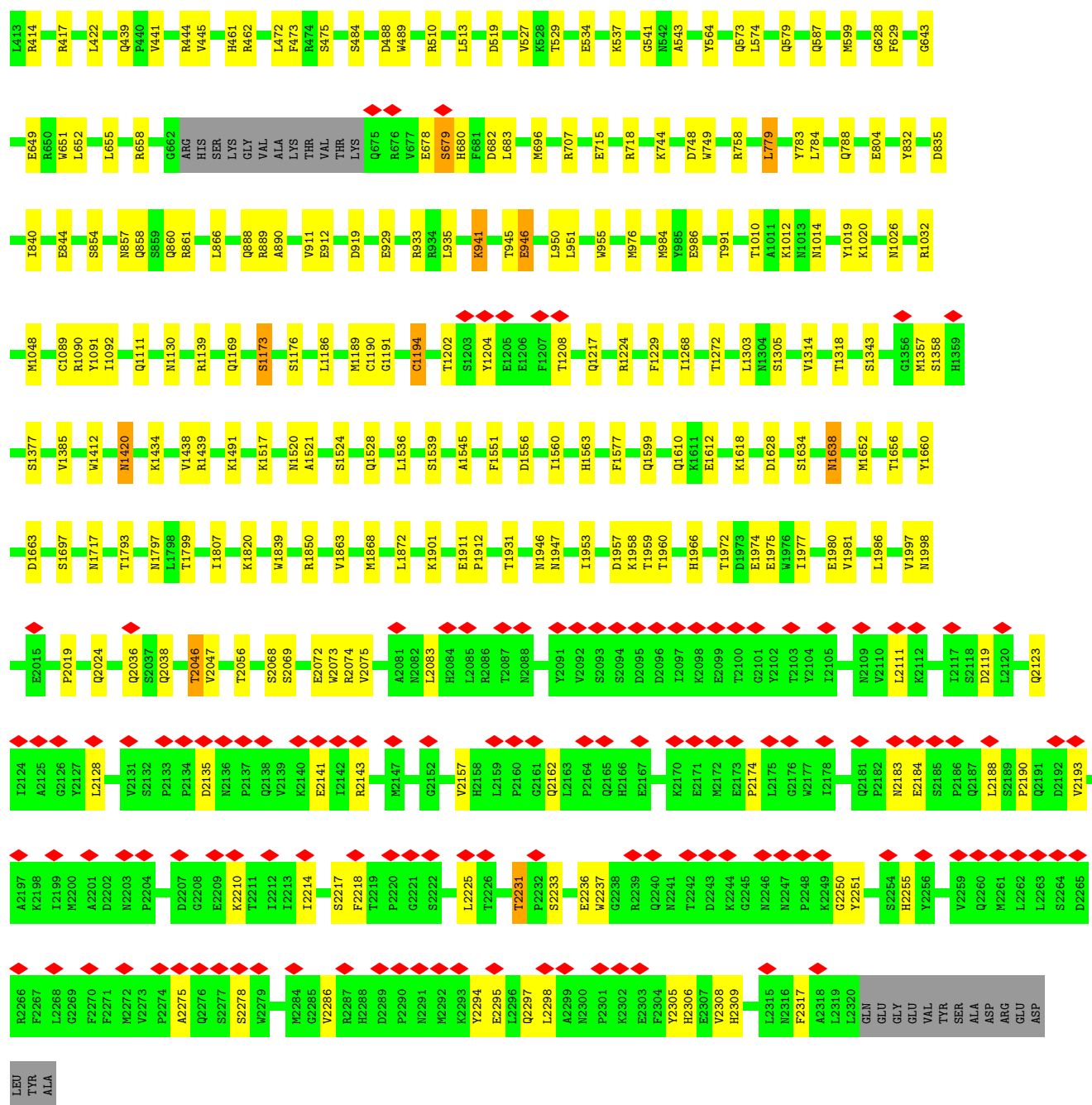


• Molecule 2: U5 snRNA



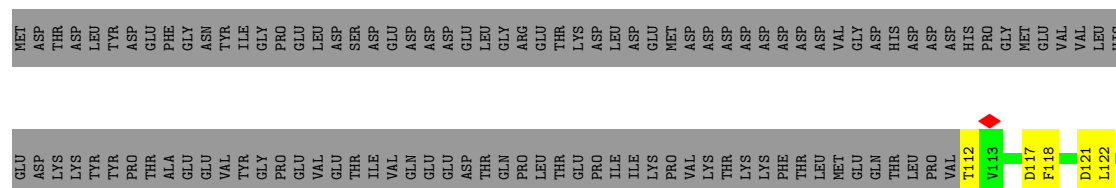
• Molecule 3: Pre-mRNA-processing-splicing factor 8

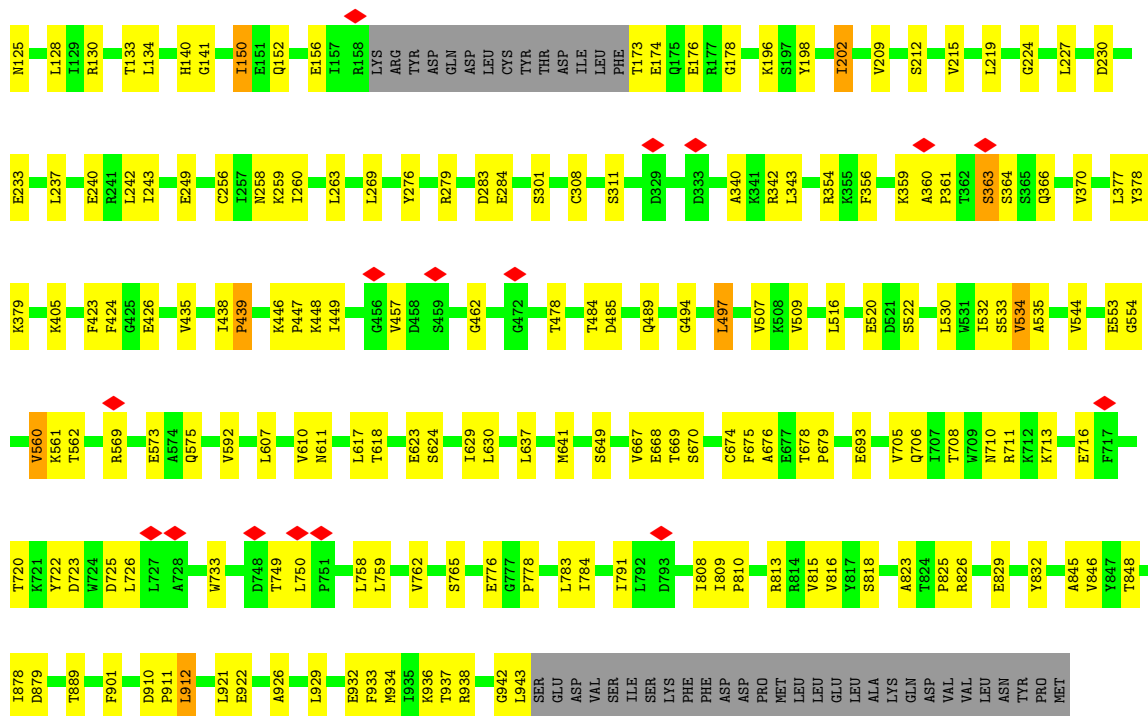




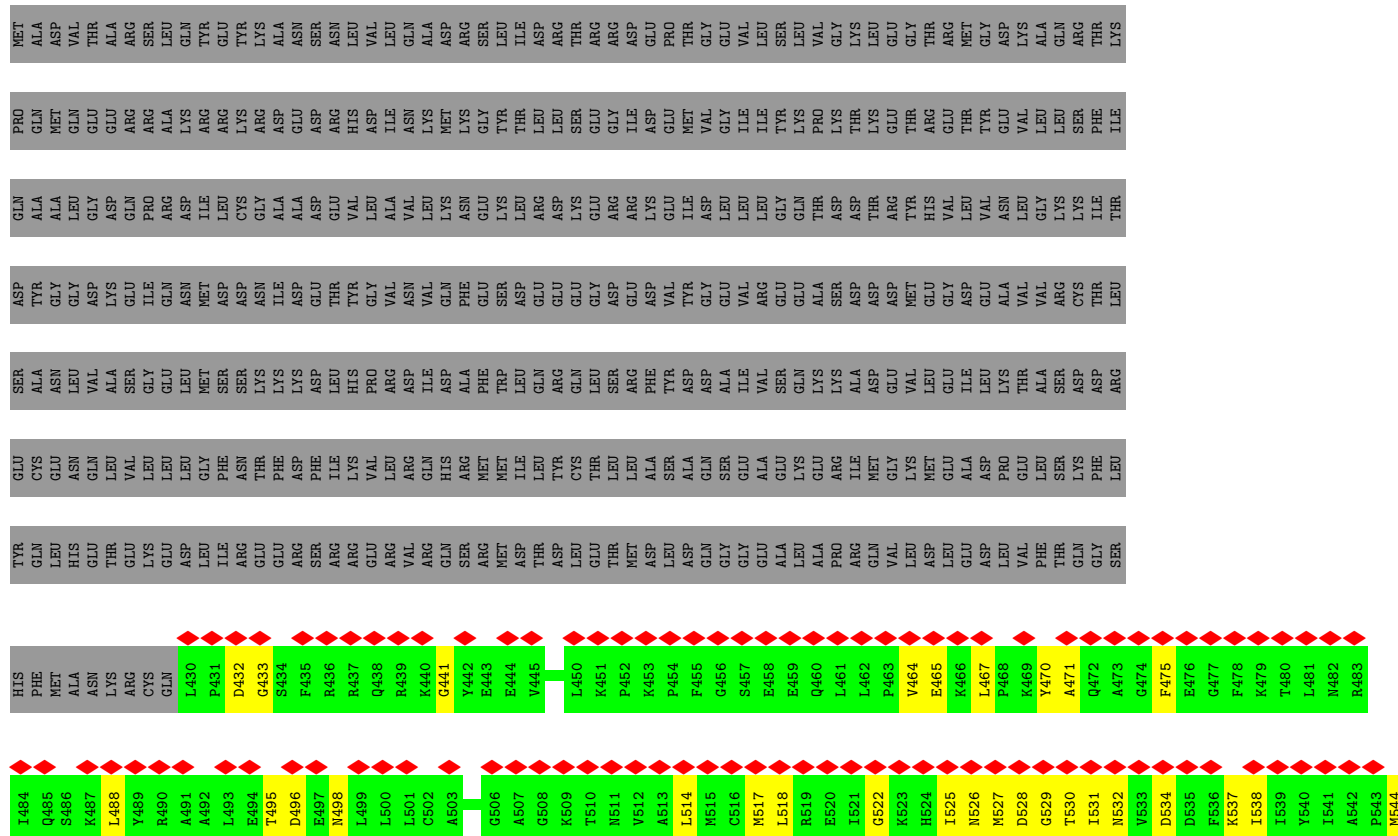
- Molecule 4: 116 kDa U5 small nuclear ribonucleoprotein component

Chain 5C:





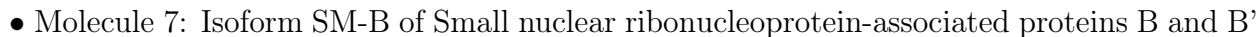
• Molecule 5: U5 small nuclear ribonucleoprotein 200 kDa helicase



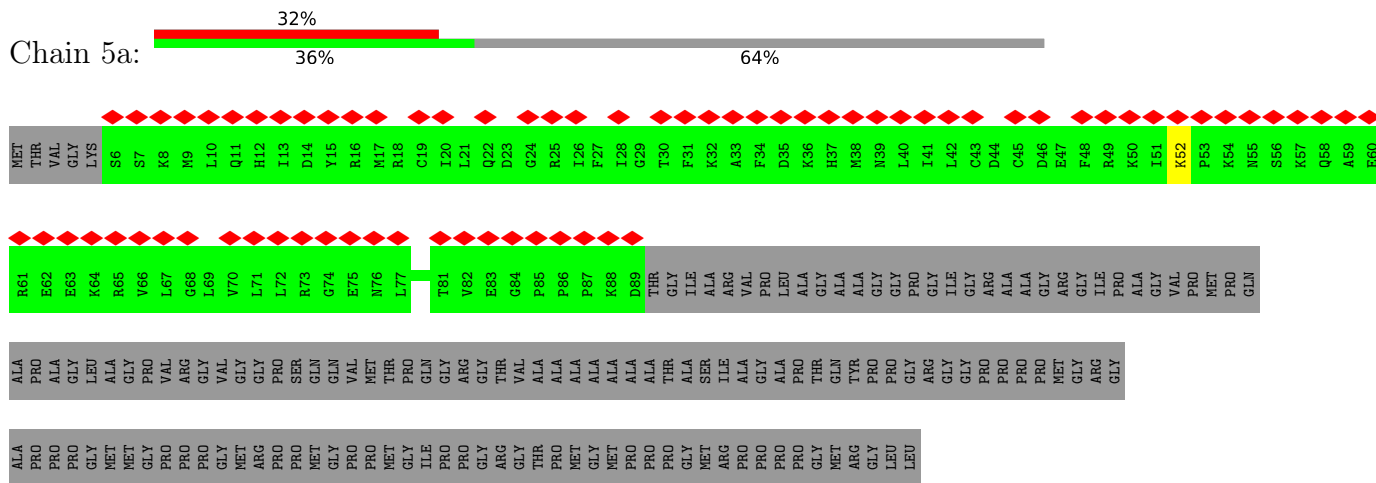
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V2124	VAL
D2125	LYS
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	ALA
	GLU
	THR
	ASP
	SER
	ASP
	SER
	ASP

- Chain 5E:

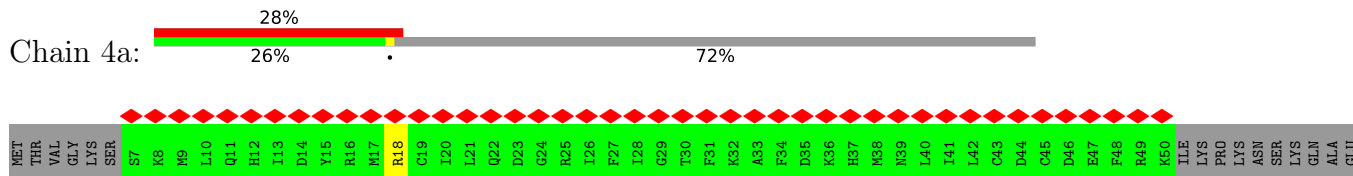


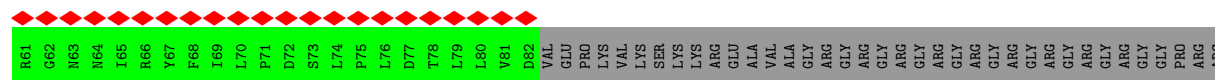
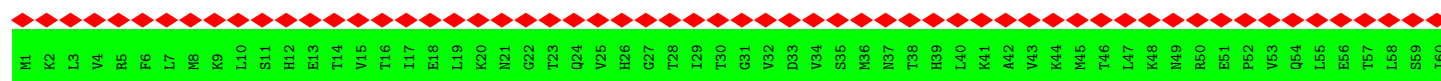
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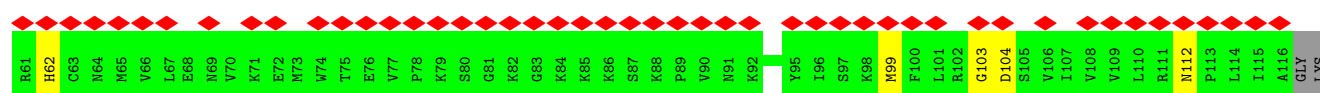
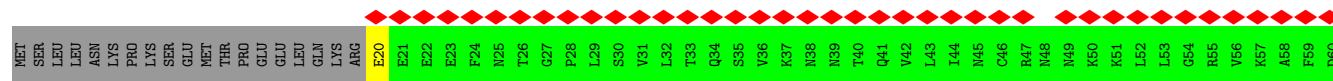
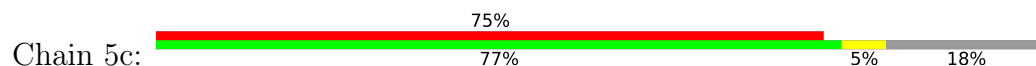
- Molecule 7: Isoform SM-B of Small nuclear ribonucleoprotein-associated proteins B and B'

Chain 4a:

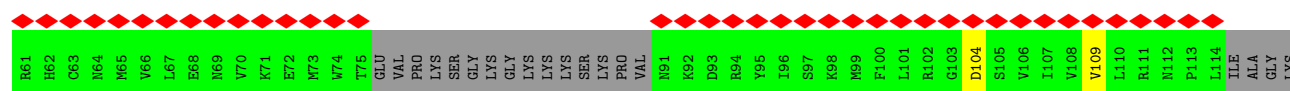
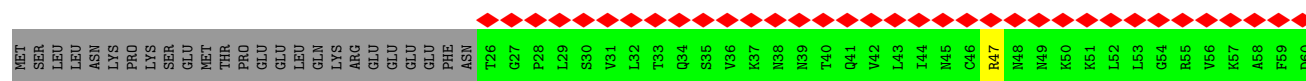




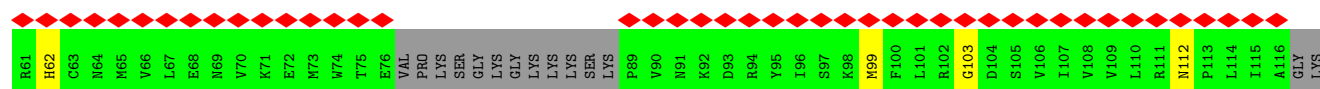
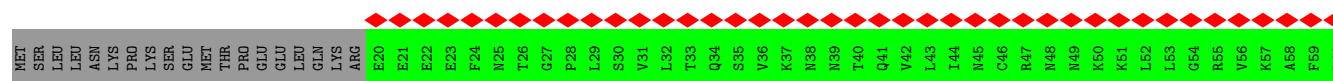
- Molecule 9: Small nuclear ribonucleoprotein Sm D2



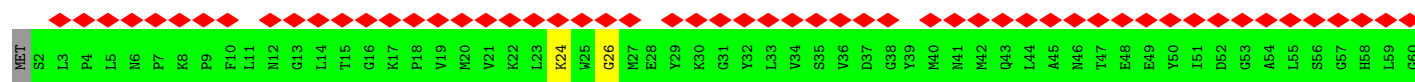
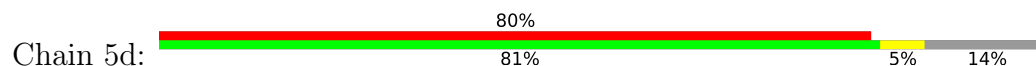
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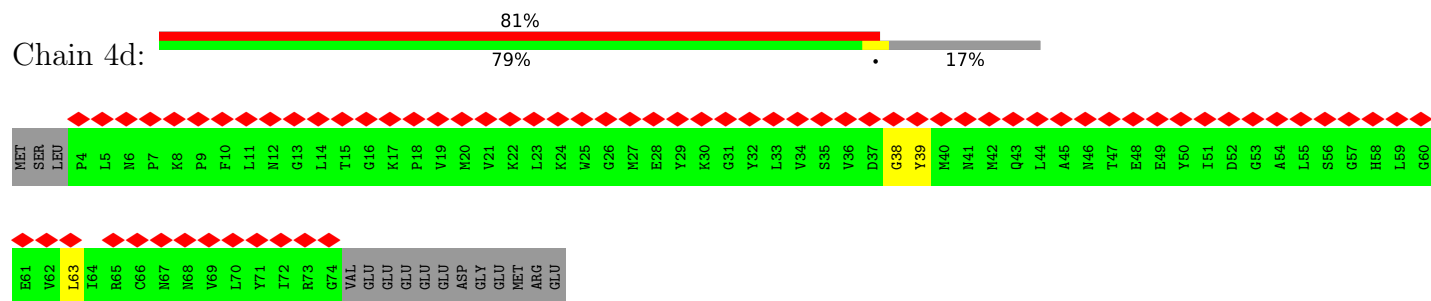
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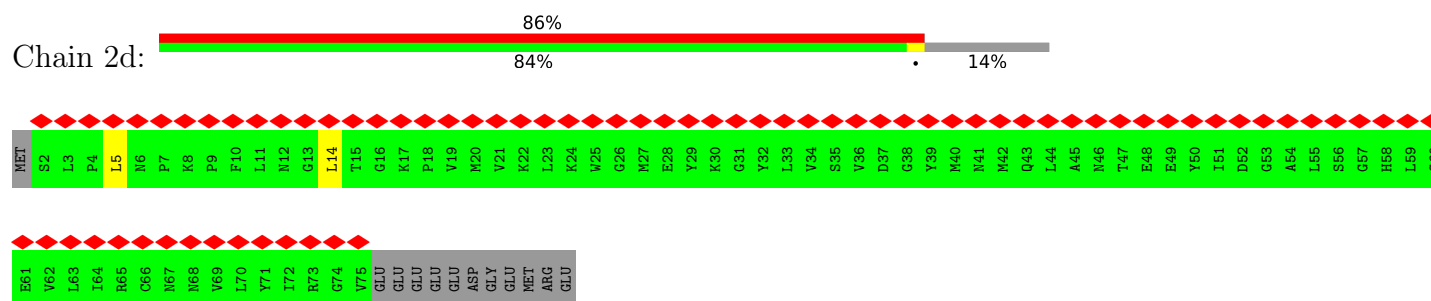
- Molecule 10: Small nuclear ribonucleoprotein F



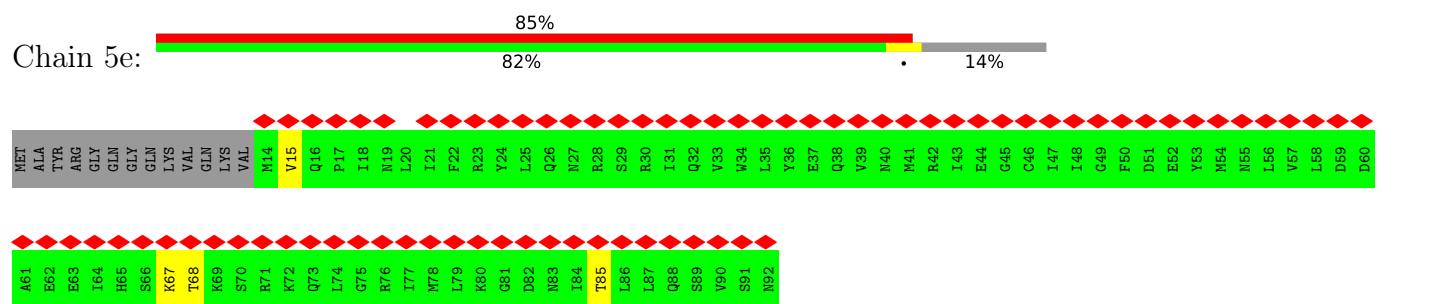
- Molecule 10: Small nuclear ribonucleoprotein F



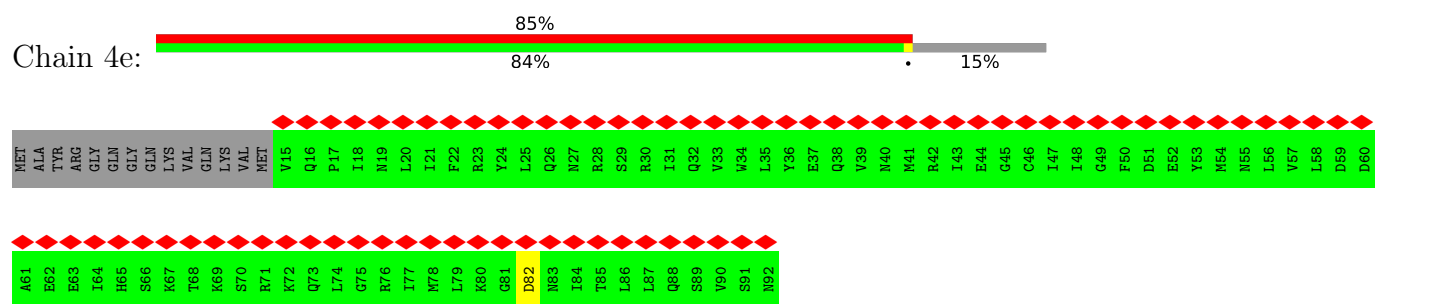
- Molecule 10: Small nuclear ribonucleoprotein F



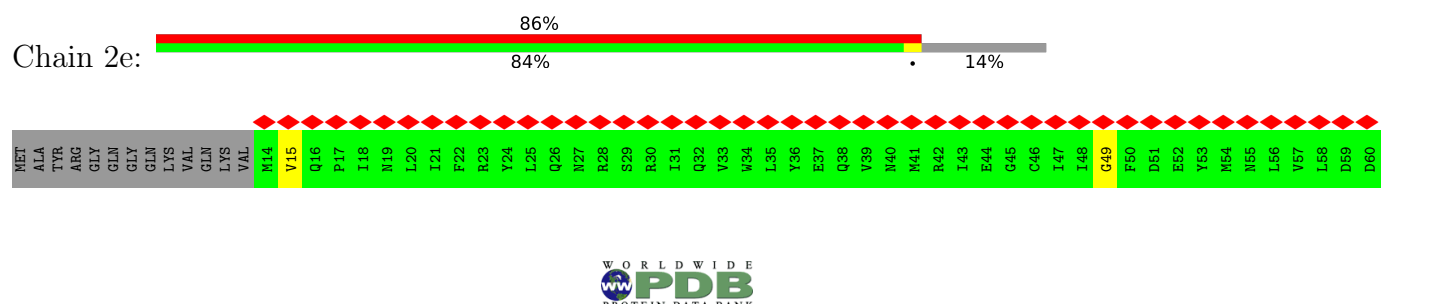
- Molecule 11: Small nuclear ribonucleoprotein E



- Molecule 11: Small nuclear ribonucleoprotein E

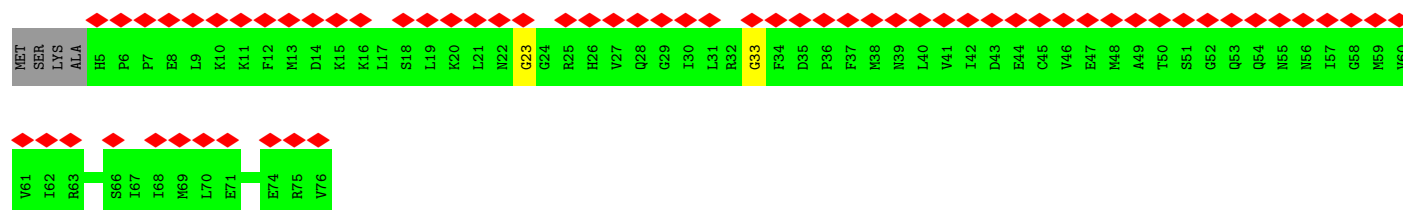
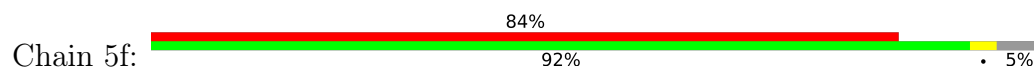


- Molecule 11: Small nuclear ribonucleoprotein E

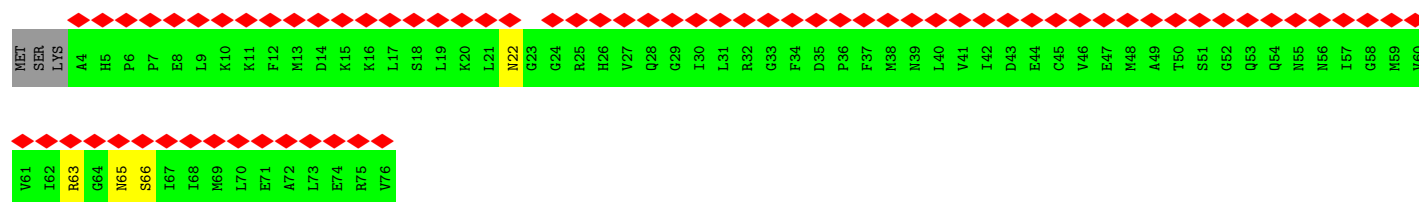
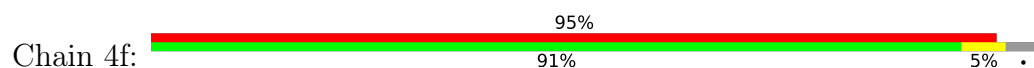




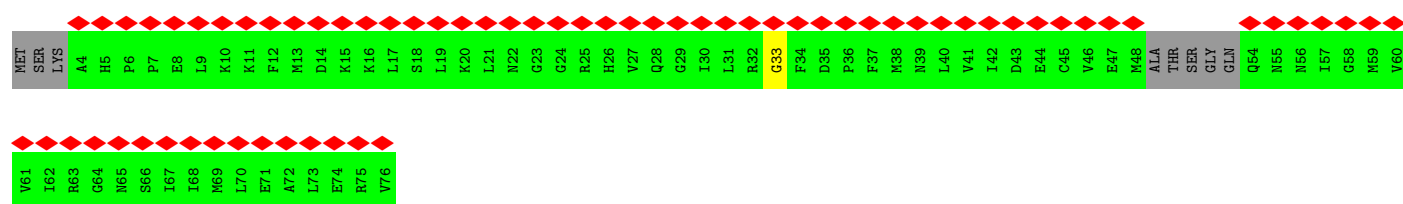
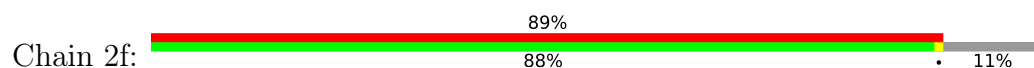
• Molecule 12: Small nuclear ribonucleoprotein G



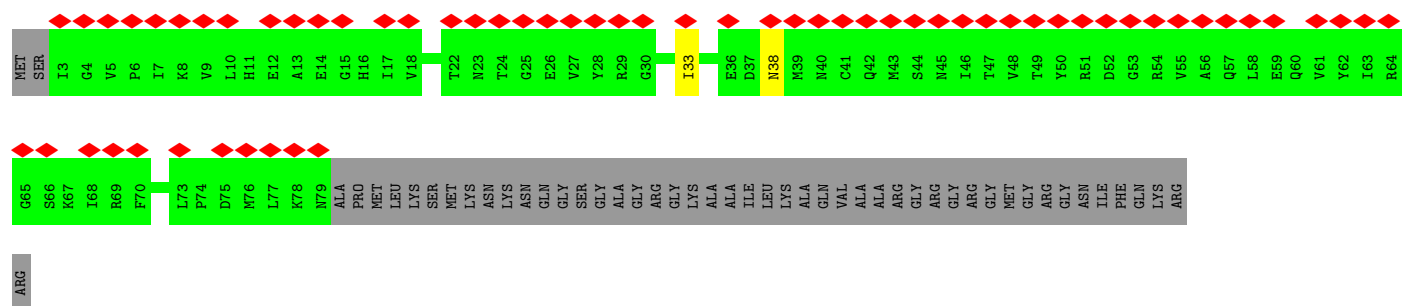
• Molecule 12: Small nuclear ribonucleoprotein G



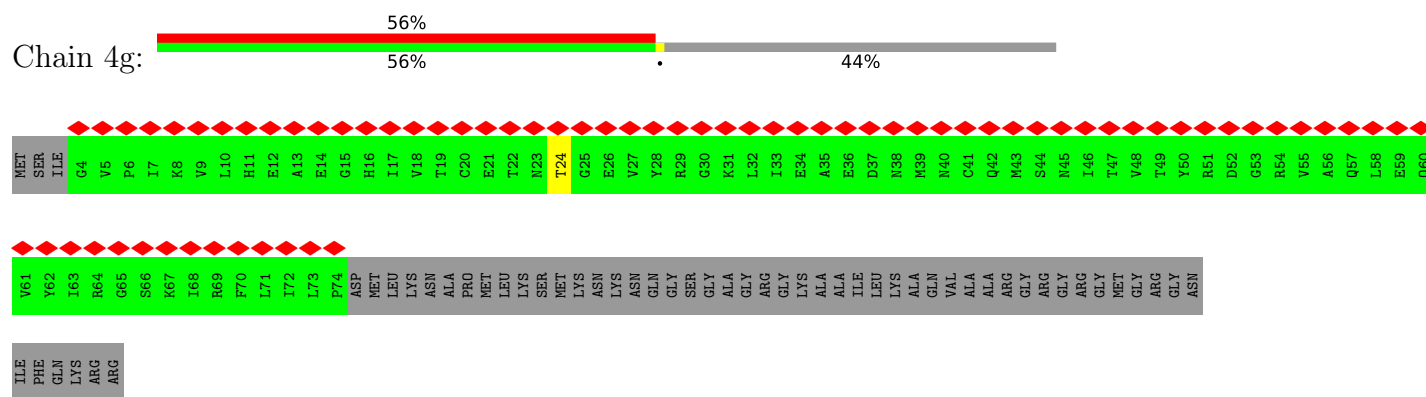
• Molecule 12: Small nuclear ribonucleoprotein G



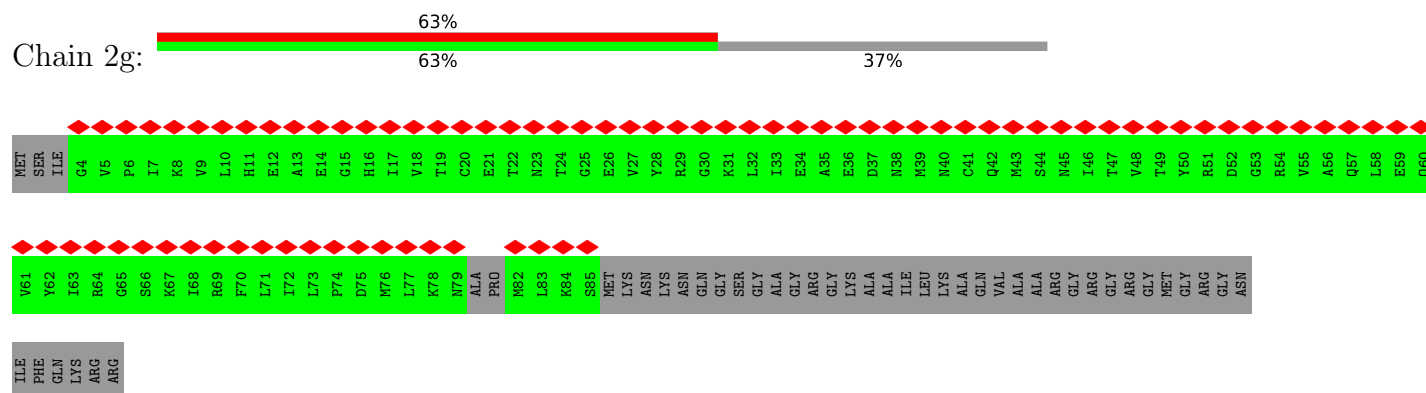
• Molecule 13: Small nuclear ribonucleoprotein Sm D3



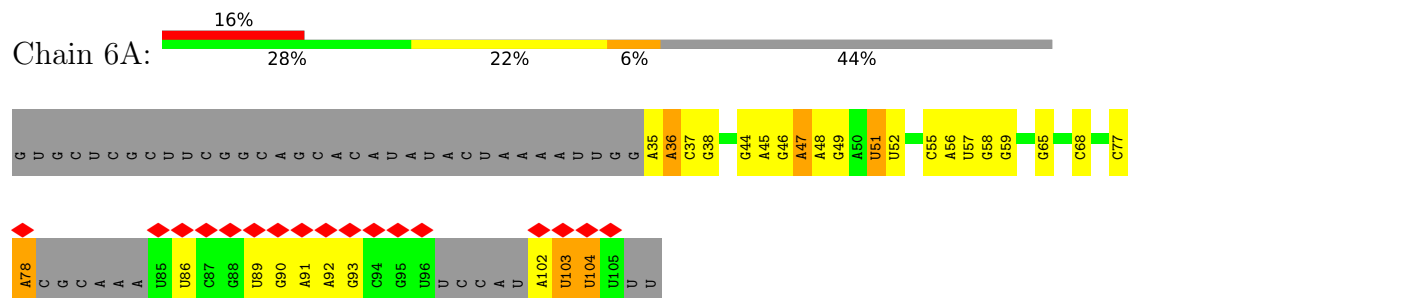
• Molecule 13: Small nuclear ribonucleoprotein Sm D3



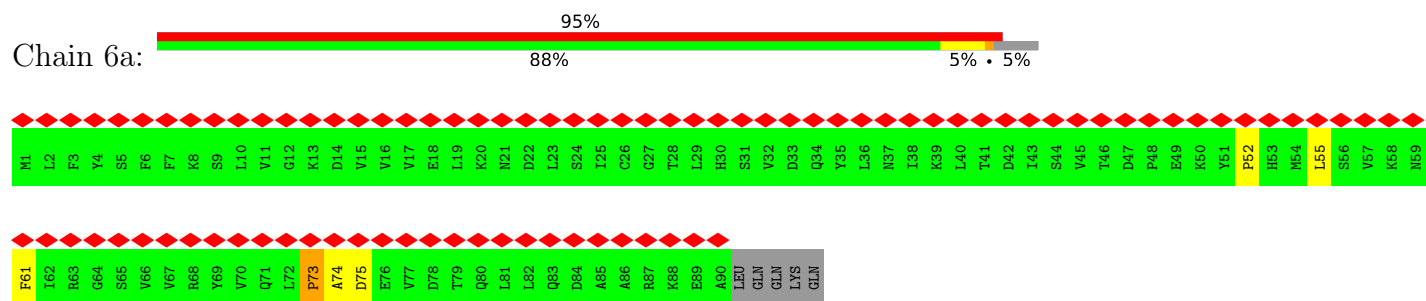
- Molecule 13: Small nuclear ribonucleoprotein Sm D3



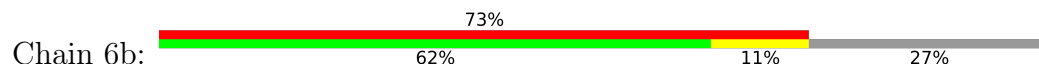
- Molecule 14: U6 snRNA



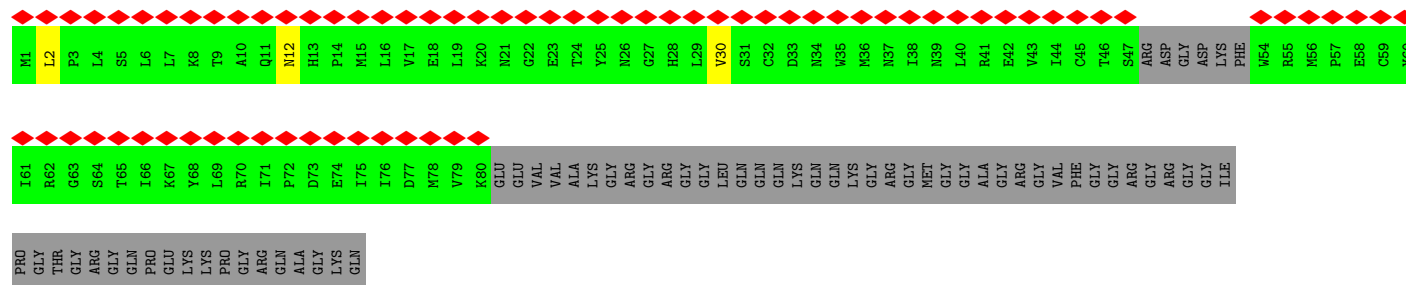
- Molecule 15: U6 snRNA-associated Sm-like protein LSm2



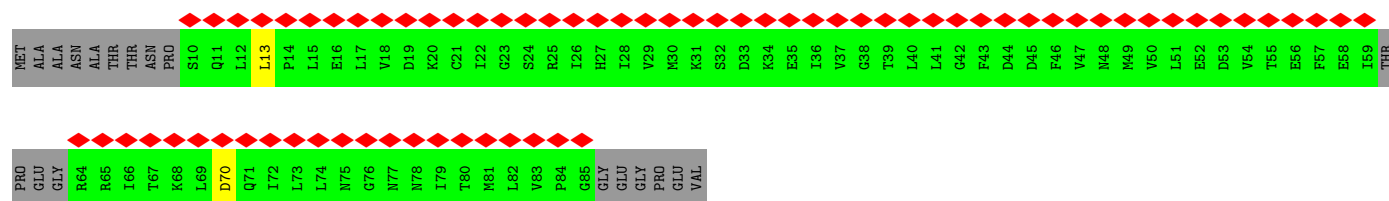
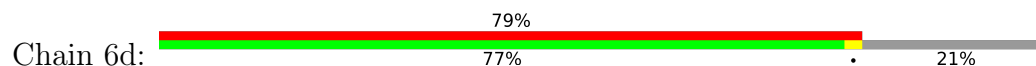
- Molecule 16: U6 snRNA-associated Sm-like protein LSm3



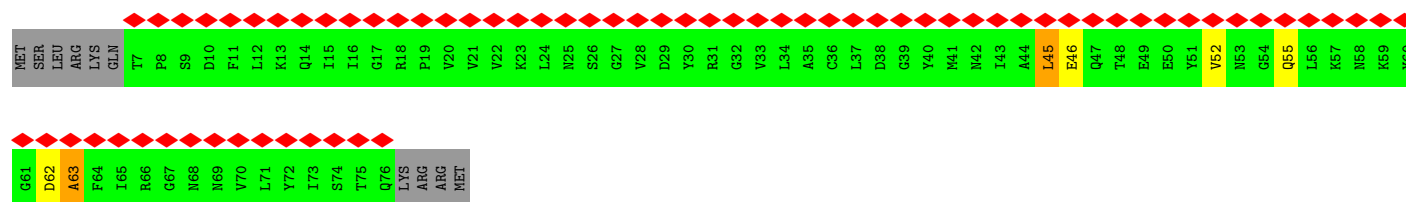
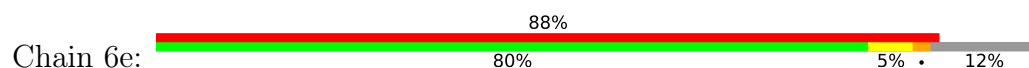
- Molecule 17: U6 snRNA-associated Sm-like protein LSm4



- Molecule 18: U6 snRNA-associated Sm-like protein LSm5



- Molecule 19: U6 snRNA-associated Sm-like protein LSm6

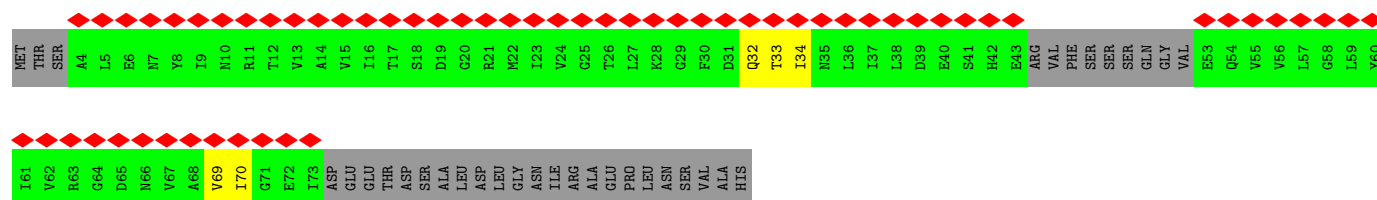


- Molecule 20: U6 snRNA-associated Sm-like protein LSm7

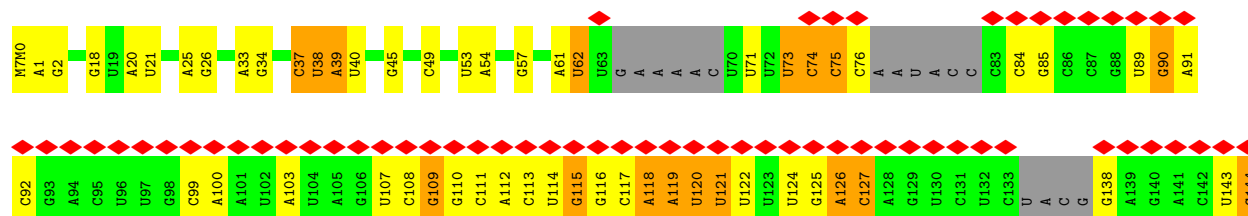




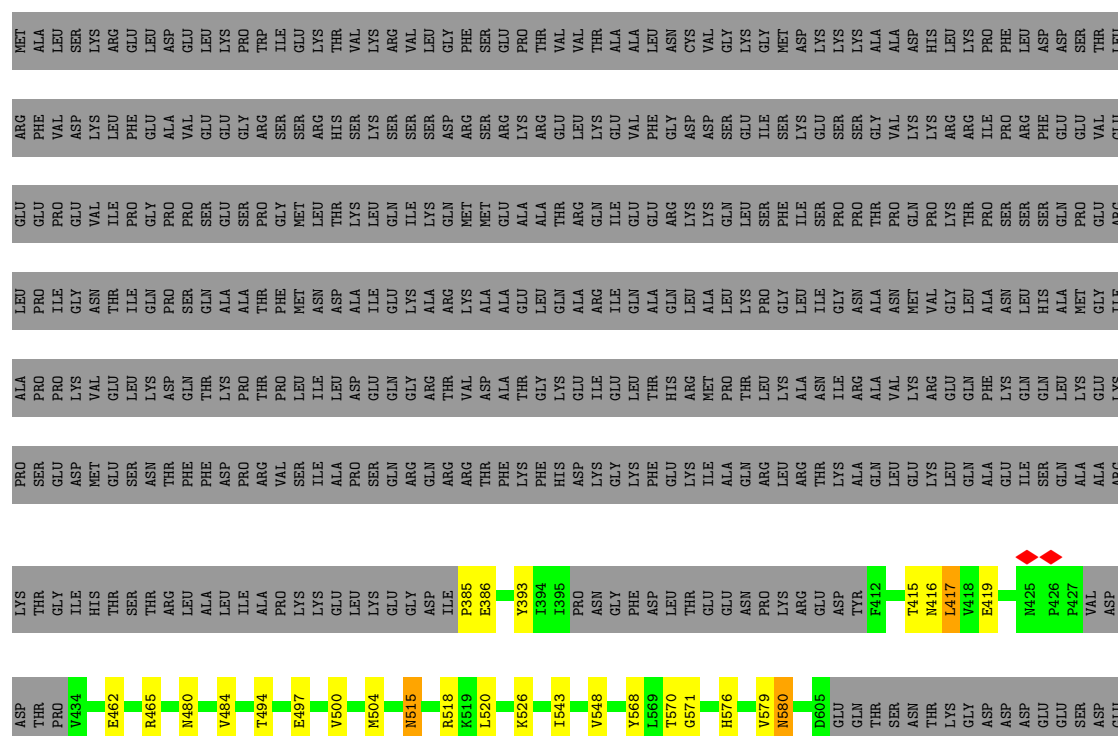
• Molecule 21: U6 snRNA-associated Sm-like protein LSm8

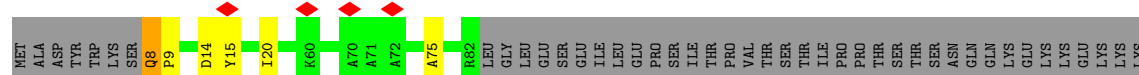


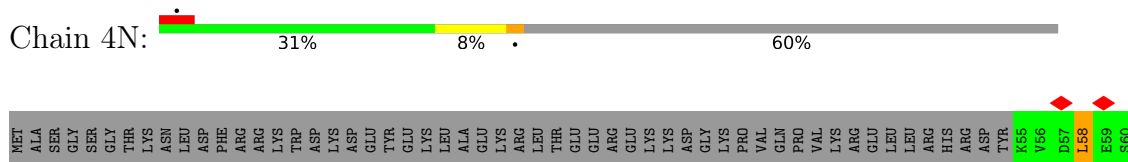
• Molecule 22: U4 snRNA



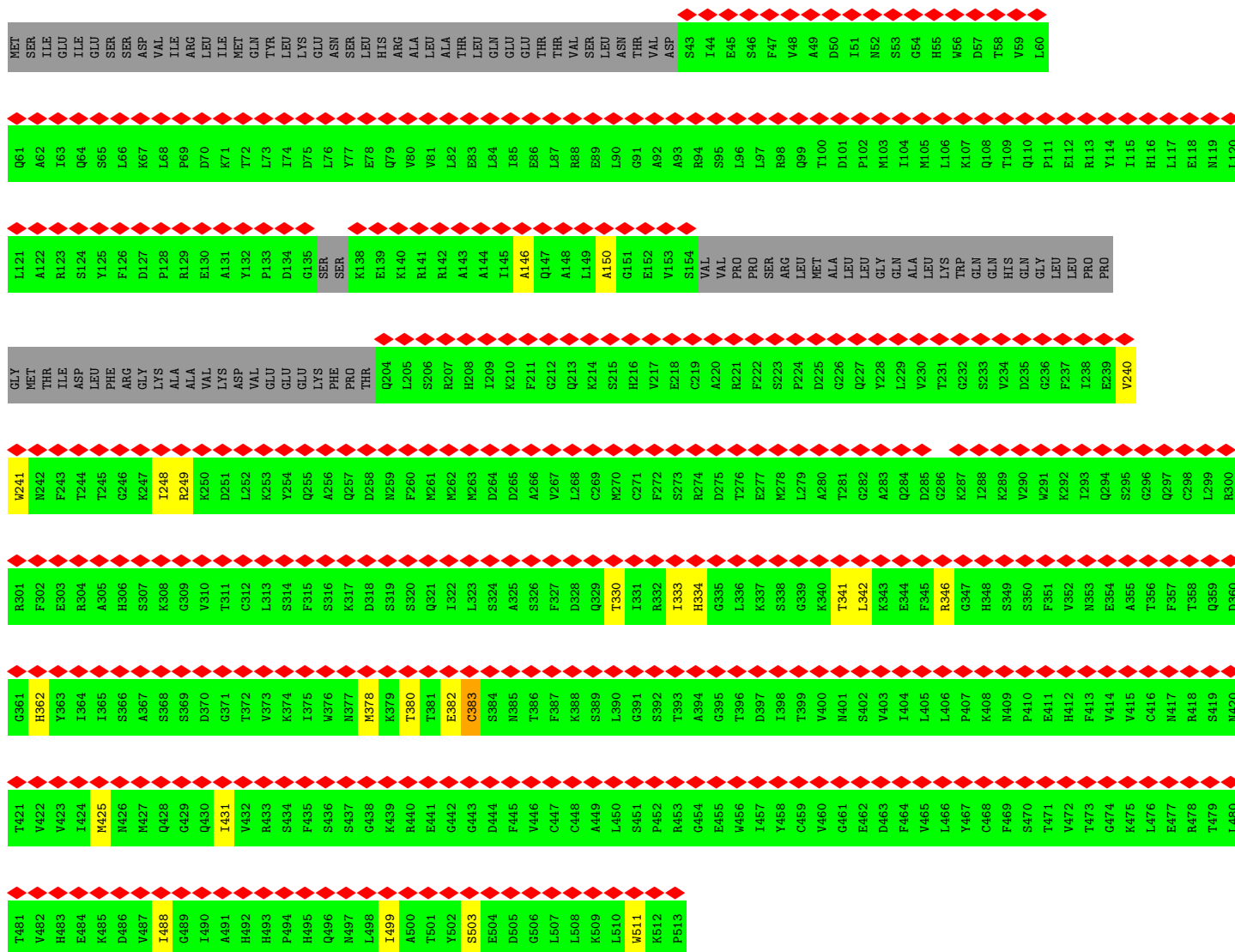
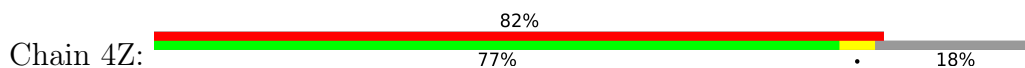
• Molecule 23: U4/U6 small nuclear ribonucleoprotein Prp3



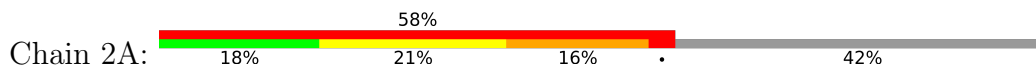


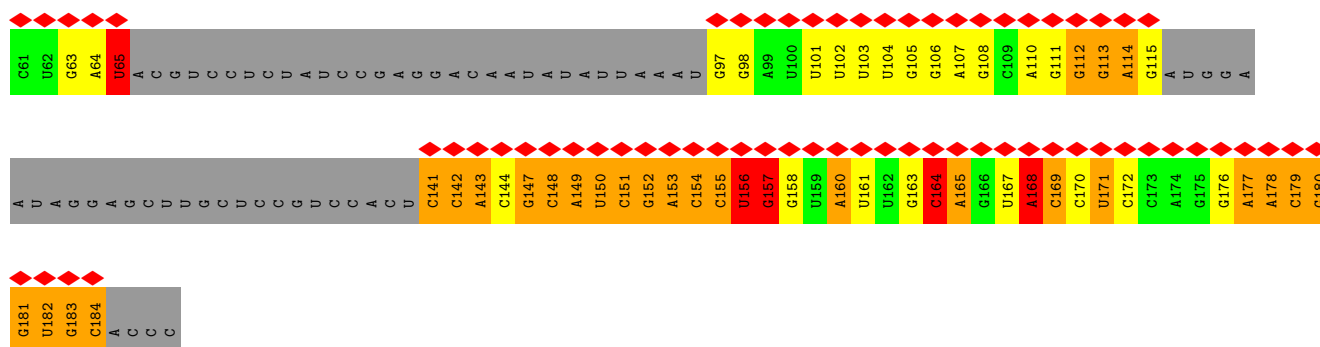


- Molecule 36: WD40 repeat-containing protein SMU1

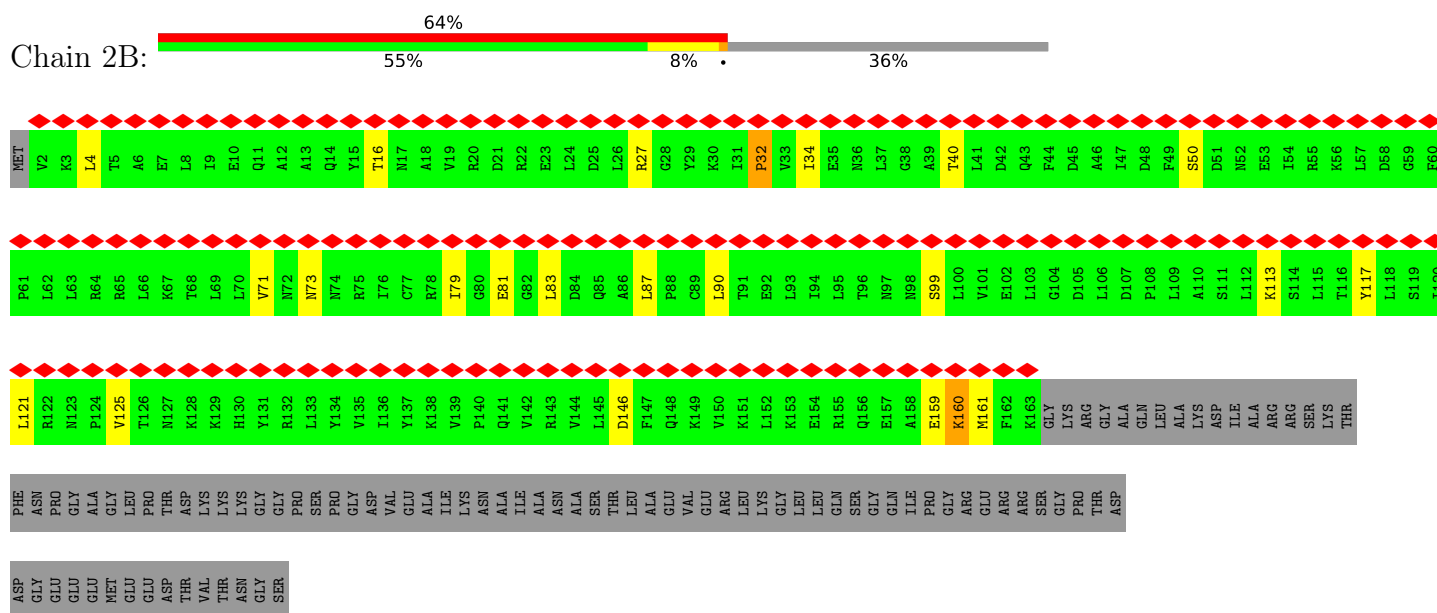


- Molecule 37: U2 snRNA

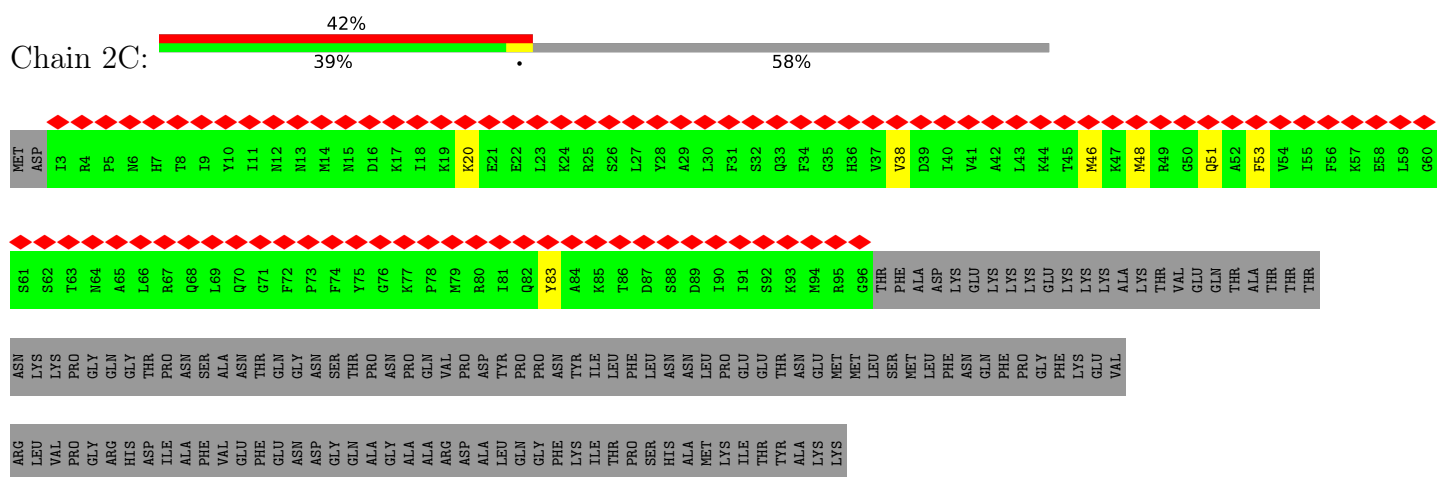




• Molecule 38: U2 small nuclear ribonucleoprotein A'



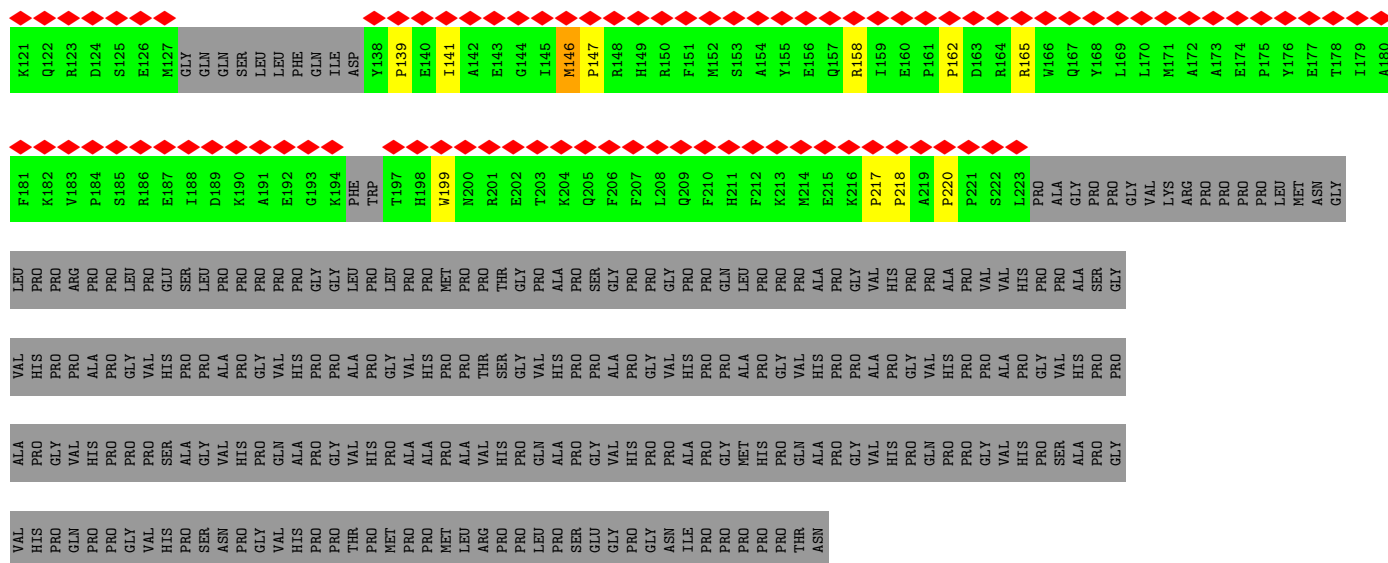
• Molecule 39: U2 small nuclear ribonucleoprotein B''



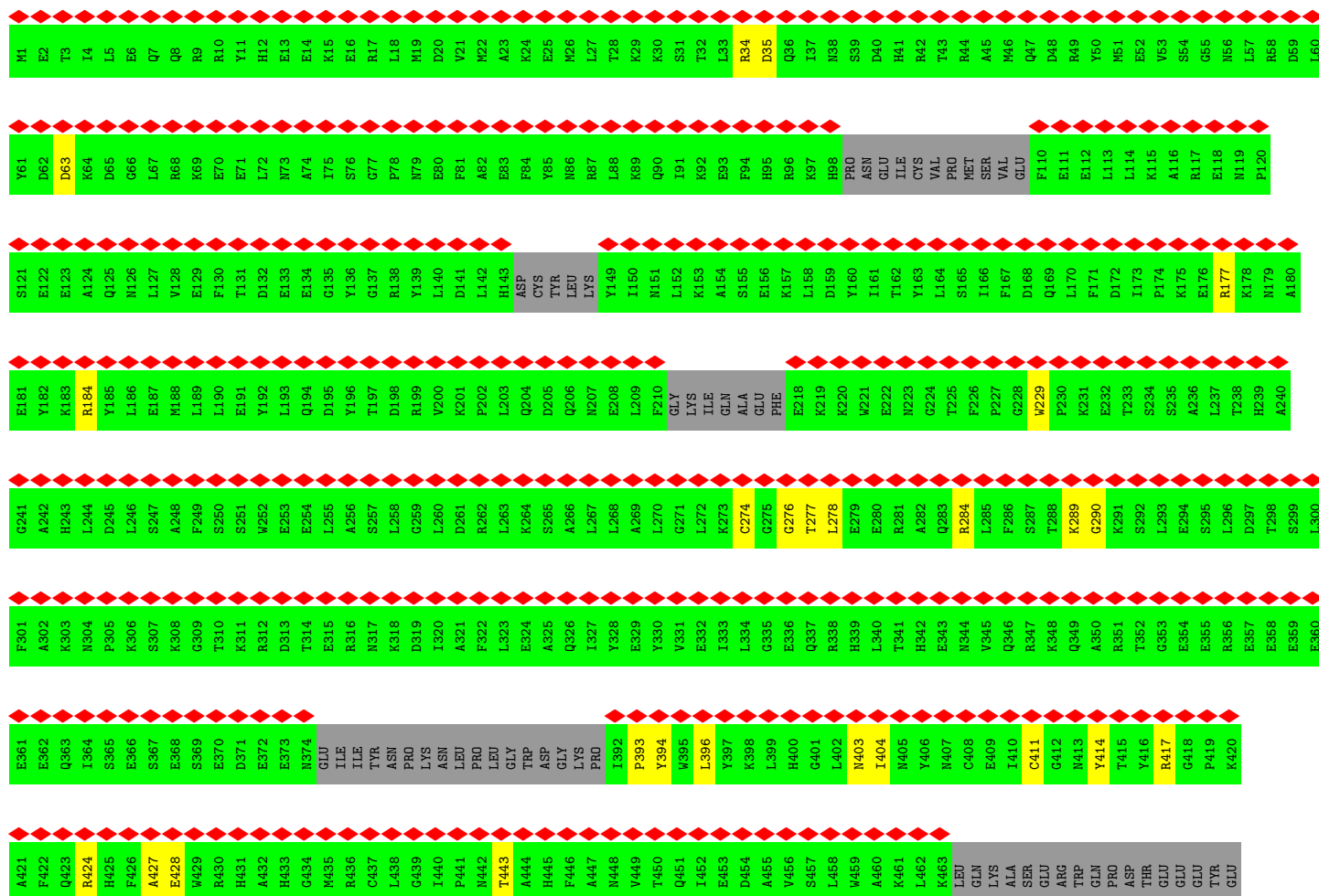
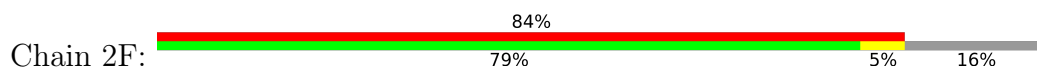
• Molecule 40: Splicing factor 3A subunit 1







• Molecule 42: Splicing factor 3A subunit 3

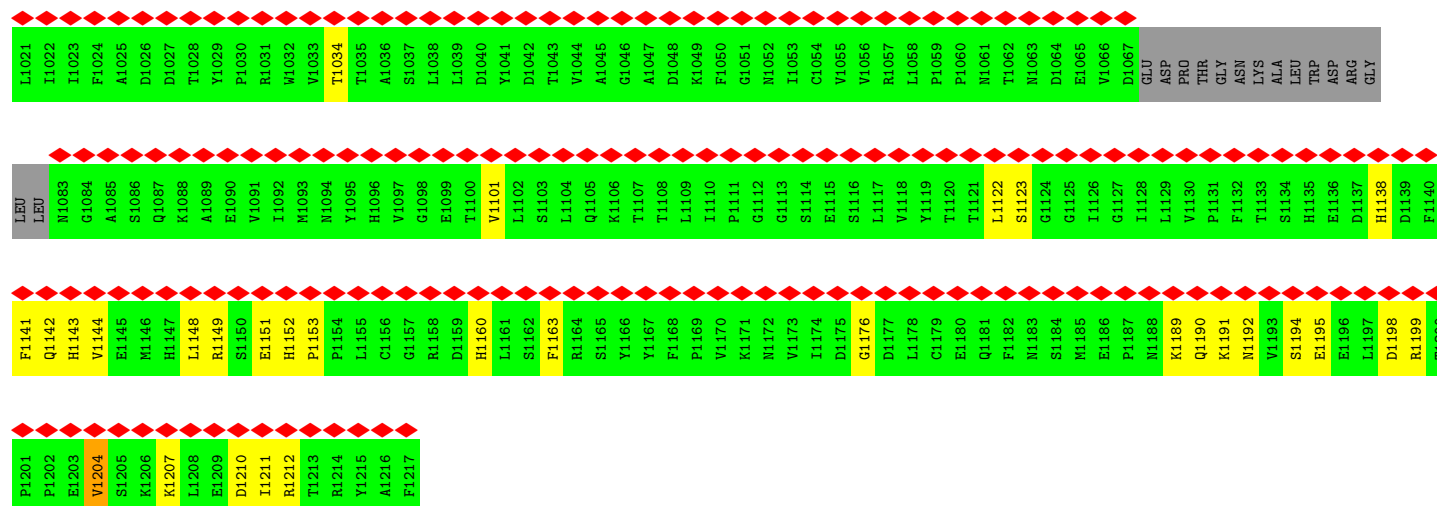


Chain 2G:

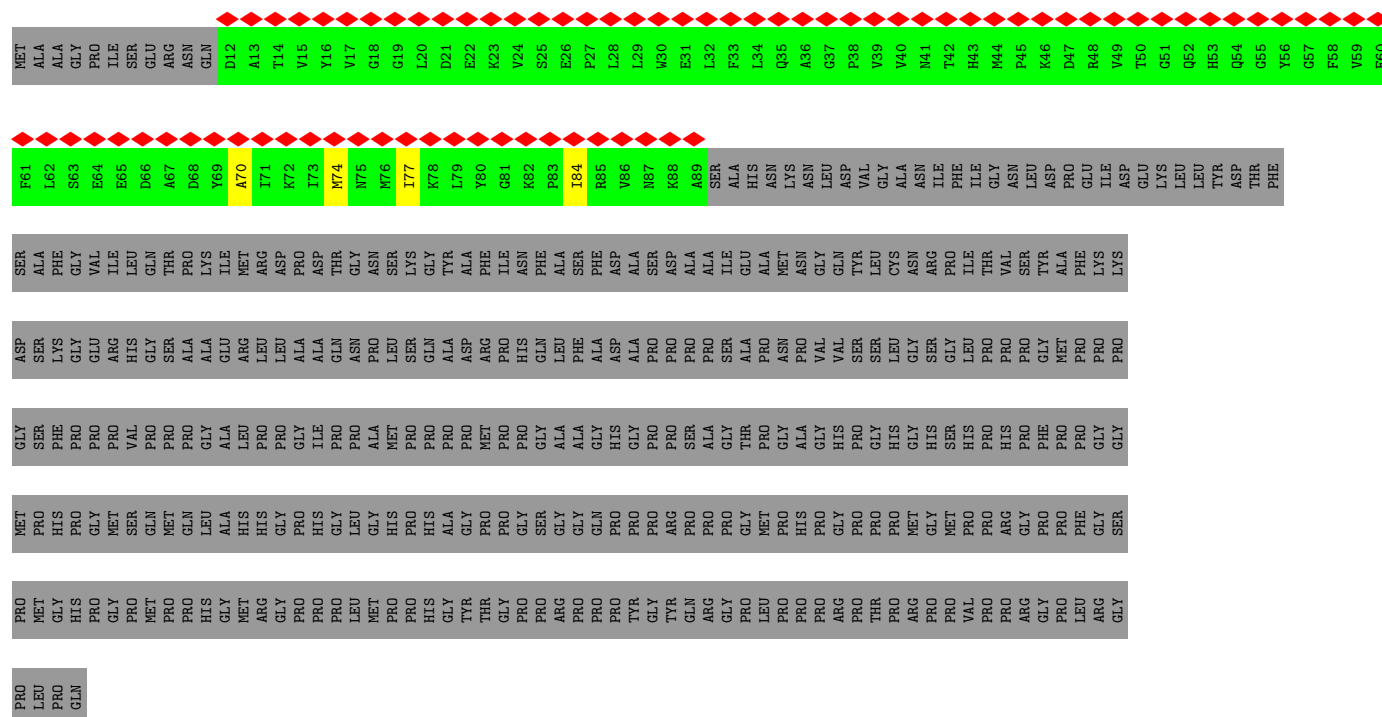




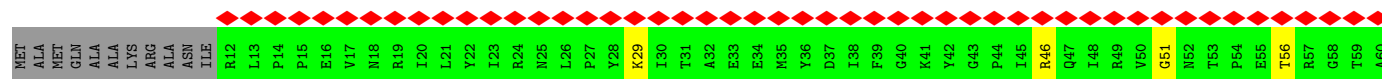
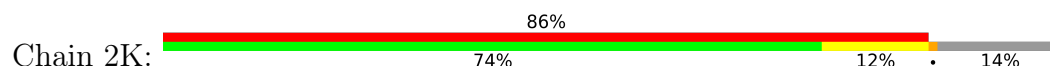
M181	F301	I361	F421	A481	K541	R601	GLY	L721	L781	A841	E901	I961
F182	L302	A362	Q422	T482	K542	S602	F662	S722	Q782	F842	D902	G962
A183	A303	H363	L423	L483	T543	R603	L663	Y723	Q783	L843	W903	V963
C184	Q304	H364	Y424	V484	I544	F604	Y664	S724	T784	H844	Y904	G964
L185	T305	G365	V425	L485	K545	L605	L665	Y725	P785	E845	W905	K965
E186	T306	D366	A426	S486	K546	A606	N666	Q726	R786	H846	L906	L966
M187	Q307	D367	C427	T487	C547	V607	T667	S727	K787	L847	Y907	L967
D188	G308	D368	G428	S488	A548	G608	G668	R728	F788	P848	W908	R968
Y189	D309	E369	R429	E489	V549	L609	L669	F729	Y789	E849	Y909	V969
E190	I310	E370	G430	T490	N550	V610	G670	H730	W790	S850	A910	Y970
E191	F311	P371	P431	V491	Q651	D611	N671	L731	H791	I851	K911	D971
A192	S252	E372	R432	E492	R652	N612	G672	T732	P792	F852	D912	L972
D193	E253	F373	S433	E493	Q653	T613	V673	P733	E793	G853	L913	G973
N194	N254	S374	S434	V494	V654	V614	L674	L734	S794	A854	I914	K974
D195	Y255	S375	L435	T495	V655	R615	L675	S735	W795	P855	L915	K975
P196	I256	A376	R436	D496	I556	T616	R676	Y736	W796	K856	N916	K976
T197	T257	M377	V437	S497	A557	T617	T677	E737	L797	A857	P917	L977
G198	Y258	PR0	L438	G498	L558	S618	V678	T738	W798	C858	R918	R978
E199	K259	LEU	R439	F499	T559	L619	L679	L739	I799	H859	S919	R979
A200	N260	GLU	HIS	L500	G560	D620	D680	E740	I800	G860	V920	K980
A201	F261	GLY	G441	G501	G561	P621	P681	F741	E801	Q861	A921	C981
A202	G262	ASP	L442	T502	E562	S622	V682	A742	T802	W862	Q922	C982
N203	D263	T384	E443	T503	L563	D623	T683	S743	D803	A863	Q923	N983
T204	Q264	F385	V444	P504	V664	C624	G684	G744	H804	S864	F924	K984
Q205	P265	F386	S445	T505	Y665	L625	D685	F745	H805	W865	Y925	H985
Q206	D266	F387	E446	L506	F566	Q626	L686	A746	A806	T866	Y926	I986
T207	I267	Q388	M447	S507	E567	P627	S687	S747	Y807	R867	T927	A987
L208	R268	P389	A448	C508	M668	L628	D688	E748	T808	W868	Y928	N988
T209	C269	R390	V449	S509	D669	S629	T689	Q749	E809	H869	K929	Y989
F210	P270	P391	S450	L510	P570	M630	R690	C750	R810	H870	Y931	I990
Y211	I271	L392	E451	L511	S571	Q631	T691	F751	T811	P871	Y931	S991
E212	P272	K393	L452	G512	G572	A632	ARG	E752	K812	L872	N932	G992
L213	R273	N394	P453	D513	Q673	L633	TYR	G753	A813	Q873	N933	I993
D214	R274	L395	G454	D514	L574	P634	LEU	L754	O814	O874	Q934	Q994
L215	R275	V396	M455	A515	N575	A635	G695	V755	R815	H875	E935	T995
G216	N276	L397	P456	L516	E576	Q636	S696	A756	K816	T876	E936	I996
E217	D277	V398	M457	V517	Y577	P637	P698	L757	Q817	L877	K937	G997
N218	L278	D399	A458	Q518	T578	E638	V699	S758	O818	D878	E938	H998
H219	D279	E400	V459	V519	E579	S639	K700	T759	H819	L879	F939	R999
V220	D280	L401	V460	Y520	R580	L640	L701	W760	A820	V880	L940	V1000
V221	P281	D402	T461	P521	K581	C641	F702	T761	E821	Q881	H941	I1001
R222	E282	S403	V462	D522	E582	I642	R703	L762	E822	Q882	K942	V1002
K223	R283	L342	R463	G523	M683	V643	W704	R763	H823	E883	T943	S1003
Y224	G284	T344	R464	I524	S584	E644	R705	L764	W824	O884	P944	D1004
S225	M285	G345	H465	R525	A585	E645	R706	L765	E825	H885	V945	V1005
E226	I286	T407	I466	H526	D586	M645	W707	A766	A826	E886	E946	Q1006
P227	F287	L408	E467	I527	V587	GLY	Q708	L767	A827	A887	E947	E1007
L228	V288	F409	D468	R528	V588	THR	G709	E768	GLY	V888	V948	S1008
E229	C289	C410	E469	A529	C589	LYS	W710	K769	GLU	F889	P949	F1009
E230	Q290	Q411	F470	D530	M690	GLN	E711	L770	ASP	S890	A950	I1010
H231	A291	I412	D471	K531	S591	ASP	A711	G771	GLU	V891	A951	W1011
G232	T292	A413	A472	R532	L592	LEU	V712	ALA	ARG	A892	I952	V1012
N233	H293	D414	Y473	V533	A593	GLY	L713	W773	LEU	W893	A953	R1013
F234	K294	L415	I474	N534	N594	GLU	A714	F774	ARG	C894	P954	Y1014
L235	T295	N355	I475	E535	V595	ARG	W715	N775	GLY	H895	F955	K1015
I236	K296	M417	V476	W536	P596	GLY	T716	Q776	SER	F896	Q956	R1016
T237	S297	E418	S477	K537	P597	ILE	T717	V777	THR	S897	G957	N1017
V238	M298	D419	F478	T538	Q598		R718	A778	GLY	H898	Q958	I1018
P239	F299	Y359	V479	P539	E599		T719	F779		T899	V959	N1019
G240	F300	Q360	M480	G540	Q600		W720	P780		O900	L960	Q1020

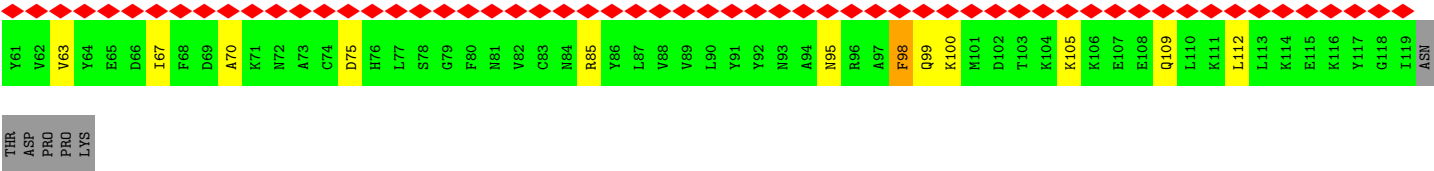


• Molecule 46: Splicing factor 3B subunit 4

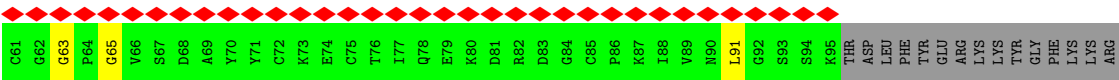
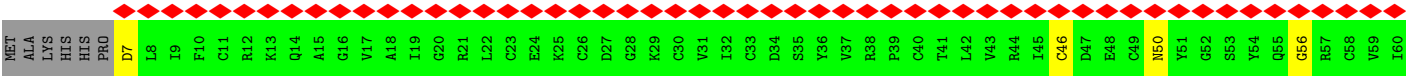
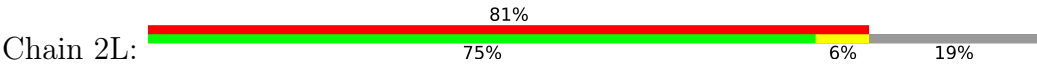


• Molecule 47: Splicing factor 3B subunit 6

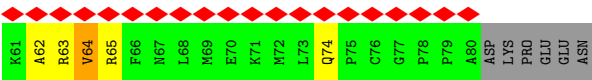
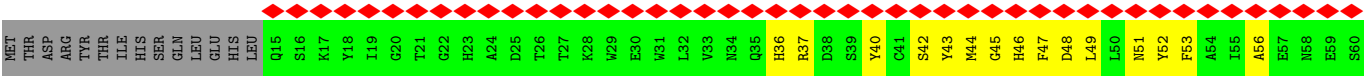
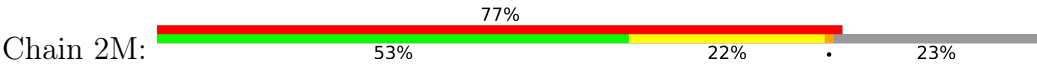




● Molecule 48: PHD finger-like domain-containing protein 5A



● Molecule 49: Splicing factor 3B subunit 5



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	414060	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	0.173	Depositor
Minimum map value	-0.110	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.01	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, M7M

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.62	6/1481 (0.4%)	0.71	2/2297 (0.1%)
2	5A	0.24	0/2698	0.43	1/4195 (0.0%)
3	5B	0.14	0/19154	0.32	1/26000 (0.0%)
4	5C	0.14	0/6573	0.36	0/8929
5	5D	0.15	0/13923	0.32	2/18868 (0.0%)
6	5E	1.08	0/1195	1.21	5/1492 (0.3%)
7	2a	0.86	0/343	1.21	3/427 (0.7%)
7	4a	0.13	0/254	0.39	0/314
7	5a	0.85	0/335	1.18	2/417 (0.5%)
8	2b	0.89	0/327	1.11	0/407
8	4b	0.15	0/333	0.46	0/416
8	5b	0.89	0/327	1.11	0/407
9	2c	1.18	0/338	1.20	1/419 (0.2%)
9	4c	0.16	0/298	0.49	0/370
9	5c	1.14	0/387	1.21	1/482 (0.2%)
10	2d	1.24	1/295 (0.3%)	1.26	0/367
10	4d	0.21	0/291	0.47	0/363
10	5d	1.23	0/295	1.26	0/367
11	2e	1.02	0/315	1.26	0/392
11	4e	0.17	0/313	0.47	0/390
11	5e	1.03	0/315	1.27	1/392 (0.3%)
12	2f	0.86	0/270	1.05	0/334
12	4f	0.24	0/297	0.59	0/371
12	5f	0.85	0/287	1.03	0/357
13	2g	0.81	0/318	1.01	0/394
13	4g	0.14	0/287	0.35	0/358
13	5g	0.78	0/307	1.01	0/382
14	6A	0.14	0/1423	0.29	0/2211
15	6a	0.69	0/359	1.28	0/447
16	6b	0.75	0/294	1.37	3/364 (0.8%)
17	6c	0.58	0/294	1.32	3/364 (0.8%)
18	6d	0.71	0/286	1.28	2/354 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
19	6e	0.71	0/279	1.40	2/347 (0.6%)
20	6f	0.60	0/258	1.14	0/319
21	6g	0.67	0/242	1.21	1/299 (0.3%)
22	4A	0.19	0/3025	0.36	0/4702
23	4B	0.12	0/2114	0.32	0/2836
24	4C	0.14	0/3452	0.33	0/4675
25	4D	0.12	0/2912	0.29	0/3924
26	4E	0.10	0/974	0.27	0/1316
27	4F	0.24	0/1198	0.47	2/1620 (0.1%)
28	4G	0.11	0/5592	0.33	2/7615 (0.0%)
29	4H	0.17	0/853	0.33	0/1188
30	4I	0.13	0/502	0.27	0/683
31	4J	0.11	0/1149	0.29	0/1542
32	4K	0.13	0/1209	0.30	0/1655
33	4L	0.14	0/1481	0.39	0/1995
34	4M	0.10	0/609	0.30	0/819
35	4N	0.17	0/646	0.37	0/859
36	4Z	0.17	0/2100	0.48	1/2926 (0.0%)
37	2A	0.71	12/2576 (0.5%)	1.11	27/4003 (0.7%)
38	2B	0.99	0/647	2.34	33/807 (4.1%)
39	2C	0.97	0/375	1.97	7/467 (1.5%)
40	2D	0.26	0/1139	0.68	2/1477 (0.1%)
41	2E	0.38	0/373	1.77	4/461 (0.9%)
42	2F	0.38	0/1688	0.92	3/2102 (0.1%)
43	2G	1.72	38/4184 (0.9%)	1.43	27/5216 (0.5%)
44	2H	1.02	0/957	1.08	2/1209 (0.2%)
45	2I	1.39	25/4664 (0.5%)	1.20	9/5816 (0.2%)
46	2J	1.02	0/311	0.99	0/387
47	2K	1.27	2/431 (0.5%)	1.27	1/537 (0.2%)
48	2L	1.16	0/355	1.11	0/442
49	2M	1.59	1/263 (0.4%)	1.23	0/327
All	All	0.60	85/100770 (0.1%)	0.69	150/136218 (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
3	5B	0	1
9	2c	0	1
9	5c	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
42	2F	0	1
43	2G	0	11
44	2H	0	3
45	2I	0	11
47	2K	0	1
49	2M	0	1
All	All	0	31

All (85) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	2G	407	MET	N-CA	22.52	1.71	1.46
43	2G	406	ALA	C-N	14.95	1.52	1.33
43	2G	1243	PRO	N-CA	-9.49	1.35	1.47
43	2G	944	SER	N-CA	-8.41	1.34	1.46
45	2I	84	SER	CA-C	-7.80	1.42	1.53
37	2A	142	C	C1'-N1	7.52	1.59	1.48
45	2I	1101	VAL	CA-C	-7.22	1.44	1.52
43	2G	868	VAL	CA-C	-7.20	1.42	1.52
45	2I	110	SER	C-O	-7.20	1.15	1.23
45	2I	82	SER	CA-C	-7.15	1.44	1.52
37	2A	182	U	C1'-N1	7.14	1.59	1.48
45	2I	1101	VAL	C-O	-7.00	1.16	1.24
37	2A	150	U	C1'-N1	6.94	1.58	1.48
37	2A	151	C	C1'-N1	6.73	1.58	1.48
37	2A	97	G	C1'-N9	-6.71	1.37	1.48
43	2G	1273	TYR	CA-C	-6.71	1.43	1.52
37	2A	141	C	C1'-N1	6.58	1.58	1.48
43	2G	939	ARG	CA-C	-6.58	1.44	1.52
45	2I	289	CYS	C-O	-6.57	1.15	1.23
37	2A	184	C	C1'-N1	6.55	1.58	1.48
45	2I	141	VAL	C-O	-6.53	1.17	1.24
37	2A	148	C	C1'-N1	6.53	1.58	1.48
45	2I	64	SER	N-CA	-6.51	1.38	1.46
47	2K	98	PHE	N-CA	-6.49	1.37	1.46
43	2G	814	PHE	CA-C	-6.20	1.45	1.52
43	2G	678	ALA	N-CA	-6.05	1.38	1.46
45	2I	64	SER	C-O	-6.03	1.16	1.23
1	A	9	U	C1'-N1	6.01	1.56	1.47
1	A	8	U	C1'-N1	6.00	1.56	1.47
45	2I	213	LEU	CA-C	-6.00	1.45	1.52
1	A	7	U	C1'-N1	6.00	1.56	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	2I	302	LEU	C-O	-5.97	1.16	1.24
43	2G	945	ALA	CA-C	-5.97	1.44	1.52
43	2G	571	VAL	CA-C	-5.92	1.45	1.52
45	2I	115	ILE	N-CA	-5.91	1.40	1.46
45	2I	167	VAL	CA-C	-5.89	1.46	1.52
43	2G	1167	TYR	CA-C	-5.89	1.45	1.52
45	2I	140	LEU	CA-C	-5.87	1.45	1.52
43	2G	893	ILE	N-CA	-5.85	1.39	1.46
37	2A	48	A	C1'-N9	-5.84	1.39	1.48
43	2G	940	LEU	CA-C	-5.81	1.45	1.52
37	2A	65	U	C1'-N1	5.74	1.57	1.48
43	2G	989	VAL	CA-C	-5.68	1.45	1.52
45	2I	1153	PRO	C-O	-5.67	1.18	1.24
43	2G	233	ASP	CA-C	-5.66	1.45	1.52
45	2I	104	GLN	CA-C	-5.66	1.46	1.52
45	2I	235	LEU	C-O	-5.66	1.16	1.23
43	2G	482	VAL	C-O	-5.64	1.17	1.24
43	2G	1177	LEU	C-O	-5.64	1.17	1.24
47	2K	95	ASN	N-CA	-5.64	1.39	1.46
43	2G	838	VAL	N-CA	-5.59	1.40	1.46
45	2I	80	VAL	C-O	-5.55	1.18	1.24
43	2G	235	THR	C-O	-5.53	1.19	1.24
1	A	11	C	C1'-N1	5.50	1.55	1.47
45	2I	1123	SER	CA-C	-5.50	1.45	1.52
37	2A	110	A	C1'-N9	-5.47	1.39	1.48
45	2I	134	ALA	C-O	-5.45	1.18	1.23
1	A	10	C	C1'-N1	5.45	1.55	1.47
45	2I	107	PHE	CA-C	-5.44	1.45	1.52
43	2G	439	GLY	CA-C	5.42	1.56	1.52
43	2G	738	HIS	N-CA	-5.41	1.39	1.45
45	2I	941	HIS	C-O	5.34	1.30	1.23
43	2G	627	THR	N-CA	-5.33	1.40	1.46
45	2I	38	LEU	CA-C	-5.32	1.46	1.52
1	A	46	U	C1'-N1	5.29	1.55	1.47
43	2G	680	LEU	C-O	-5.28	1.19	1.24
43	2G	721	ILE	N-CA	-5.25	1.40	1.46
43	2G	864	TYR	CA-C	-5.23	1.46	1.52
45	2I	1034	THR	CA-C	-5.20	1.47	1.53
43	2G	898	TYR	C-N	-5.18	1.27	1.33
43	2G	415	LEU	C-N	5.18	1.39	1.33
43	2G	672	ALA	CA-C	-5.17	1.46	1.52
43	2G	776	GLU	CA-C	-5.16	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	2G	407	MET	C-O	-5.16	1.18	1.23
49	2M	44	MET	C-O	-5.15	1.18	1.24
43	2G	601	ALA	N-CA	-5.14	1.40	1.46
37	2A	60	U	C1'-N1	5.12	1.56	1.48
43	2G	1279	ALA	CA-C	-5.12	1.46	1.52
43	2G	1281	ILE	CA-C	-5.12	1.46	1.52
43	2G	944	SER	CA-C	5.09	1.59	1.53
43	2G	899	ALA	N-CA	-5.09	1.40	1.46
10	2d	14	LEU	CA-C	5.07	1.59	1.52
45	2I	68	PHE	N-CA	-5.05	1.40	1.46
43	2G	739	ARG	N-CA	-5.03	1.40	1.46
43	2G	1253	GLY	N-CA	-5.03	1.39	1.45

All (150) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	2E	146	MET	CA-C-N	21.07	146.17	119.84
41	2E	146	MET	C-N-CA	21.07	146.17	119.84
43	2G	406	ALA	CA-C-N	17.67	147.39	120.89
43	2G	406	ALA	C-N-CA	17.67	147.39	120.89
43	2G	406	ALA	CA-C-O	-13.04	105.77	120.24
43	2G	108	ARG	CA-C-N	12.13	132.88	120.38
43	2G	108	ARG	C-N-CA	12.13	132.88	120.38
45	2I	916	ASN	CA-C-N	9.51	131.72	119.84
45	2I	916	ASN	C-N-CA	9.51	131.72	119.84
43	2G	114	ASP	N-CA-C	9.45	121.35	111.14
37	2A	180	G	O3'-P-O5'	-8.65	91.02	104.00
37	2A	149	A	O3'-P-O5'	-8.65	91.03	104.00
37	2A	182	U	O3'-P-O5'	-8.62	91.06	104.00
37	2A	183	G	O3'-P-O5'	-8.59	91.11	104.00
37	2A	148	C	O3'-P-O5'	-8.59	91.12	104.00
37	2A	141	C	O3'-P-O5'	-8.57	91.14	104.00
37	2A	150	U	O3'-P-O5'	-8.55	91.17	104.00
37	2A	113	G	O3'-P-O5'	-8.54	91.19	104.00
37	2A	181	G	O3'-P-O5'	-8.54	91.19	104.00
19	6e	45	LEU	N-CA-C	8.53	123.56	112.12
37	2A	114	A	O3'-P-O5'	-8.53	91.21	104.00
28	4G	707	ASP	CA-C-N	8.18	136.43	121.70
28	4G	707	ASP	C-N-CA	8.18	136.43	121.70
38	2B	16	THR	CA-C-O	-8.01	111.79	120.36
38	2B	99	SER	N-CA-C	8.01	122.84	112.26
5	5D	583	THR	CA-C-N	7.79	136.07	121.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	5D	583	THR	C-N-CA	7.79	136.07	121.81
38	2B	117	TYR	CA-C-O	7.76	128.55	120.40
37	2A	168	A	P-O5'-C5'	-7.62	109.47	120.90
36	4Z	380	THR	N-CA-C	7.36	121.68	111.74
37	2A	167	U	O3'-P-O5'	-7.27	93.09	104.00
38	2B	71	VAL	CA-C-N	7.19	131.60	120.75
38	2B	71	VAL	C-N-CA	7.19	131.60	120.75
43	2G	613	MET	N-CA-C	7.18	121.75	112.92
43	2G	1100	ASN	N-CA-C	7.16	119.22	110.41
43	2G	407	MET	N-CA-C	7.05	121.96	111.04
37	2A	170	C	C3'-C2'-O2'	-7.02	104.07	114.60
3	5B	1194	CYS	CA-CB-SG	6.94	130.36	114.40
40	2D	199	ARG	CA-C-N	6.91	127.87	120.47
40	2D	199	ARG	C-N-CA	6.91	127.87	120.47
42	2F	290	GLY	N-CA-C	6.88	120.98	112.73
38	2B	121	LEU	CA-C-O	6.87	128.85	121.44
38	2B	4	LEU	N-CA-C	-6.85	98.05	108.67
39	2C	53	PHE	CA-C-O	-6.83	112.80	120.32
41	2E	158	ARG	N-CA-C	6.75	118.72	111.36
43	2G	1120	ALA	CA-C-N	-6.69	111.34	120.44
43	2G	1120	ALA	C-N-CA	-6.69	111.34	120.44
37	2A	164	C	C5'-C4'-O4'	-6.57	99.25	109.10
47	2K	85	ARG	N-CA-C	6.52	120.03	109.40
38	2B	87	LEU	CA-C-N	6.41	126.17	119.05
38	2B	87	LEU	C-N-CA	6.41	126.17	119.05
43	2G	406	ALA	O-C-N	6.41	130.56	122.23
37	2A	168	A	C5'-C4'-C3'	-6.33	106.51	116.00
38	2B	40	THR	CA-C-N	6.24	131.44	122.40
38	2B	40	THR	C-N-CA	6.24	131.44	122.40
43	2G	406	ALA	N-CA-C	6.23	119.35	111.69
37	2A	169	C	P-O3'-C3'	6.23	129.54	120.20
43	2G	1180	ARG	N-CA-C	-6.16	103.27	111.96
38	2B	73	ASN	N-CA-C	6.16	119.85	111.17
44	2H	559	PRO	N-CA-C	6.11	120.07	111.33
43	2G	1275	GLY	N-CA-C	-6.11	104.91	111.93
38	2B	79	ILE	CA-C-N	6.05	125.85	120.10
38	2B	79	ILE	C-N-CA	6.05	125.85	120.10
43	2G	415	LEU	O-C-N	-6.02	114.40	121.32
2	5A	77	G	P-O3'-C3'	-5.96	111.26	120.20
39	2C	46	MET	N-CA-C	-5.94	104.71	111.07
17	6c	2	LEU	CA-C-N	5.87	127.17	119.84
17	6c	2	LEU	C-N-CA	5.87	127.17	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	2B	113	LYS	N-CA-C	5.85	118.41	111.33
37	2A	163	G	O3'-P-O5'	-5.85	95.23	104.00
43	2G	465	PRO	N-CA-C	-5.84	106.51	114.80
38	2B	50	SER	CA-C-O	5.83	127.73	121.55
18	6d	13	LEU	CA-C-N	5.82	125.95	119.32
18	6d	13	LEU	C-N-CA	5.82	125.95	119.32
38	2B	27	ARG	CA-C-N	5.74	128.78	120.11
38	2B	27	ARG	C-N-CA	5.74	128.78	120.11
45	2I	679	LEU	N-CA-C	5.73	119.43	110.32
19	6e	63	ALA	N-CA-C	5.71	118.08	109.23
37	2A	164	C	P-O3'-C3'	5.70	128.75	120.20
45	2I	887	ALA	N-CA-C	-5.68	101.64	110.10
43	2G	942	ASN	CA-C-N	-5.64	114.77	124.82
43	2G	942	ASN	C-N-CA	-5.64	114.77	124.82
7	2a	52	LYS	CA-C-N	-5.64	114.12	119.76
7	2a	52	LYS	C-N-CA	-5.64	114.12	119.76
37	2A	160	A	P-O5'-C5'	-5.62	112.46	120.90
38	2B	71	VAL	O-C-N	-5.62	115.54	122.57
43	2G	942	ASN	N-CA-C	-5.60	98.86	110.80
38	2B	32	PRO	CA-C-N	5.59	130.76	122.99
38	2B	32	PRO	C-N-CA	5.59	130.76	122.99
7	5a	52	LYS	CA-C-N	-5.56	114.20	119.76
7	5a	52	LYS	C-N-CA	-5.56	114.20	119.76
27	4F	78	PRO	N-CD-CG	-5.55	94.88	103.20
38	2B	34	ILE	CA-C-O	-5.53	114.21	120.74
6	5E	322	LYS	N-CA-C	-5.52	98.20	108.02
37	2A	168	A	O4'-C1'-C2'	-5.50	102.10	107.60
6	5E	284	PHE	N-CA-C	5.49	119.48	112.34
37	2A	157	G	P-O5'-C5'	-5.49	112.66	120.90
37	2A	165	A	N9-C1'-C2'	5.49	120.23	112.00
38	2B	159	GLU	N-CA-C	-5.48	104.95	111.69
7	2a	5	LYS	N-CA-C	5.48	118.17	111.82
6	5E	281	VAL	N-CA-C	5.46	116.17	108.36
38	2B	16	THR	O-C-N	5.45	129.43	123.22
16	6b	49	HIS	N-CA-C	-5.45	106.71	113.19
43	2G	1128	VAL	N-CA-C	5.45	117.90	111.09
44	2H	511	LEU	N-CA-C	5.44	117.53	108.99
43	2G	1105	GLU	N-CA-C	5.43	117.58	108.73
45	2I	488	GLY	N-CA-C	-5.42	106.37	115.80
1	A	28	G	C4'-C3'-O3'	-5.41	104.88	113.00
1	A	28	G	C2'-C3'-O3'	-5.41	105.59	113.70
38	2B	40	THR	N-CA-C	-5.39	106.20	112.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	5E	156	SER	N-CA-C	5.38	116.70	108.42
6	5E	237	SER	N-CA-C	5.37	117.87	110.35
41	2E	199	TRP	N-CA-C	5.35	117.36	107.73
38	2B	125	VAL	CA-C-N	5.35	127.98	120.28
38	2B	125	VAL	C-N-CA	5.35	127.98	120.28
17	6c	30	VAL	N-CA-C	5.33	116.22	111.90
16	6b	92	VAL	N-CA-C	5.32	115.95	109.30
43	2G	1106	ARG	N-CA-C	5.28	118.86	111.74
38	2B	146	ASP	CA-C-N	5.26	130.03	122.40
38	2B	146	ASP	C-N-CA	5.26	130.03	122.40
45	2I	4	TYR	N-CA-C	-5.25	102.52	110.28
42	2F	289	LYS	N-CA-C	5.24	121.96	110.80
21	6g	69	VAL	N-CA-C	5.23	115.44	108.27
37	2A	171	U	C2'-C3'-O3'	-5.23	105.86	113.70
37	2A	170	C	O4'-C1'-C2'	-5.23	100.57	105.80
39	2C	20	LYS	N-CA-C	5.21	117.36	111.11
16	6b	44	HIS	N-CA-C	-5.18	107.02	113.55
43	2G	415	LEU	CA-C-N	5.14	125.67	120.38
43	2G	415	LEU	C-N-CA	5.14	125.67	120.38
9	5c	99	MET	N-CA-C	5.14	116.88	108.76
39	2C	51	GLN	N-CA-C	5.13	117.48	109.52
37	2A	155	C	P-O3'-C3'	5.12	127.88	120.20
27	4F	78	PRO	CA-N-CD	-5.11	104.84	112.00
39	2C	48	MET	N-CA-C	5.11	119.52	113.28
38	2B	90	LEU	O-C-N	5.11	129.39	122.59
11	5e	85	THR	N-CA-C	-5.11	105.89	112.68
39	2C	38	VAL	O-C-N	5.10	127.09	121.83
38	2B	90	LEU	CA-C-O	-5.10	113.22	120.51
37	2A	160	A	N9-C1'-C2'	5.10	119.65	112.00
38	2B	83	LEU	N-CA-C	5.09	117.50	111.33
9	2c	99	MET	N-CA-C	5.09	116.80	108.76
37	2A	156	U	C4'-C3'-C2'	5.08	107.69	102.60
39	2C	83	TYR	CA-C-O	-5.08	115.25	121.05
45	2I	404	LEU	N-CA-C	-5.08	105.82	111.36
45	2I	9	GLN	N-CA-C	-5.07	101.49	109.25
38	2B	81	GLU	N-CA-C	5.05	118.59	112.23
45	2I	445	SER	N-CA-C	-5.04	104.03	110.53
43	2G	1002	ASN	CA-C-N	-5.02	118.05	122.97
43	2G	1002	ASN	C-N-CA	-5.02	118.05	122.97
42	2F	274	CYS	N-CA-C	5.01	116.56	111.14

There are no chirality outliers.

All (31) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
42	2F	443	THR	Peptide
43	2G	1025	LYS	Peptide
43	2G	1122	THR	Peptide
43	2G	1127	THR	Peptide
43	2G	1179	ASP	Peptide
43	2G	1199	VAL	Peptide
43	2G	220	GLN	Peptide
43	2G	415	LEU	Mainchain,Peptide
43	2G	689	ILE	Peptide
43	2G	941	ASN	Peptide
43	2G	944	SER	Peptide
44	2H	553	MET	Peptide
44	2H	558	ARG	Peptide
44	2H	571	LEU	Peptide
45	2I	261	PHE	Peptide
45	2I	366	ASP	Peptide
45	2I	468	ASP	Peptide
45	2I	530	ASP	Peptide
45	2I	534	ASN	Peptide
45	2I	552	ARG	Peptide
45	2I	670	GLN	Peptide
45	2I	678	VAL	Peptide
45	2I	74	THR	Peptide
45	2I	980	LYS	Peptide
45	2I	986	ILE	Peptide
47	2K	29	LYS	Peptide
49	2M	74	GLN	Peptide
9	2c	112	ASN	Peptide
3	5B	941	LYS	Peptide
9	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	1334	0	681	160	0
2	5A	2420	0	1226	82	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	5B	18639	0	18495	192	0
4	5C	6430	0	6446	114	0
5	5D	13633	0	13769	315	0
6	5E	1196	0	337	2	0
7	2a	344	0	93	4	0
7	4a	256	0	70	2	0
7	5a	336	0	89	0	0
8	2b	328	0	89	0	0
8	4b	334	0	92	1	0
8	5b	328	0	89	5	0
9	2c	340	0	87	1	0
9	4c	300	0	80	5	0
9	5c	388	0	102	7	0
10	2d	296	0	87	1	0
10	4d	292	0	93	7	0
10	5d	296	0	87	10	0
11	2e	316	0	85	2	0
11	4e	314	0	86	3	0
11	5e	316	0	85	4	0
12	2f	272	0	75	1	0
12	4f	298	0	89	5	0
12	5f	288	0	82	5	0
13	2g	320	0	88	0	0
13	4g	288	0	84	1	0
13	5g	308	0	86	5	0
14	6A	1273	0	641	31	0
15	6a	360	0	95	2	0
16	6b	296	0	76	5	0
17	6c	296	0	77	0	0
18	6d	288	0	78	0	0
19	6e	280	0	81	8	0
20	6f	260	0	75	0	0
21	6g	244	0	71	3	0
22	4A	2744	0	1395	65	0
23	4B	2076	0	2148	29	0
24	4C	3370	0	3300	46	0
25	4D	2874	0	2856	25	0
26	4E	962	0	1012	2	0
27	4F	1169	0	1139	9	0
28	4G	5504	0	4772	47	0
29	4H	844	0	426	6	0
30	4I	494	0	384	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	4J	1144	0	1094	10	0
32	4K	1192	0	841	9	0
33	4L	1452	0	1465	31	0
34	4M	599	0	613	5	0
35	4N	640	0	664	16	0
36	4Z	2092	0	992	15	0
37	2A	2311	0	1170	144	0
38	2B	648	0	167	1	0
39	2C	376	0	102	0	0
40	2D	1134	0	764	8	0
41	2E	376	0	85	0	0
42	2F	1693	0	454	22	0
43	2G	4192	0	1110	234	0
44	2H	959	0	417	11	0
45	2I	4672	0	1260	71	0
46	2J	312	0	87	3	0
47	2K	432	0	114	6	0
48	2L	356	0	105	4	0
49	2M	264	0	70	11	0
50	5B	36	0	6	0	0
51	5C	32	0	12	2	0
52	5C	1	0	0	0	0
53	4I	1	0	0	0	0
53	4N	1	0	0	0	0
All	All	98459	0	72990	1644	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 (1644) 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)
43:2G:407:MET:N	43:2G:407:MET:CA	1.71	1.53
1:A:30:C:C2'	1:A:31:C:H5''	1.54	1.35
30:4I:8:GLN:HE21	30:4I:8:GLN:N	1.33	1.24
1:A:30:C:N4	1:A:31:C:C4	2.10	1.18
1:A:38:C:H4'	1:A:39:U:OP1	1.42	1.18
1:A:30:C:C4	1:A:31:C:C5	2.34	1.16
1:A:22:C:O2'	1:A:23:G:H5'	1.45	1.15
1:A:34:G:C8	1:A:35:U:C5	2.34	1.15
22:4A:119:A:H5''	10:4d:39:TYR:CA	1.75	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:C:H2'	1:A:31:C:C5'	1.78	1.13
3:5B:2038:GLN:CB	5:5D:1035:LEU:CD1	2.26	1.12
37:2A:156:U:H6	37:2A:156:U:H5''	1.09	1.09
3:5B:2038:GLN:CB	5:5D:1035:LEU:HD12	1.83	1.08
37:2A:105:G:H2'	37:2A:106:G:H5''	1.37	1.06
2:5A:90:U:C5	13:5g:38:ASN:O	2.09	1.06
1:A:30:C:C3'	1:A:31:C:H5''	1.84	1.04
1:A:40:U:H4'	1:A:41:U:H5'	1.38	1.04
22:4A:118:A:C2	22:4A:119:A:N6	2.25	1.03
22:4A:126:A:C2	9:4c:104:ASP:CA	2.41	1.03
3:5B:2036:GLN:O	5:5D:1035:LEU:HD13	1.58	1.02
1:A:30:C:H2'	1:A:31:C:H5''	1.03	1.02
1:A:34:G:C8	1:A:35:U:C4	2.47	1.02
3:5B:2038:GLN:N	5:5D:1035:LEU:HD11	1.73	1.01
2:5A:95:G:H1'	10:5d:24:LYS:CA	1.90	1.01
1:A:30:C:C3'	1:A:31:C:C5'	2.40	1.00
22:4A:91:A:H2	22:4A:110:G:N2	1.61	0.98
37:2A:168:A:C8	37:2A:168:A:H5''	1.98	0.97
1:A:31:C:C2	37:2A:33:G:N1	2.32	0.97
1:A:30:C:C2'	1:A:31:C:C5'	2.38	0.96
36:4Z:333:ILE:O	36:4Z:342:LEU:N	1.98	0.96
43:2G:501:LEU:O	43:2G:504:ILE:N	1.98	0.96
3:5B:2038:GLN:N	5:5D:1035:LEU:CD1	2.29	0.96
1:A:31:C:C2	37:2A:33:G:C6	2.53	0.95
1:A:31:C:O2	37:2A:33:G:C6	2.20	0.94
2:5A:93:U:H1'	9:5c:104:ASP:CA	1.96	0.94
30:4I:8:GLN:N	30:4I:8:GLN:NE2	2.16	0.93
37:2A:156:U:H5''	37:2A:156:U:C6	2.02	0.93
43:2G:86:ALA:O	43:2G:89:ALA:N	2.02	0.91
2:5A:95:G:H21	2:5A:96:A:H5''	1.36	0.89
37:2A:54:U:OP1	42:2F:428:GLU:CA	2.20	0.89
1:A:23:G:H1	37:2A:39:U:H3	1.20	0.89
1:A:34:G:N7	1:A:35:U:C4	2.40	0.89
2:5A:93:U:O4	10:5d:66:CYS:N	2.06	0.89
1:A:40:U:O2'	1:A:41:U:OP2	1.89	0.88
43:2G:793:LYS:O	43:2G:797:GLY:HA3	1.72	0.88
2:5A:67:A:O2'	2:5A:68:C:OP1	1.89	0.87
3:5B:2036:GLN:C	5:5D:1035:LEU:HD13	1.98	0.87
3:5B:2038:GLN:CB	5:5D:1035:LEU:HD11	2.04	0.87
22:4A:120:U:H2'	11:4e:82:ASP:CA	2.04	0.87
2:5A:93:U:C1'	9:5c:104:ASP:CA	2.52	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2A:154:C:O2	37:2A:176:G:N2	2.07	0.87
1:A:12:U:OP2	1:A:12:U:H2'	1.74	0.87
5:5D:1519:ARG:NH2	5:5D:1691:ALA:O	2.07	0.86
37:2A:40:C:H5''	37:2A:40:C:H6	1.39	0.86
37:2A:156:U:H6	37:2A:156:U:C5'	1.89	0.86
2:5A:90:U:H5	13:5g:38:ASN:O	1.53	0.86
5:5D:1622:GLU:OE2	5:5D:1649:SER:OG	1.93	0.86
22:4A:118:A:H2	22:4A:119:A:H62	1.22	0.86
27:4F:22:GLU:OE1	27:4F:22:GLU:N	2.08	0.86
37:2A:168:A:H5''	37:2A:168:A:H8	1.36	0.86
1:A:38:C:OP1	1:A:39:U:P	2.34	0.85
22:4A:121:U:H3	12:4f:63:ARG:CA	1.88	0.85
5:5D:471:ALA:HB1	5:5D:518:LEU:HD13	1.58	0.85
28:4G:354:PRO:O	28:4G:357:THR:OG1	1.93	0.85
43:2G:728:LEU:O	43:2G:731:LEU:N	2.10	0.85
1:A:11:C:H2'	1:A:11:C:O2	1.75	0.84
1:A:30:C:H3'	1:A:31:C:C5'	2.04	0.84
22:4A:118:A:N3	22:4A:119:A:N6	2.23	0.84
22:4A:119:A:C5'	10:4d:39:TYR:CA	2.56	0.84
4:5C:256:CYS:HA	4:5C:308:CYS:HB3	1.60	0.83
1:A:36:C:H1'	1:A:37:C:OP1	1.78	0.83
3:5B:1412:TRP:O	3:5B:1420:ASN:ND2	2.10	0.83
37:2A:152:G:N2	37:2A:153:A:N7	2.27	0.83
1:A:30:C:C5	1:A:31:C:C5	2.67	0.83
3:5B:2038:GLN:H	5:5D:1035:LEU:CD1	1.90	0.83
35:4N:125:ARG:O	35:4N:129:ASN:ND2	2.11	0.82
1:A:99:C:O2'	1:A:100:C:OP2	1.96	0.82
19:6e:46:GLU:CA	19:6e:63:ALA:N	2.43	0.82
22:4A:49:C:OP1	28:4G:172:ARG:NH1	2.12	0.82
36:4Z:334:HIS:HA	36:4Z:341:THR:HA	1.62	0.81
25:4D:115:ARG:O	25:4D:119:SER:OG	1.98	0.81
37:2A:105:G:C2'	37:2A:106:G:H5''	2.10	0.81
43:2G:648:LEU:O	43:2G:651:VAL:N	2.13	0.81
45:2I:839:ALA:O	45:2I:843:LEU:N	2.13	0.81
3:5B:292:ASP:OD1	3:5B:1139:ARG:NH1	2.13	0.81
1:A:31:C:O2	37:2A:33:G:N1	2.13	0.81
5:5D:991:TYR:OH	5:5D:1097:GLU:OE2	1.97	0.81
1:A:36:C:H4'	1:A:37:C:H5	1.44	0.81
37:2A:152:G:H5''	37:2A:153:A:OP2	1.80	0.81
1:A:34:G:C2	1:A:35:U:H2'	2.16	0.81
1:A:27:U:OP2	43:2G:1106:ARG:CA	2.30	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:U:O2	37:2A:42:G:C2	2.35	0.80
33:4L:29:ILE:HD11	33:4L:71:LEU:HD22	1.62	0.80
2:5A:92:U:H3	8:5b:36:MET:CA	1.93	0.80
22:4A:108:C:O2'	22:4A:109:G:H5'	1.81	0.80
1:A:34:G:N9	1:A:35:U:C5	2.49	0.80
1:A:28:G:H5'	1:A:28:G:H8	1.45	0.79
1:A:32:C:O2	37:2A:31:G:N1	2.11	0.79
37:2A:101:U:H5''	37:2A:102:U:H5'	1.65	0.79
3:5B:1793:THR:OG1	3:5B:1797:ASN:OD1	1.99	0.79
5:5D:1151:GLU:OE2	5:5D:1151:GLU:N	2.16	0.79
4:5C:623:GLU:OE1	4:5C:624:SER:OG	2.00	0.79
2:5A:94:U:H1'	2:5A:95:G:OP1	1.82	0.79
48:2L:56:GLY:O	48:2L:65:GLY:N	2.12	0.79
1:A:23:G:N2	37:2A:39:U:O2	2.14	0.79
37:2A:54:U:OP1	42:2F:424:ARG:O	2.00	0.79
43:2G:669:GLN:O	43:2G:672:ALA:N	2.16	0.79
1:A:28:G:H5'	1:A:28:G:C8	2.18	0.79
1:A:30:C:N4	1:A:31:C:N4	2.31	0.78
3:5B:1217:GLN:OE1	3:5B:1224:ARG:NH1	2.15	0.78
1:A:31:C:H1'	37:2A:33:G:N2	1.99	0.78
1:A:34:G:H2'	1:A:35:U:C6	2.19	0.78
3:5B:1972:THR:OG1	3:5B:1975:GLU:OE1	1.99	0.78
1:A:36:C:H4'	1:A:37:C:C5	2.18	0.78
45:2I:523:GLY:HA3	45:2I:536:TRP:O	1.83	0.78
5:5D:1090:ARG:NH1	22:4A:75:C:O2'	2.17	0.78
4:5C:569:ARG:O	4:5C:569:ARG:NH1	2.16	0.78
1:A:31:C:O2	37:2A:33:G:C2	2.37	0.77
45:2I:914:ILE:O	45:2I:918:ARG:CA	2.32	0.77
28:4G:724:MET:HA	28:4G:724:MET:HE2	1.65	0.77
43:2G:428:ALA:O	43:2G:432:THR:N	2.17	0.77
1:A:115:U:H2'	1:A:116:G:C8	2.19	0.77
3:5B:2188:LEU:O	3:5B:2251:TYR:OH	2.01	0.77
5:5D:880:LEU:O	5:5D:884:ASN:ND2	2.17	0.77
37:2A:177:A:H5''	37:2A:178:A:OP1	1.84	0.77
1:A:8:U:O2	1:A:8:U:H2'	1.84	0.77
4:5C:826:ARG:NH2	4:5C:910:ASP:OD2	2.18	0.77
37:2A:153:A:H2'	37:2A:154:C:H5'	1.65	0.76
43:2G:1246:MET:O	43:2G:1249:TYR:N	2.18	0.76
1:A:34:G:H3'	1:A:35:U:H5''	1.67	0.76
1:A:40:U:H4'	1:A:41:U:C5'	2.13	0.76
22:4A:121:U:N3	12:4f:63:ARG:CA	2.48	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:C:H1'	37:2A:33:G:C2	2.20	0.76
24:4C:262:ASP:OD2	24:4C:264:ASN:ND2	2.19	0.76
24:4C:513:ASP:OD1	28:4G:802:LYS:NZ	2.18	0.76
43:2G:531:LEU:O	43:2G:534:GLN:N	2.18	0.76
42:2F:276:GLY:C	42:2F:278:LEU:H	1.92	0.75
33:4L:166:GLN:OE1	33:4L:166:GLN:N	2.19	0.75
22:4A:1:A:OP1	23:4B:526:LYS:NZ	2.19	0.75
43:2G:1016:LEU:O	43:2G:1019:ARG:N	2.19	0.75
5:5D:1342:SER:O	5:5D:1486:ARG:NH2	2.20	0.75
1:A:17:G:H1	37:2A:44:U:H3	1.33	0.75
37:2A:153:A:C2'	37:2A:154:C:H5'	2.17	0.75
1:A:30:C:C4	1:A:31:C:C6	2.76	0.74
37:2A:143:A:H3'	37:2A:143:A:N3	2.01	0.74
4:5C:561:LYS:NZ	4:5C:611:ASN:O	2.21	0.74
2:5A:59:G:OP1	3:5B:417:ARG:NH2	2.20	0.74
33:4L:155:GLU:OE2	33:4L:155:GLU:N	2.19	0.74
43:2G:1270:ASN:O	43:2G:1273:TYR:N	2.21	0.74
45:2I:304:GLN:CA	45:2I:309:ASP:O	2.36	0.74
22:4A:57:G:N7	25:4D:354:ARG:NH1	2.35	0.74
42:2F:184:ARG:O	7:2a:85:PRO:N	2.21	0.74
1:A:31:C:O2	37:2A:33:G:C5	2.41	0.74
2:5A:93:U:O4	10:5d:65:ARG:CA	2.35	0.73
22:4A:91:A:H2	22:4A:110:G:H22	0.82	0.73
24:4C:104:ASP:OD1	24:4C:106:SER:OG	2.04	0.73
43:2G:874:LYS:O	43:2G:877:GLY:N	2.20	0.73
45:2I:442:LEU:O	45:2I:735:SER:N	2.19	0.73
1:A:38:C:OP1	1:A:39:U:OP1	2.06	0.73
1:A:34:G:H2'	1:A:35:U:H6	1.52	0.73
2:5A:117:A:N1	10:5d:26:GLY:HA3	2.03	0.73
3:5B:138:PRO:O	3:5B:142:SER:OG	2.07	0.73
43:2G:660:ALA:O	43:2G:663:THR:N	2.22	0.73
5:5D:730:GLU:O	5:5D:734:THR:HG22	1.89	0.73
42:2F:276:GLY:O	42:2F:278:LEU:N	2.20	0.73
37:2A:179:C:H2'	37:2A:180:G:H8	1.54	0.72
3:5B:510:ARG:NH2	28:4G:35:GLY:O	2.22	0.72
37:2A:106:G:H21	37:2A:107:A:N6	1.87	0.72
19:6e:46:GLU:N	19:6e:63:ALA:H	1.87	0.72
33:4L:18:GLN:OE1	33:4L:30:TYR:OH	2.05	0.72
45:2I:753:GLY:HA3	45:2I:765:LEU:O	1.88	0.72
5:5D:441:GLY:O	5:5D:693:THR:OG1	2.08	0.72
5:5D:622:ASP:OD1	5:5D:623:ASP:N	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2G:1055:TRP:O	43:2G:1058:ILE:N	2.22	0.72
2:5A:96:A:H61	12:5f:23:GLY:H	1.38	0.72
5:5D:1945:LEU:HA	5:5D:1948:MET:HE3	1.72	0.72
1:A:15:A:H2'	1:A:16:A:O4'	1.89	0.72
1:A:19:U:H3	37:2A:42:G:H1	1.37	0.72
3:5B:105:ASN:ND2	3:5B:131:GLU:OE1	2.23	0.72
4:5C:196:LYS:HA	13:5g:33:ILE:O	1.90	0.72
43:2G:87:PRO:O	43:2G:91:LEU:N	2.21	0.72
43:2G:535:ILE:O	43:2G:538:LEU:N	2.23	0.72
1:A:21:U:H1'	1:A:22:C:OP1	1.90	0.72
3:5B:919:ASP:OD2	3:5B:1012:LYS:NZ	2.22	0.72
27:4F:107:GLU:OE1	27:4F:107:GLU:N	2.17	0.72
43:2G:994:LEU:O	43:2G:997:LEU:N	2.22	0.71
3:5B:2295:GLU:OE2	3:5B:2295:GLU:N	2.22	0.71
43:2G:122:HIS:O	43:2G:125:THR:N	2.22	0.71
43:2G:791:VAL:O	43:2G:794:GLN:N	2.23	0.71
37:2A:106:G:H4'	37:2A:107:A:O4'	1.89	0.71
2:5A:96:A:H4'	2:5A:97:G:H5''	1.72	0.71
3:5B:189:GLU:O	3:5B:564:TYR:OH	2.08	0.71
37:2A:153:A:H2'	37:2A:154:C:C5'	2.19	0.71
1:A:38:C:OP1	1:A:39:U:OP2	2.09	0.71
14:6A:86:U:H3	37:2A:12:G:H1	1.39	0.71
19:6e:46:GLU:N	19:6e:63:ALA:N	2.38	0.71
2:5A:92:U:N3	8:5b:36:MET:CA	2.53	0.70
3:5B:2278:SER:OG	3:5B:2309:HIS:NE2	2.22	0.70
29:4H:20:GLY:N	29:4H:168:PRO:O	2.24	0.70
35:4N:122:VAL:HG12	35:4N:126:PHE:CE2	2.26	0.70
2:5A:87:A:N6	2:5A:92:U:P	2.64	0.70
3:5B:2038:GLN:CA	5:5D:1035:LEU:HD11	2.22	0.70
37:2A:54:U:OP1	42:2F:427:ALA:O	2.10	0.70
2:5A:94:U:C1'	2:5A:95:G:OP1	2.39	0.70
4:5C:198:TYR:CE2	4:5C:435:VAL:HG11	2.27	0.70
43:2G:700:LYS:O	43:2G:703:THR:N	2.24	0.70
44:2H:479:ASP:O	44:2H:482:ALA:N	2.25	0.70
5:5D:1041:LEU:HD23	5:5D:1041:LEU:O	1.90	0.70
5:5D:1699:GLU:OE2	5:5D:1701:ARG:NH1	2.25	0.70
4:5C:269:LEU:O	4:5C:378:TYR:OH	2.08	0.70
14:6A:103:U:O4	21:6g:32:GLN:O	2.10	0.70
37:2A:40:C:H6	37:2A:40:C:C5'	2.05	0.69
45:2I:545:VAL:N	45:2I:557:ALA:O	2.25	0.69
37:2A:154:C:H2'	37:2A:155:C:C6	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:5B:2036:GLN:O	5:5D:1035:LEU:CD1	2.40	0.69
5:5D:1201:GLU:N	5:5D:1201:GLU:OE1	2.26	0.69
5:5D:731:THR:HG23	5:5D:810:VAL:HG12	1.74	0.69
5:5D:816:ALA:O	5:5D:855:ARG:NH2	2.26	0.69
37:2A:153:A:N6	37:2A:177:A:C2	2.60	0.69
2:5A:93:U:O4	10:5d:65:ARG:C	2.36	0.69
32:4K:350:ASP:OD1	32:4K:351:GLU:N	2.25	0.69
48:2L:7:ASP:O	48:2L:91:LEU:N	2.25	0.69
1:A:30:C:H41	1:A:31:C:N4	1.91	0.69
5:5D:1186:LEU:HD21	5:5D:1270:VAL:HG23	1.75	0.69
45:2I:558:LEU:O	45:2I:561:GLY:N	2.24	0.69
22:4A:120:U:C2'	11:4e:82:ASP:CA	2.70	0.69
14:6A:65:G:H21	23:4B:515:ASN:HD21	1.41	0.68
14:6A:102:A:O2'	21:6g:33:THR:CA	2.41	0.68
2:5A:87:A:N6	2:5A:92:U:OP2	2.26	0.68
37:2A:30:A:N3	37:2A:30:A:H2'	2.06	0.68
14:6A:103:U:H3'	14:6A:104:U:H5''	1.75	0.68
1:A:30:C:C4	1:A:31:C:C4	2.69	0.68
4:5C:249:GLU:OE2	4:5C:249:GLU:O	2.10	0.68
3:5B:1610:GLN:NE2	3:5B:1612:GLU:OE1	2.27	0.67
5:5D:1980:GLU:N	5:5D:1980:GLU:OE1	2.27	0.67
3:5B:1977:ILE:O	3:5B:1981:VAL:HG23	1.94	0.67
37:2A:143:A:H2'	37:2A:144:C:H6	1.59	0.67
1:A:36:C:C4'	1:A:37:C:H5	2.07	0.67
5:5D:748:LEU:HD23	5:5D:748:LEU:O	1.94	0.67
44:2H:596:GLU:C	44:2H:598:GLU:H	2.00	0.67
2:5A:97:G:H1	2:5A:116:U:H3	1.41	0.67
37:2A:152:G:O3'	37:2A:153:A:O4'	2.11	0.67
1:A:22:C:O5'	1:A:22:C:H6	1.78	0.67
2:5A:95:G:H21	2:5A:96:A:C5'	2.06	0.67
3:5B:2237:TRP:NE1	3:5B:2250:GLY:O	2.28	0.67
45:2I:1148:LEU:O	45:2I:1152:HIS:N	2.27	0.67
1:A:31:C:H5'	1:A:31:C:H6	1.58	0.67
5:5D:569:LEU:HB2	5:5D:575:LEU:HD12	1.77	0.67
23:4B:674:LEU:O	23:4B:678:VAL:HG23	1.95	0.67
33:4L:135:ARG:NH2	33:4L:159:ASP:OD1	2.26	0.67
36:4Z:362:HIS:O	36:4Z:378:MET:N	2.26	0.67
37:2A:151:C:C2	37:2A:152:G:C8	2.83	0.67
1:A:30:C:N4	1:A:31:C:C5	2.50	0.67
22:4A:111:C:H6	22:4A:111:C:O5'	1.78	0.67
4:5C:623:GLU:OE2	4:5C:623:GLU:N	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2A:150:U:H3	37:2A:181:G:H1	1.41	0.66
5:5D:1218:SER:HB3	5:5D:1240:LEU:HD21	1.76	0.66
28:4G:513:CYS:O	28:4G:517:GLY:N	2.27	0.66
3:5B:2278:SER:HG	3:5B:2309:HIS:HE2	1.37	0.66
5:5D:1943:MET:HE1	5:5D:2065:TRP:HB2	1.77	0.66
37:2A:151:C:H2'	37:2A:152:G:H8	1.60	0.66
43:2G:758:ASP:O	43:2G:762:ALA:N	2.28	0.66
43:2G:1280:LEU:O	43:2G:1283:HIS:N	2.22	0.66
43:2G:400:SER:O	43:2G:404:LEU:N	2.28	0.66
44:2H:487:LEU:O	44:2H:490:HIS:N	2.28	0.66
45:2I:753:GLY:CA	45:2I:765:LEU:O	2.44	0.66
3:5B:1974:GLU:N	3:5B:1974:GLU:OE1	2.27	0.66
28:4G:921:ASN:HD22	28:4G:921:ASN:C	2.03	0.66
37:2A:168:A:C8	37:2A:168:A:C5'	2.75	0.66
3:5B:861:ARG:NH2	28:4G:178:LYS:O	2.28	0.66
28:4G:297:LEU:O	28:4G:301:VAL:HG23	1.96	0.66
37:2A:151:C:O2	37:2A:152:G:C8	2.48	0.66
2:5A:93:U:O4'	9:5c:104:ASP:CA	2.42	0.66
33:4L:83:GLU:O	33:4L:87:ILE:HD12	1.95	0.66
43:2G:1243:PRO:O	43:2G:1246:MET:N	2.29	0.66
14:6A:103:U:H4'	14:6A:104:U:OP2	1.95	0.66
1:A:36:C:H1'	1:A:37:C:P	2.36	0.66
37:2A:54:U:OP1	42:2F:427:ALA:C	2.39	0.65
1:A:8:U:O2	1:A:8:U:C2'	2.44	0.65
37:2A:153:A:C3'	37:2A:154:C:H5'	2.25	0.65
3:5B:162:LYS:O	3:5B:573:GLN:NE2	2.30	0.65
4:5C:152:GLN:NE2	4:5C:426:GLU:O	2.29	0.65
40:2D:418:GLU:N	40:2D:418:GLU:OE1	2.30	0.65
3:5B:1931:THR:OG1	23:4B:497:GLU:OE2	2.14	0.65
33:4L:120:LEU:CB	33:4L:152:LEU:HD11	2.27	0.65
43:2G:658:TRP:O	43:2G:661:ARG:N	2.30	0.65
24:4C:241:PRO:O	24:4C:286:THR:OG1	2.13	0.65
1:A:32:C:OP2	1:A:32:C:H3'	1.96	0.65
5:5D:1538:ARG:NH1	5:5D:1665:ASP:OD1	2.30	0.65
5:5D:1948:MET:O	5:5D:1952:ALA:N	2.30	0.65
28:4G:326:GLN:O	28:4G:330:ASN:ND2	2.29	0.65
1:A:11:C:O2	1:A:11:C:C2'	2.45	0.64
2:5A:89:U:H2'	2:5A:90:U:H5''	1.79	0.64
3:5B:858:GLN:OE1	3:5B:861:ARG:NH1	2.30	0.64
5:5D:769:CYS:SG	5:5D:770:LYS:N	2.69	0.64
43:2G:886:HIS:O	43:2G:889:GLU:N	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5D:488:LEU:HD12	5:5D:488:LEU:O	1.98	0.64
45:2I:325:ILE:O	45:2I:375:SER:N	2.30	0.64
1:A:36:C:C4'	1:A:37:C:C5	2.79	0.64
5:5D:526:ASN:O	5:5D:529:GLY:N	2.30	0.64
22:4A:117:C:O5'	22:4A:117:C:H6	1.80	0.64
37:2A:114:A:H61	37:2A:142:C:H42	1.44	0.64
2:5A:85:C:OP1	9:5c:20:GLU:CA	2.46	0.64
43:2G:1109:ARG:O	43:2G:1110:VAL:C	2.41	0.64
49:2M:40:TYR:O	49:2M:43:TYR:N	2.31	0.64
1:A:22:C:O2'	1:A:23:G:C5'	2.37	0.64
1:A:22:C:C2'	1:A:23:G:H5'	2.28	0.64
28:4G:493:SER:O	28:4G:497:ASN:N	2.31	0.64
5:5D:1936:LEU:HD23	5:5D:1937:SER:N	2.12	0.64
22:4A:120:U:OP2	10:4d:39:TYR:O	2.16	0.64
36:4Z:334:HIS:CA	36:4Z:341:THR:HA	2.27	0.64
3:5B:2072:GLU:HB2	3:5B:2075:VAL:HG22	1.80	0.64
1:A:99:C:HO2'	1:A:100:C:P	2.21	0.64
37:2A:147:G:H2'	37:2A:148:C:H6	1.63	0.64
40:2D:413:SER:OG	40:2D:416:THR:O	2.09	0.64
44:2H:491:LEU:O	44:2H:494:THR:N	2.30	0.64
5:5D:1383:GLU:N	5:5D:1383:GLU:OE1	2.31	0.64
37:2A:154:C:H2'	37:2A:155:C:H6	1.63	0.63
45:2I:868:VAL:O	45:2I:877:LEU:N	2.30	0.63
1:A:35:U:OP1	48:2L:63:GLY:HA3	1.98	0.63
3:5B:715:GLU:OE1	3:5B:718:ARG:NH1	2.31	0.63
28:4G:426:ALA:O	28:4G:430:CYS:N	2.30	0.63
37:2A:152:G:C2	37:2A:153:A:C5	2.87	0.63
1:A:20:U:H5'	1:A:21:U:OP2	1.99	0.63
43:2G:749:ALA:O	43:2G:752:TYR:N	2.31	0.63
43:2G:1018:PRO:O	43:2G:1021:THR:N	2.30	0.63
45:2I:563:LEU:N	45:2I:581:LYS:O	2.27	0.63
45:2I:645:MET:N	45:2I:662:PHE:O	2.28	0.63
3:5B:2038:GLN:CA	5:5D:1035:LEU:CD1	2.76	0.63
22:4A:127:C:O2	9:4c:47:ARG:O	2.17	0.63
1:A:31:C:N3	37:2A:33:G:C6	2.66	0.63
37:2A:164:C:H6	37:2A:164:C:H5'	1.63	0.63
2:5A:88:A:H2'	2:5A:88:A:N3	2.14	0.63
5:5D:793:ASP:O	5:5D:797:VAL:HG23	1.98	0.63
4:5C:283:ASP:OD1	4:5C:284:GLU:N	2.32	0.63
22:4A:108:C:H2'	22:4A:109:G:H8	1.63	0.63
37:2A:153:A:H3'	37:2A:154:C:H5'	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5A:90:U:H5	13:5g:38:ASN:C	2.06	0.63
5:5D:602:GLU:OE1	5:5D:606:THR:OG1	2.16	0.63
4:5C:359:LYS:HD2	4:5C:359:LYS:O	1.98	0.63
22:4A:89:U:C2'	22:4A:90:G:H5'	2.29	0.63
22:4A:89:U:O2'	22:4A:90:G:H5'	1.99	0.63
28:4G:11:MET:SD	28:4G:11:MET:N	2.72	0.63
33:4L:166:GLN:O	33:4L:167:LYS:HD3	1.98	0.63
37:2A:156:U:C6	37:2A:156:U:C5'	2.72	0.63
4:5C:198:TYR:CD2	4:5C:435:VAL:HG11	2.33	0.62
22:4A:91:A:O5'	22:4A:91:A:H8	1.82	0.62
25:4D:399:LEU:O	28:4G:289:ASN:ND2	2.32	0.62
43:2G:1264:VAL:O	43:2G:1267:LYS:N	2.32	0.62
45:2I:1191:LYS:O	45:2I:1194:SER:N	2.32	0.62
5:5D:760:GLU:O	5:5D:764:THR:HG23	1.99	0.62
33:4L:176:GLN:OE1	33:4L:176:GLN:N	2.33	0.62
1:A:31:C:C2	1:A:32:C:C5	2.87	0.62
3:5B:143:GLN:NE2	3:5B:207:PHE:O	2.32	0.62
5:5D:537:LYS:N	5:5D:608:LEU:O	2.32	0.62
4:5C:260:ILE:HD12	4:5C:263:LEU:HD12	1.82	0.62
5:5D:1960:LEU:HD12	5:5D:1982:VAL:HG22	1.82	0.62
43:2G:179:GLY:O	43:2G:182:LYS:N	2.33	0.62
1:A:31:C:H2'	1:A:32:C:H6	1.65	0.62
3:5B:235:MET:HA	3:5B:235:MET:HE3	1.81	0.62
24:4C:128:GLU:OE2	40:2D:442:ARG:NH2	2.32	0.62
37:2A:143:A:H2'	37:2A:144:C:C6	2.35	0.62
1:A:31:C:C2'	1:A:32:C:H5'	2.30	0.62
2:5A:95:G:N3	2:5A:95:G:H2'	2.15	0.62
3:5B:2231:THR:OG1	3:5B:2255:HIS:O	2.16	0.61
4:5C:484:THR:HG21	4:5C:489:GLN:NE2	2.15	0.61
23:4B:386:GLU:OE1	23:4B:386:GLU:N	2.33	0.61
37:2A:112:G:H2'	37:2A:113:G:H8	1.65	0.61
43:2G:914:PHE:O	43:2G:917:VAL:N	2.32	0.61
45:2I:586:ASP:O	45:2I:610:VAL:N	2.32	0.61
46:2J:77:ILE:O	46:2J:84:ILE:N	2.32	0.61
5:5D:774:LEU:CD2	5:5D:778:LEU:HD11	2.30	0.61
40:2D:252:PHE:CA	42:2F:63:ASP:CA	2.79	0.61
43:2G:88:VAL:CA	43:2G:92:ASN:H	2.13	0.61
5:5D:1849:ILE:HD13	5:5D:1923:ILE:CD1	2.30	0.61
43:2G:784:MET:O	43:2G:787:ILE:N	2.34	0.61
5:5D:639:ILE:HD11	5:5D:646:VAL:HG22	1.83	0.61
37:2A:142:C:C2'	37:2A:143:A:H5'	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2G:897:LEU:O	43:2G:900:PHE:N	2.34	0.61
1:A:31:C:O2'	1:A:32:C:H5'	2.00	0.61
4:5C:118:PHE:O	4:5C:122:LEU:HD12	2.01	0.61
4:5C:933:PHE:O	4:5C:937:THR:OG1	2.08	0.61
5:5D:949:LEU:O	5:5D:953:ARG:NH1	2.34	0.61
45:2I:973:GLY:HA3	45:2I:976:LYS:O	2.00	0.61
1:A:40:U:H5''	1:A:41:U:H5''	1.82	0.61
3:5B:1169:GLN:O	3:5B:1173:SER:OG	2.19	0.61
4:5C:112:THR:HG22	4:5C:112:THR:O	2.01	0.61
33:4L:107:MET:HE2	33:4L:107:MET:HA	1.81	0.61
37:2A:157:G:H5''	37:2A:157:G:H8	1.65	0.61
3:5B:840:ILE:HG22	3:5B:844:GLU:OE2	2.00	0.61
43:2G:895:GLY:O	43:2G:898:TYR:N	2.34	0.61
43:2G:981:TYR:O	43:2G:984:GLU:N	2.20	0.61
1:A:35:U:H4'	1:A:36:C:OP2	1.98	0.61
1:A:116:G:H22	14:6A:38:G:H22	1.49	0.61
23:4B:480:ASN:OD1	23:4B:480:ASN:O	2.18	0.61
35:4N:133:MET:SD	35:4N:134:GLU:N	2.74	0.61
43:2G:173:ALA:C	43:2G:176:ALA:H	2.09	0.61
5:5D:1456:VAL:HG22	5:5D:1491:SER:HB3	1.83	0.61
5:5D:1428:THR:HG22	5:5D:1429:PRO:HD2	1.83	0.60
43:2G:862:GLU:O	43:2G:865:ARG:N	2.33	0.60
2:5A:19:A:O2'	2:5A:21:A:N1	2.30	0.60
3:5B:2141:GLU:OE1	3:5B:2143:ARG:NH2	2.34	0.60
1:A:13:U:H2'	1:A:14:G:H8	1.66	0.60
5:5D:1078:MET:CE	5:5D:1082:VAL:HG23	2.30	0.60
43:2G:551:LEU:O	43:2G:554:LYS:N	2.34	0.60
45:2I:550:ASN:N	45:2I:553:GLN:O	2.27	0.60
1:A:10:C:O2'	1:A:11:C:OP2	2.16	0.60
5:5D:1604:LEU:HD13	5:5D:1609:LEU:HD22	1.83	0.60
1:A:31:C:H2'	1:A:32:C:C6	2.36	0.60
1:A:116:G:H22	14:6A:38:G:H1	1.49	0.60
5:5D:789:MET:O	5:5D:794:ARG:NH1	2.35	0.60
43:2G:953:ASP:O	43:2G:956:SER:N	2.34	0.60
43:2G:1125:PRO:O	43:2G:1128:VAL:N	2.35	0.60
1:A:21:U:H1'	1:A:22:C:P	2.41	0.60
3:5B:388:LEU:O	4:5C:379:LYS:NZ	2.18	0.60
5:5D:1569:THR:OG1	5:5D:1645:VAL:HG12	2.02	0.60
4:5C:130:ARG:NH2	4:5C:439:PRO:O	2.35	0.60
5:5D:1037:LEU:HG	5:5D:1052:ILE:HD11	1.83	0.60
5:5D:1561:VAL:HG22	5:5D:1662:ILE:HB	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:4A:118:A:H2	22:4A:119:A:N6	1.84	0.60
30:4I:14:ASP:OD1	30:4I:15:TYR:N	2.34	0.60
43:2G:610:ILE:O	43:2G:613:MET:N	2.34	0.60
22:4A:20:A:OP2	25:4D:423:THR:HG23	2.01	0.60
37:2A:153:A:N6	37:2A:177:A:H2	1.98	0.60
45:2I:664:TYR:CA	45:2I:677:THR:O	2.50	0.60
1:A:13:U:O5'	1:A:13:U:H6	1.84	0.59
3:5B:888:GLN:NE2	3:5B:890:ALA:O	2.35	0.59
4:5C:607:LEU:O	4:5C:610:VAL:HG22	2.02	0.59
5:5D:1725:GLU:OE2	5:5D:1763:ARG:NH2	2.34	0.59
43:2G:929:LEU:O	43:2G:932:ILE:N	2.34	0.59
1:A:31:C:O2	37:2A:33:G:C4	2.56	0.59
3:5B:306:GLN:NE2	4:5C:879:ASP:OD1	2.34	0.59
19:6e:46:GLU:CA	19:6e:62:ASP:C	2.74	0.59
36:4Z:334:HIS:HA	36:4Z:342:LEU:H	1.67	0.59
37:2A:106:G:N2	37:2A:107:A:C6	2.67	0.59
45:2I:15:SER:N	45:2I:33:SER:O	2.35	0.59
5:5D:1248:ASP:OD1	5:5D:1248:ASP:N	2.35	0.59
2:5A:95:G:N2	2:5A:96:A:H5''	2.13	0.59
3:5B:194:GLU:N	3:5B:194:GLU:OE1	2.35	0.59
5:5D:548:VAL:O	5:5D:552:VAL:HG23	2.02	0.59
5:5D:551:MET:HA	5:5D:551:MET:HE2	1.84	0.59
43:2G:1109:ARG:O	43:2G:1112:THR:N	2.36	0.59
43:2G:1149:LYS:O	43:2G:1152:SER:N	2.36	0.59
28:4G:921:ASN:C	28:4G:921:ASN:ND2	2.61	0.59
43:2G:1182:LEU:O	43:2G:1185:ARG:N	2.35	0.59
36:4Z:334:HIS:CB	36:4Z:341:THR:HA	2.33	0.59
2:5A:95:G:O2'	10:5d:24:LYS:C	2.46	0.59
47:2K:67:ILE:O	47:2K:70:ALA:N	2.36	0.59
2:5A:87:A:N6	2:5A:91:U:O3'	2.36	0.58
14:6A:103:U:C3'	14:6A:104:U:H5''	2.31	0.58
43:2G:745:ALA:O	43:2G:748:LYS:N	2.36	0.58
4:5C:759:LEU:HA	4:5C:762:VAL:HG22	1.85	0.58
28:4G:118:GLU:OE2	28:4G:119:ARG:NH1	2.35	0.58
1:A:22:C:HO2'	1:A:23:G:H5'	1.65	0.58
2:5A:53:U:OP1	28:4G:123:ARG:NH1	2.36	0.58
3:5B:1357:MET:SD	3:5B:1358:SER:N	2.75	0.58
24:4C:403:LEU:HD12	24:4C:403:LEU:O	2.03	0.58
43:2G:811:LEU:O	43:2G:814:PHE:N	2.36	0.58
45:2I:931:VAL:O	45:2I:936:LYS:N	2.31	0.58
1:A:117:G:H5''	35:4N:101:GLY:HA3	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2D:411:LEU:N	40:2D:419:LYS:HZ2	2.01	0.58
43:2G:424:ILE:O	43:2G:428:ALA:N	2.36	0.58
4:5C:215:VAL:HG11	4:5C:242:LEU:CD2	2.33	0.58
5:5D:465:GLU:N	5:5D:465:GLU:OE1	2.36	0.58
19:6e:46:GLU:H	19:6e:63:ALA:N	2.01	0.58
1:A:30:C:H3'	1:A:31:C:H5'	1.83	0.58
24:4C:120:THR:HG22	24:4C:129:ARG:NH1	2.19	0.58
3:5B:1208:THR:HG23	3:5B:1208:THR:O	2.03	0.58
5:5D:552:VAL:HG21	5:5D:568:GLU:HB2	1.86	0.58
43:2G:929:LEU:O	43:2G:930:PRO:C	2.46	0.58
44:2H:596:GLU:O	44:2H:598:GLU:N	2.37	0.58
1:A:35:U:O2	1:A:35:U:O2'	2.22	0.58
22:4A:110:G:O5'	22:4A:110:G:H8	1.87	0.58
23:4B:416:ASN:ND2	24:4C:170:GLY:O	2.36	0.58
43:2G:308:SER:O	43:2G:311:ALA:N	2.35	0.58
1:A:30:C:N3	1:A:31:C:C6	2.72	0.58
1:A:117:G:H2'	1:A:118:A:C8	2.39	0.58
22:4A:108:C:C2'	22:4A:109:G:H5'	2.34	0.58
5:5D:675:TYR:OH	5:5D:885:GLN:OE1	2.10	0.58
5:5D:1197:THR:O	5:5D:1198:LEU:HD12	2.04	0.58
22:4A:111:C:H2'	22:4A:112:A:H8	1.69	0.58
45:2I:523:GLY:CA	45:2I:536:TRP:O	2.51	0.58
49:2M:48:ASP:O	49:2M:51:ASN:N	2.37	0.58
43:2G:892:LEU:O	43:2G:895:GLY:N	2.37	0.57
36:4Z:382:GLU:O	36:4Z:383:CYS:CB	2.52	0.57
43:2G:491:GLU:O	43:2G:494:GLU:N	2.32	0.57
45:2I:1160:HIS:O	45:2I:1163:PHE:N	2.37	0.57
1:A:36:C:C5'	1:A:37:C:H5	2.17	0.57
24:4C:200:LYS:O	24:4C:207:ARG:NH1	2.36	0.57
31:4J:352:GLU:OE2	31:4J:352:GLU:N	2.38	0.57
5:5D:930:LEU:HD23	5:5D:949:LEU:HD12	1.86	0.57
22:4A:37:C:H1'	22:4A:38:U:H2'	1.85	0.57
42:2F:184:ARG:CA	7:2a:85:PRO:CA	2.82	0.57
45:2I:638:GLU:N	45:2I:668:GLY:O	2.32	0.57
4:5C:922:GLU:N	4:5C:922:GLU:OE1	2.37	0.57
37:2A:152:G:N2	37:2A:153:A:C5	2.73	0.57
1:A:34:G:C4	1:A:35:U:C6	2.93	0.57
5:5D:1071:LYS:HA	5:5D:1071:LYS:HE2	1.87	0.57
5:5D:1825:ASN:OD1	5:5D:1827:THR:N	2.38	0.57
5:5D:1828:THR:OG1	5:5D:1853:ALA:N	2.35	0.57
5:5D:1971:ILE:O	5:5D:1975:THR:HG23	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:2I:914:ILE:O	45:2I:918:ARG:C	2.47	0.57
5:5D:1752:VAL:HG11	32:4K:208:ASP:CB	2.34	0.57
22:4A:126:A:N1	9:4c:104:ASP:CA	2.67	0.57
1:A:34:G:N9	1:A:35:U:C6	2.72	0.57
2:5A:96:A:N6	12:5f:23:GLY:H	2.02	0.57
22:4A:121:U:C2	12:4f:63:ARG:CA	2.88	0.57
1:A:31:C:C1'	37:2A:33:G:N2	2.68	0.57
3:5B:1556:ASP:OD2	14:6A:44:G:N2	2.33	0.57
23:4B:415:THR:HG23	23:4B:417:LEU:HG	1.87	0.57
24:4C:426:SER:OG	24:4C:428:ASP:OD1	2.23	0.57
37:2A:152:G:N2	37:2A:153:A:C8	2.73	0.57
45:2I:1204:VAL:O	45:2I:1207:LYS:N	2.37	0.57
1:A:20:U:O2	37:2A:42:G:N2	2.38	0.56
5:5D:739:ARG:NE	5:5D:740:ASP:OD1	2.37	0.56
37:2A:141:C:C2	37:2A:142:C:C5	2.93	0.56
43:2G:937:LEU:O	43:2G:940:LEU:N	2.38	0.56
45:2I:973:GLY:HA3	45:2I:976:LYS:C	2.31	0.56
1:A:31:C:N4	1:A:32:C:H41	2.03	0.56
2:5A:81:U:H2'	2:5A:81:U:O2	2.05	0.56
2:5A:87:A:C6	2:5A:92:U:OP2	2.59	0.56
3:5B:541:GLY:N	28:4G:33:ASP:OD2	2.38	0.56
4:5C:693:GLU:HA	4:5C:693:GLU:OE2	2.05	0.56
1:A:12:U:H2'	1:A:12:U:P	2.45	0.56
3:5B:1660:TYR:OH	3:5B:1717:ASN:O	2.16	0.56
37:2A:154:C:O2'	37:2A:155:C:H5'	2.04	0.56
42:2F:184:ARG:O	7:2a:85:PRO:CA	2.53	0.56
1:A:10:C:O2'	1:A:11:C:P	2.64	0.56
2:5A:38:C:O2'	32:4K:386:SER:O	2.23	0.56
3:5B:227:ARG:O	3:5B:229:GLN:NE2	2.39	0.56
25:4D:177:GLN:N	25:4D:177:GLN:OE1	2.39	0.56
2:5A:110:C:H2'	2:5A:111:A:H8	1.70	0.56
3:5B:151:MET:SD	3:5B:628:GLY:O	2.64	0.56
5:5D:544:MET:HE1	22:4A:73:U:H5''	1.87	0.56
45:2I:287:PHE:CA	45:2I:304:GLN:O	2.53	0.56
45:2I:931:VAL:O	45:2I:935:GLU:N	2.39	0.56
5:5D:470:TYR:O	5:5D:562:TYR:OH	2.12	0.56
37:2A:181:G:H2'	37:2A:182:U:H6	1.71	0.56
43:2G:968:GLU:O	43:2G:971:MET:N	2.39	0.56
3:5B:488:ASP:OD1	3:5B:489:TRP:N	2.39	0.56
4:5C:230:ASP:OD1	4:5C:233:GLU:N	2.32	0.56
5:5D:1725:GLU:OE1	5:5D:1763:ARG:NE	2.30	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:4C:189:ALA:O	24:4C:193:LEU:HD12	2.06	0.56
45:2I:42:ARG:N	45:2I:51:HIS:O	2.32	0.56
47:2K:98:PHE:O	47:2K:100:LYS:N	2.39	0.56
24:4C:363:GLY:O	24:4C:390:ARG:NH2	2.39	0.56
26:4E:24:ASP:OD2	26:4E:28:GLN:NE2	2.38	0.56
1:A:36:C:O2'	1:A:37:C:OP1	2.24	0.55
2:5A:67:A:HO2'	2:5A:68:C:P	2.25	0.55
5:5D:774:LEU:HD21	5:5D:778:LEU:HD11	1.88	0.55
5:5D:1058:LYS:NZ	5:5D:1080:ASP:OD2	2.27	0.55
37:2A:149:A:H2'	37:2A:150:U:H6	1.70	0.55
1:A:21:U:C1'	1:A:22:C:P	2.94	0.55
5:5D:1402:ASN:O	5:5D:1402:ASN:ND2	2.37	0.55
22:4A:113:C:O5'	22:4A:113:C:H6	1.88	0.55
43:2G:1124:SER:O	43:2G:1127:THR:N	2.34	0.55
4:5C:140:HIS:N	51:5C:1500:GTP:O2B	2.38	0.55
5:5D:1078:MET:HE1	5:5D:1082:VAL:HG23	1.88	0.55
5:5D:1092:MET:HE3	5:5D:1092:MET:O	2.07	0.55
19:6e:46:GLU:CA	19:6e:62:ASP:CA	2.85	0.55
35:4N:83:ASN:OD1	35:4N:84:VAL:N	2.39	0.55
40:2D:174:VAL:O	40:2D:178:GLY:HA2	2.05	0.55
1:A:34:G:C2'	1:A:35:U:C6	2.88	0.55
5:5D:877:GLN:OE1	5:5D:877:GLN:N	2.40	0.55
5:5D:1535:THR:HG21	5:5D:1676:TYR:CE2	2.42	0.55
45:2I:303:ALA:O	45:2I:310:ILE:CA	2.55	0.55
1:A:31:C:N3	37:2A:33:G:O6	2.40	0.55
1:A:36:C:O2'	1:A:36:C:O2	2.24	0.55
2:5A:110:C:H2'	2:5A:111:A:C8	2.42	0.55
4:5C:516:LEU:HD13	4:5C:575:GLN:OE1	2.06	0.55
5:5D:1186:LEU:HD21	5:5D:1270:VAL:CG2	2.36	0.55
5:5D:1636:PHE:HD2	5:5D:1656:VAL:HG21	1.70	0.55
5:5D:1943:MET:HE1	5:5D:2065:TRP:CB	2.37	0.55
33:4L:120:LEU:HB3	33:4L:152:LEU:HD11	1.89	0.55
37:2A:183:G:C4	37:2A:184:C:C5	2.94	0.55
43:2G:747:LEU:O	43:2G:748:LYS:C	2.48	0.55
47:2K:109:GLN:O	47:2K:112:LEU:N	2.39	0.55
1:A:36:C:C1'	1:A:37:C:P	2.94	0.55
2:5A:117:A:C2	10:5d:26:GLY:HA3	2.41	0.55
5:5D:475:PHE:HE1	5:5D:514:LEU:HD23	1.72	0.55
37:2A:141:C:H2'	37:2A:142:C:H6	1.71	0.55
37:2A:150:U:C2	37:2A:151:C:C5	2.94	0.55
37:2A:150:U:H2'	37:2A:151:C:H6	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2G:874:LYS:O	43:2G:877:GLY:CA	2.54	0.55
45:2I:1195:GLU:C	45:2I:1198:ASP:H	2.14	0.55
5:5D:1802:ILE:HD12	5:5D:1810:VAL:CG1	2.36	0.55
27:4F:110:GLN:NE2	27:4F:114:ASP:OD1	2.40	0.55
43:2G:578:ILE:O	43:2G:581:LEU:N	2.39	0.55
3:5B:180:ASP:OD1	3:5B:180:ASP:C	2.50	0.55
5:5D:2037:VAL:HG13	5:5D:2092:LEU:CD2	2.37	0.55
5:5D:1029:VAL:HG13	5:5D:1029:VAL:O	2.07	0.55
22:4A:73:U:O2'	22:4A:74:C:OP2	2.22	0.55
22:4A:108:C:H2'	22:4A:109:G:C8	2.41	0.55
37:2A:149:A:C4	37:2A:150:U:C5	2.95	0.55
37:2A:183:G:H2'	37:2A:184:C:H6	1.71	0.55
43:2G:86:ALA:C	43:2G:89:ALA:H	2.11	0.55
43:2G:557:ASP:O	43:2G:560:LEU:N	2.40	0.55
5:5D:1854:GLU:N	5:5D:1854:GLU:OE1	2.40	0.54
5:5D:1970:HIS:CE1	5:5D:1997:LEU:HD13	2.41	0.54
37:2A:147:G:C4	37:2A:148:C:C5	2.95	0.54
5:5D:2098:ALA:O	5:5D:2099:THR:HG22	2.06	0.54
43:2G:699:GLN:O	43:2G:700:LYS:C	2.48	0.54
43:2G:849:ILE:O	43:2G:852:ARG:N	2.38	0.54
5:5D:2037:VAL:HG13	5:5D:2092:LEU:HD21	1.90	0.54
43:2G:517:ARG:O	43:2G:520:THR:N	2.41	0.54
43:2G:641:ILE:O	43:2G:644:LEU:N	2.40	0.54
45:2I:488:GLY:C	45:2I:490:THR:H	2.14	0.54
1:A:34:G:C3'	1:A:35:U:H5''	2.35	0.54
3:5B:1305:SER:O	3:5B:1305:SER:OG	2.18	0.54
4:5C:117:ASP:O	4:5C:121:ASP:OD1	2.26	0.54
5:5D:687:GLN:OE1	5:5D:689:TYR:OH	2.24	0.54
36:4Z:330:THR:HA	36:4Z:346:ARG:HA	1.88	0.54
43:2G:1205:GLU:O	43:2G:1208:LEU:N	2.41	0.54
45:2I:785:PRO:CA	45:2I:800:ILE:O	2.56	0.54
1:A:31:C:C2	37:2A:33:G:C2	2.95	0.54
4:5C:938:ARG:O	4:5C:942:GLY:N	2.41	0.54
19:6e:46:GLU:H	19:6e:63:ALA:CA	2.21	0.54
37:2A:181:G:C4	37:2A:182:U:C5	2.95	0.54
5:5D:1425:ILE:N	5:5D:1425:ILE:HD12	2.22	0.54
25:4D:311:SER:O	25:4D:311:SER:OG	2.24	0.54
37:2A:179:C:H2'	37:2A:180:G:C8	2.39	0.54
3:5B:2135:ASP:CG	3:5B:2135:ASP:O	2.50	0.54
5:5D:1405:VAL:HG23	5:5D:1424:ILE:HB	1.89	0.54
14:6A:57:U:C2	14:6A:58:G:C8	2.95	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:4H:110:LEU:O	29:4H:141:PHE:N	2.41	0.54
3:5B:1545:ALA:HB2	3:5B:1563:HIS:CD2	2.43	0.54
4:5C:354:ARG:O	4:5C:354:ARG:HG3	2.08	0.54
4:5C:377:LEU:HD21	4:5C:424:PHE:HZ	1.73	0.54
5:5D:615:ASP:OD1	5:5D:616:GLU:N	2.41	0.54
5:5D:1074:GLY:HA3	35:4N:71:THR:HG23	1.90	0.54
24:4C:417:PRO:HG3	24:4C:459:PRO:O	2.07	0.54
22:4A:119:A:H5''	10:4d:39:TYR:N	2.23	0.54
4:5C:520:GLU:N	4:5C:520:GLU:OE1	2.38	0.54
5:5D:1139:VAL:HG21	5:5D:1174:ILE:HD11	1.89	0.54
22:4A:61:A:H2'	22:4A:62:U:O4'	2.08	0.54
37:2A:147:G:H2'	37:2A:148:C:C6	2.43	0.54
5:5D:713:MET:HE3	5:5D:713:MET:HA	1.89	0.53
28:4G:97:ASP:OD1	28:4G:97:ASP:N	2.41	0.53
45:2I:589:CYS:O	45:2I:608:GLY:N	2.30	0.53
5:5D:1986:MET:O	5:5D:1993:ARG:NH2	2.41	0.53
37:2A:153:A:H3'	37:2A:154:C:C5'	2.37	0.53
43:2G:1026:ASN:O	43:2G:1028:HIS:N	2.41	0.53
2:5A:67:A:O2'	2:5A:68:C:P	2.66	0.53
4:5C:825:PRO:HG2	4:5C:912:LEU:HD11	1.90	0.53
5:5D:1736:PHE:HE1	5:5D:1751:ALA:HB1	1.73	0.53
37:2A:153:A:C3'	37:2A:154:C:C5'	2.85	0.53
43:2G:1132:LEU:O	43:2G:1135:GLU:N	2.41	0.53
1:A:10:C:HO2'	1:A:11:C:P	2.32	0.53
3:5B:519:ASP:OD1	3:5B:519:ASP:C	2.52	0.53
24:4C:356:GLU:OE2	24:4C:356:GLU:N	2.41	0.53
28:4G:651:LEU:O	28:4G:655:ASN:N	2.42	0.53
43:2G:663:THR:O	43:2G:666:LYS:N	2.42	0.53
1:A:15:A:O2'	1:A:16:A:H5'	2.09	0.53
2:5A:99:C:H2'	2:5A:100:C:C6	2.43	0.53
2:5A:108:G:H3'	2:5A:109:G:H8	1.73	0.53
3:5B:2046:THR:OG1	3:5B:2047:VAL:N	2.40	0.53
30:4I:8:GLN:HE21	30:4I:8:GLN:CA	2.16	0.53
23:4B:480:ASN:OD1	23:4B:484:VAL:HG23	2.08	0.53
3:5B:744:LYS:O	3:5B:748:ASP:OD1	2.27	0.53
5:5D:1886:ASP:OD1	5:5D:1888:HIS:ND1	2.40	0.53
24:4C:290:ASP:N	24:4C:290:ASP:OD1	2.41	0.53
28:4G:771:LEU:C	28:4G:771:LEU:HD23	2.34	0.53
43:2G:1280:LEU:O	43:2G:1282:ALA:N	2.42	0.53
3:5B:75:ASP:OD1	3:5B:75:ASP:N	2.41	0.53
1:A:22:C:C2'	1:A:23:G:C5'	2.87	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5C:227:LEU:HD22	4:5C:243:ILE:CG2	2.38	0.53
5:5D:1157:ASN:OD1	5:5D:1159:ASN:N	2.41	0.53
25:4D:89:GLU:OE1	25:4D:211:ARG:NH1	2.42	0.53
33:4L:134:ASN:ND2	33:4L:140:GLU:OE2	2.41	0.53
37:2A:54:U:P	42:2F:424:ARG:O	2.67	0.53
45:2I:1195:GLU:O	45:2I:1198:ASP:N	2.41	0.53
5:5D:1143:ILE:CD1	5:5D:1165:ILE:HD12	2.39	0.53
16:6b:47:ASP:O	16:6b:50:LEU:N	2.39	0.53
16:6b:48:GLN:C	16:6b:50:LEU:H	2.14	0.53
23:4B:646:MET:HE2	23:4B:646:MET:HA	1.90	0.53
32:4K:341:TYR:O	34:4M:15:ARG:NH2	2.41	0.53
28:4G:707:ASP:HA	28:4G:708:PHE:C	2.33	0.52
43:2G:244:THR:O	43:2G:247:ALA:N	2.43	0.52
1:A:41:U:H2'	1:A:41:U:O2	2.09	0.52
3:5B:439:GLN:O	3:5B:444:ARG:NH1	2.41	0.52
4:5C:713:LYS:O	4:5C:713:LYS:HD3	2.09	0.52
5:5D:890:GLU:OE2	5:5D:928:ARG:NH2	2.43	0.52
33:4L:4:ARG:O	33:4L:79:GLN:NE2	2.38	0.52
4:5C:209:VAL:O	4:5C:212:SER:OG	2.25	0.52
23:4B:385:PRO:HG2	24:4C:437:ARG:NH1	2.25	0.52
43:2G:1025:LYS:O	43:2G:1027:ARG:N	2.42	0.52
2:5A:95:G:N3	2:5A:95:G:C2'	2.73	0.52
3:5B:832:TYR:OH	3:5B:929:GLU:OE2	2.25	0.52
5:5D:471:ALA:CB	5:5D:518:LEU:HD13	2.35	0.52
5:5D:785:HIS:HB3	5:5D:809:LEU:HD21	1.91	0.52
5:5D:824:HIS:ND1	5:5D:862:ASP:OD1	2.36	0.52
43:2G:978:LEU:O	43:2G:979:TYR:C	2.51	0.52
49:2M:36:HIS:O	49:2M:37:ARG:C	2.53	0.52
1:A:36:C:C5'	1:A:37:C:C5	2.91	0.52
1:A:38:C:O2	1:A:38:C:H2'	2.08	0.52
22:4A:118:A:H8	22:4A:118:A:OP2	1.92	0.52
36:4Z:425:MET:HA	36:4Z:431:ILE:HA	1.92	0.52
43:2G:841:ALA:O	43:2G:843:LYS:N	2.41	0.52
24:4C:393:ASP:O	24:4C:397:GLY:N	2.42	0.52
2:5A:87:A:H61	2:5A:92:U:P	2.32	0.52
5:5D:1320:LEU:HD22	5:5D:1396:LYS:HG2	1.91	0.52
5:5D:1735:HIS:O	5:5D:1739:GLU:HG3	2.10	0.52
5:5D:933:PRO:HG3	5:5D:943:LEU:HD12	1.91	0.52
23:4B:417:LEU:HD12	23:4B:417:LEU:O	2.10	0.52
29:4H:66:HIS:N	29:4H:75:GLN:O	2.42	0.52
42:2F:411:CYS:O	42:2F:414:TYR:N	2.37	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2G:407:MET:CA	43:2G:407:MET:H	2.06	0.52
43:2G:423:PRO:O	43:2G:427:PRO:N	2.43	0.52
43:2G:1280:LEU:O	43:2G:1281:ILE:C	2.51	0.52
3:5B:2183:ASN:OD1	3:5B:2183:ASN:C	2.52	0.52
5:5D:1001:TYR:OH	5:5D:1091:LEU:HD12	2.09	0.52
43:2G:1207:SER:O	43:2G:1210:HIS:N	2.43	0.52
23:4B:570:THR:HG22	23:4B:571:GLY:N	2.25	0.52
37:2A:107:A:C6	37:2A:108:G:C5	2.98	0.52
3:5B:248:ASP:N	3:5B:248:ASP:OD1	2.43	0.51
3:5B:1957:ASP:OD1	3:5B:1958:LYS:N	2.42	0.51
24:4C:259:SER:O	24:4C:263:CYS:N	2.43	0.51
3:5B:2184:GLU:OE1	3:5B:2217:SER:CB	2.59	0.51
4:5C:141:GLY:N	51:5C:1500:GTP:O2B	2.33	0.51
5:5D:1127:CYS:SG	5:5D:1143:ILE:HG21	2.50	0.51
23:4B:674:LEU:O	23:4B:677:SER:OG	2.23	0.51
33:4L:82:PRO:HG2	33:4L:87:ILE:HD11	1.91	0.51
43:2G:1109:ARG:O	43:2G:1111:CYS:N	2.43	0.51
2:5A:50:G:O2'	2:5A:51:A:H5'	2.10	0.51
5:5D:597:THR:HG21	5:5D:634:ARG:HD2	1.91	0.51
5:5D:734:THR:HG23	5:5D:810:VAL:HG11	1.93	0.51
5:5D:1617:VAL:HG12	5:5D:1643:VAL:HB	1.93	0.51
5:5D:2084:LEU:HD23	5:5D:2084:LEU:H	1.76	0.51
43:2G:1129:LEU:O	43:2G:1132:LEU:N	2.44	0.51
45:2I:673:VAL:CA	45:2I:691:THR:H	2.24	0.51
4:5C:340:ALA:HA	4:5C:343:LEU:HD12	1.92	0.51
5:5D:1819:ALA:HB2	5:5D:1829:ILE:HG21	1.91	0.51
22:4A:120:U:O2'	11:4e:82:ASP:CA	2.58	0.51
33:4L:94:GLU:O	33:4L:94:GLU:OE1	2.28	0.51
33:4L:130:ILE:HD11	33:4L:142:MET:HB3	1.92	0.51
43:2G:720:GLY:O	43:2G:721:ILE:C	2.54	0.51
43:2G:1094:LEU:O	43:2G:1098:LEU:N	2.41	0.51
43:2G:1110:VAL:O	43:2G:1113:THR:N	2.43	0.51
2:5A:96:A:N6	12:5f:23:GLY:N	2.58	0.51
4:5C:776:GLU:OE1	4:5C:776:GLU:HA	2.09	0.51
5:5D:1433:ASP:OD1	5:5D:1473:ARG:NH2	2.43	0.51
5:5D:1837:ASN:OD1	5:5D:1840:THR:N	2.43	0.51
37:2A:111:G:O3'	37:2A:112:G:O4'	2.29	0.51
43:2G:103:PRO:C	43:2G:106:GLU:H	2.18	0.51
3:5B:353:ASP:OD1	3:5B:353:ASP:N	2.44	0.51
3:5B:651:TRP:CZ3	3:5B:652:LEU:HD23	2.45	0.51
5:5D:1295:TYR:OH	5:5D:1763:ARG:NH1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5D:1931:SER:HA	5:5D:2076:LEU:HD23	1.93	0.51
23:4B:579:VAL:HG23	23:4B:579:VAL:O	2.11	0.51
28:4G:891:GLU:CD	28:4G:891:GLU:H	2.19	0.51
1:A:36:C:C1'	1:A:37:C:OP1	2.55	0.51
2:5A:67:A:H2'	2:5A:68:C:C5	2.46	0.51
5:5D:1277:SER:O	5:5D:1277:SER:OG	2.28	0.51
45:2I:546:LYS:O	45:2I:556:ILE:CA	2.58	0.51
3:5B:310:THR:HG22	3:5B:314:ILE:HD12	1.92	0.51
45:2I:699:VAL:CA	45:2I:715:MET:O	2.59	0.51
2:5A:85:C:OP1	9:5c:20:GLU:N	2.44	0.51
3:5B:1901:LYS:NZ	3:5B:1966:HIS:O	2.36	0.51
5:5D:1301:LEU:HD11	5:5D:1518:VAL:HG13	1.93	0.51
5:5D:1943:MET:HE1	5:5D:2065:TRP:CG	2.45	0.51
22:4A:111:C:H2'	22:4A:112:A:C8	2.46	0.51
4:5C:173:THR:N	4:5C:176:GLU:OE1	2.44	0.51
4:5C:809:ILE:HG13	4:5C:810:PRO:HD3	1.92	0.51
5:5D:1222:TRP:NE1	5:5D:1273:ASP:OD1	2.36	0.51
5:5D:1622:GLU:N	5:5D:1622:GLU:OE1	2.44	0.51
43:2G:528:ALA:O	43:2G:531:LEU:N	2.44	0.51
47:2K:46:ARG:N	47:2K:63:VAL:O	2.44	0.51
49:2M:37:ARG:O	49:2M:40:TYR:N	2.44	0.51
1:A:31:C:H2'	1:A:32:C:H5'	1.91	0.50
3:5B:678:GLU:HA	3:5B:749:TRP:HZ2	1.76	0.50
4:5C:778:PRO:HD3	4:5C:784:ILE:HD11	1.91	0.50
31:4J:184:LEU:HD12	31:4J:184:LEU:C	2.36	0.50
37:2A:164:C:H5'	37:2A:164:C:C6	2.44	0.50
43:2G:629:ALA:O	43:2G:632:PHE:N	2.45	0.50
2:5A:98:G:H2'	2:5A:99:C:C6	2.47	0.50
5:5D:570:THR:HG23	5:5D:572:ASP:H	1.76	0.50
25:4D:102:GLU:OE2	25:4D:102:GLU:C	2.55	0.50
5:5D:565:THR:O	5:5D:583:THR:OG1	2.26	0.50
14:6A:58:G:C2	14:6A:59:G:C8	2.99	0.50
24:4C:458:GLU:HG2	24:4C:459:PRO:HD2	1.93	0.50
43:2G:804:ASN:O	43:2G:807:LYS:N	2.44	0.50
43:2G:1243:PRO:O	43:2G:1244:CYS:C	2.55	0.50
5:5D:1345:ASN:OD1	5:5D:1487:ILE:HD12	2.11	0.50
7:4a:18:ARG:N	7:4a:81:THR:O	2.40	0.50
43:2G:771:LEU:O	43:2G:774:ILE:N	2.43	0.50
43:2G:939:ARG:O	43:2G:940:LEU:C	2.51	0.50
1:A:40:U:HO2'	1:A:41:U:P	2.24	0.50
24:4C:230:ASP:OD1	24:4C:231:ASP:N	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2G:862:GLU:O	43:2G:863:GLN:C	2.55	0.50
43:2G:892:LEU:O	43:2G:893:ILE:C	2.54	0.50
1:A:34:G:H21	1:A:35:U:H5'	1.77	0.50
1:A:37:C:H3'	1:A:37:C:H6	1.75	0.50
2:5A:100:C:H2'	2:5A:101:U:C6	2.46	0.50
5:5D:1947:GLN:NE2	5:5D:2114:MET:SD	2.85	0.50
43:2G:963:LYS:O	43:2G:966:GLN:N	2.30	0.50
43:2G:1035:CYS:O	43:2G:1038:LEU:N	2.44	0.50
43:2G:1188:ALA:O	43:2G:1191:VAL:N	2.45	0.50
5:5D:781:GLY:O	5:5D:806:ILE:HG23	2.11	0.50
5:5D:1767:ASN:OD1	5:5D:1770:TYR:HB2	2.12	0.50
5:5D:1899:LEU:HD22	5:5D:1948:MET:HG3	1.93	0.50
43:2G:1268:ILE:O	43:2G:1271:SER:N	2.44	0.50
1:A:25:G:H1	37:2A:37:U:H3	1.60	0.50
1:A:34:G:C2'	1:A:35:U:H6	2.23	0.50
1:A:102:U:N3	3:5B:587:GLN:OE1	2.44	0.50
2:5A:73:C:H2'	2:5A:74:U:C6	2.47	0.50
3:5B:1010:THR:HG22	25:4D:261:GLY:O	2.12	0.50
5:5D:1092:MET:HE3	5:5D:1092:MET:HA	1.93	0.50
28:4G:634:ALA:O	28:4G:638:ASN:N	2.40	0.50
22:4A:143:U:H2'	22:4A:144:G:H5''	1.92	0.50
28:4G:739:CYS:HB3	28:4G:740:PRO:HA	1.94	0.50
28:4G:744:PRO:O	28:4G:748:LEU:HD23	2.11	0.50
3:5B:411:PHE:CD1	3:5B:411:PHE:N	2.76	0.49
3:5B:1091:TYR:O	3:5B:1092:ILE:C	2.54	0.49
5:5D:1092:MET:HE3	5:5D:1092:MET:CA	2.41	0.49
11:5e:15:VAL:O	12:5f:33:GLY:HA3	2.12	0.49
22:4A:120:U:H3'	22:4A:120:U:H6	1.77	0.49
30:4I:14:ASP:OD1	30:4I:14:ASP:C	2.55	0.49
43:2G:708:ALA:O	43:2G:709:ILE:C	2.54	0.49
43:2G:1080:THR:O	43:2G:1083:TYR:N	2.44	0.49
1:A:37:C:O2'	1:A:38:C:O5'	2.30	0.49
1:A:116:G:N2	14:6A:38:G:H22	2.10	0.49
5:5D:534:ASP:O	5:5D:534:ASP:OD1	2.30	0.49
5:5D:1609:LEU:C	5:5D:1609:LEU:HD23	2.37	0.49
23:4B:543:ILE:HD11	23:4B:638:ALA:HB3	1.94	0.49
24:4C:404:GLU:N	24:4C:404:GLU:OE1	2.45	0.49
33:4L:49:ASP:OD1	33:4L:49:ASP:C	2.55	0.49
37:2A:30:A:N3	37:2A:30:A:C2'	2.73	0.49
43:2G:501:LEU:O	43:2G:502:LEU:C	2.55	0.49
43:2G:665:ILE:O	43:2G:666:LYS:C	2.56	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2G:974:LEU:O	43:2G:975:GLY:C	2.54	0.49
45:2I:1194:SER:O	45:2I:1199:ARG:N	2.35	0.49
3:5B:352:PHE:CD1	4:5C:269:LEU:HD22	2.47	0.49
25:4D:282:SER:O	25:4D:282:SER:OG	2.30	0.49
4:5C:845:ALA:O	4:5C:848:THR:HG22	2.13	0.49
5:5D:1411:GLU:OE2	5:5D:1413:SER:OG	2.21	0.49
24:4C:195:GLU:OE2	24:4C:195:GLU:O	2.30	0.49
5:5D:642:THR:HG21	5:5D:644:GLU:OE2	2.12	0.49
16:6b:48:GLN:C	16:6b:50:LEU:N	2.69	0.49
37:2A:107:A:C2	37:2A:108:G:C4	3.01	0.49
43:2G:693:GLY:O	43:2G:694:LEU:C	2.55	0.49
43:2G:833:LEU:O	43:2G:834:VAL:C	2.56	0.49
45:2I:596:PRO:O	45:2I:598:GLY:N	2.46	0.49
3:5B:1638:ASN:OD1	3:5B:1652:MET:O	2.31	0.49
5:5D:1624:LEU:O	5:5D:1629:ARG:NH1	2.46	0.49
5:5D:1830:GLU:OE2	5:5D:1830:GLU:HA	2.12	0.49
22:4A:138:G:OP2	13:4g:24:THR:O	2.31	0.49
11:2e:15:VAL:O	12:2f:33:GLY:HA3	2.12	0.49
2:5A:115:C:OP1	11:5e:67:LYS:O	2.30	0.49
5:5D:815:LEU:HD23	5:5D:815:LEU:O	2.12	0.49
43:2G:553:VAL:O	43:2G:556:ILE:N	2.46	0.49
2:5A:98:G:H2'	2:5A:99:C:H6	1.77	0.49
5:5D:1462:GLU:O	5:5D:1463:ASN:OD1	2.31	0.49
5:5D:1628:GLU:CD	5:5D:1628:GLU:H	2.20	0.49
5:5D:2043:ARG:NE	5:5D:2045:GLU:O	2.44	0.49
43:2G:849:ILE:O	43:2G:850:ILE:C	2.54	0.49
49:2M:48:ASP:O	49:2M:49:LEU:C	2.54	0.49
1:A:31:C:C2	1:A:32:C:H5	2.30	0.49
3:5B:955:TRP:CZ3	3:5B:976:MET:HE1	2.48	0.49
4:5C:237:LEU:O	4:5C:240:GLU:HG2	2.13	0.49
4:5C:423:PHE:CD1	4:5C:423:PHE:C	2.88	0.49
4:5C:765:SER:HB2	4:5C:808:ILE:HG21	1.94	0.49
5:5D:877:GLN:HA	5:5D:880:LEU:HD12	1.95	0.49
43:2G:793:LYS:O	43:2G:797:GLY:CA	2.54	0.49
3:5B:347:LEU:HD23	3:5B:348:PRO:HD2	1.95	0.49
3:5B:2275:ALA:HB2	3:5B:2297:GLN:HB2	1.95	0.49
5:5D:694:GLU:O	5:5D:700:ARG:NH2	2.46	0.49
6:5E:255:MET:C	6:5E:257:ASN:H	2.21	0.49
37:2A:143:A:N3	37:2A:143:A:C3'	2.73	0.49
43:2G:177:LYS:O	43:2G:180:GLU:N	2.46	0.49
43:2G:663:THR:O	43:2G:664:GLY:C	2.56	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:2I:430:GLY:O	45:2I:433:SER:N	2.31	0.49
3:5B:171:ASP:OD1	3:5B:171:ASP:N	2.41	0.48
3:5B:2111:LEU:HD21	3:5B:2225:LEU:HD11	1.95	0.48
5:5D:995:ASN:O	5:5D:998:VAL:HG22	2.12	0.48
24:4C:119:ILE:HG23	24:4C:120:THR:HG23	1.95	0.48
43:2G:1227:ILE:O	43:2G:1230:VAL:N	2.46	0.48
2:5A:92:U:H3'	2:5A:92:U:H6	1.77	0.48
5:5D:1946:ALA:O	5:5D:1949:VAL:HG12	2.14	0.48
14:6A:35:A:H2'	14:6A:36:A:C8	2.48	0.48
24:4C:228:ILE:HD13	24:4C:515:THR:HG22	1.94	0.48
43:2G:237:GLY:O	43:2G:239:ALA:N	2.45	0.48
43:2G:944:SER:O	43:2G:946:LYS:N	2.38	0.48
45:2I:930:LEU:C	45:2I:934:GLY:HA2	2.38	0.48
3:5B:1019:TYR:O	3:5B:1020:LYS:C	2.55	0.48
3:5B:1850:ARG:NH2	44:2H:800:MET:O	2.41	0.48
4:5C:125:ASN:OD1	4:5C:128:LEU:N	2.38	0.48
5:5D:525:ILE:O	5:5D:526:ASN:OD1	2.31	0.48
5:5D:1039:LYS:HA	5:5D:1039:LYS:HD3	1.44	0.48
25:4D:98:ASN:OD1	25:4D:99:LEU:N	2.47	0.48
43:2G:955:ILE:O	43:2G:956:SER:C	2.57	0.48
44:2H:491:LEU:O	44:2H:493:ALA:N	2.46	0.48
45:2I:672:GLY:O	45:2I:695:GLY:N	2.46	0.48
4:5C:342:ARG:NH2	4:5C:356:PHE:O	2.46	0.48
5:5D:938:ILE:HD13	5:5D:949:LEU:HD21	1.95	0.48
5:5D:1693:ARG:NH2	5:5D:1697:ASP:OD1	2.47	0.48
5:5D:1815:LEU:HD12	5:5D:1829:ILE:HG13	1.95	0.48
43:2G:953:ASP:O	43:2G:954:LEU:C	2.56	0.48
1:A:34:G:H3'	1:A:34:G:N3	2.28	0.48
3:5B:1618:LYS:NZ	3:5B:1628:ASP:OD2	2.46	0.48
4:5C:710:ASN:OD1	4:5C:713:LYS:HB3	2.14	0.48
33:4L:167:LYS:O	33:4L:171:LEU:HD23	2.13	0.48
37:2A:54:U:C5'	42:2F:424:ARG:O	2.62	0.48
43:2G:226:HIS:O	43:2G:229:SER:N	2.46	0.48
43:2G:625:ARG:O	43:2G:628:THR:N	2.46	0.48
43:2G:631:ALA:O	43:2G:634:VAL:N	2.46	0.48
3:5B:888:GLN:O	3:5B:889:ARG:NH1	2.44	0.48
3:5B:1521:ALA:O	3:5B:1524:SER:OG	2.26	0.48
3:5B:2074:ARG:NH2	5:5D:1044:VAL:O	2.41	0.48
5:5D:528:ASP:OD1	5:5D:528:ASP:N	2.45	0.48
5:5D:1369:LEU:HD23	5:5D:1369:LEU:O	2.14	0.48
5:5D:1970:HIS:HE1	5:5D:1996:LEU:HD23	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:4G:729:ARG:NH1	28:4G:753:GLU:OE1	2.46	0.48
43:2G:994:LEU:O	43:2G:995:GLY:C	2.56	0.48
47:2K:98:PHE:C	47:2K:100:LYS:N	2.72	0.48
2:5A:78:U:H1'	2:5A:79:C:H6	1.79	0.48
3:5B:2184:GLU:OE1	3:5B:2217:SER:OG	2.26	0.48
5:5D:1777:SER:OG	5:5D:1780:HIS:ND1	2.45	0.48
37:2A:153:A:C2'	37:2A:154:C:C5'	2.86	0.48
1:A:17:G:H2'	1:A:18:C:H6	1.78	0.48
4:5C:733:TRP:HZ3	4:5C:791:ILE:HD12	1.79	0.48
5:5D:1358:ILE:HG22	5:5D:1362:PHE:CE1	2.48	0.48
15:6a:61:PHE:N	21:6g:70:ILE:O	2.45	0.48
43:2G:667:ILE:O	43:2G:668:VAL:C	2.53	0.48
3:5B:1202:THR:HG23	3:5B:1204:TYR:CE2	2.49	0.48
3:5B:2128:LEU:HD11	3:5B:2214:ILE:HD12	1.96	0.48
4:5C:725:ASP:OD1	4:5C:726:LEU:N	2.47	0.48
14:6A:55:C:H2'	14:6A:56:A:O4'	2.14	0.48
14:6A:78:A:N3	14:6A:78:A:H2'	2.29	0.48
24:4C:242:ASN:C	24:4C:242:ASN:OD1	2.57	0.48
43:2G:705:SER:O	43:2G:706:ALA:C	2.54	0.48
1:A:38:C:H4'	1:A:38:C:OP1	2.14	0.48
2:5A:67:A:C2'	2:5A:68:C:OP1	2.62	0.48
3:5B:1528:GLN:OE1	3:5B:1528:GLN:HA	2.14	0.48
5:5D:1787:GLU:C	5:5D:1787:GLU:OE1	2.56	0.48
24:4C:458:GLU:OE1	24:4C:462:GLY:N	2.47	0.48
43:2G:803:ALA:O	43:2G:804:ASN:C	2.54	0.48
3:5B:1130:ASN:N	3:5B:1130:ASN:OD1	2.47	0.47
5:5D:517:MET:HG2	5:5D:538:ILE:HD13	1.96	0.47
5:5D:713:MET:HA	5:5D:716:ALA:HB2	1.95	0.47
5:5D:996:ASP:OD1	5:5D:997:THR:N	2.46	0.47
5:5D:1039:LYS:HD2	5:5D:1043:ARG:NH2	2.29	0.47
5:5D:1625:SER:HB3	5:5D:1628:GLU:OE1	2.14	0.47
2:5A:111:A:H2'	2:5A:112:A:C8	2.49	0.47
3:5B:933:ARG:O	3:5B:935:LEU:N	2.48	0.47
3:5B:1111:GLN:OE1	3:5B:1111:GLN:HA	2.13	0.47
4:5C:174:GLU:O	4:5C:178:GLY:N	2.48	0.47
4:5C:449:ILE:HD11	4:5C:497:LEU:CD1	2.44	0.47
5:5D:641:MET:HG2	5:5D:1582:ALA:HB1	1.95	0.47
5:5D:1968:SER:HA	5:5D:1971:ILE:HD12	1.95	0.47
22:4A:20:A:H2'	22:4A:21:U:C6	2.48	0.47
22:4A:110:G:H2'	22:4A:111:C:C6	2.49	0.47
37:2A:151:C:C2	37:2A:152:G:N7	2.82	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:G:H1	14:6A:38:G:H1	1.61	0.47
5:5D:1739:GLU:OE2	5:5D:1754:TYR:CZ	2.67	0.47
36:4Z:499:ILE:N	36:4Z:511:TRP:O	2.43	0.47
1:A:28:G:H22	37:2A:34:U:H3	1.61	0.47
1:A:116:G:H2'	1:A:117:G:C8	2.49	0.47
5:5D:1737:ASN:O	5:5D:1740:ILE:HG22	2.14	0.47
5:5D:1740:ILE:HD12	5:5D:1745:ILE:HG22	1.96	0.47
5:5D:1849:ILE:HD13	5:5D:1923:ILE:HD12	1.96	0.47
37:2A:150:U:H2'	37:2A:151:C:C6	2.50	0.47
43:2G:1110:VAL:O	43:2G:1111:CYS:C	2.57	0.47
44:2H:573:ASP:O	44:2H:577:LYS:N	2.44	0.47
3:5B:1343:SER:O	3:5B:1491:LYS:NZ	2.48	0.47
5:5D:467:LEU:HD12	5:5D:467:LEU:N	2.30	0.47
5:5D:1424:ILE:C	5:5D:1425:ILE:HD12	2.40	0.47
43:2G:660:ALA:O	43:2G:661:ARG:C	2.53	0.47
45:2I:558:LEU:O	45:2I:561:GLY:CA	2.63	0.47
3:5B:475:SER:HB3	28:4G:108:LEU:HD11	1.96	0.47
5:5D:1845:LEU:O	5:5D:1849:ILE:HD12	2.15	0.47
5:5D:1961:LYS:HD3	5:5D:1971:ILE:HD11	1.97	0.47
5:5D:2041:LEU:O	5:5D:2087:LYS:HA	2.15	0.47
24:4C:174:LEU:HD11	24:4C:178:ARG:HE	1.80	0.47
45:2I:923:GLY:HA3	45:2I:947:GLU:O	2.14	0.47
49:2M:42:SER:O	49:2M:45:GLY:N	2.48	0.47
2:5A:74:U:H2'	2:5A:75:G:C8	2.50	0.47
2:5A:117:A:C2	10:5d:26:GLY:O	2.68	0.47
3:5B:461:HIS:O	3:5B:462:ARG:NH1	2.48	0.47
3:5B:1014:ASN:ND2	3:5B:1026:ASN:O	2.42	0.47
5:5D:716:ALA:HB1	5:5D:751:PHE:CE1	2.50	0.47
5:5D:1027:ILE:HG21	5:5D:1059:ILE:HD11	1.95	0.47
5:5D:1157:ASN:O	5:5D:1161:ILE:N	2.39	0.47
23:4B:518:ARG:O	23:4B:518:ARG:HG2	2.14	0.47
24:4C:316:VAL:O	24:4C:317:ALA:C	2.58	0.47
33:4L:29:ILE:HG23	33:4L:72:CYS:SG	2.55	0.47
37:2A:153:A:C8	37:2A:154:C:H5'	2.50	0.47
37:2A:183:G:H2'	37:2A:184:C:C6	2.50	0.47
43:2G:993:ILE:O	43:2G:994:LEU:C	2.56	0.47
43:2G:1264:VAL:O	43:2G:1265:TYR:C	2.56	0.47
4:5C:534:VAL:O	4:5C:535:ALA:C	2.58	0.47
5:5D:1357:THR:O	5:5D:1361:GLU:HG3	2.15	0.47
5:5D:2052:ILE:HG22	5:5D:2054:PRO:HD3	1.96	0.47
2:5A:67:A:O2'	2:5A:68:C:C6	2.68	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:5B:1959:THR:O	3:5B:1960:THR:C	2.57	0.47
5:5D:1561:VAL:HB	5:5D:1645:VAL:HG22	1.97	0.47
22:4A:109:G:H2'	22:4A:110:G:C8	2.50	0.47
31:4J:284:GLU:CD	31:4J:284:GLU:O	2.58	0.47
43:2G:567:VAL:O	43:2G:568:ARG:C	2.58	0.47
43:2G:865:ARG:O	43:2G:866:LYS:C	2.56	0.47
45:2I:44:ASP:O	45:2I:48:GLY:HA2	2.15	0.47
46:2J:70:ALA:O	46:2J:74:MET:N	2.40	0.47
3:5B:330:THR:O	3:5B:330:THR:OG1	2.31	0.47
4:5C:360:ALA:N	4:5C:361:PRO:CD	2.79	0.47
4:5C:711:ARG:HB3	4:5C:711:ARG:NH1	2.30	0.47
4:5C:889:THR:O	32:4K:406:TRP:HA	2.15	0.47
5:5D:1920:ILE:HD11	5:5D:1950:THR:CG2	2.45	0.47
28:4G:800:MET:HE1	28:4G:813:LEU:HD22	1.96	0.47
43:2G:471:ASP:O	43:2G:472:ILE:C	2.57	0.47
43:2G:645:LEU:O	43:2G:646:PRO:C	2.56	0.47
45:2I:1148:LEU:O	45:2I:1149:ARG:C	2.57	0.47
3:5B:233:PRO:O	3:5B:237:THR:OG1	2.33	0.46
4:5C:921:LEU:N	4:5C:922:GLU:OE1	2.47	0.46
35:4N:118:THR:O	35:4N:122:VAL:HG23	2.15	0.46
3:5B:214:ARG:HB3	3:5B:214:ARG:CZ	2.45	0.46
25:4D:275:TYR:HA	25:4D:280:VAL:HG11	1.98	0.46
33:4L:71:LEU:O	33:4L:71:LEU:HD23	2.16	0.46
37:2A:141:C:H2'	37:2A:142:C:C6	2.50	0.46
43:2G:952:ALA:O	43:2G:953:ASP:C	2.57	0.46
5:5D:591:GLU:OE1	5:5D:992:TYR:CE2	2.68	0.46
5:5D:1432:TRP:HE1	5:5D:1474:MET:HE2	1.80	0.46
5:5D:1802:ILE:HD12	5:5D:1810:VAL:HG13	1.97	0.46
28:4G:95:GLU:OE1	28:4G:95:GLU:N	2.49	0.46
37:2A:107:A:C6	37:2A:108:G:C6	3.04	0.46
43:2G:693:GLY:O	43:2G:695:VAL:N	2.48	0.46
43:2G:810:ILE:O	43:2G:811:LEU:C	2.59	0.46
43:2G:872:ILE:O	43:2G:873:GLU:C	2.57	0.46
1:A:7:U:H4'	1:A:8:U:OP1	2.15	0.46
2:5A:28:A:O2'	3:5B:643:GLY:HA3	2.16	0.46
5:5D:1455:GLU:N	5:5D:1490:LEU:O	2.47	0.46
5:5D:1672:LYS:HD2	5:5D:1672:LYS:N	2.30	0.46
33:4L:166:GLN:O	33:4L:167:LYS:CD	2.62	0.46
2:5A:99:C:H2'	2:5A:100:C:H6	1.79	0.46
5:5D:935:LEU:H	5:5D:935:LEU:HD12	1.81	0.46
33:4L:108:ARG:NH1	33:4L:163:PRO:O	2.39	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2G:745:ALA:O	43:2G:746:PHE:C	2.59	0.46
43:2G:867:MET:O	43:2G:868:VAL:C	2.57	0.46
43:2G:1165:TYR:O	43:2G:1166:ILE:C	2.59	0.46
5:5D:639:ILE:HD11	5:5D:646:VAL:CG2	2.46	0.46
4:5C:560:VAL:O	4:5C:561:LYS:C	2.59	0.46
5:5D:617:ILE:HD12	5:5D:628:LEU:HD13	1.98	0.46
5:5D:1183:LYS:O	5:5D:1184:LEU:HD12	2.15	0.46
5:5D:1914:GLU:O	5:5D:1917:SER:OG	2.30	0.46
16:6b:19:ASP:C	16:6b:21:ILE:H	2.23	0.46
23:4B:580:ASN:N	23:4B:580:ASN:OD1	2.49	0.46
24:4C:101:VAL:HG21	24:4C:134:ARG:HB2	1.97	0.46
37:2A:3:C:H2'	37:2A:4:G:C8	2.51	0.46
43:2G:429:ARG:O	43:2G:432:THR:N	2.46	0.46
43:2G:1119:VAL:O	43:2G:1122:THR:N	2.49	0.46
43:2G:1129:LEU:O	43:2G:1130:PRO:C	2.59	0.46
43:2G:1256:HIS:O	43:2G:1257:PRO:C	2.58	0.46
3:5B:1618:LYS:NZ	3:5B:1663:ASP:OD1	2.46	0.46
3:5B:2069:SER:O	3:5B:2072:GLU:HG3	2.16	0.46
5:5D:475:PHE:CE1	5:5D:514:LEU:HD23	2.51	0.46
5:5D:531:ILE:HD12	5:5D:531:ILE:N	2.31	0.46
5:5D:757:ALA:O	5:5D:761:VAL:HG23	2.16	0.46
5:5D:1825:ASN:N	5:5D:1854:GLU:OE2	2.37	0.46
37:2A:149:A:H2'	37:2A:150:U:C6	2.50	0.46
43:2G:257:THR:O	43:2G:259:SER:N	2.49	0.46
1:A:28:G:C2	37:2A:35:A:C2	3.04	0.46
4:5C:215:VAL:HG11	4:5C:242:LEU:HD21	1.98	0.46
4:5C:405:LYS:O	4:5C:405:LYS:HD3	2.15	0.46
5:5D:2003:GLN:O	5:5D:2007:VAL:HG23	2.16	0.46
15:6a:73:PRO:O	15:6a:75:ASP:N	2.49	0.46
42:2F:403:ASN:N	42:2F:417:ARG:O	2.49	0.46
43:2G:210:ALA:O	43:2G:213:LYS:N	2.48	0.46
3:5B:941:LYS:HG2	3:5B:951:LEU:HD13	1.97	0.46
5:5D:1868:LEU:HD11	5:5D:1890:LYS:HE3	1.97	0.46
2:5A:96:A:H61	12:5f:23:GLY:N	2.07	0.45
3:5B:2174:PRO:O	3:5B:2210:LYS:NZ	2.44	0.45
4:5C:674:CYS:SG	4:5C:675:PHE:N	2.87	0.45
4:5C:926:ALA:HA	4:5C:929:LEU:HD23	1.96	0.45
5:5D:1742:THR:O	5:5D:1742:THR:HG22	2.16	0.45
5:5D:1920:ILE:HD11	5:5D:1950:THR:HG23	1.99	0.45
28:4G:15:LEU:HD22	28:4G:15:LEU:H	1.80	0.45
28:4G:711:LEU:H	28:4G:711:LEU:HD22	1.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2G:841:ALA:C	43:2G:843:LYS:N	2.73	0.45
49:2M:62:ALA:O	49:2M:65:ARG:N	2.50	0.45
2:5A:17:U:H2'	2:5A:18:C:C6	2.50	0.45
3:5B:1517:LYS:O	3:5B:1517:LYS:HG2	2.16	0.45
3:5B:1957:ASP:O	3:5B:1960:THR:OG1	2.30	0.45
5:5D:1672:LYS:NZ	5:5D:1860:ILE:HG21	2.32	0.45
5:5D:1753:ASP:O	5:5D:1756:THR:HG22	2.16	0.45
22:4A:0:M7M:HBZB	22:4A:1:A:N6	2.32	0.45
32:4K:401:SER:OG	32:4K:403:ASP:OD1	2.16	0.45
37:2A:152:G:O2'	37:2A:153:A:H1'	2.16	0.45
42:2F:394:TYR:C	42:2F:396:LEU:H	2.24	0.45
1:A:34:G:N3	1:A:35:U:H5''	2.31	0.45
4:5C:832:TYR:HD1	4:5C:901:PHE:HA	1.82	0.45
5:5D:1768:PRO:HG3	5:5D:1776:ILE:HG22	1.98	0.45
23:4B:462:GLU:OE1	23:4B:465:ARG:NH1	2.50	0.45
43:2G:914:PHE:O	43:2G:915:GLY:C	2.58	0.45
49:2M:46:HIS:O	49:2M:47:PHE:C	2.59	0.45
1:A:38:C:C4'	1:A:39:U:OP1	2.35	0.45
4:5C:283:ASP:OD1	4:5C:283:ASP:C	2.59	0.45
5:5D:2084:LEU:HD12	5:5D:2086:GLN:O	2.17	0.45
42:2F:276:GLY:C	42:2F:278:LEU:N	2.60	0.45
4:5C:723:ASP:C	4:5C:723:ASP:OD1	2.59	0.45
5:5D:567:ALA:HB1	5:5D:575:LEU:HD21	1.98	0.45
23:4B:646:MET:HE2	23:4B:646:MET:CA	2.47	0.45
25:4D:112:LYS:O	25:4D:116:ASP:OD1	2.34	0.45
37:2A:180:G:H2'	37:2A:181:G:H8	1.81	0.45
43:2G:1031:VAL:O	43:2G:1032:GLN:C	2.60	0.45
43:2G:687:VAL:O	43:2G:690:ILE:N	2.50	0.45
43:2G:889:GLU:O	43:2G:890:GLU:C	2.57	0.45
45:2I:672:GLY:O	45:2I:691:THR:N	2.49	0.45
1:A:31:C:C4	1:A:32:C:N4	2.73	0.45
1:A:32:C:N3	37:2A:31:G:O6	2.50	0.45
2:5A:92:U:N3	8:5b:36:MET:N	2.64	0.45
3:5B:206:TRP:CD1	3:5B:213:LEU:HD21	2.52	0.45
4:5C:716:GLU:O	4:5C:720:THR:HG23	2.16	0.45
5:5D:801:PHE:HB3	5:5D:821:LEU:HD21	1.98	0.45
5:5D:1167:MET:HA	5:5D:1167:MET:HE3	1.98	0.45
5:5D:1290:ILE:HG23	5:5D:1290:ILE:O	2.17	0.45
5:5D:1425:ILE:N	5:5D:1425:ILE:CD1	2.79	0.45
5:5D:1868:LEU:HD13	5:5D:1890:LYS:HG2	1.98	0.45
28:4G:892:GLU:C	28:4G:892:GLU:OE1	2.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4J:332:SER:O	31:4J:332:SER:OG	2.29	0.45
43:2G:830:TYR:O	43:2G:831:ARG:C	2.57	0.45
45:2I:1141:PHE:O	45:2I:1144:VAL:N	2.49	0.45
48:2L:46:CYS:O	48:2L:50:ASN:N	2.43	0.45
3:5B:658:ARG:NH2	28:4G:102:ASP:OD2	2.47	0.45
4:5C:156:GLU:OE1	4:5C:156:GLU:N	2.47	0.45
5:5D:1300:GLU:OE1	5:5D:1300:GLU:N	2.36	0.45
5:5D:2036:VAL:HG23	5:5D:2093:ASP:OD1	2.17	0.45
22:4A:115:G:H2'	22:4A:116:G:C8	2.52	0.45
37:2A:114:A:H2'	37:2A:115:G:H8	1.81	0.45
43:2G:1078:VAL:O	43:2G:1081:PHE:N	2.50	0.45
3:5B:857:ASN:ND2	3:5B:860:GLN:OE1	2.50	0.45
4:5C:676:ALA:HB3	4:5C:815:VAL:HB	1.98	0.45
23:4B:416:ASN:CG	23:4B:416:ASN:O	2.60	0.45
42:2F:394:TYR:C	42:2F:396:LEU:N	2.75	0.45
43:2G:708:ALA:O	43:2G:711:ALA:N	2.49	0.45
45:2I:663:LEU:O	45:2I:678:VAL:CA	2.65	0.45
3:5B:198:GLU:OE1	3:5B:198:GLU:N	2.43	0.45
3:5B:1189:MET:O	3:5B:1191:GLY:N	2.50	0.45
3:5B:1194:CYS:HA	3:5B:1229:PHE:O	2.17	0.45
3:5B:1638:ASN:ND2	3:5B:1656:THR:HG22	2.32	0.45
5:5D:1464:GLY:N	5:5D:1465:PRO:CD	2.80	0.45
22:4A:118:A:OP2	22:4A:118:A:C8	2.70	0.45
24:4C:109:LYS:O	24:4C:119:ILE:HD11	2.16	0.45
28:4G:921:ASN:ND2	28:4G:921:ASN:O	2.37	0.45
33:4L:57:VAL:O	33:4L:132:SER:HA	2.17	0.45
33:4L:146:GLU:OE2	33:4L:146:GLU:N	2.49	0.45
37:2A:59:A:H2'	37:2A:60:U:O4'	2.17	0.45
43:2G:629:ALA:O	43:2G:630:ARG:C	2.56	0.45
43:2G:791:VAL:O	43:2G:792:VAL:C	2.60	0.45
45:2I:215:LEU:O	45:2I:218:ASN:N	2.50	0.45
45:2I:1141:PHE:O	45:2I:1142:GLN:C	2.60	0.45
45:2I:1191:LYS:O	45:2I:1192:ASN:C	2.59	0.45
4:5C:726:LEU:HD23	4:5C:726:LEU:O	2.18	0.44
5:5D:1037:LEU:CG	5:5D:1052:ILE:HD11	2.47	0.44
28:4G:122:GLN:O	28:4G:126:GLU:HG3	2.16	0.44
43:2G:1013:ILE:O	43:2G:1014:LYS:C	2.60	0.44
43:2G:1128:VAL:O	43:2G:1129:LEU:C	2.60	0.44
45:2I:672:GLY:C	45:2I:691:THR:H	2.25	0.44
1:A:33:U:O3'	1:A:34:G:O4'	2.35	0.44
1:A:118:A:P	35:4N:101:GLY:HA2	2.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:5B:2019:PRO:O	3:5B:2024:GLN:NE2	2.50	0.44
14:6A:35:A:O2'	14:6A:36:A:O5'	2.28	0.44
14:6A:91:A:H2'	14:6A:92:A:H8	1.82	0.44
22:4A:91:A:H2'	22:4A:92:C:C6	2.53	0.44
31:4J:284:GLU:O	31:4J:284:GLU:CG	2.65	0.44
37:2A:54:U:H5'	42:2F:424:ARG:CA	2.47	0.44
43:2G:658:TRP:O	43:2G:659:GLN:C	2.60	0.44
43:2G:669:GLN:O	43:2G:670:GLN:C	2.60	0.44
43:2G:749:ALA:O	43:2G:750:ILE:C	2.60	0.44
43:2G:937:LEU:O	43:2G:938:TRP:C	2.59	0.44
2:5A:81:U:O5'	2:5A:81:U:C6	2.70	0.44
4:5C:276:TYR:O	4:5C:279:ARG:NH2	2.50	0.44
5:5D:597:THR:HG21	5:5D:634:ARG:CD	2.48	0.44
7:4a:80:MET:O	8:4b:59:SER:N	2.44	0.44
37:2A:143:A:OP2	37:2A:143:A:C2	2.71	0.44
43:2G:935:THR:O	43:2G:936:VAL:C	2.58	0.44
43:2G:1246:MET:O	43:2G:1247:LEU:C	2.59	0.44
2:5A:117:A:C6	10:5d:26:GLY:HA3	2.52	0.44
3:5B:835:ASP:OD1	3:5B:835:ASP:N	2.49	0.44
5:5D:569:LEU:HD13	5:5D:575:LEU:HB2	1.98	0.44
5:5D:1015:PHE:CE2	5:5D:1063:LEU:HD23	2.53	0.44
5:5D:1499:ASP:OD2	5:5D:1763:ARG:NH1	2.42	0.44
14:6A:90:G:H2'	14:6A:91:A:H8	1.82	0.44
14:6A:91:A:H2'	14:6A:92:A:C8	2.53	0.44
22:4A:18:G:C2	25:4D:358:ARG:HD2	2.53	0.44
22:4A:122:U:H1'	12:4f:65:ASN:CA	2.47	0.44
24:4C:180:TRP:O	24:4C:183:ASN:OD1	2.36	0.44
24:4C:275:ASN:O	24:4C:301:ALA:N	2.50	0.44
29:4H:45:GLN:O	29:4H:49:GLY:N	2.51	0.44
30:4I:8:GLN:HB2	30:4I:9:PRO:CD	2.47	0.44
12:4f:22:ASN:N	12:4f:66:SER:O	2.49	0.44
2:5A:92:U:C4	8:5b:36:MET:N	2.85	0.44
3:5B:441:VAL:O	3:5B:445:VAL:HG23	2.18	0.44
3:5B:529:THR:OG1	34:4M:45:LYS:NZ	2.43	0.44
3:5B:534:GLU:HA	3:5B:537:LYS:HE2	1.99	0.44
3:5B:1839:TRP:CH2	28:4G:301:VAL:HG22	2.52	0.44
3:5B:2298:LEU:CD2	5:5D:1265:GLN:OE1	2.66	0.44
22:4A:127:C:H1'	9:4c:47:ARG:C	2.42	0.44
24:4C:458:GLU:CG	24:4C:459:PRO:HD2	2.47	0.44
33:4L:87:ILE:HD12	33:4L:87:ILE:H	1.81	0.44
34:4M:8:ASP:OD1	34:4M:8:ASP:O	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2G:834:VAL:O	43:2G:835:ASP:C	2.60	0.44
43:2G:874:LYS:O	43:2G:875:ILE:C	2.60	0.44
3:5B:1524:SER:O	3:5B:1528:GLN:HG2	2.17	0.44
4:5C:829:GLU:OE2	4:5C:878:ILE:HG22	2.18	0.44
5:5D:783:ALA:HB3	5:5D:806:ILE:HG21	2.00	0.44
5:5D:1845:LEU:HA	5:5D:1848:ILE:HG22	2.00	0.44
5:5D:1846:ILE:HG22	5:5D:1892:ASN:OD1	2.18	0.44
5:5D:1919:ALA:O	5:5D:1923:ILE:HG12	2.18	0.44
5:5D:2041:LEU:HD23	5:5D:2108:PHE:CZ	2.52	0.44
31:4J:264:ASP:OD1	31:4J:264:ASP:C	2.60	0.44
37:2A:112:G:H2'	37:2A:113:G:C8	2.50	0.44
43:2G:429:ARG:C	43:2G:432:THR:H	2.26	0.44
43:2G:631:ALA:O	43:2G:632:PHE:C	2.58	0.44
43:2G:831:ARG:O	43:2G:832:GLN:C	2.58	0.44
3:5B:1946:ASN:O	3:5B:1947:ASN:HB3	2.18	0.44
3:5B:1953:ILE:HD12	3:5B:1986:LEU:HD12	2.00	0.44
3:5B:1980:GLU:OE2	23:4B:494:THR:OG1	2.35	0.44
4:5C:457:VAL:HA	4:5C:462:GLY:HA3	2.00	0.44
5:5D:1784:HIS:O	5:5D:1788:LEU:HG	2.18	0.44
22:4A:127:C:O5'	22:4A:127:C:C6	2.70	0.44
23:4B:576:HIS:HB3	23:4B:579:VAL:HG23	1.99	0.44
29:4H:152:ARG:CB	30:4I:75:ALA:HB2	2.48	0.44
9:4c:109:VAL:N	10:4d:63:LEU:O	2.42	0.44
37:2A:40:C:C5'	37:2A:40:C:C6	2.92	0.44
37:2A:113:G:H2'	37:2A:114:A:H8	1.82	0.44
37:2A:153:A:H2'	37:2A:154:C:H5''	1.99	0.44
43:2G:1223:SER:O	43:2G:1224:PRO:C	2.60	0.44
2:5A:71:C:H2'	2:5A:72:U:O4'	2.17	0.44
3:5B:246:LEU:HD11	3:5B:411:PHE:HE2	1.81	0.44
3:5B:1314:VAL:O	3:5B:1318:THR:OG1	2.24	0.44
4:5C:670:SER:HA	4:5C:823:ALA:HA	1.99	0.44
24:4C:220:SER:O	24:4C:220:SER:OG	2.25	0.44
25:4D:212:MET:HE1	25:4D:232:MET:SD	2.58	0.44
25:4D:346:PRO:O	27:4F:121:ARG:NH2	2.51	0.44
27:4F:117:GLU:OE1	27:4F:121:ARG:NH1	2.50	0.44
31:4J:270:GLU:N	31:4J:270:GLU:OE1	2.51	0.44
37:2A:182:U:H2'	37:2A:183:G:H8	1.81	0.44
43:2G:578:ILE:O	43:2G:579:GLU:C	2.57	0.44
43:2G:606:LEU:O	43:2G:609:MET:N	2.51	0.44
45:2I:406:PRO:CA	45:2I:1122:LEU:O	2.65	0.44
3:5B:543:ALA:HB3	3:5B:651:TRP:CE2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:5B:564:TYR:CG	3:5B:574:LEU:HD22	2.53	0.44
5:5D:616:GLU:HA	5:5D:616:GLU:OE1	2.18	0.44
5:5D:1604:LEU:HD13	5:5D:1609:LEU:CD2	2.47	0.44
5:5D:2039:VAL:HB	5:5D:2090:VAL:HG13	2.00	0.44
35:4N:58:LEU:HD22	35:4N:58:LEU:H	1.83	0.44
43:2G:1029:GLU:O	43:2G:1032:GLN:N	2.51	0.44
45:2I:676:ARG:O	45:2I:686:LEU:CA	2.65	0.44
1:A:34:G:C5	1:A:35:U:C4	3.05	0.43
1:A:35:U:O2'	1:A:36:C:C5	2.71	0.43
1:A:117:G:OP1	35:4N:103:LYS:HB3	2.17	0.43
4:5C:260:ILE:HG22	4:5C:311:SER:OG	2.18	0.43
4:5C:573:GLU:N	4:5C:573:GLU:OE1	2.51	0.43
5:5D:765:GLU:N	5:5D:765:GLU:OE1	2.51	0.43
43:2G:1230:VAL:O	43:2G:1233:ALA:N	2.51	0.43
1:A:116:G:N2	14:6A:38:G:H1	2.15	0.43
1:A:116:G:H4'	35:4N:98:HIS:CE1	2.53	0.43
3:5B:2162:GLN:O	3:5B:2294:TYR:OH	2.18	0.43
3:5B:2317:PHE:CE2	5:5D:1070:LEU:HD11	2.52	0.43
5:5D:526:ASN:ND2	5:5D:531:ILE:O	2.51	0.43
5:5D:815:LEU:HD21	5:5D:821:LEU:HB3	2.00	0.43
25:4D:99:LEU:O	25:4D:99:LEU:HD23	2.18	0.43
45:2I:1148:LEU:O	45:2I:1151:GLU:N	2.51	0.43
4:5C:224:GLY:HA3	4:5C:438:ILE:HD12	2.00	0.43
4:5C:813:ARG:O	4:5C:816:VAL:HG12	2.18	0.43
5:5D:1360:ALA:HB2	5:5D:1490:LEU:HD11	2.00	0.43
14:6A:92:A:H2'	14:6A:93:G:H8	1.83	0.43
34:4M:69:GLU:OE2	34:4M:69:GLU:N	2.51	0.43
37:2A:98:G:H5'	37:2A:104:U:OP2	2.19	0.43
37:2A:154:C:O2'	37:2A:155:C:C5'	2.66	0.43
37:2A:181:G:H2'	37:2A:182:U:C6	2.50	0.43
43:2G:792:VAL:O	43:2G:793:LYS:C	2.59	0.43
4:5C:668:GLU:OE2	4:5C:669:THR:HG22	2.19	0.43
5:5D:1628:GLU:CD	5:5D:1628:GLU:N	2.76	0.43
5:5D:1844:GLY:O	5:5D:1848:ILE:HG22	2.18	0.43
28:4G:800:MET:HE2	28:4G:804:LEU:HG	2.00	0.43
1:A:17:G:H2'	1:A:18:C:C6	2.53	0.43
1:A:117:G:H1	14:6A:37:C:N4	2.15	0.43
2:5A:92:U:O4	8:5b:34:VAL:O	2.37	0.43
3:5B:65:HIS:O	3:5B:69:ILE:HG13	2.17	0.43
3:5B:1357:MET:SD	3:5B:1357:MET:C	3.02	0.43
3:5B:2275:ALA:HB3	3:5B:2295:GLU:OE1	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5C:484:THR:OG1	4:5C:485:ASP:N	2.51	0.43
14:6A:51:U:O2'	14:6A:52:U:H5'	2.18	0.43
24:4C:184:TYR:CD1	24:4C:184:TYR:C	2.97	0.43
35:4N:115:GLU:N	35:4N:115:GLU:CD	2.77	0.43
35:4N:122:VAL:HG12	35:4N:126:PHE:CZ	2.52	0.43
49:2M:64:VAL:O	49:2M:65:ARG:C	2.59	0.43
1:A:20:U:C2	37:2A:42:G:C2	3.04	0.43
3:5B:1090:ARG:HG2	3:5B:1091:TYR:O	2.19	0.43
4:5C:618:THR:HB	4:5C:630:LEU:HB2	2.01	0.43
5:5D:1518:VAL:O	5:5D:1518:VAL:CG1	2.67	0.43
36:4Z:488:ILE:H	36:4Z:503:SER:HA	1.83	0.43
37:2A:40:C:H5''	37:2A:40:C:C6	2.32	0.43
37:2A:148:C:H2'	37:2A:149:A:H8	1.82	0.43
43:2G:82:PRO:O	43:2G:86:ALA:N	2.42	0.43
43:2G:310:TRP:O	43:2G:311:ALA:C	2.62	0.43
43:2G:625:ARG:O	43:2G:626:ASN:C	2.61	0.43
43:2G:1262:ARG:O	43:2G:1263:ASP:C	2.61	0.43
2:5A:89:U:C2'	2:5A:90:U:H5''	2.47	0.43
3:5B:147:MET:HG3	3:5B:151:MET:HE3	2.01	0.43
5:5D:530:THR:CB	5:5D:531:ILE:HD12	2.48	0.43
5:5D:595:ILE:HD12	5:5D:992:TYR:HB2	2.01	0.43
24:4C:99:ILE:HG22	24:4C:101:VAL:HG23	2.01	0.43
37:2A:142:C:H2'	37:2A:143:A:H5'	1.97	0.43
43:2G:665:ILE:O	43:2G:668:VAL:N	2.52	0.43
45:2I:318:ASP:N	45:2I:321:MET:O	2.27	0.43
3:5B:97:HIS:ND1	3:5B:649:GLU:OE1	2.51	0.43
3:5B:1807:ILE:HB	3:5B:1820:LYS:HB3	2.00	0.43
4:5C:405:LYS:HA	4:5C:405:LYS:HE2	1.99	0.43
4:5C:705:VAL:O	4:5C:706:GLN:C	2.62	0.43
5:5D:1518:VAL:O	5:5D:1518:VAL:HG12	2.17	0.43
5:5D:1960:LEU:CD1	5:5D:1982:VAL:HG22	2.48	0.43
14:6A:89:U:H2'	14:6A:90:G:C8	2.53	0.43
24:4C:92:ARG:HA	24:4C:92:ARG:NE	2.34	0.43
27:4F:29:ARG:HD3	27:4F:79:CYS:SG	2.58	0.43
28:4G:668:ALA:O	28:4G:672:ALA:N	2.46	0.43
43:2G:782:GLU:O	43:2G:783:GLU:C	2.62	0.43
43:2G:889:GLU:O	43:2G:892:LEU:N	2.51	0.43
43:2G:916:THR:O	43:2G:917:VAL:C	2.61	0.43
43:2G:981:TYR:C	43:2G:983:GLY:N	2.75	0.43
45:2I:147:ASP:N	45:2I:151:ARG:O	2.42	0.43
3:5B:683:LEU:HD21	27:4F:43:GLU:HG2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:6b:19:ASP:C	16:6b:21:ILE:N	2.77	0.43
23:4B:672:LEU:HD22	24:4C:446:PRO:HG2	2.01	0.43
25:4D:61:ALA:HB2	25:4D:106:GLU:OE1	2.19	0.43
45:2I:430:GLY:O	45:2I:431:PRO:C	2.61	0.43
45:2I:886:GLU:CA	45:2I:910:ALA:O	2.67	0.43
1:A:116:G:HO2'	35:4N:98:HIS:HD1	1.66	0.43
5:5D:534:ASP:OD1	5:5D:534:ASP:C	2.62	0.43
5:5D:831:THR:CG2	5:5D:869:LEU:HD11	2.48	0.43
14:6A:89:U:H2'	14:6A:90:G:H8	1.84	0.43
22:4A:120:U:C6	22:4A:120:U:C3'	3.01	0.43
24:4C:499:ASP:OD1	24:4C:500:ILE:N	2.52	0.43
25:4D:270:HIS:O	25:4D:271:THR:HG23	2.18	0.43
43:2G:627:THR:O	43:2G:630:ARG:N	2.52	0.43
45:2I:5:ASN:O	45:2I:1176:GLY:HA3	2.19	0.43
1:A:117:G:H1	14:6A:37:C:H42	1.66	0.42
3:5B:113:ILE:CD1	3:5B:187:PRO:HG3	2.49	0.42
5:5D:1196:SER:O	5:5D:1196:SER:OG	2.34	0.42
5:5D:1923:ILE:HG21	5:5D:1946:ALA:HB2	2.01	0.42
14:6A:45:A:C6	14:6A:47:A:N6	2.87	0.42
24:4C:282:HIS:N	24:4C:295:ASN:O	2.46	0.42
37:2A:178:A:N3	37:2A:178:A:H2'	2.34	0.42
43:2G:854:VAL:O	43:2G:856:ASP:N	2.52	0.42
43:2G:928:TYR:O	43:2G:929:LEU:C	2.61	0.42
43:2G:1016:LEU:O	43:2G:1017:LEU:C	2.62	0.42
43:2G:1090:PRO:O	43:2G:1091:HIS:C	2.62	0.42
1:A:37:C:C2'	1:A:38:C:O5'	2.67	0.42
3:5B:579:GLN:HG3	3:5B:629:PHE:H	1.84	0.42
3:5B:2038:GLN:CB	5:5D:1035:LEU:CG	2.95	0.42
4:5C:446:LYS:HB3	4:5C:447:PRO:HD3	2.01	0.42
5:5D:464:VAL:HA	5:5D:467:LEU:HD13	2.02	0.42
5:5D:848:ASP:O	5:5D:852:MET:HG3	2.20	0.42
5:5D:1569:THR:CG2	5:5D:1570:ARG:N	2.82	0.42
14:6A:92:A:H2'	14:6A:93:G:C8	2.54	0.42
22:4A:90:G:H2'	22:4A:91:A:C8	2.55	0.42
27:4F:30:PHE:HB3	27:4F:63:ILE:HD11	2.01	0.42
37:2A:64:A:H2'	37:2A:65:U:C6	2.54	0.42
43:2G:682:HIS:O	43:2G:683:LEU:C	2.61	0.42
43:2G:723:SER:C	43:2G:725:ASP:H	2.26	0.42
43:2G:948:ARG:O	43:2G:949:GLN:C	2.60	0.42
45:2I:1189:LYS:O	45:2I:1190:GLN:C	2.62	0.42
3:5B:1189:MET:O	3:5B:1190:CYS:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5C:478:THR:HA	4:5C:494:GLY:HA3	2.00	0.42
5:5D:525:ILE:O	5:5D:526:ASN:C	2.62	0.42
5:5D:1074:GLY:CA	35:4N:71:THR:HG23	2.49	0.42
25:4D:384:GLU:OE1	25:4D:395:SER:OG	2.36	0.42
28:4G:309:PRO:N	28:4G:310:PRO:CD	2.82	0.42
28:4G:773:ASN:HB2	28:4G:774:PRO:HA	2.00	0.42
37:2A:107:A:N1	37:2A:108:G:C5	2.88	0.42
43:2G:981:TYR:O	43:2G:983:GLY:N	2.53	0.42
47:2K:51:GLY:HA3	47:2K:56:THR:O	2.19	0.42
49:2M:62:ALA:O	49:2M:63:ARG:C	2.62	0.42
3:5B:679:SER:O	3:5B:680:HIS:C	2.61	0.42
4:5C:509:VAL:O	4:5C:522:SER:HA	2.19	0.42
5:5D:495:THR:HG22	5:5D:496:ASP:N	2.35	0.42
5:5D:642:THR:O	5:5D:642:THR:HG22	2.19	0.42
5:5D:1857:ASN:OD1	5:5D:1857:ASN:C	2.62	0.42
22:4A:110:G:O5'	22:4A:110:G:C8	2.70	0.42
22:4A:119:A:H5''	10:4d:38:GLY:O	2.19	0.42
23:4B:568:TYR:O	23:4B:641:ARG:NH2	2.53	0.42
37:2A:142:C:O2'	37:2A:143:A:H5'	2.18	0.42
43:2G:632:PHE:O	43:2G:633:ALA:C	2.59	0.42
43:2G:950:GLN:O	43:2G:951:ALA:C	2.61	0.42
1:A:37:C:O2'	1:A:38:C:O4'	2.38	0.42
3:5B:122:ILE:HD12	3:5B:122:ILE:HA	1.94	0.42
3:5B:173:GLU:OE2	33:4L:164:ARG:NH1	2.52	0.42
3:5B:599:MET:HE3	3:5B:599:MET:HA	2.01	0.42
3:5B:2298:LEU:HD21	5:5D:1265:GLN:OE1	2.19	0.42
22:4A:119:A:H5''	10:4d:38:GLY:C	2.44	0.42
24:4C:184:TYR:OH	24:4C:188:ARG:NH1	2.49	0.42
26:4E:87:GLN:NE2	40:2D:426:GLN:OE1	2.51	0.42
28:4G:891:GLU:HA	28:4G:894:GLN:OE1	2.19	0.42
31:4J:250:SER:OG	31:4J:252:ARG:NH1	2.53	0.42
38:2B:160:LYS:O	38:2B:161:MET:C	2.63	0.42
2:5A:95:G:C1'	10:5d:24:LYS:CA	2.80	0.42
3:5B:707:ARG:HG2	3:5B:707:ARG:HH11	1.84	0.42
4:5C:758:LEU:N	4:5C:758:LEU:HD22	2.35	0.42
5:5D:1936:LEU:HD23	5:5D:1936:LEU:C	2.43	0.42
5:5D:2098:ALA:C	5:5D:2099:THR:HG22	2.45	0.42
29:4H:158:PRO:O	29:4H:165:PRO:HA	2.20	0.42
34:4M:28:LYS:NZ	34:4M:42:ILE:O	2.37	0.42
37:2A:157:G:H2'	37:2A:158:G:O4'	2.19	0.42
43:2G:574:ILE:O	43:2G:575:LEU:C	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2G:1205:GLU:O	43:2G:1206:ASP:C	2.61	0.42
43:2G:1279:ALA:O	43:2G:1280:LEU:C	2.60	0.42
1:A:33:U:O2'	1:A:34:G:C8	2.70	0.42
3:5B:472:LEU:O	3:5B:473:PHE:HB2	2.20	0.42
3:5B:513:LEU:HG	3:5B:513:LEU:O	2.20	0.42
3:5B:1139:ARG:HA	3:5B:1186:LEU:HD11	2.02	0.42
3:5B:1434:LYS:O	3:5B:1439:ARG:NH2	2.47	0.42
3:5B:2233:SER:O	3:5B:2236:GLU:HG3	2.20	0.42
4:5C:363:SER:O	4:5C:364:SER:OG	2.27	0.42
4:5C:560:VAL:HG12	4:5C:561:LYS:H	1.85	0.42
4:5C:845:ALA:O	4:5C:846:VAL:C	2.61	0.42
5:5D:467:LEU:HD12	5:5D:467:LEU:H	1.84	0.42
5:5D:1613:LEU:CD1	5:5D:1641:ILE:HG21	2.50	0.42
5:5D:1943:MET:HE3	5:5D:2109:MET:HB2	2.01	0.42
23:4B:393:TYR:CD1	23:4B:393:TYR:C	2.97	0.42
33:4L:42:LEU:O	33:4L:80:ILE:HD11	2.19	0.42
43:2G:710:ALA:O	43:2G:711:ALA:C	2.61	0.42
43:2G:1078:VAL:O	43:2G:1079:ASN:C	2.63	0.42
43:2G:1115:ALA:O	43:2G:1116:ILE:C	2.61	0.42
1:A:22:C:H2'	1:A:23:G:C5'	2.49	0.42
3:5B:214:ARG:HB3	3:5B:214:ARG:NH1	2.35	0.42
3:5B:1911:GLU:HA	3:5B:1911:GLU:OE2	2.20	0.42
5:5D:514:LEU:HD22	5:5D:558:ARG:HD3	2.01	0.42
5:5D:938:ILE:HD11	5:5D:952:ARG:HG2	2.01	0.42
5:5D:1369:LEU:HD23	5:5D:1369:LEU:C	2.45	0.42
5:5D:1847:GLU:OE1	5:5D:1847:GLU:C	2.63	0.42
24:4C:458:GLU:OE1	24:4C:461:HIS:HB3	2.20	0.42
25:4D:292:ALA:O	25:4D:293:ARG:C	2.62	0.42
28:4G:369:LEU:O	28:4G:371:GLN:N	2.50	0.42
33:4L:145:ASP:CG	33:4L:146:GLU:OE2	2.63	0.42
37:2A:155:C:H2'	37:2A:156:U:H5''	2.02	0.42
40:2D:420:ILE:HD11	40:2D:425:MET:HA	2.01	0.42
43:2G:854:VAL:C	43:2G:856:ASP:H	2.28	0.42
43:2G:997:LEU:O	43:2G:998:LYS:C	2.62	0.42
44:2H:805:ILE:HG12	44:2H:806:TYR:N	2.34	0.42
1:A:20:U:H5''	1:A:20:U:H6	1.85	0.42
2:5A:18:C:H2'	2:5A:19:A:O4'	2.19	0.42
4:5C:258:ASN:OD1	4:5C:259:LYS:N	2.50	0.42
4:5C:932:GLU:OE2	4:5C:936:LYS:NZ	2.37	0.42
5:5D:625:GLY:N	5:5D:626:PRO:CD	2.83	0.42
28:4G:862:GLU:C	28:4G:862:GLU:OE1	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:4N:84:VAL:O	35:4N:85:CYS:SG	2.77	0.42
36:4Z:334:HIS:HA	36:4Z:342:LEU:N	2.34	0.42
43:2G:887:LYS:O	43:2G:888:LEU:C	2.63	0.42
45:2I:1211:ILE:O	45:2I:1212:ARG:C	2.62	0.42
1:A:10:C:C2	1:A:10:C:OP2	2.73	0.42
3:5B:1997:VAL:HG12	3:5B:1998:ASN:N	2.35	0.42
3:5B:2286:VAL:O	3:5B:2286:VAL:HG22	2.20	0.42
4:5C:530:LEU:HD21	4:5C:544:VAL:HG21	2.01	0.42
4:5C:553:GLU:OE2	4:5C:554:GLY:N	2.53	0.42
5:5D:573:HIS:C	5:5D:575:LEU:H	2.27	0.42
5:5D:690:VAL:HG11	5:5D:707:ILE:HD13	2.01	0.42
5:5D:692:ILE:HG21	5:5D:700:ARG:HG3	2.02	0.42
22:4A:74:C:N3	22:4A:75:C:N4	2.68	0.42
31:4J:352:GLU:C	31:4J:353:GLN:OE1	2.63	0.42
36:4Z:241:TRP:HA	36:4Z:248:ILE:HA	2.01	0.42
42:2F:34:ARG:O	42:2F:35:ASP:C	2.62	0.42
43:2G:704:ILE:O	43:2G:705:SER:C	2.61	0.42
43:2G:806:ILE:O	43:2G:807:LYS:C	2.62	0.42
46:2J:77:ILE:O	46:2J:84:ILE:CA	2.68	0.42
2:5A:93:U:C4'	9:5c:104:ASP:CA	2.97	0.41
2:5A:116:U:OP2	11:5e:68:THR:CA	2.67	0.41
3:5B:783:TYR:CD1	3:5B:783:TYR:C	2.98	0.41
3:5B:2306:HIS:CD2	3:5B:2308:VAL:HG22	2.55	0.41
4:5C:134:LEU:CD2	4:5C:202:ILE:HG23	2.49	0.41
4:5C:617:LEU:HD11	4:5C:629:ILE:CG2	2.50	0.41
25:4D:222:ILE:HG22	25:4D:223:ILE:HG23	2.01	0.41
37:2A:103:U:C3'	37:2A:104:U:H5'	2.50	0.41
43:2G:91:LEU:O	43:2G:94:ILE:N	2.53	0.41
43:2G:862:GLU:O	43:2G:864:TYR:N	2.53	0.41
43:2G:1038:LEU:O	43:2G:1039:VAL:C	2.62	0.41
1:A:30:C:C5	1:A:31:C:H5	2.32	0.41
3:5B:409:ARG:HA	3:5B:412:ASN:OD1	2.20	0.41
3:5B:2190:PRO:HA	3:5B:2193:VAL:HG12	2.01	0.41
4:5C:133:THR:HG21	4:5C:219:LEU:HD23	2.03	0.41
4:5C:637:LEU:O	4:5C:641:MET:HG2	2.20	0.41
5:5D:641:MET:HG2	5:5D:1582:ALA:CB	2.50	0.41
5:5D:1166:ARG:CZ	5:5D:1166:ARG:HB2	2.49	0.41
5:5D:1536:GLN:O	5:5D:1540:LEU:HG	2.20	0.41
5:5D:1970:HIS:ND1	5:5D:1974:CYS:SG	2.89	0.41
22:4A:107:U:H2'	22:4A:108:C:H6	1.85	0.41
36:4Z:146:ALA:O	36:4Z:150:ALA:CB	2.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:4Z:240:VAL:O	36:4Z:249:ARG:N	2.52	0.41
37:2A:153:A:H62	37:2A:177:A:H2	1.67	0.41
43:2G:318:ARG:O	43:2G:321:ASP:N	2.52	0.41
43:2G:1169:VAL:O	43:2G:1172:LEU:N	2.54	0.41
1:A:108:G:N1	3:5B:1551:PHE:O	2.50	0.41
3:5B:422:LEU:N	3:5B:422:LEU:HD12	2.35	0.41
3:5B:682:ASP:OD1	3:5B:749:TRP:CZ3	2.74	0.41
5:5D:592:LYS:O	5:5D:595:ILE:HG22	2.19	0.41
24:4C:223:ASN:OD1	24:4C:224:PHE:N	2.53	0.41
33:4L:116:CYS:O	33:4L:120:LEU:HB2	2.21	0.41
37:2A:54:U:H5'	42:2F:424:ARG:C	2.45	0.41
42:2F:404:ILE:N	42:2F:417:ARG:O	2.44	0.41
43:2G:600:LEU:O	43:2G:604:ALA:N	2.35	0.41
43:2G:998:LYS:O	43:2G:1001:VAL:N	2.51	0.41
43:2G:1082:GLY:O	43:2G:1083:TYR:C	2.61	0.41
44:2H:504:TRP:C	44:2H:506:PHE:H	2.27	0.41
45:2I:127:GLY:O	45:2I:128:ARG:C	2.63	0.41
2:5A:115:C:OP1	11:5e:67:LYS:CA	2.67	0.41
4:5C:711:ARG:HB3	4:5C:711:ARG:CZ	2.51	0.41
5:5D:1936:LEU:HD21	5:5D:1940:LEU:HD11	2.02	0.41
5:5D:2042:GLU:HA	5:5D:2087:LYS:HB3	2.02	0.41
28:4G:714:MET:SD	28:4G:718:ILE:HD13	2.60	0.41
33:4L:96:PHE:CD1	33:4L:96:PHE:N	2.88	0.41
37:2A:63:G:H2'	37:2A:64:A:C8	2.56	0.41
2:5A:78:U:O2'	2:5A:79:C:H3'	2.21	0.41
3:5B:784:LEU:O	3:5B:788:GLN:HG3	2.20	0.41
3:5B:946:GLU:HB2	3:5B:950:LEU:HD23	2.03	0.41
3:5B:1560:ILE:HD11	3:5B:1577:PHE:CE2	2.55	0.41
5:5D:1351:PRO:HG3	5:5D:1516:PRO:HA	2.01	0.41
5:5D:1492:SER:OG	5:5D:1493:SER:N	2.53	0.41
5:5D:1665:ASP:O	5:5D:1667:GLN:N	2.48	0.41
25:4D:377:ARG:O	25:4D:397:GLY:HA3	2.20	0.41
43:2G:86:ALA:O	43:2G:89:ALA:CA	2.67	0.41
43:2G:1040:GLY:O	43:2G:1041:ARG:C	2.63	0.41
1:A:40:U:O4'	1:A:41:U:C5	2.72	0.41
2:5A:90:U:C5	13:5g:38:ASN:C	2.85	0.41
4:5C:708:THR:O	4:5C:708:THR:HG22	2.19	0.41
5:5D:573:HIS:O	5:5D:575:LEU:N	2.53	0.41
5:5D:769:CYS:SG	5:5D:771:ASN:N	2.93	0.41
37:2A:152:G:H2'	37:2A:153:A:C1'	2.51	0.41
45:2I:1210:ASP:O	45:2I:1211:ILE:C	2.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:5B:232:LEU:HD21	3:5B:414:ARG:HD3	2.03	0.41
3:5B:274:PRO:O	32:4K:400:THR:HA	2.21	0.41
3:5B:2119:ASP:OD2	3:5B:2305:TYR:OH	2.39	0.41
24:4C:266:LEU:C	24:4C:267:HIS:CG	2.98	0.41
27:4F:48:ILE:CG2	27:4F:109:LYS:HB2	2.50	0.41
32:4K:336:LYS:NZ	32:4K:367:ASP:O	2.46	0.41
43:2G:301:ARG:O	43:2G:302:ASP:C	2.63	0.41
43:2G:594:ARG:O	43:2G:595:GLU:C	2.61	0.41
1:A:113:U:H4'	30:4I:20:ILE:HD13	2.01	0.41
3:5B:986:GLU:OE1	3:5B:986:GLU:N	2.53	0.41
3:5B:1268:ILE:O	3:5B:1272:THR:OG1	2.30	0.41
4:5C:366:GLN:HG2	4:5C:370:VAL:HG11	2.02	0.41
4:5C:668:GLU:O	4:5C:823:ALA:HB1	2.21	0.41
5:5D:699:LYS:HD2	5:5D:699:LYS:HA	1.92	0.41
28:4G:108:LEU:HD12	28:4G:108:LEU:HA	1.97	0.41
37:2A:112:G:O5'	37:2A:112:G:H8	2.04	0.41
43:2G:1182:LEU:O	43:2G:1183:VAL:C	2.63	0.41
45:2I:1143:HIS:O	45:2I:1144:VAL:C	2.64	0.41
1:A:103:A:H2'	1:A:104:C:O4'	2.21	0.41
3:5B:150:MET:CE	3:5B:153:ARG:HE	2.33	0.41
3:5B:758:ARG:HD3	3:5B:779:LEU:HD11	2.02	0.41
3:5B:2123:GLN:HB2	3:5B:2157:VAL:HG13	2.03	0.41
4:5C:240:GLU:HA	4:5C:243:ILE:HG12	2.02	0.41
4:5C:911:PRO:O	4:5C:934:MET:HE3	2.20	0.41
5:5D:488:LEU:HD12	5:5D:488:LEU:C	2.46	0.41
5:5D:1375:ARG:NH1	5:5D:1447:ASN:O	2.54	0.41
5:5D:1631:LEU:HD23	5:5D:1631:LEU:C	2.46	0.41
5:5D:1748:LYS:NZ	5:5D:1790:GLU:OE1	2.46	0.41
5:5D:1920:ILE:HG22	5:5D:1924:GLN:OE1	2.21	0.41
5:5D:1943:MET:HE3	5:5D:2109:MET:CB	2.51	0.41
5:5D:2098:ALA:O	5:5D:2099:THR:CG2	2.68	0.41
6:5E:255:MET:O	6:5E:257:ASN:N	2.54	0.41
19:6e:45:LEU:N	19:6e:63:ALA:O	2.37	0.41
23:4B:419:GLU:OE1	24:4C:167:TYR:OH	2.31	0.41
37:2A:152:G:H2'	37:2A:152:G:N3	2.36	0.41
37:2A:171:U:H2'	37:2A:172:C:O4'	2.21	0.41
43:2G:647:PHE:O	43:2G:648:LEU:C	2.63	0.41
43:2G:712:LEU:O	43:2G:713:ALA:C	2.64	0.41
43:2G:750:ILE:O	43:2G:751:GLY:C	2.63	0.41
43:2G:1018:PRO:O	43:2G:1019:ARG:C	2.63	0.41
45:2I:811:THR:C	45:2I:813:ALA:N	2.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5A:49:A:C5	2:5A:50:G:N7	2.89	0.41
4:5C:150:ILE:HD12	4:5C:535:ALA:HB2	2.03	0.41
5:5D:526:ASN:O	5:5D:527:MET:C	2.64	0.41
5:5D:1036:GLU:OE1	5:5D:1075:PHE:HA	2.21	0.41
25:4D:189:GLU:C	25:4D:189:GLU:OE2	2.63	0.41
37:2A:149:A:C6	37:2A:150:U:C4	3.09	0.41
43:2G:758:ASP:O	43:2G:761:TYR:N	2.54	0.41
44:2H:596:GLU:C	44:2H:598:GLU:N	2.67	0.41
45:2I:437:VAL:O	45:2I:776:GLN:CA	2.69	0.41
3:5B:104:GLU:HG2	3:5B:422:LEU:HD11	2.02	0.40
3:5B:696:MET:HE3	3:5B:696:MET:HB3	1.99	0.40
3:5B:1911:GLU:O	3:5B:1912:PRO:C	2.64	0.40
4:5C:249:GLU:OE1	4:5C:448:LYS:NZ	2.51	0.40
4:5C:722:TYR:O	4:5C:723:ASP:OD1	2.39	0.40
5:5D:730:GLU:OE2	5:5D:829:LYS:NZ	2.50	0.40
5:5D:1006:LYS:O	5:5D:1107:LEU:HD22	2.21	0.40
5:5D:1165:ILE:O	5:5D:1165:ILE:HG22	2.22	0.40
23:4B:500:VAL:O	23:4B:504:MET:HG3	2.20	0.40
32:4K:382:ASN:O	32:4K:383:PHE:C	2.64	0.40
42:2F:184:ARG:CA	7:2a:85:PRO:C	2.94	0.40
43:2G:301:ARG:O	43:2G:304:PRO:N	2.54	0.40
43:2G:771:LEU:O	43:2G:772:ILE:C	2.65	0.40
43:2G:1149:LYS:O	43:2G:1150:SER:C	2.63	0.40
45:2I:672:GLY:N	45:2I:697:ARG:O	2.54	0.40
3:5B:655:LEU:HD12	3:5B:655:LEU:HA	1.98	0.40
4:5C:678:THR:O	4:5C:679:PRO:C	2.64	0.40
5:5D:782:PHE:N	5:5D:782:PHE:CD1	2.89	0.40
5:5D:1382:MET:HE2	5:5D:1652:TRP:CG	2.56	0.40
5:5D:1598:ILE:N	5:5D:1599:PRO:CD	2.85	0.40
22:4A:38:U:H4'	22:4A:39:A:OP1	2.21	0.40
25:4D:193:MET:O	25:4D:196:GLU:HG2	2.21	0.40
28:4G:371:GLN:N	28:4G:371:GLN:OE1	2.54	0.40
33:4L:21:VAL:HG13	33:4L:160:ILE:HD11	2.04	0.40
43:2G:706:ALA:O	43:2G:707:LEU:C	2.61	0.40
49:2M:52:TYR:O	49:2M:53:PHE:C	2.62	0.40
3:5B:651:TRP:HZ3	3:5B:652:LEU:HD23	1.85	0.40
3:5B:1863:VAL:HG11	3:5B:1868:MET:HB3	2.03	0.40
3:5B:2083:LEU:HD21	3:5B:2218:PHE:CE2	2.56	0.40
4:5C:750:LEU:HD23	4:5C:750:LEU:C	2.46	0.40
5:5D:537:LYS:NZ	5:5D:583:THR:O	2.53	0.40
5:5D:1437:ARG:CD	5:5D:1738:ALA:HB1	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5D:1559:VAL:N	5:5D:1642:GLN:O	2.49	0.40
5:5D:1962:GLN:OE1	5:5D:2114:MET:N	2.48	0.40
5:5D:1988:MET:HE1	5:5D:1996:LEU:HD13	2.03	0.40
22:4A:33:A:H2'	22:4A:34:G:O4'	2.20	0.40
43:2G:951:ALA:O	43:2G:952:ALA:C	2.61	0.40
43:2G:1169:VAL:O	43:2G:1170:THR:C	2.65	0.40
9:2c:62:HIS:O	9:2c:103:GLY:HA3	2.21	0.40
3:5B:186:GLU:N	3:5B:186:GLU:OE1	2.54	0.40
3:5B:804:GLU:OE1	3:5B:804:GLU:N	2.51	0.40
4:5C:713:LYS:HE3	4:5C:713:LYS:HA	2.02	0.40
5:5D:518:LEU:O	5:5D:522:GLY:N	2.52	0.40
5:5D:530:THR:HB	5:5D:531:ILE:HD12	2.03	0.40
5:5D:531:ILE:HG22	5:5D:532:ASN:N	2.37	0.40
5:5D:792:VAL:O	5:5D:795:THR:HG22	2.22	0.40
5:5D:1946:ALA:O	5:5D:1950:THR:HG23	2.20	0.40
14:6A:68:C:P	23:4B:520:LEU:HD11	2.62	0.40
31:4J:352:GLU:O	31:4J:353:GLN:C	2.65	0.40
37:2A:183:G:C6	37:2A:184:C:N4	2.89	0.40
43:2G:899:ALA:O	43:2G:900:PHE:C	2.64	0.40
10:2d:5:LEU:O	11:2e:49:GLY:HA3	2.21	0.40
2:5A:107:U:H2'	2:5A:108:G:O4'	2.22	0.40
3:5B:911:VAL:HG12	3:5B:912:GLU:N	2.35	0.40
3:5B:984:MET:HE3	3:5B:1048:MET:CE	2.51	0.40
5:5D:432:ASP:OD1	5:5D:433:GLY:N	2.52	0.40
5:5D:498:ASN:OD1	5:5D:498:ASN:N	2.55	0.40
5:5D:1214:VAL:HG23	5:5D:1215:HIS:N	2.36	0.40
5:5D:1240:LEU:C	5:5D:1240:LEU:HD23	2.47	0.40
5:5D:1860:ILE:HD12	5:5D:1890:LYS:HD3	2.04	0.40
9:5c:62:HIS:O	9:5c:103:GLY:HA3	2.21	0.40
24:4C:459:PRO:HB2	24:4C:460:ILE:H	1.71	0.40
37:2A:160:A:H2'	37:2A:161:U:O4'	2.22	0.40
43:2G:705:SER:O	43:2G:708:ALA:N	2.55	0.40
43:2G:750:ILE:O	43:2G:753:LEU:N	2.54	0.40
43:2G:1062:LEU:O	43:2G:1064:GLU:N	2.54	0.40
43:2G:1187:THR:O	43:2G:1188:ALA:C	2.64	0.40
43:2G:1188:ALA:O	43:2G:1189:SER:C	2.63	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	5B	2249/2335 (96%)	2156 (96%)	93 (4%)	0	100	100
4	5C	814/972 (84%)	755 (93%)	58 (7%)	1 (0%)	48	73
5	5D	1694/2136 (79%)	1618 (96%)	75 (4%)	1 (0%)	48	73
6	5E	297/357 (83%)	272 (92%)	16 (5%)	9 (3%)	3	8
7	2a	84/231 (36%)	82 (98%)	2 (2%)	0	100	100
7	4a	60/231 (26%)	57 (95%)	3 (5%)	0	100	100
7	5a	82/231 (36%)	80 (98%)	2 (2%)	0	100	100
8	2b	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
8	4b	80/119 (67%)	76 (95%)	4 (5%)	0	100	100
8	5b	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
9	2c	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
9	4c	70/118 (59%)	68 (97%)	2 (3%)	0	100	100
9	5c	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
10	2d	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
10	4d	69/86 (80%)	67 (97%)	2 (3%)	0	100	100
10	5d	72/86 (84%)	69 (96%)	3 (4%)	0	100	100
11	2e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
11	4e	76/92 (83%)	70 (92%)	6 (8%)	0	100	100
11	5e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
12	2f	64/76 (84%)	62 (97%)	2 (3%)	0	100	100
12	4f	71/76 (93%)	67 (94%)	4 (6%)	0	100	100
12	5f	70/76 (92%)	68 (97%)	2 (3%)	0	100	100
13	2g	76/126 (60%)	75 (99%)	1 (1%)	0	100	100
13	4g	69/126 (55%)	69 (100%)	0	0	100	100
13	5g	75/126 (60%)	73 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	6a	88/95 (93%)	77 (88%)	7 (8%)	4 (4%)	2	4
16	6b	70/102 (69%)	64 (91%)	3 (4%)	3 (4%)	2	4
17	6c	70/139 (50%)	63 (90%)	6 (9%)	1 (1%)	9	23
18	6d	68/91 (75%)	63 (93%)	4 (6%)	1 (2%)	8	22
19	6e	68/80 (85%)	64 (94%)	2 (3%)	2 (3%)	3	9
20	6f	61/103 (59%)	56 (92%)	5 (8%)	0	100	100
21	6g	57/96 (59%)	52 (91%)	4 (7%)	1 (2%)	6	18
23	4B	248/683 (36%)	235 (95%)	13 (5%)	0	100	100
24	4C	422/522 (81%)	393 (93%)	28 (7%)	1 (0%)	43	68
25	4D	372/499 (74%)	353 (95%)	19 (5%)	0	100	100
26	4E	122/128 (95%)	115 (94%)	7 (6%)	0	100	100
27	4F	139/142 (98%)	134 (96%)	5 (4%)	0	100	100
28	4G	795/941 (84%)	747 (94%)	48 (6%)	0	100	100
29	4H	167/177 (94%)	158 (95%)	9 (5%)	0	100	100
30	4I	73/376 (19%)	73 (100%)	0	0	100	100
31	4J	142/800 (18%)	136 (96%)	6 (4%)	0	100	100
32	4K	184/439 (42%)	174 (95%)	10 (5%)	0	100	100
33	4L	173/312 (55%)	165 (95%)	6 (4%)	2 (1%)	10	27
34	4M	71/73 (97%)	66 (93%)	5 (7%)	0	100	100
35	4N	78/199 (39%)	77 (99%)	0	1 (1%)	9	25
36	4Z	414/513 (81%)	401 (97%)	12 (3%)	1 (0%)	43	68
38	2B	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	9	25
39	2C	92/225 (41%)	90 (98%)	2 (2%)	0	100	100
40	2D	196/793 (25%)	180 (92%)	10 (5%)	6 (3%)	3	8
41	2E	88/464 (19%)	63 (72%)	16 (18%)	9 (10%)	0	0
42	2F	413/501 (82%)	367 (89%)	41 (10%)	5 (1%)	10	27
43	2G	1032/1304 (79%)	844 (82%)	166 (16%)	22 (2%)	5	15
44	2H	199/895 (22%)	179 (90%)	16 (8%)	4 (2%)	6	16
45	2I	1152/1217 (95%)	1053 (91%)	89 (8%)	10 (1%)	14	35
46	2J	76/424 (18%)	75 (99%)	1 (1%)	0	100	100
47	2K	106/125 (85%)	85 (80%)	18 (17%)	3 (3%)	4	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	2L	87/110 (79%)	74 (85%)	13 (15%)	0	100	100
49	2M	64/86 (74%)	55 (86%)	7 (11%)	2 (3%)	3	8
All	All	14181/21253 (67%)	13204 (93%)	886 (6%)	91 (1%)	23	44

All (91) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	5D	1086	GLN
6	5E	193	THR
15	6a	55	LEU
16	6b	84	MET
18	6d	70	ASP
19	6e	52	VAL
19	6e	55	GLN
24	4C	459	PRO
36	4Z	383	CYS
40	2D	301	PRO
41	2E	139	PRO
41	2E	141	ILE
41	2E	146	MET
41	2E	162	PRO
41	2E	165	ARG
41	2E	218	PRO
42	2F	284	ARG
43	2G	208	PRO
43	2G	416	PRO
43	2G	418	PRO
43	2G	456	VAL
43	2G	717	THR
43	2G	941	ASN
43	2G	1107	GLN
45	2I	405	SER
45	2I	919	SER
47	2K	99	GLN
47	2K	105	LYS
15	6a	74	ALA
16	6b	97	PRO
17	6c	12	ASN
38	2B	160	LYS
40	2D	223	LYS
40	2D	280	VAL

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Mol	Chain	Res	Type
42	2F	277	THR
43	2G	113	ALA
43	2G	1110	VAL
44	2H	597	PHE
45	2I	917	PRO
6	5E	60	MET
6	5E	88	ARG
6	5E	256	ASP
33	4L	39	CYS
42	2F	177	ARG
42	2F	393	PRO
44	2H	510	TYR
6	5E	162	ARG
16	6b	96	ALA
38	2B	32	PRO
40	2D	300	THR
43	2G	112	ILE
43	2G	437	PRO
43	2G	523	ALA
43	2G	909	VAL
43	2G	1006	MET
44	2H	463	ALA
44	2H	574	ALA
45	2I	529	ALA
45	2I	578	THR
47	2K	75	ASP
6	5E	159	PRO
15	6a	73	PRO
35	4N	85	CYS
41	2E	147	PRO
41	2E	217	PRO
43	2G	1047	ALA
43	2G	1075	ARG
43	2G	1186	GLN
45	2I	95	SER
45	2I	229	GLU
6	5E	270	LYS
21	6g	34	ILE
33	4L	65	ILE
41	2E	220	PRO
43	2G	326	THR
43	2G	932	ILE

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Mol	Chain	Res	Type
45	2I	918	ARG
45	2I	1138	HIS
49	2M	56	ALA
6	5E	149	GLY
43	2G	417	PRO
40	2D	221	PRO
43	2G	223	THR
42	2F	229	TRP
45	2I	1204	VAL
4	5C	439	PRO
6	5E	324	PRO
40	2D	298	PRO
43	2G	1031	VAL
49	2M	64	VAL
15	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	
3	5B	2033/2108 (96%)	1986 (98%)	47 (2%)	44	73
4	5C	717/866 (83%)	698 (97%)	19 (3%)	40	70
5	5D	1517/1908 (80%)	1513 (100%)	4 (0%)	86	94
23	4B	225/599 (38%)	220 (98%)	5 (2%)	45	74
24	4C	362/442 (82%)	350 (97%)	12 (3%)	33	63
25	4D	299/424 (70%)	290 (97%)	9 (3%)	36	66
26	4E	108/111 (97%)	105 (97%)	3 (3%)	38	68
27	4F	129/130 (99%)	124 (96%)	5 (4%)	28	57
28	4G	417/792 (53%)	405 (97%)	12 (3%)	37	67
29	4H	10/148 (7%)	10 (100%)	0	100	100
30	4I	32/333 (10%)	31 (97%)	1 (3%)	35	65
31	4J	112/681 (16%)	110 (98%)	2 (2%)	51	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
32	4K	66/395 (17%)	63 (96%)	3 (4%)	24	52	
33	4L	159/293 (54%)	153 (96%)	6 (4%)	29	58	
34	4M	66/66 (100%)	64 (97%)	2 (3%)	36	66	
35	4N	75/181 (41%)	70 (93%)	5 (7%)	15	36	
36	4Z	11/450 (2%)	11 (100%)	0	100	100	
40	2D	70/709 (10%)	69 (99%)	1 (1%)	59	82	
44	2H	26/776 (3%)	25 (96%)	1 (4%)	29	58	
All	All	6434/11412 (56%)	6297 (98%)	137 (2%)	46	75	

All (137) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	5B	81	PHE
3	5B	87	VAL
3	5B	104	GLU
3	5B	142	SER
3	5B	147	MET
3	5B	183	LEU
3	5B	200	ASP
3	5B	223	SER
3	5B	236	SER
3	5B	248	ASP
3	5B	282	LEU
3	5B	322	ASN
3	5B	330	THR
3	5B	351	TYR
3	5B	353	ASP
3	5B	484	SER
3	5B	527	VAL
3	5B	679	SER
3	5B	779	LEU
3	5B	854	SER
3	5B	866	LEU
3	5B	945	THR
3	5B	946	GLU
3	5B	991	THR
3	5B	1032	ARG
3	5B	1089	CYS
3	5B	1173	SER
3	5B	1176	SER

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Mol	Chain	Res	Type
3	5B	1303	LEU
3	5B	1377	SER
3	5B	1385	VAL
3	5B	1420	ASN
3	5B	1438	VAL
3	5B	1520	ASN
3	5B	1536	LEU
3	5B	1539	SER
3	5B	1599	GLN
3	5B	1634	SER
3	5B	1638	ASN
3	5B	1697	SER
3	5B	1799	THR
3	5B	1872	LEU
3	5B	2046	THR
3	5B	2056	THR
3	5B	2068	SER
3	5B	2073	TRP
3	5B	2231	THR
4	5C	150	ILE
4	5C	202	ILE
4	5C	301	SER
4	5C	363	SER
4	5C	497	LEU
4	5C	507	VAL
4	5C	532	ILE
4	5C	533	SER
4	5C	534	VAL
4	5C	560	VAL
4	5C	562	THR
4	5C	592	VAL
4	5C	649	SER
4	5C	667	VAL
4	5C	749	THR
4	5C	783	LEU
4	5C	818	SER
4	5C	912	LEU
4	5C	943	LEU
5	5D	778	LEU
5	5D	984	LEU
5	5D	1039	LYS
5	5D	1705	MET

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Mol	Chain	Res	Type
23	4B	417	LEU
23	4B	515	ASN
23	4B	548	VAL
23	4B	580	ASN
23	4B	675	SER
24	4C	98	GLN
24	4C	206	THR
24	4C	235	SER
24	4C	292	LYS
24	4C	304	SER
24	4C	334	SER
24	4C	378	SER
24	4C	399	CYS
24	4C	430	THR
24	4C	436	LEU
24	4C	460	ILE
24	4C	461	HIS
25	4D	119	SER
25	4D	163	THR
25	4D	168	SER
25	4D	214	PHE
25	4D	260	SER
25	4D	311	SER
25	4D	395	SER
25	4D	398	HIS
25	4D	427	THR
26	4E	81	VAL
26	4E	85	SER
26	4E	122	SER
27	4F	25	VAL
27	4F	80	THR
27	4F	94	LEU
27	4F	132	SER
27	4F	138	THR
28	4G	15	LEU
28	4G	102	ASP
28	4G	108	LEU
28	4G	199	SER
28	4G	205	THR
28	4G	343	GLU
28	4G	357	THR
28	4G	373	VAL

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Mol	Chain	Res	Type
28	4G	718	ILE
28	4G	750	SER
28	4G	752	LEU
28	4G	921	ASN
30	4I	8	GLN
31	4J	250	SER
31	4J	288	VAL
32	4K	358	ARG
32	4K	359	ASP
32	4K	400	THR
33	4L	24	ILE
33	4L	60	VAL
33	4L	72	CYS
33	4L	74	THR
33	4L	75	LEU
33	4L	108	ARG
34	4M	23	THR
34	4M	49	THR
35	4N	58	LEU
35	4N	61	LYS
35	4N	70	LYS
35	4N	84	VAL
35	4N	88	VAL
40	2D	482	THR
44	2H	803	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (79) such sidechains are listed below:

Mol	Chain	Res	Type
3	5B	65	HIS
3	5B	73	HIS
3	5B	105	ASN
3	5B	229	GLN
3	5B	326	HIS
3	5B	357	ASN
3	5B	434	HIS
3	5B	509	HIS
3	5B	542	ASN
3	5B	654	ASN
3	5B	680	HIS
3	5B	857	ASN
3	5B	1018	ASN

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Mol	Chain	Res	Type
3	5B	1172	ASN
3	5B	1218	ASN
3	5B	1367	ASN
3	5B	1457	HIS
3	5B	1466	ASN
3	5B	1487	HIS
3	5B	1563	HIS
3	5B	1586	HIS
3	5B	1595	GLN
3	5B	1638	ASN
3	5B	1691	ASN
3	5B	1717	ASN
3	5B	1835	GLN
3	5B	1944	HIS
3	5B	1966	HIS
3	5B	1995	ASN
3	5B	1996	ASN
3	5B	2021	GLN
3	5B	2024	GLN
3	5B	2032	GLN
3	5B	2241	ASN
3	5B	2255	HIS
3	5B	2288	HIS
4	5C	140	HIS
4	5C	245	HIS
4	5C	335	ASN
4	5C	538	HIS
4	5C	627	HIS
4	5C	642	HIS
5	5D	715	HIS
5	5D	785	HIS
5	5D	902	ASN
5	5D	911	GLN
5	5D	1002	ASN
5	5D	1288	HIS
5	5D	1515	HIS
5	5D	1553	HIS
5	5D	1655	ASN
5	5D	1667	GLN
5	5D	1690	HIS
5	5D	1733	HIS
5	5D	1784	HIS

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Mol	Chain	Res	Type
5	5D	1896	GLN
5	5D	2003	GLN
23	4B	423	GLN
23	4B	511	HIS
24	4C	282	HIS
24	4C	295	ASN
24	4C	322	HIS
24	4C	479	HIS
25	4D	111	HIS
25	4D	270	HIS
25	4D	376	ASN
26	4E	17	HIS
26	4E	77	ASN
26	4E	87	GLN
27	4F	89	HIS
28	4G	173	ASN
28	4G	308	HIS
28	4G	326	GLN
28	4G	741	HIS
28	4G	773	ASN
28	4G	805	GLN
33	4L	143	HIS
33	4L	153	HIS
44	2H	804	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	62/144 (43%)	37 (59%)	12 (19%)
14	6A	56/107 (52%)	10 (17%)	1 (1%)
2	5A	114/117 (97%)	30 (26%)	5 (4%)
22	4A	124/145 (85%)	33 (26%)	2 (1%)
37	2A	105/188 (55%)	22 (20%)	3 (2%)
All	All	461/701 (65%)	132 (28%)	23 (4%)

All (132) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	U
1	A	9	U
1	A	10	C

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Mol	Chain	Res	Type
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
1	A	100	C
1	A	102	U
1	A	103	A
1	A	106	A
1	A	108	G
1	A	110	G
1	A	111	A
1	A	116	G
1	A	117	G
1	A	118	A
2	5A	8	G
2	5A	10	U
2	5A	17	U
2	5A	21	A
2	5A	22	U
2	5A	24	G
2	5A	25	C
2	5A	26	A

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Mol	Chain	Res	Type
2	5A	28	A
2	5A	35	U
2	5A	36	C
2	5A	40	U
2	5A	45	C
2	5A	52	U
2	5A	68	C
2	5A	69	A
2	5A	78	U
2	5A	79	C
2	5A	80	U
2	5A	83	A
2	5A	88	A
2	5A	89	U
2	5A	90	U
2	5A	92	U
2	5A	93	U
2	5A	94	U
2	5A	95	G
2	5A	96	A
2	5A	97	G
2	5A	109	G
14	6A	36	A
14	6A	46	G
14	6A	47	A
14	6A	48	A
14	6A	49	G
14	6A	51	U
14	6A	77	C
14	6A	78	A
14	6A	103	U
14	6A	104	U
22	4A	2	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	54	A

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Mol	Chain	Res	Type
22	4A	62	U
22	4A	71	U
22	4A	73	U
22	4A	74	C
22	4A	75	C
22	4A	76	C
22	4A	84	C
22	4A	85	G
22	4A	90	G
22	4A	100	A
22	4A	103	A
22	4A	109	G
22	4A	114	U
22	4A	115	G
22	4A	118	A
22	4A	119	A
22	4A	120	U
22	4A	121	U
22	4A	124	U
22	4A	125	G
22	4A	126	A
22	4A	127	C
22	4A	144	G
37	2A	31	G
37	2A	37	U
37	2A	40	C
37	2A	45	C
37	2A	47	U
37	2A	51	A
37	2A	65	U
37	2A	112	G
37	2A	143	A
37	2A	147	G
37	2A	152	G
37	2A	153	A
37	2A	154	C
37	2A	156	U
37	2A	157	G
37	2A	164	C
37	2A	165	A
37	2A	168	A
37	2A	169	C

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Mol	Chain	Res	Type
37	2A	177	A
37	2A	178	A
37	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
1	A	99	C
1	A	116	G
1	A	117	G
2	5A	67	A
2	5A	78	U
2	5A	79	C
2	5A	94	U
2	5A	96	A
14	6A	77	C
22	4A	99	C
22	4A	114	U
37	2A	156	U
37	2A	164	C
37	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

Of 5 ligands modelled in this entry, 3 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
51	GTP	5C	1500	52	33,34,34	0.94	1 (3%)	50,54,54	1.57	8 (16%)
50	IHP	5B	3000	-	36,36,36	0.76	0	60,60,60	1.20	3 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
51	GTP	5C	1500	52	-	8/22/38/38	0/3/3/3
50	IHP	5B	3000	-	-	2/30/54/54	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	5C	1500	GTP	C2-N3	2.19	1.38	1.33

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	5C	1500	GTP	C5-C4-N3	-5.07	120.32	128.39
51	5C	1500	GTP	C2-N3-C4	4.69	120.38	112.30
51	5C	1500	GTP	N9-C4-N3	3.13	132.22	125.95
51	5C	1500	GTP	C2-N1-C6	-2.97	119.73	125.11
51	5C	1500	GTP	N9-C8-N7	-2.67	108.45	113.40
51	5C	1500	GTP	C8-N7-C5	2.59	108.87	104.26
51	5C	1500	GTP	C5-C6-N1	2.54	119.73	113.25
50	5B	3000	IHP	C5-C4-C3	2.46	115.82	110.43
51	5C	1500	GTP	O6-C6-C5	-2.37	120.28	126.53
50	5B	3000	IHP	C6-C5-C4	2.24	115.35	110.43

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	5B	3000	IHP	P5-O15-C5	-2.05	117.95	123.43

There are no chirality outliers.

All (10) torsion outliers are listed below:

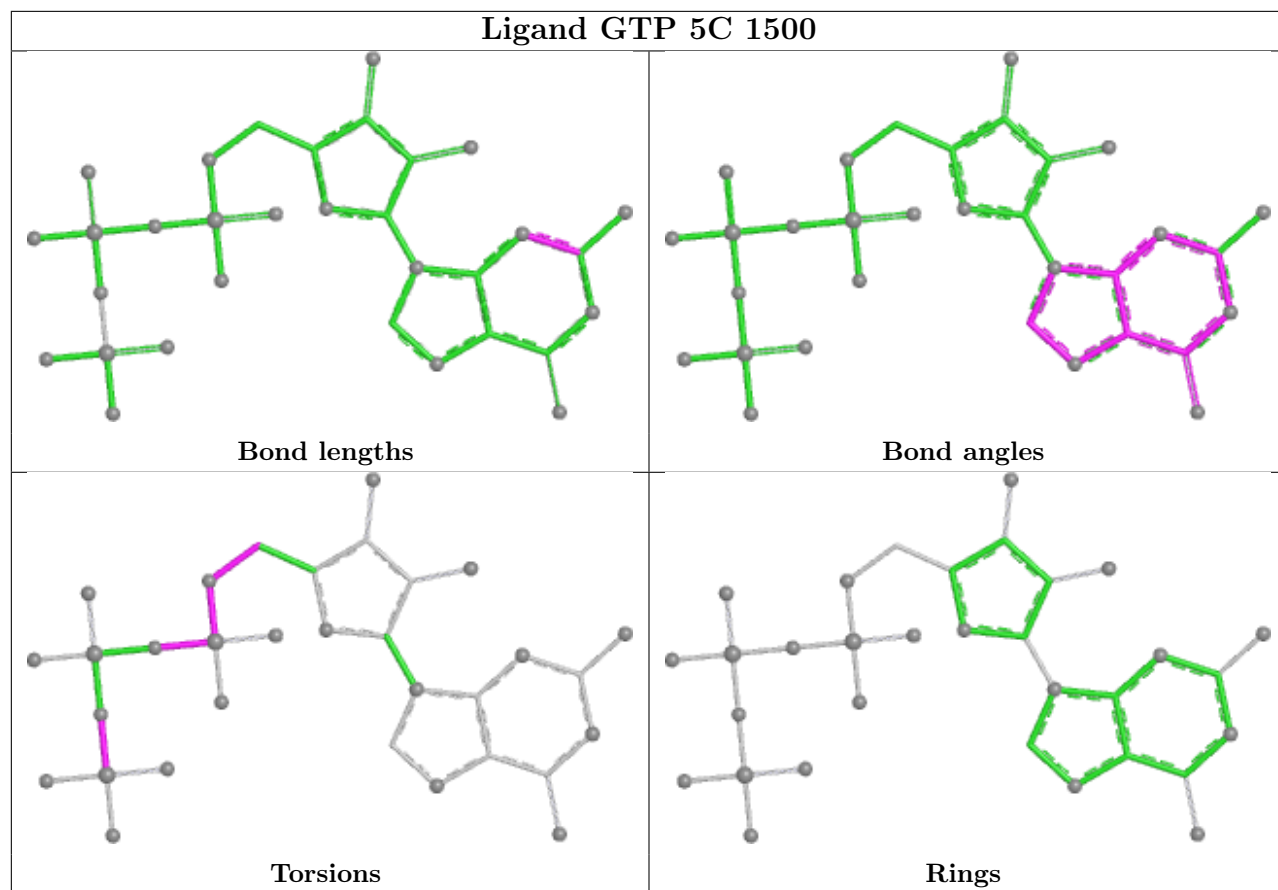
Mol	Chain	Res	Type	Atoms
51	5C	1500	GTP	C5'-O5'-PA-O3A
51	5C	1500	GTP	C5'-O5'-PA-O1A
51	5C	1500	GTP	C5'-O5'-PA-O2A
51	5C	1500	GTP	PB-O3A-PA-O5'
50	5B	3000	IHP	C4-O14-P4-O44
51	5C	1500	GTP	C4'-C5'-O5'-PA
51	5C	1500	GTP	PB-O3B-PG-O1G
51	5C	1500	GTP	PB-O3B-PG-O2G
51	5C	1500	GTP	PB-O3B-PG-O3G
50	5B	3000	IHP	C3-O13-P3-O43

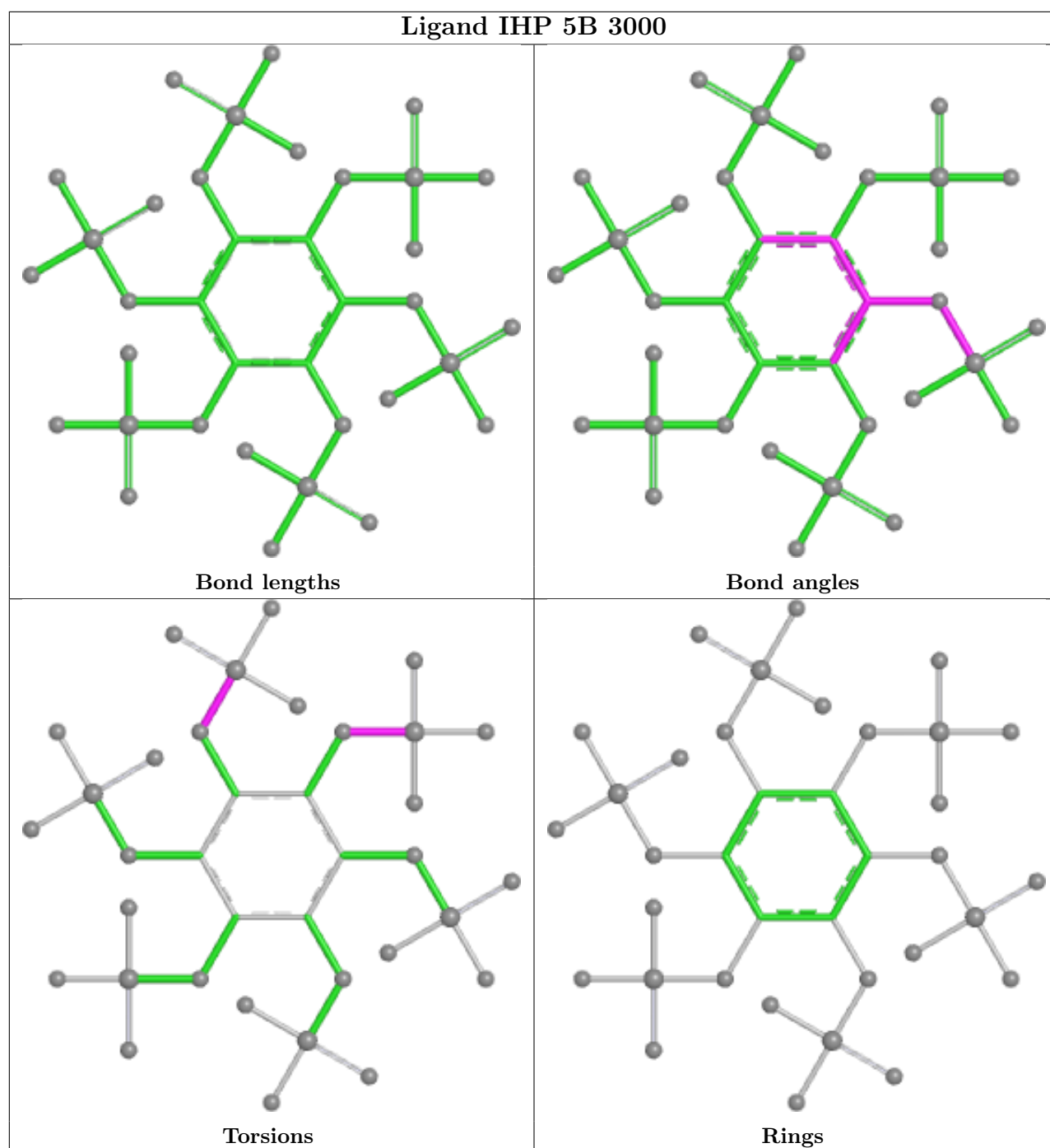
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
51	5C	1500	GTP	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.





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.

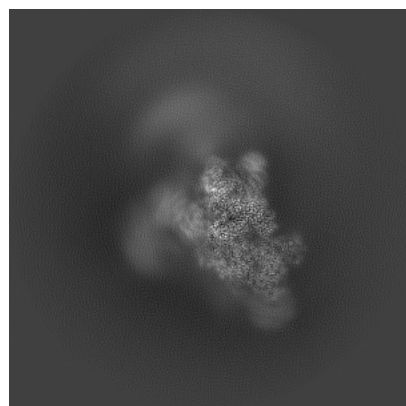
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34507. These allow visual inspection of the internal detail of the map and identification of artifacts.

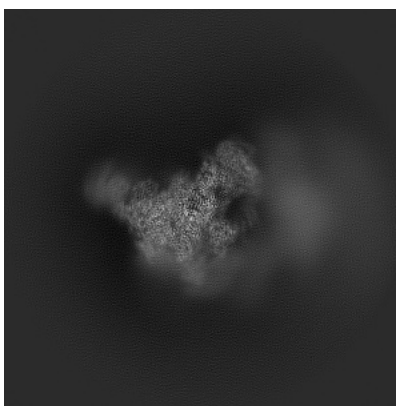
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

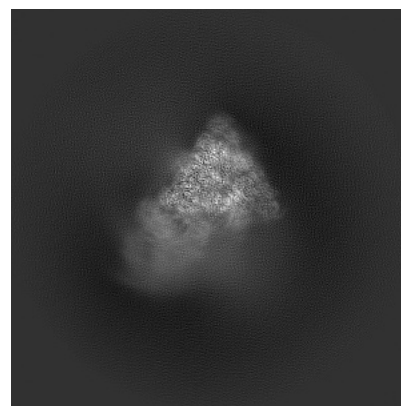
6.1.1 Primary map



X

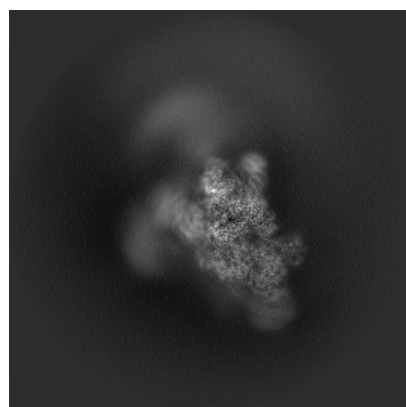


Y

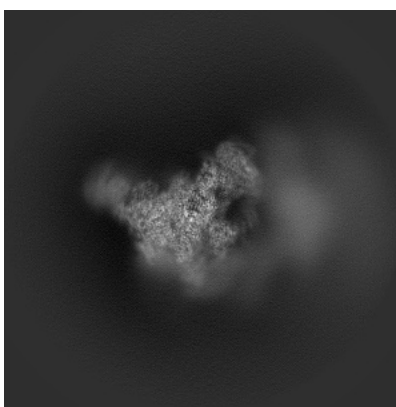


Z

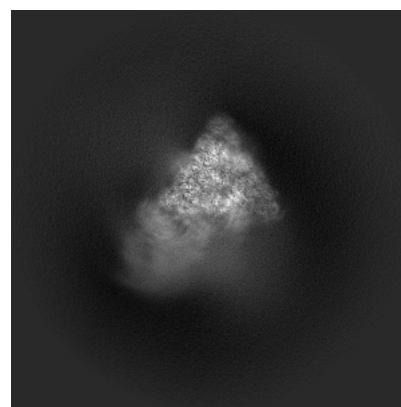
6.1.2 Raw map



X



Y

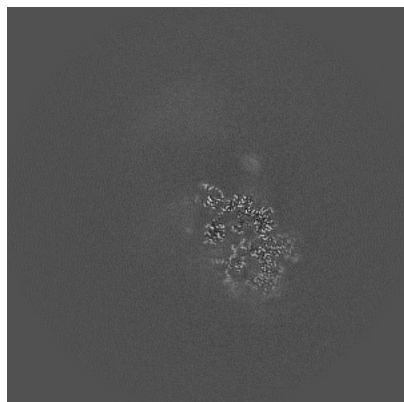


Z

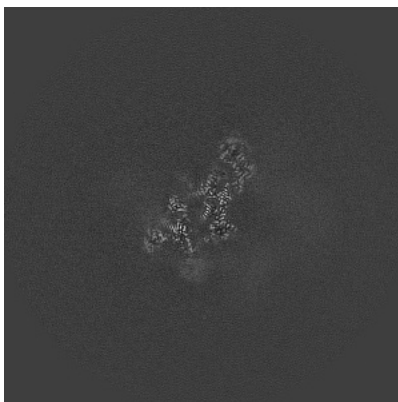
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

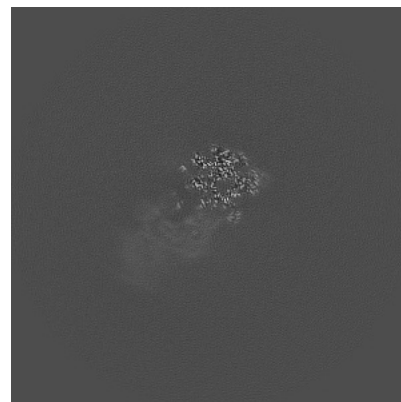
6.2.1 Primary map



X Index: 256

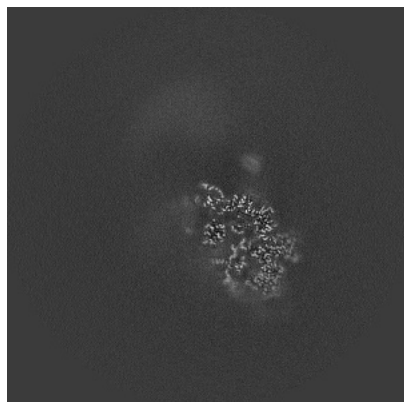


Y Index: 256

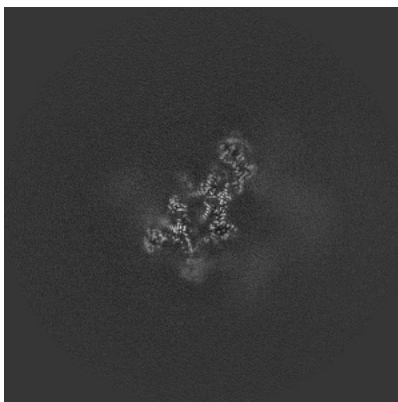


Z Index: 256

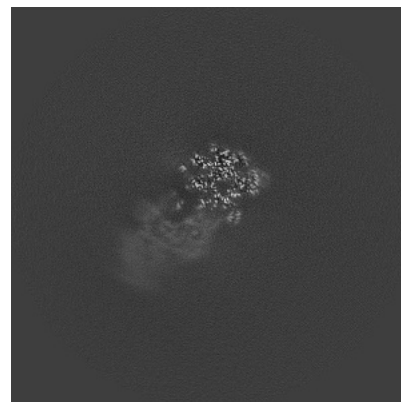
6.2.2 Raw map



X Index: 256



Y Index: 256

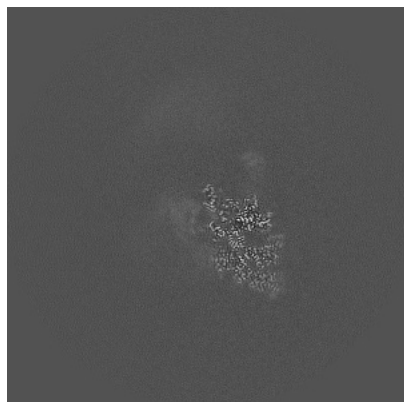


Z Index: 256

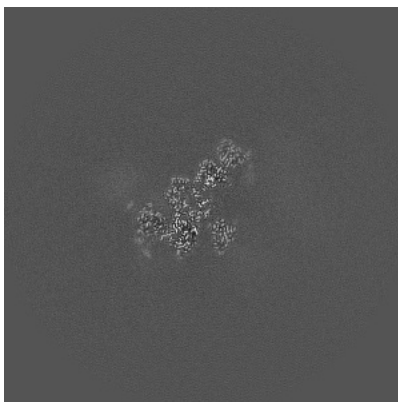
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

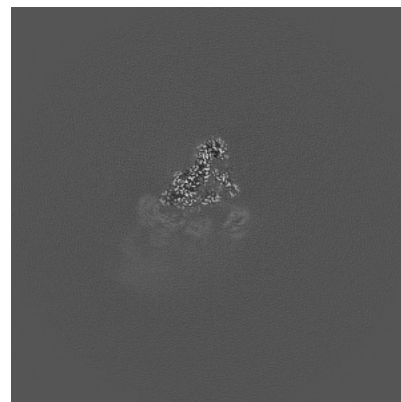
6.3.1 Primary map



X Index: 245

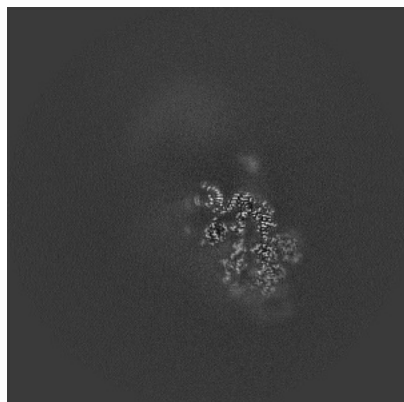


Y Index: 277

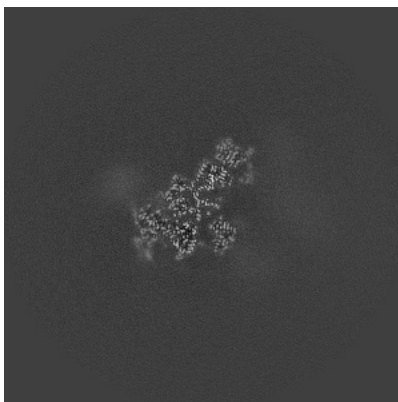


Z Index: 234

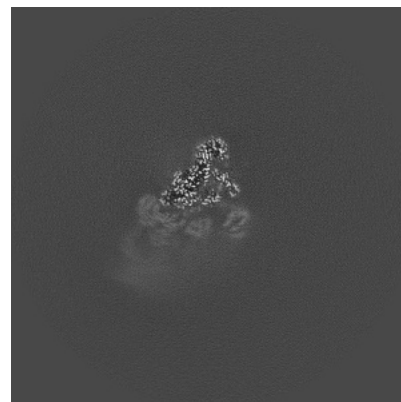
6.3.2 Raw map



X Index: 259



Y Index: 274

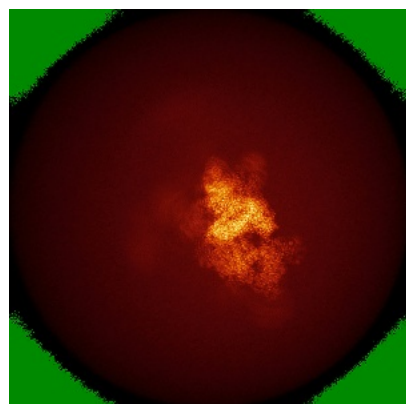


Z Index: 234

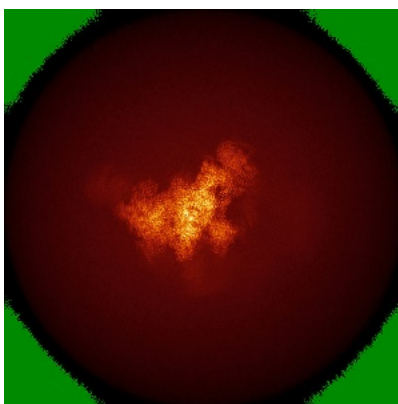
The images above show the largest variance slices of the map in three orthogonal directions.

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

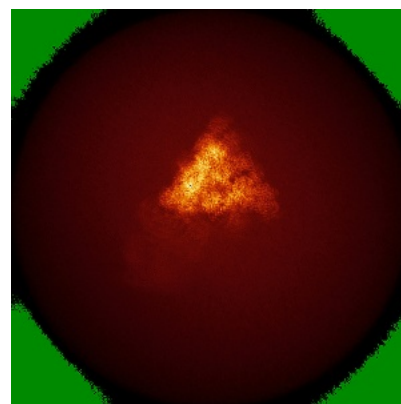
6.4.1 Primary map



X

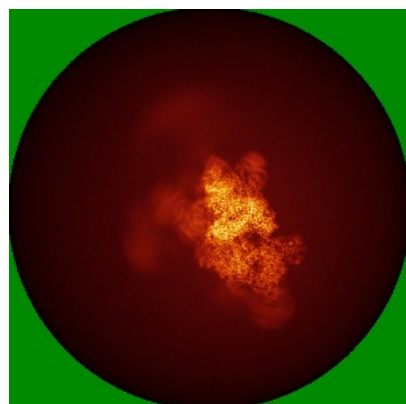


Y

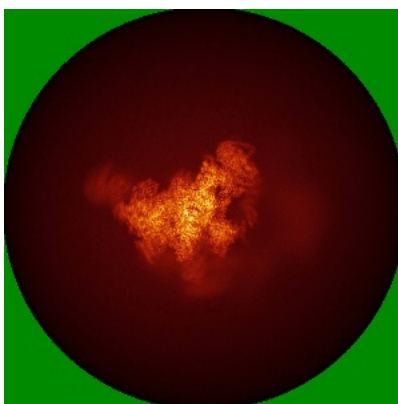


Z

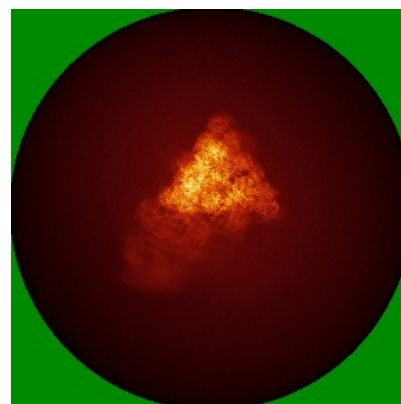
6.4.2 Raw map



X



Y

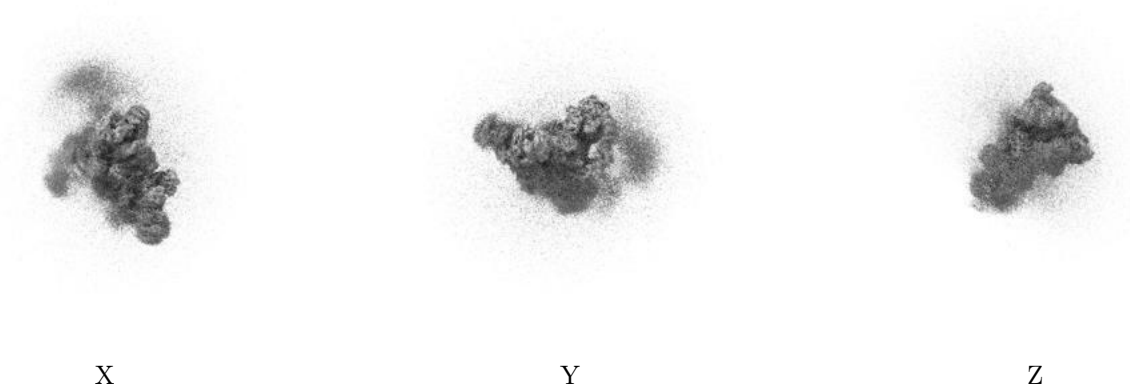


Z

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.

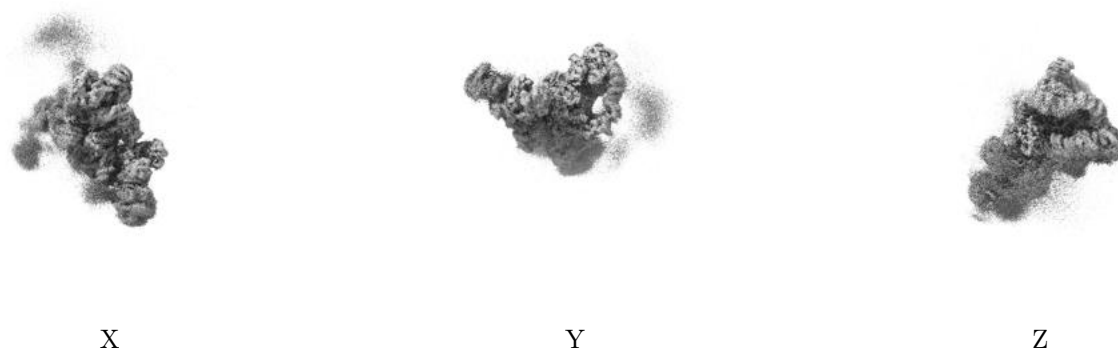
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

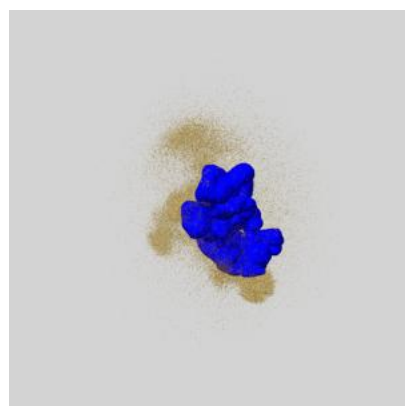
6.6 Mask visualisation [i](#)

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

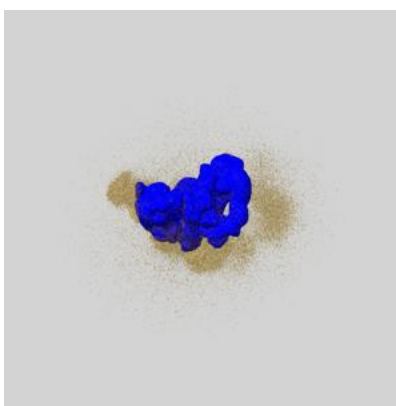
A mask typically either:

- 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_34507_msk_1.map [i](#)



X



Y

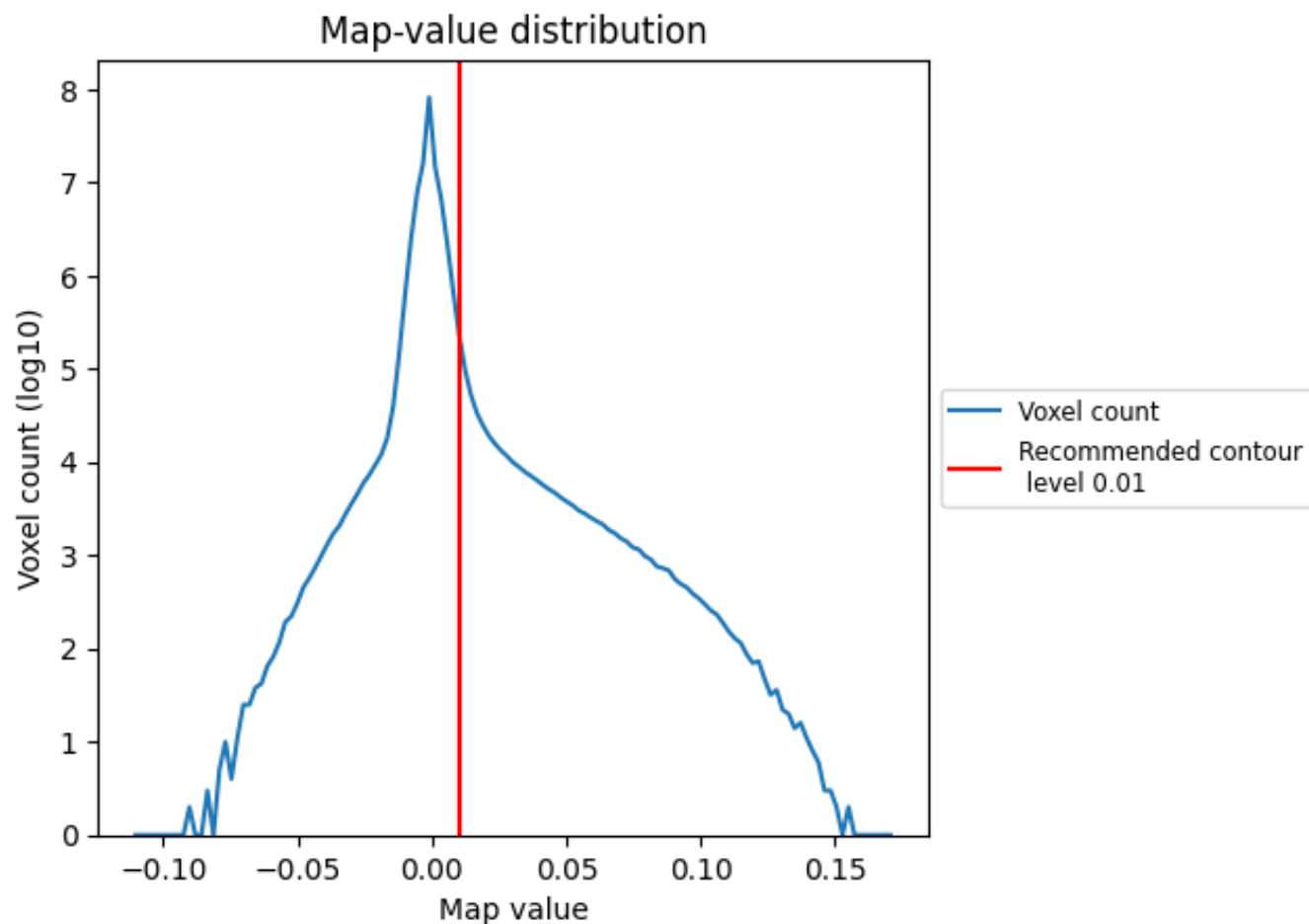


Z

7 Map analysis [i](#)

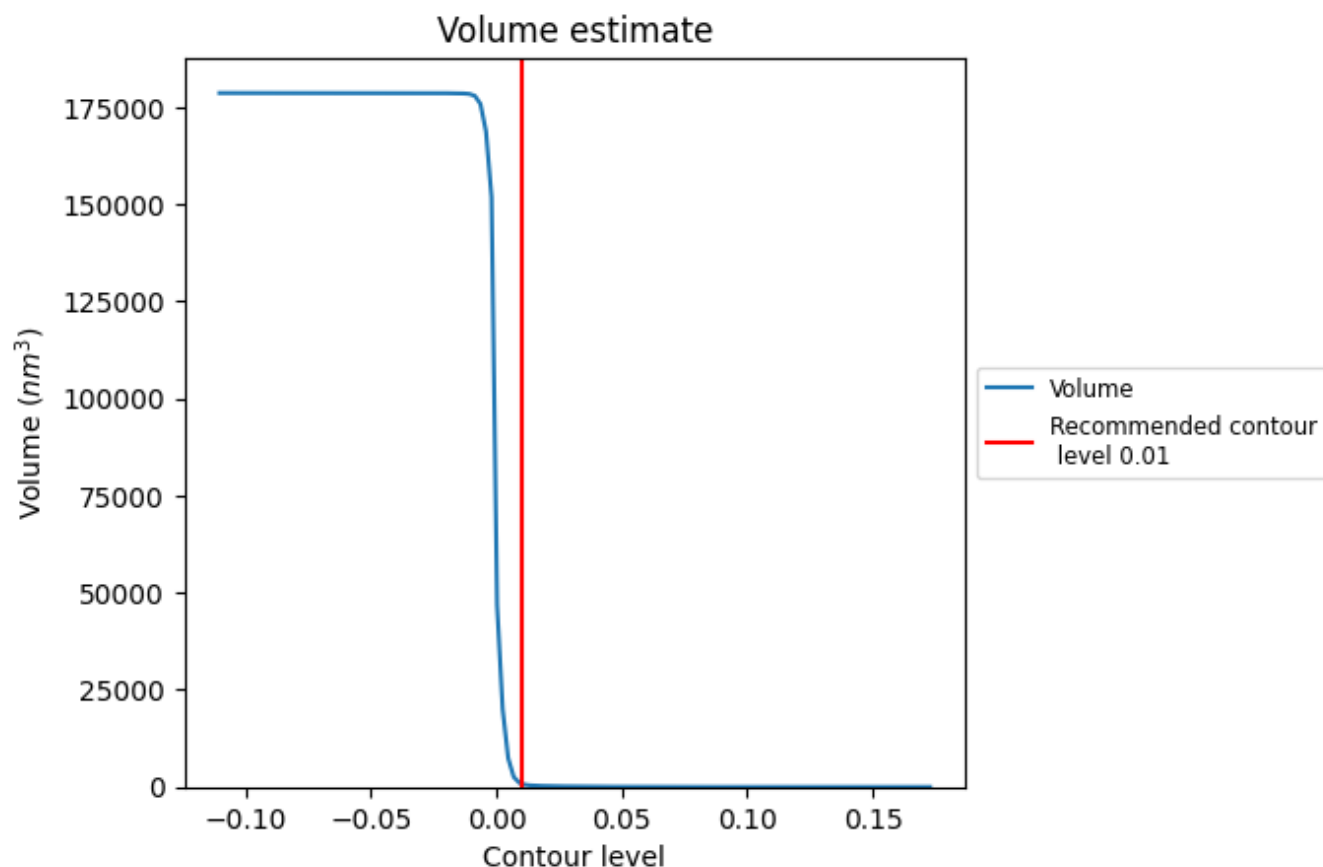
This section contains the results of statistical analysis of the map.

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.

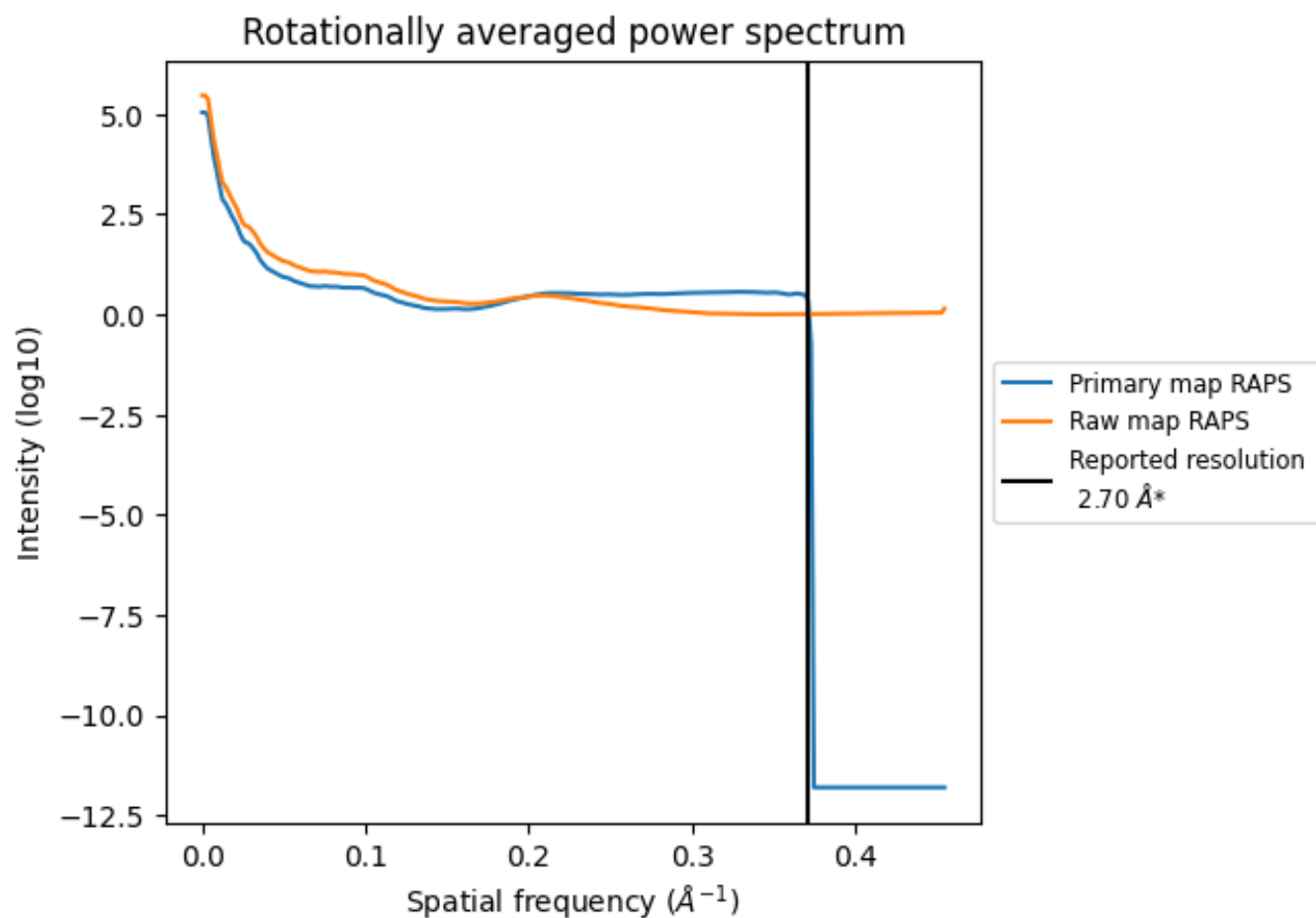
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 875 nm^3 ; this corresponds to an approximate mass of 791 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 ⓘ

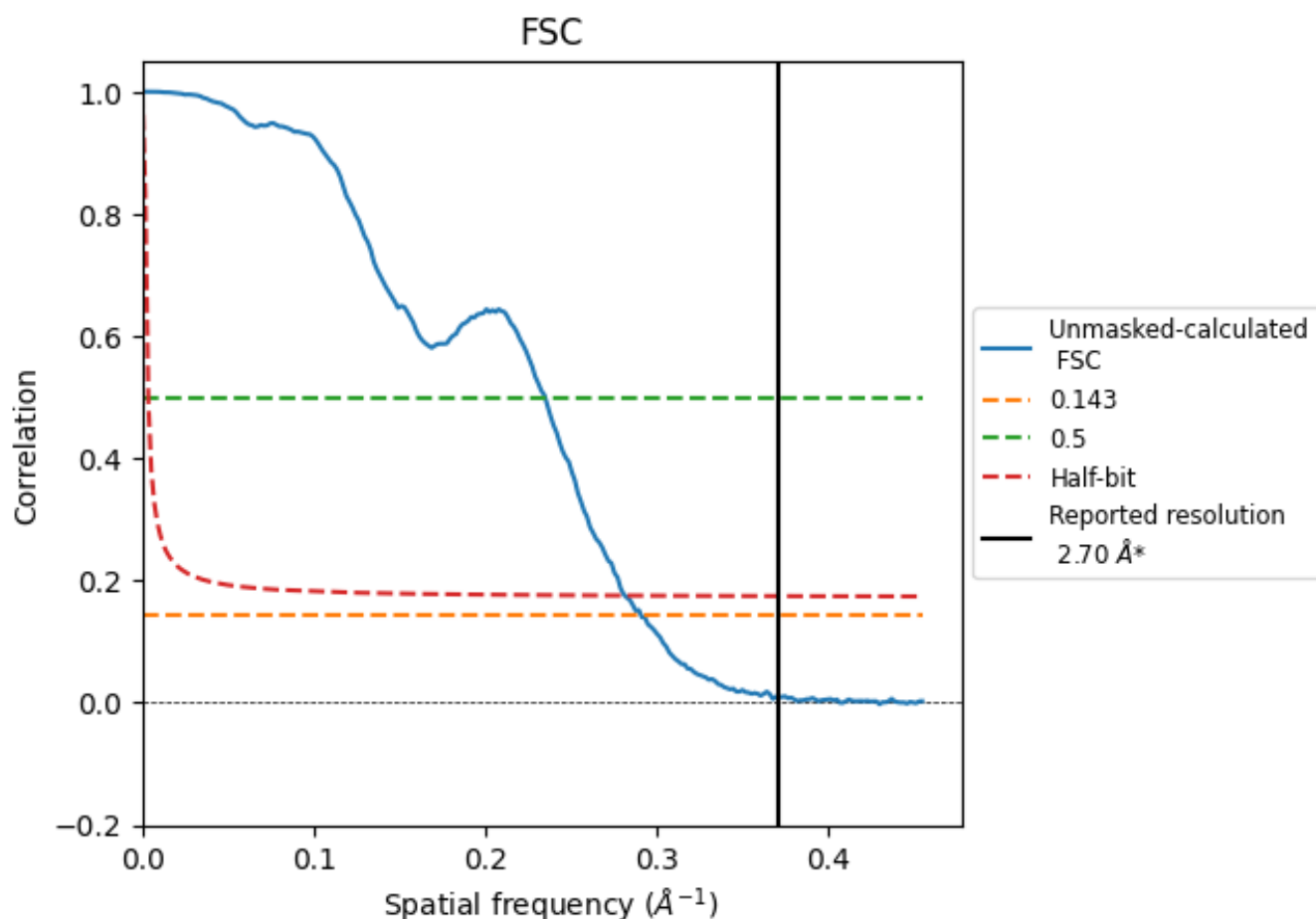


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

8.2 Resolution estimates [i](#)

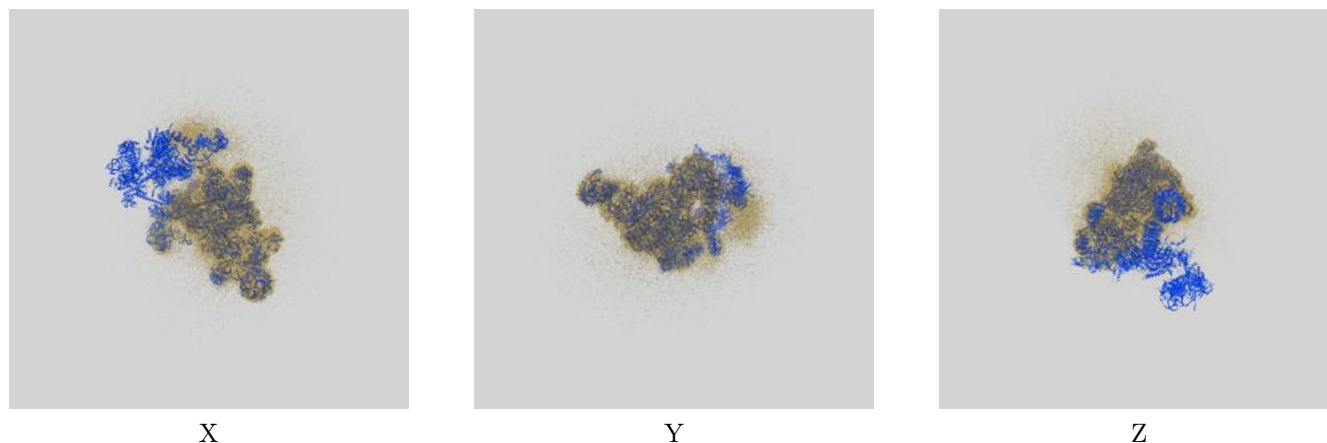
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.44	4.26	3.55

*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 3.44 differs from the reported value 2.7 by more than 10 %

9 Map-model fit [i](#)

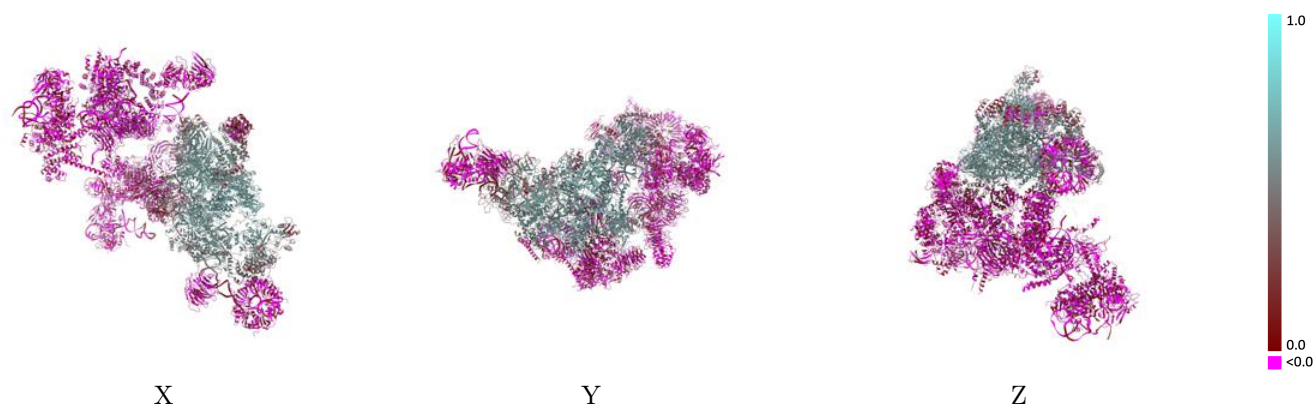
This section contains information regarding the fit between EMDB map EMD-34507 and PDB model 8H6K. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



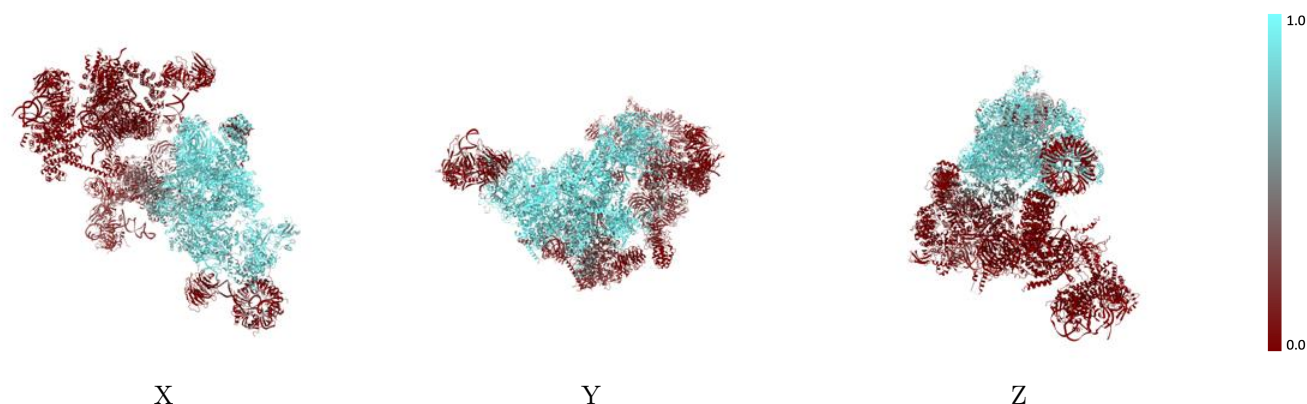
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



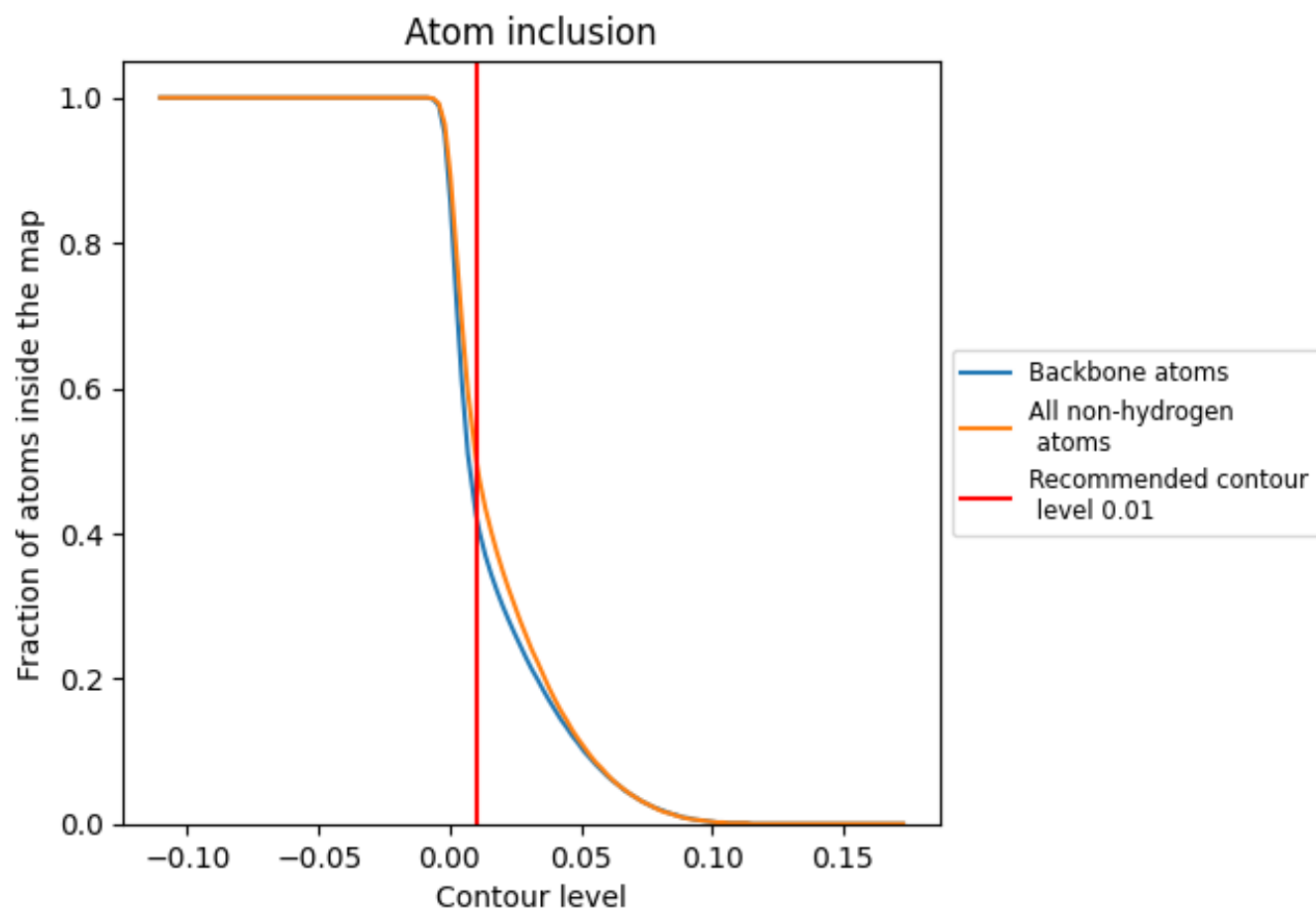
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 43% of all backbone atoms, 50% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5030	 0.2790
2A	 0.0020	 -0.0150
2B	 0.0000	 0.0460
2C	 0.0000	 0.0250
2D	 0.4950	 0.2890
2E	 0.0000	 0.0250
2F	 0.0000	 0.0160
2G	 0.0020	 0.0060
2H	 0.2270	 0.1180
2I	 0.0000	 0.0020
2J	 0.0030	 0.0230
2K	 0.0000	 -0.0020
2L	 0.0000	 -0.0190
2M	 0.0000	 -0.0220
2a	 0.0000	 -0.0370
2b	 0.0000	 -0.0030
2c	 0.0000	 -0.0640
2d	 0.0000	 0.0100
2e	 0.0000	 -0.0200
2f	 0.0000	 0.0370
2g	 0.0000	 0.0170
4A	 0.5220	 0.3060
4B	 0.9070	 0.5190
4C	 0.9190	 0.5180
4D	 0.9380	 0.5700
4E	 0.9780	 0.6280
4F	 0.9790	 0.6330
4G	 0.8120	 0.4270
4H	 0.8040	 0.2910
4I	 0.7400	 0.3700
4J	 0.8570	 0.5110
4K	 0.6850	 0.3810
4L	 0.9440	 0.5510
4M	 0.9900	 0.6420
4N	 0.7960	 0.4350



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Chain	Atom inclusion	Q-score
4Z	 0.0240	 0.0010
4a	 0.0120	 -0.0050
4b	 0.0180	 -0.0060
4c	 0.0130	 -0.0090
4d	 0.0410	 0.0560
4e	 0.0480	 0.0060
4f	 0.0270	 -0.0200
4g	 0.0380	 -0.0290
5A	 0.5990	 0.3000
5B	 0.8960	 0.5420
5C	 0.8770	 0.4650
5D	 0.1830	 0.0350
5E	 0.0320	 -0.0090
5a	 0.1370	 0.0100
5b	 0.0730	 0.0010
5c	 0.1080	 0.0050
5d	 0.1010	 0.0190
5e	 0.0730	 -0.0220
5f	 0.1250	 0.0070
5g	 0.1720	 -0.0110
6A	 0.7020	 0.4220
6a	 0.0080	 0.0260
6b	 0.0000	 -0.0270
6c	 0.0000	 -0.0050
6d	 0.0000	 -0.0560
6e	 0.0110	 0.0270
6f	 0.0000	 0.0110
6g	 0.0000	 -0.0170
A	 0.3350	 0.1550