



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 10:43 PM UTC

PDB ID : 7JQB / pdb_00007jqb
EMDB ID : EMD-22432
Title : SARS-CoV-2 Nsp1 and rabbit 40S ribosome complex
Authors : Yuan, S.; Xiong, Y.
Deposited on : 2020-08-10
Resolution : 2.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

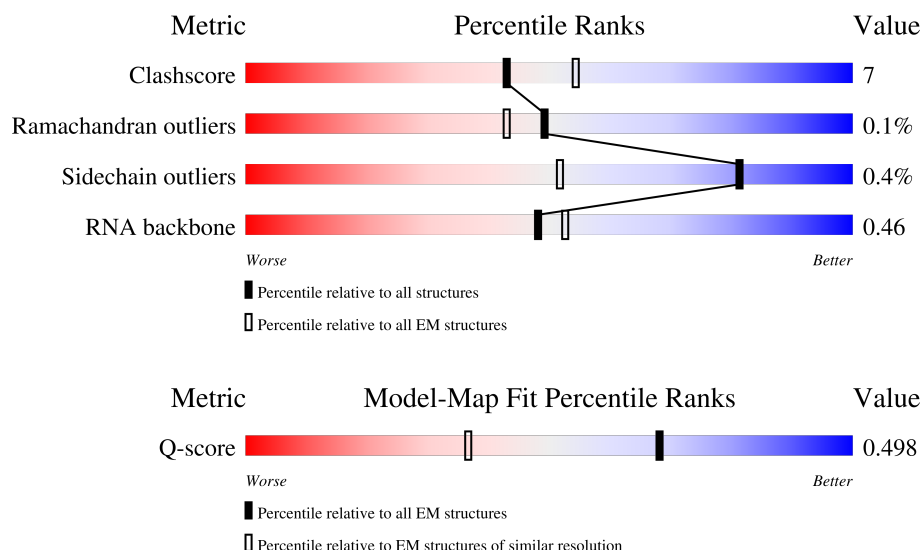
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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.



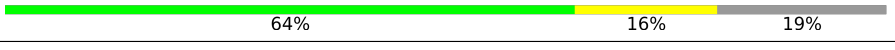
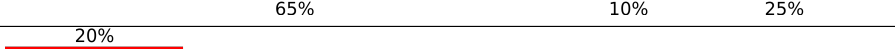
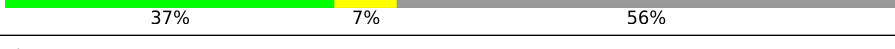
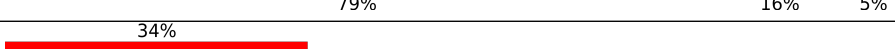
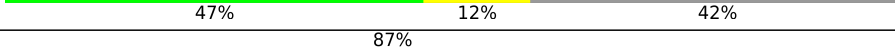
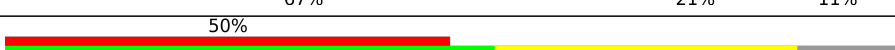
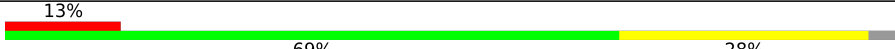
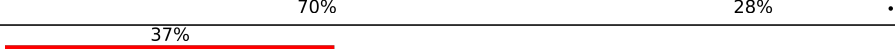
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10327 (2.20 - 3.20)

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	1869	
2	a	125	
3	B	295	

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Mol	Chain	Length	Quality of chain
4	b	115	
5	C	264	
6	D	293	
7	d	69	
8	E	243	
9	f	133	
10	G	204	
11	g	156	
12	H	249	
13	h	317	
14	I	194	
15	J	208	
16	K	194	
17	L	165	
18	N	132	
19	Q	145	
20	R	146	
21	S	135	
22	T	152	
23	U	145	
24	V	119	
25	W	83	
26	Z	130	
27	F	36	
28	M	263	

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Mol	Chain	Length	Quality of chain
29	O	158	15% 86% 13%
30	P	151	84% 15%
31	X	168	64% 17% 19%
32	Y	130	85% 14%
33	c	143	85% 15%
34	e	84	5% 87% 12%

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 74976 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 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 2 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	a	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 3 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	114	THR	ALA	conflict	UNP G1TLT8

- Molecule 4 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	b	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	28	ARG	CYS	conflict	UNP G1TFE8
b	56	ALA	VAL	conflict	UNP G1TFE8
b	109	ARG	PRO	conflict	UNP G1TFE8

- Molecule 5 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 6 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 7 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	d	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 8 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 9 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	f	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 10 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 11 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	g	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 12 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 13 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	h	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 14 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 15 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 16 is a protein called uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 17 is a protein called S10_pectin domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 18 is a protein called eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 19 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	129	Total	C	N	O	S	0	0
			1058	670	201	180	7		

- Molecule 20 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 21 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 22 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 23 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 24 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 25 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	3	ASN	SER	conflict	UNP G1TM82
W	4	ASP	ASN	conflict	UNP G1TM82
W	33	GLN	PRO	conflict	UNP G1TM82
W	50	PHE	SER	conflict	UNP G1TM82
W	75	ALA	SER	conflict	UNP G1TM82
W	76	ASP	HIS	conflict	UNP G1TM82
W	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 26 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 27 is a protein called Host translation inhibitor nsp1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	F	36	Total	C	N	O	S	0	0
			280	171	50	58	1		

- Molecule 28 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	M	263	Total	C	N	O	S	0	0
			2083	1329	385	359	10		

- Molecule 29 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	O	158	Total	C	N	O	S	0	0
			1296	827	241	221	7		

- Molecule 30 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	P	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 31 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	X	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 32 is a protein called uS8.

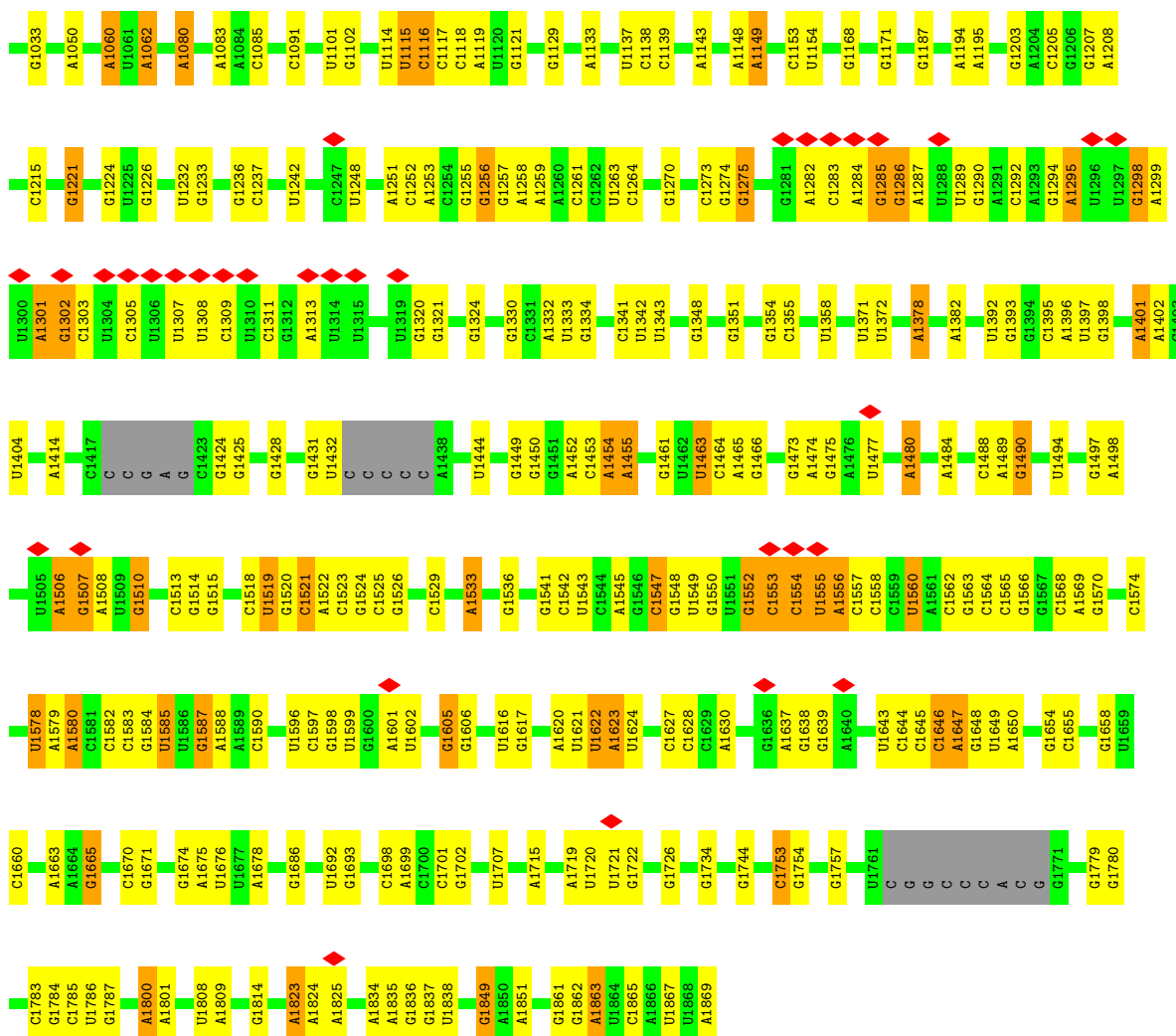
Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 33 is a protein called Uncharacterized protein.

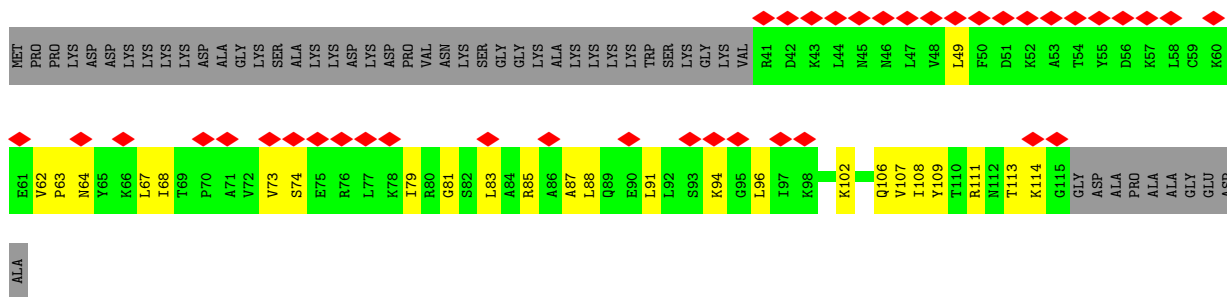
Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	142	Total	C	N	O	S	0	0
			1106	698	220	184	4		

- Molecule 34 is a protein called eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	e	84	Total	C	N	O	S	0	0
			659	413	122	116	8		



• Molecule 2: eS25



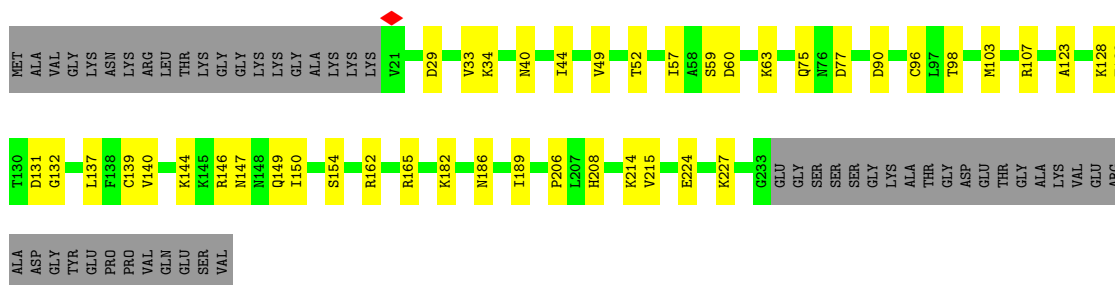
• Molecule 3: 40S ribosomal protein SA



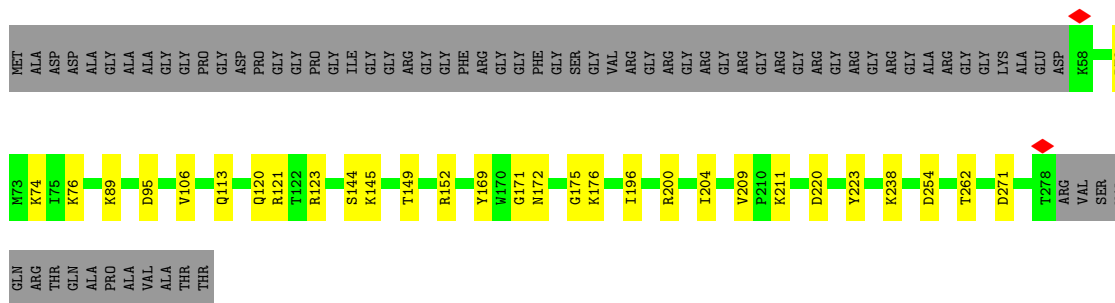
- Molecule 4: 40S ribosomal protein S26



- Molecule 5: eS1



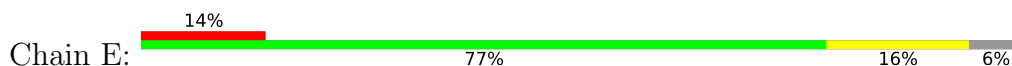
- Molecule 6: uS5

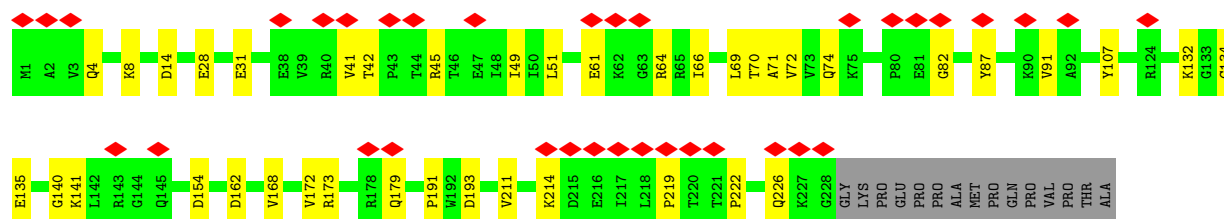


- Molecule 7: eS28

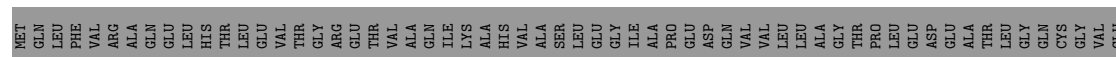
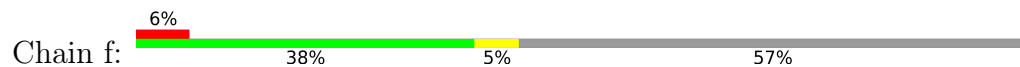


- Molecule 8: Ribosomal protein S3

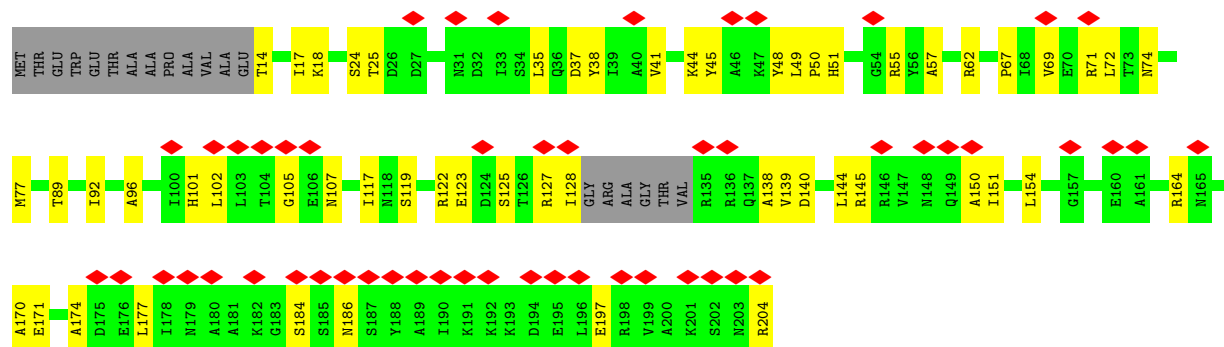




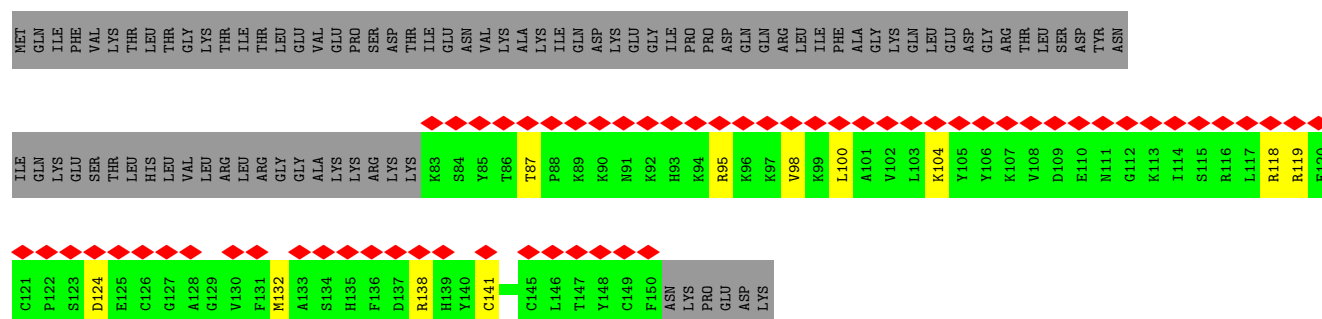
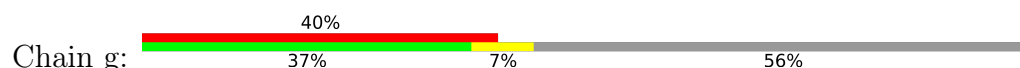
• Molecule 9: eS30



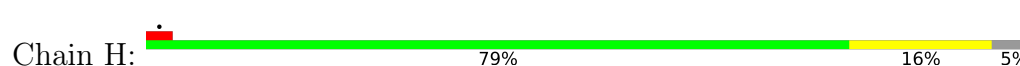
• Molecule 10: uS7

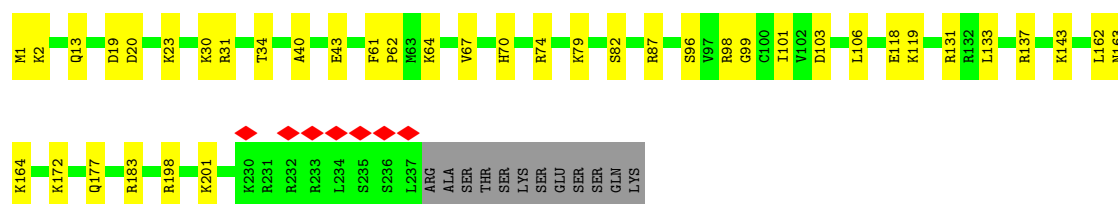


• Molecule 11: eS31

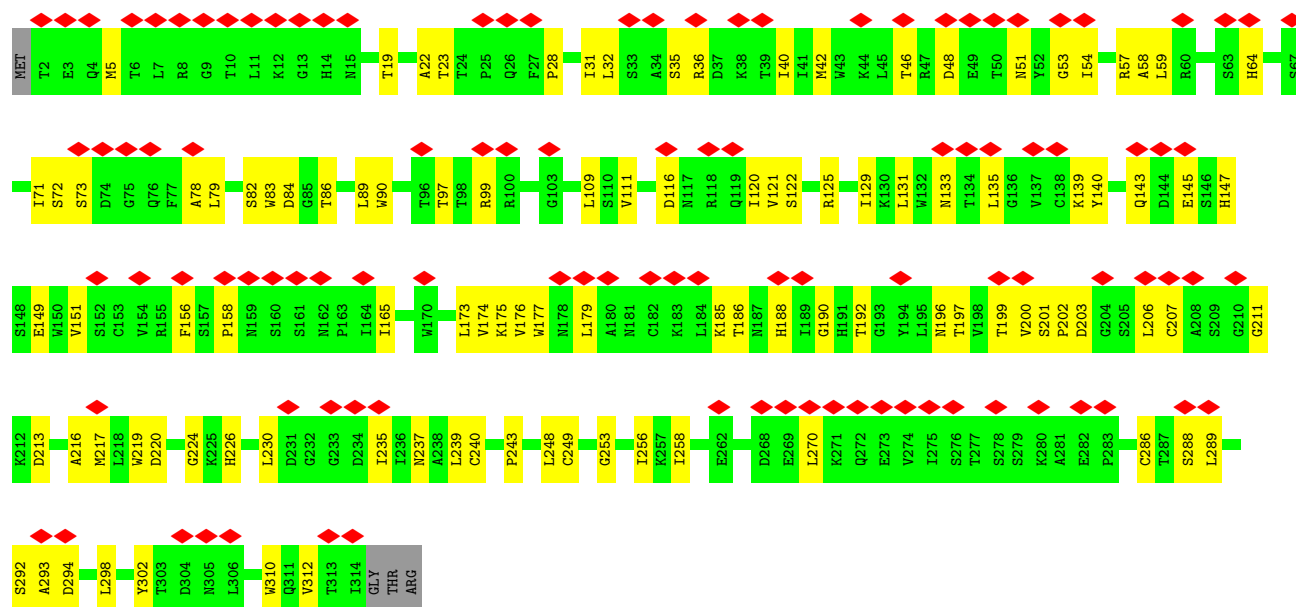


• Molecule 12: eS6

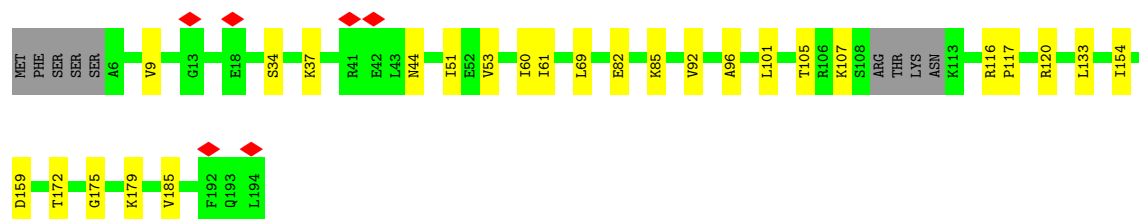
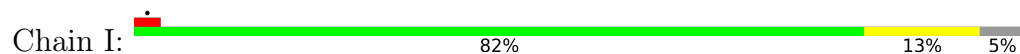




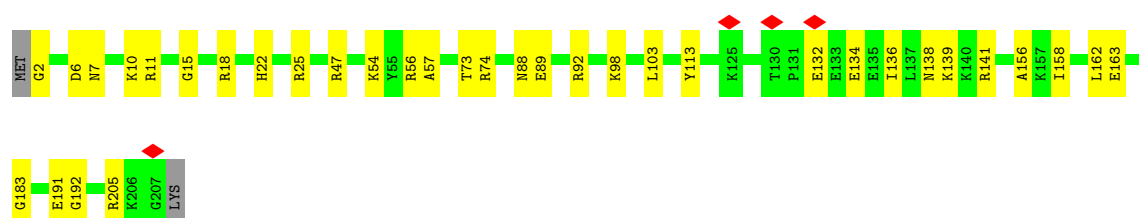
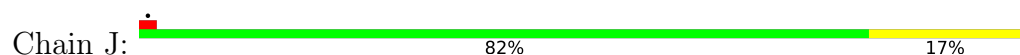
• Molecule 13: RACK1



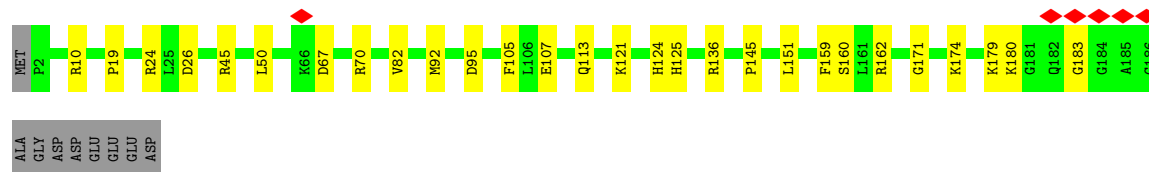
• Molecule 14: eS7



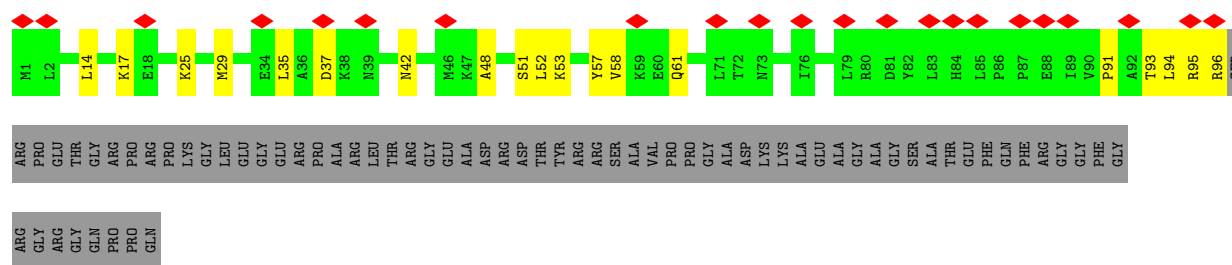
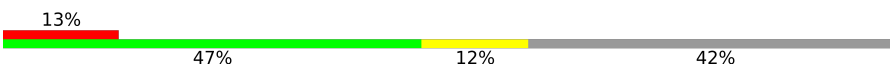
• Molecule 15: eS8



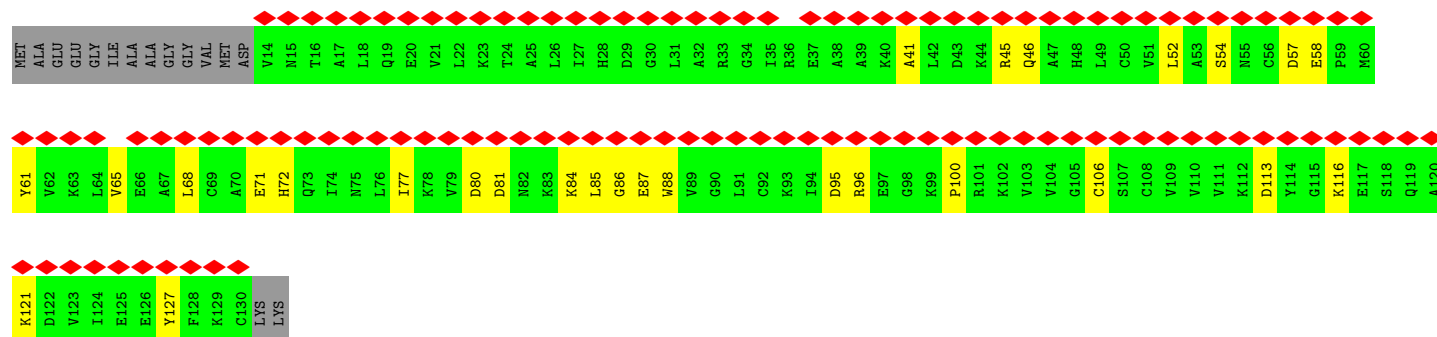
• Molecule 16: uS4

Chain K: 

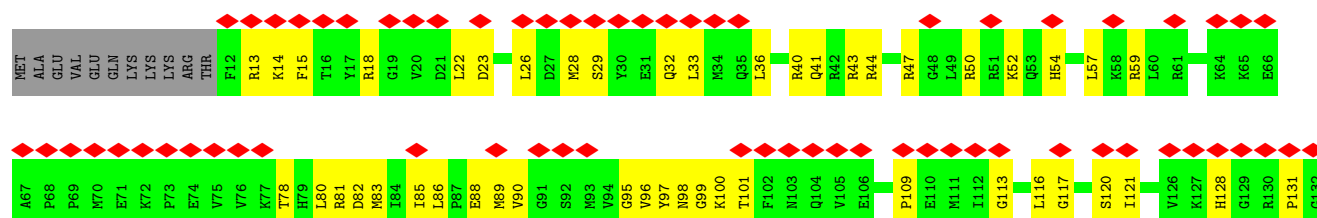
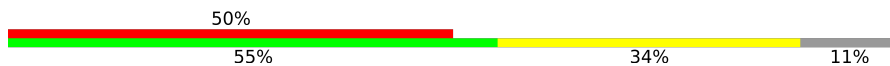
• Molecule 17: S10_plectin domain-containing protein

Chain L: 

• Molecule 18: eS12

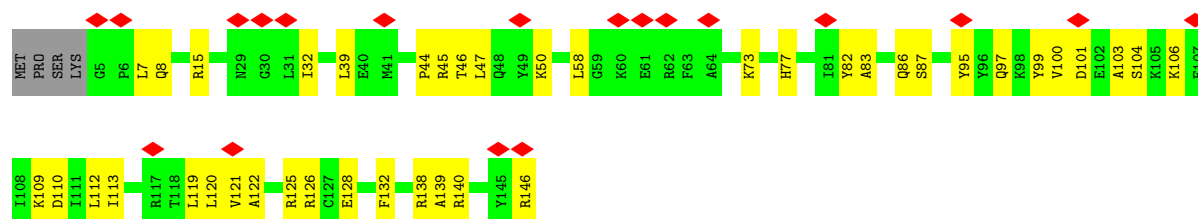
Chain N: 

• Molecule 19: uS19

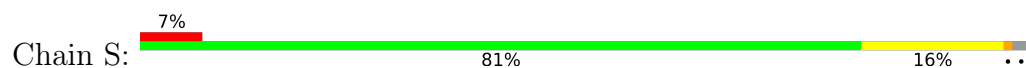
Chain Q: 



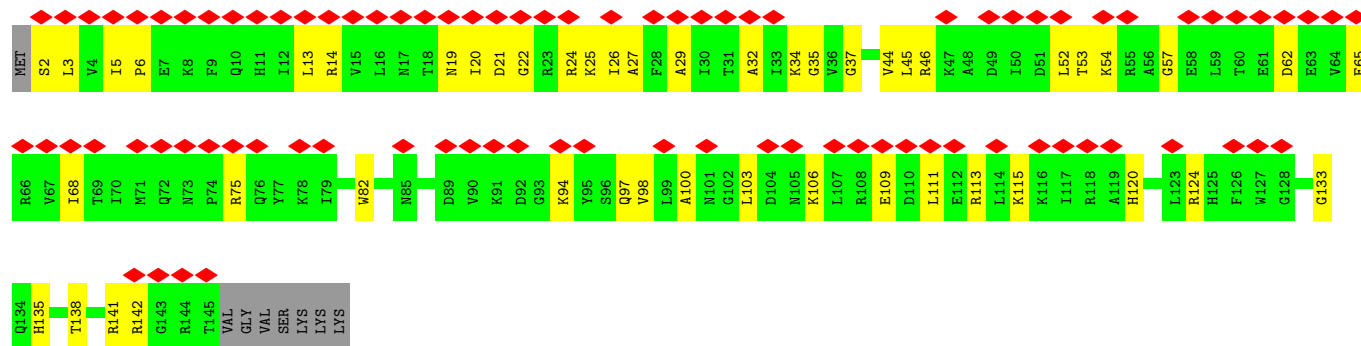
- Molecule 20: Uncharacterized protein



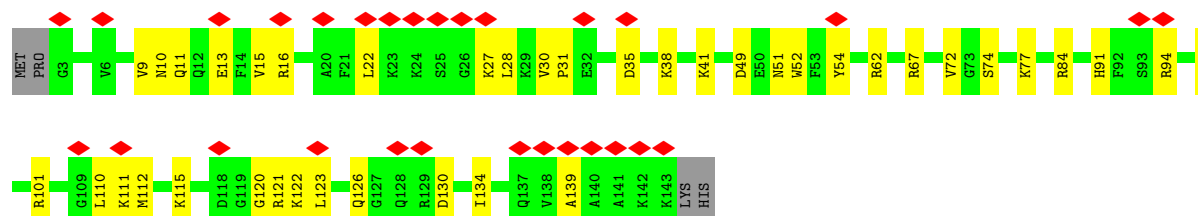
- Molecule 21: eS17



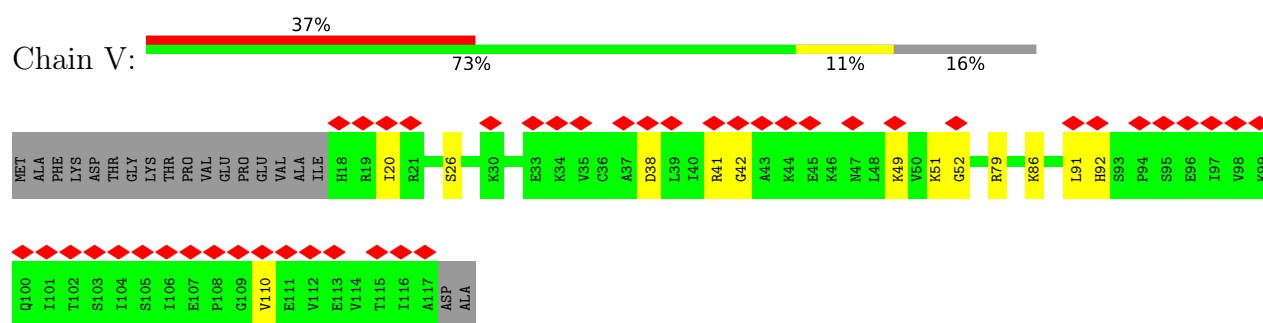
- Molecule 22: uS13



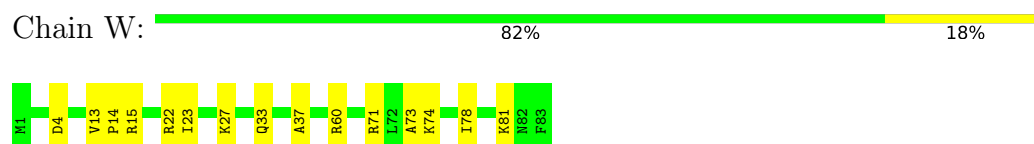
- Molecule 23: Uncharacterized protein



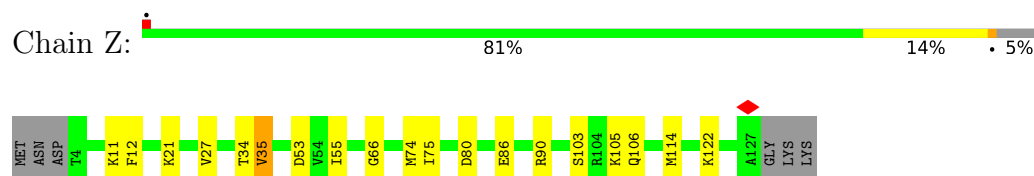
- Molecule 24: uS10



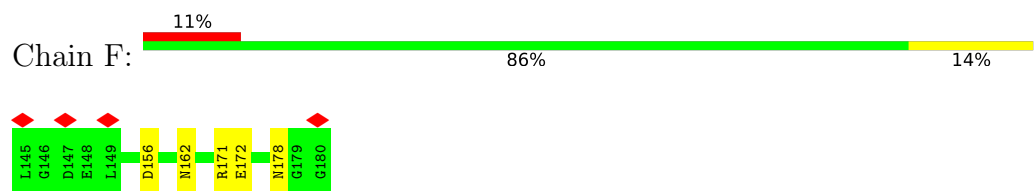
- Molecule 25: 40S ribosomal protein S21



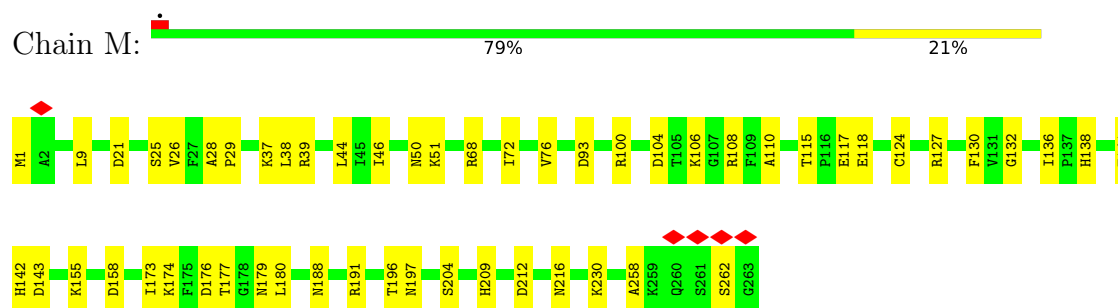
- Molecule 26: 40S ribosomal protein S24



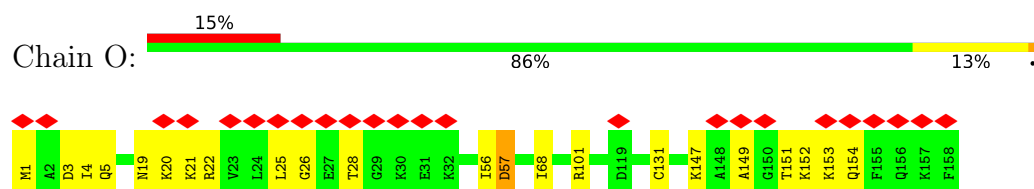
- Molecule 27: Host translation inhibitor nsp1



- Molecule 28: 40S ribosomal protein S4

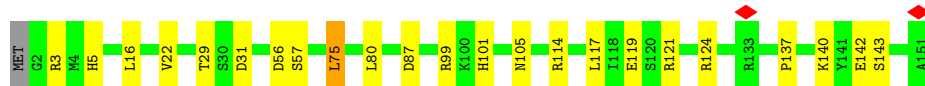


- Molecule 29: uS17



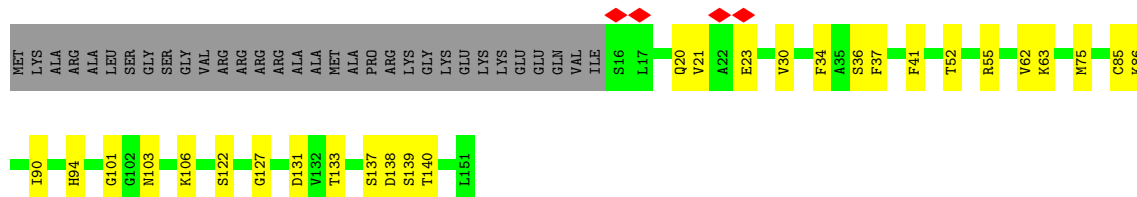
- Molecule 30: uS15

Chain P: 



- Molecule 31: Uncharacterized protein

Chain X: 



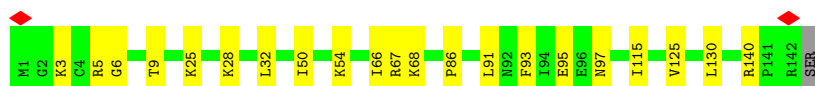
- Molecule 32: uS8

Chain Y: 



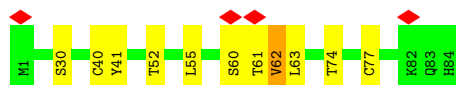
- Molecule 33: Uncharacterized protein

Chain c: 



- Molecule 34: eS27

Chain e: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	353927	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	5.392	Depositor
Minimum map value	-2.806	Depositor
Average map value	0.013	Depositor
Map value standard deviation	0.131	Depositor
Recommended contour level	0.35	Depositor
Map size ($\text{\AA}$)	341.75998, 341.75998, 341.75998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.068, 1.068, 1.068	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.39	0/40509	0.37	5/63128 (0.0%)
2	a	0.23	0/604	0.61	0/810
3	B	0.37	0/1747	0.44	0/2374
4	b	0.41	0/828	0.54	0/1109
5	C	0.35	0/1756	0.47	0/2350
6	D	0.41	0/1753	0.46	0/2369
7	d	0.18	0/490	0.42	0/656
8	E	0.27	1/1796 (0.1%)	0.48	0/2417
9	f	0.33	0/462	0.44	0/607
10	G	0.20	0/1492	0.48	0/2005
11	g	0.19	0/567	0.51	0/753
12	H	0.30	0/1946	0.45	0/2590
13	h	0.20	0/2493	0.48	0/3394
14	I	0.31	0/1510	0.51	0/2022
15	J	0.38	0/1715	0.47	0/2287
16	K	0.40	0/1550	0.46	0/2069
17	L	0.19	0/834	0.45	0/1125
18	N	0.23	0/918	0.63	0/1233
19	Q	0.19	0/1079	0.50	0/1441
20	R	0.22	0/1146	0.53	0/1534
21	S	0.25	0/1082	0.47	0/1452
22	T	0.23	0/1208	0.59	0/1618
23	U	0.19	0/1115	0.44	0/1493
24	V	0.19	0/805	0.46	0/1081
25	W	0.37	0/643	0.44	0/860
26	Z	0.38	0/1028	0.49	0/1366
27	F	0.33	0/285	0.44	0/384
28	M	0.42	0/2125	0.58	0/2856
29	O	0.42	0/1319	0.68	3/1761 (0.2%)
30	P	0.39	0/1232	0.58	3/1656 (0.2%)
31	X	0.36	0/1029	0.77	1/1380 (0.1%)
32	Y	0.48	0/1051	0.55	0/1406
33	c	0.42	0/1124	0.62	0/1500
34	e	0.38	0/673	0.62	0/902

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.36	1/79914 (0.0%)	0.45	12/115988 (0.0%)

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	B	0	1
5	C	0	1
8	E	0	1
28	M	0	1
29	O	0	2
30	P	0	1
31	X	0	3
33	c	0	1
34	e	0	2
All	All	0	13

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	E	162	ASP	C-N	5.13	1.39	1.34

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	P	22	VAL	C-N-CD	-5.51	108.48	120.60
29	O	26	GLY	CA-C-N	5.33	131.30	121.70
29	O	26	GLY	C-N-CA	5.33	131.30	121.70
1	A	688	U	P-O3'-C3'	5.27	128.10	120.20
1	A	688	U	C2'-C3'-O3'	5.16	117.24	109.50
31	X	138	ASP	N-CA-C	5.13	117.53	110.35
30	P	22	VAL	CA-C-N	5.12	139.29	127.00
30	P	22	VAL	C-N-CA	5.12	139.29	127.00
1	A	110	U	C2'-C3'-O3'	5.09	121.33	113.70
29	O	57	ASP	N-CA-C	5.09	117.38	111.02
1	A	627	U	P-O3'-C3'	5.05	127.77	120.20
1	A	752	G	P-O3'-C3'	5.00	127.70	120.20

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	43	SER	Peptide
5	C	189	ILE	Peptide
8	E	41	VAL	Peptide
28	M	204	SER	Peptide
29	O	147	LYS	Peptide
29	O	4	ILE	Peptide
30	P	137	PRO	Peptide
31	X	127	GLY	Peptide
31	X	137	SER	Peptide
31	X	55	ARG	Peptide
33	c	86	PRO	Peptide
34	e	61	THR	Peptide
34	e	62	VAL	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	36229	0	18300	225	0
2	a	598	0	656	19	0
3	B	1710	0	1708	14	0
4	b	814	0	867	11	0
5	C	1729	0	1803	29	0
6	D	1716	0	1806	20	0
7	d	488	0	514	14	0
8	E	1768	0	1866	26	0
9	f	457	0	502	6	0
10	G	1471	0	1522	42	0
11	g	555	0	567	10	0
12	H	1923	0	2089	30	0
13	h	2436	0	2393	65	0
14	I	1488	0	1582	15	0
15	J	1686	0	1772	23	0
16	K	1525	0	1640	23	0
17	L	810	0	836	13	0
18	N	908	0	939	19	0
19	Q	1058	0	1104	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	R	1128	0	1195	31	0
21	S	1068	0	1121	21	0
22	T	1190	0	1249	35	0
23	U	1097	0	1132	32	0
24	V	795	0	862	9	0
25	W	636	0	637	10	0
26	Z	1011	0	1083	15	0
27	F	280	0	250	4	0
28	M	2083	0	2189	36	0
29	O	1296	0	1374	11	0
30	P	1208	0	1294	16	0
31	X	1016	0	1039	17	0
32	Y	1034	0	1080	12	0
33	c	1106	0	1179	12	0
34	e	659	0	683	6	0
All	All	74976	0	58833	750	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (750) 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)
1:A:1091:C:HO2'	32:Y:2:VAL:N	1.79	0.81
1:A:925:G:H1	1:A:1017:U:H3	1.34	0.76
1:A:928:G:H1	1:A:1013:U:H3	1.38	0.72
7:d:29:GLN:HE22	7:d:67:ARG:HA	1.57	0.69
34:e:62:VAL:HG13	34:e:63:LEU:HB2	1.76	0.67
1:A:1286:G:H21	1:A:1313:A:H62	1.44	0.65
5:C:149:GLN:HE22	5:C:154:SER:HB3	1.61	0.64
2:a:68:ILE:HB	2:a:109:TYR:HB2	1.80	0.64
19:Q:98:ASN:ND2	19:Q:121:ILE:O	2.31	0.63
1:A:1497:G:N7	17:L:25:LYS:NZ	2.46	0.63
8:E:49:ILE:HG12	8:E:87:TYR:HB2	1.80	0.63
1:A:94:G:OP2	28:M:1:MET:N	2.32	0.63
1:A:1547:C:H1'	1:A:1670:C:H4'	1.81	0.63
6:D:196:ILE:HB	6:D:223:TYR:HB2	1.81	0.62
13:h:286:CYS:HA	13:h:302:TYR:HA	1.81	0.62
14:I:53:VAL:HG21	14:I:172:THR:HA	1.81	0.62
5:C:224:GLU:HG3	5:C:227:LYS:H	1.64	0.62
1:A:1693:G:H21	1:A:1834:A:H8	1.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1290:G:OP2	11:g:95:ARG:NH2	2.33	0.61
10:G:72:LEU:HD11	10:G:154:LEU:HD11	1.82	0.61
13:h:256:ILE:HD12	13:h:289:LEU:HD13	1.83	0.61
16:K:121:LYS:H	16:K:125:HIS:HD2	1.46	0.61
21:S:31:ASN:OD1	21:S:31:ASN:N	2.34	0.60
1:A:1834:A:H2	1:A:1837:G:H1	1.50	0.60
29:O:25:LEU:H	29:O:28:THR:HG23	1.67	0.60
21:S:31:ASN:HA	21:S:34:VAL:HB	1.83	0.59
1:A:64:A:H2	1:A:83:A:H62	1.50	0.59
1:A:1566:G:N7	23:U:101:ARG:NH2	2.50	0.59
12:H:98:ARG:NH2	12:H:103:ASP:OD1	2.34	0.59
29:O:149:ALA:HB1	29:O:152:LYS:HE3	1.85	0.59
1:A:1450:G:H5''	21:S:33:ARG:HH22	1.68	0.59
28:M:100:ARG:NH2	28:M:118:GLU:O	2.36	0.59
1:A:1473:G:H2'	1:A:1475:G:H22	1.67	0.59
1:A:583:A:OP1	16:K:162:ARG:NH2	2.36	0.59
31:X:34:PHE:HB3	31:X:41:PHE:HB2	1.85	0.59
1:A:1024:A:OP2	30:P:124:ARG:NH2	2.33	0.58
7:d:20:ARG:NH1	7:d:28:THR:OG1	2.36	0.58
3:B:77:ILE:HG12	3:B:99:ILE:HB	1.85	0.58
20:R:132:PHE:O	20:R:140:ARG:NH2	2.36	0.58
34:e:40:CYS:SG	34:e:41:TYR:N	2.75	0.58
17:L:91:PRO:HD2	17:L:94:LEU:HD12	1.85	0.58
8:E:28:GLU:HG2	17:L:61:GLN:HG2	1.86	0.58
1:A:1605:G:OP1	23:U:84:ARG:NH2	2.37	0.58
23:U:13:GLU:HA	23:U:16:ARG:HE	1.67	0.58
28:M:21:ASP:N	28:M:21:ASP:OD1	2.37	0.58
1:A:1259:A:N6	1:A:1519:U:OP1	2.34	0.58
10:G:92:ILE:HG23	10:G:170:ALA:HA	1.85	0.58
17:L:29:MET:SD	17:L:42:ASN:ND2	2.77	0.58
6:D:171:GLY:O	32:Y:98:GLN:NE2	2.37	0.58
7:d:29:GLN:NE2	7:d:66:ARG:O	2.36	0.58
1:A:1285:G:H4'	11:g:100:LEU:HD21	1.86	0.57
1:A:1674:G:OP1	10:G:51:HIS:NE2	2.37	0.57
13:h:82:SER:OG	13:h:83:TRP:N	2.36	0.57
1:A:1543:U:OP2	23:U:62:ARG:NH1	2.33	0.57
19:Q:44:ARG:NH1	19:Q:82:ASP:O	2.37	0.57
18:N:95:ASP:HB3	18:N:100:PRO:HA	1.86	0.57
1:A:1568:C:O2	1:A:1627:C:O2'	2.23	0.57
1:A:1005:G:OP2	5:C:162:ARG:NH1	2.38	0.57
1:A:1414:A:N6	1:A:1425:G:O6	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1658:G:OP2	1:A:1660:C:N4	2.38	0.57
26:Z:21:LYS:HD2	26:Z:75:ILE:HD11	1.87	0.57
1:A:1299:A:OP2	19:Q:59:ARG:NH2	2.38	0.56
19:Q:18:ARG:NH1	19:Q:36:LEU:O	2.38	0.56
1:A:1587:G:H1	23:U:74:SER:HG	1.52	0.56
3:B:13:GLU:HA	3:B:16:LEU:HD12	1.87	0.56
20:R:110:ASP:HA	20:R:113:ILE:HB	1.88	0.56
1:A:1515:G:N2	19:Q:99:GLY:O	2.36	0.56
13:h:202:PRO:HG2	13:h:243:PRO:HA	1.88	0.56
14:I:51:ILE:HG21	14:I:179:LYS:HG2	1.87	0.56
5:C:60:ASP:OD1	5:C:60:ASP:N	2.38	0.56
28:M:173:ILE:HG23	28:M:230:LYS:HE3	1.86	0.56
33:c:67:ARG:HG3	33:c:115:ILE:HG12	1.86	0.56
1:A:1261:C:OP1	1:A:1518:C:N4	2.39	0.56
1:A:1566:G:N2	1:A:1569:A:OP2	2.35	0.56
4:b:32:LYS:O	4:b:37:LYS:NZ	2.39	0.56
14:I:34:SER:O	14:I:37:LYS:NZ	2.38	0.56
8:E:134:CYS:SG	8:E:135:GLU:N	2.79	0.56
10:G:50:PRO:HB3	10:G:69:VAL:HG13	1.87	0.56
24:V:38:ASP:HB2	24:V:41:ARG:HH21	1.70	0.56
28:M:158:ASP:OD1	28:M:158:ASP:N	2.38	0.56
15:J:89:GLU:OE2	15:J:92:ARG:NH2	2.38	0.56
28:M:197:ASN:HB3	28:M:209:HIS:HB2	1.86	0.56
4:b:60:ASP:OD1	4:b:60:ASP:N	2.38	0.56
8:E:45:ARG:NH2	8:E:82:GLY:O	2.38	0.56
19:Q:81:ARG:NH2	19:Q:117:GLY:O	2.39	0.56
5:C:33:VAL:HG13	5:C:44:ILE:HB	1.88	0.55
5:C:150:ILE:HD13	21:S:129:LYS:HB2	1.88	0.55
30:P:5:HIS:HD2	30:P:121:ARG:HE	1.54	0.55
4:b:45:VAL:HG11	4:b:53:ILE:HG13	1.88	0.55
14:I:117:PRO:HG2	14:I:120:ARG:HD3	1.89	0.55
22:T:35:GLY:O	22:T:97:GLN:NE2	2.39	0.55
1:A:126:G:OP1	12:H:198:ARG:NH2	2.39	0.55
13:h:109:LEU:HD21	13:h:125:ARG:HE	1.72	0.55
1:A:1597:C:OP2	2:a:85:ARG:NH1	2.39	0.55
19:Q:41:GLN:NE2	19:Q:113:GLY:O	2.39	0.55
19:Q:81:ARG:NH1	19:Q:97:TYR:O	2.37	0.55
1:A:1646:C:O5'	20:R:138:ARG:NH1	2.39	0.55
1:A:1863:A:OP2	4:b:4:LYS:NZ	2.39	0.55
23:U:72:VAL:HG21	23:U:101:ARG:HG3	1.89	0.55
23:U:111:LYS:HB2	23:U:126:GLN:HE21	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:C:O2'	1:A:1194:A:N1	2.40	0.55
13:h:201:SER:OG	13:h:203:ASP:OD1	2.22	0.55
19:Q:136:THR:H	19:Q:139:SER:HB2	1.72	0.55
22:T:25:LYS:HE3	22:T:53:THR:HA	1.89	0.55
1:A:146:G:OP1	12:H:143:LYS:NZ	2.39	0.55
1:A:1628:C:OP1	23:U:38:LYS:NZ	2.40	0.55
1:A:1678:A:H62	10:G:57:ALA:HB1	1.72	0.55
25:W:74:LYS:O	25:W:81:LYS:NZ	2.39	0.55
8:E:154:ASP:OD1	8:E:154:ASP:N	2.40	0.54
21:S:99:ASP:OD1	21:S:99:ASP:N	2.36	0.54
22:T:138:THR:HA	22:T:141:ARG:HH21	1.70	0.54
1:A:952:G:H21	31:X:52:THR:HG21	1.71	0.54
1:A:1647:A:OP1	20:R:138:ARG:NH2	2.40	0.54
22:T:75:ARG:HH22	22:T:94:LYS:HB3	1.72	0.54
1:A:1719:A:N6	1:A:1814:G:O2'	2.40	0.54
5:C:182:LYS:O	5:C:186:ASN:ND2	2.40	0.54
13:h:5:MET:HG2	13:h:312:VAL:HG22	1.90	0.54
19:Q:100:LYS:HG3	19:Q:101:THR:HG23	1.90	0.54
17:L:53:LYS:HB3	17:L:58:VAL:HG23	1.90	0.54
19:Q:23:ASP:HA	19:Q:26:LEU:HD23	1.88	0.54
22:T:2:SER:OG	22:T:3:LEU:N	2.39	0.54
22:T:98:VAL:HB	22:T:103:LEU:HD13	1.90	0.54
1:A:561:A:H5'	16:K:171:GLY:HA3	1.88	0.54
3:B:211:GLU:HA	3:B:214:GLU:HB2	1.89	0.54
4:b:51:ARG:NH2	7:d:37:ASP:OD2	2.40	0.54
12:H:118:GLU:HG2	12:H:119:LYS:HG3	1.90	0.54
19:Q:28:MET:SD	19:Q:32:GLN:NE2	2.81	0.54
10:G:24:SER:O	10:G:107:ASN:ND2	2.41	0.54
1:A:587:A:H5'	1:A:592:C:H41	1.72	0.54
1:A:1292:C:O2	11:g:138:ARG:NH1	2.39	0.53
8:E:172:VAL:O	8:E:173:ARG:NH1	2.41	0.53
10:G:25:THR:OG1	10:G:41:VAL:O	2.26	0.53
22:T:13:LEU:HB2	22:T:20:ILE:HG13	1.90	0.53
1:A:381:C:OP2	15:J:54:LYS:NZ	2.39	0.53
1:A:1678:A:N6	10:G:57:ALA:O	2.42	0.53
20:R:101:ASP:OD2	20:R:104:SER:N	2.42	0.53
27:F:171:ARG:NH2	27:F:172:GLU:OE2	2.41	0.53
31:X:30:VAL:HG12	31:X:94:HIS:HB2	1.90	0.53
1:A:1455:A:H4'	21:S:28:PHE:HB2	1.89	0.53
1:A:1808:U:H2'	1:A:1809:A:H8	1.73	0.53
8:E:132:LYS:HE3	8:E:191:PRO:HA	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:M:127:ARG:HD3	28:M:142:HIS:HA	1.90	0.53
28:M:176:ASP:OD1	28:M:179:ASN:ND2	2.40	0.53
1:A:1521:C:OP1	22:T:124:ARG:NH1	2.39	0.53
10:G:127:ARG:NH2	10:G:128:ILE:O	2.41	0.53
11:g:104:LYS:O	11:g:118:ARG:NH1	2.41	0.53
22:T:22:GLY:O	22:T:57:GLY:N	2.41	0.53
1:A:847:A:O2'	28:M:106:LYS:NZ	2.41	0.53
10:G:89:THR:HA	10:G:92:ILE:HD12	1.91	0.53
13:h:206:LEU:HA	13:h:220:ASP:HA	1.91	0.53
22:T:27:ALA:HB2	22:T:52:LEU:HB3	1.91	0.53
1:A:351:G:OP1	15:J:7:ASN:ND2	2.40	0.53
1:A:1115:U:H1'	1:A:1116:C:H2'	1.90	0.53
2:a:111:ARG:HB3	2:a:114:LYS:HE2	1.90	0.53
13:h:216:ALA:HB3	13:h:230:LEU:HB2	1.90	0.53
19:Q:13:ARG:NH1	19:Q:14:LYS:O	2.41	0.53
30:P:29:THR:OG1	30:P:31:ASP:OD1	2.27	0.53
3:B:85:ARG:NH1	3:B:203:PHE:O	2.42	0.53
13:h:90:TRP:HA	13:h:97:THR:HA	1.91	0.53
15:J:134:GLU:O	15:J:138:ASN:ND2	2.40	0.53
1:A:1334:G:H5'	8:E:140:GLY:HA2	1.90	0.52
23:U:122:LYS:NZ	23:U:123:LEU:O	2.38	0.52
30:P:87:ASP:OD1	30:P:87:ASP:N	2.41	0.52
1:A:1564:C:OP1	23:U:121:ARG:NH1	2.43	0.52
13:h:78:ALA:O	13:h:90:TRP:N	2.41	0.52
1:A:1545:A:N6	1:A:1655:C:O2'	2.42	0.52
14:I:53:VAL:HG23	14:I:175:GLY:HA3	1.91	0.52
18:N:113:ASP:OD2	18:N:113:ASP:N	2.41	0.52
19:Q:33:LEU:HA	19:Q:36:LEU:HB2	1.92	0.52
1:A:433:A:H5''	15:J:22:HIS:HB3	1.91	0.52
1:A:1358:U:OP2	6:D:123:ARG:NH1	2.43	0.52
1:A:1461:G:H3'	1:A:1463:U:H3	1.75	0.52
18:N:58:GLU:HB3	18:N:61:TYR:HB3	1.90	0.52
20:R:8:GLN:HB3	20:R:95:TYR:HE1	1.74	0.52
31:X:103:ASN:ND2	31:X:140:THR:O	2.42	0.52
14:I:60:ILE:HB	14:I:92:VAL:HG12	1.91	0.52
26:Z:114:MET:O	26:Z:122:LYS:NZ	2.42	0.52
3:B:142:LEU:O	25:W:60:ARG:NH2	2.43	0.52
1:A:888:U:H2'	1:A:889:U:H4'	1.91	0.52
1:A:1506:A:H4'	1:A:1507:G:H3'	1.90	0.52
1:A:1678:A:OP1	10:G:145:ARG:NH1	2.43	0.52
21:S:77:GLU:O	21:S:81:ARG:NH2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:h:40:ILE:HB	13:h:59:LEU:HB2	1.91	0.52
28:M:177:THR:HG23	28:M:196:THR:HA	1.92	0.52
15:J:88:ASN:HB3	15:J:205:ARG:HH21	1.75	0.51
16:K:95:ASP:OD2	16:K:95:ASP:N	2.43	0.51
15:J:139:LYS:O	15:J:141:ARG:NH2	2.44	0.51
3:B:76:VAL:HG12	3:B:123:VAL:HB	1.93	0.51
23:U:22:LEU:HD13	23:U:28:LEU:HD21	1.92	0.51
26:Z:80:ASP:OD1	26:Z:80:ASP:N	2.40	0.51
1:A:522:A:OP2	16:K:45:ARG:NH2	2.39	0.51
18:N:81:ASP:O	18:N:84:LYS:NZ	2.42	0.51
23:U:77:LYS:HE2	23:U:94:ARG:HH22	1.76	0.51
34:e:74:THR:OG1	34:e:77:CYS:SG	2.67	0.51
1:A:1552:G:OP1	1:A:1578:U:N3	2.44	0.51
6:D:95:ASP:OD1	6:D:95:ASP:N	2.39	0.51
10:G:37:ASP:OD1	10:G:44:LYS:NZ	2.42	0.51
1:A:1252:C:N4	20:R:146:ARG:OXT	2.44	0.51
13:h:298:LEU:HB3	13:h:310:TRP:HB2	1.93	0.51
18:N:85:LEU:HA	18:N:88:TRP:HB2	1.92	0.51
1:A:1753:C:H2'	1:A:1754:G:H8	1.75	0.51
16:K:136:ARG:HD3	16:K:160:SER:HA	1.93	0.51
1:A:1285:G:N1	18:N:57:ASP:O	2.41	0.51
1:A:1299:A:O2'	1:A:1301:A:OP1	2.28	0.51
17:L:91:PRO:HB2	17:L:93:THR:HG22	1.91	0.51
26:Z:86:GLU:OE2	26:Z:90:ARG:NH1	2.43	0.51
8:E:61:GLU:H	8:E:64:ARG:HB3	1.76	0.51
10:G:55:ARG:O	10:G:62:ARG:NH1	2.44	0.51
12:H:23:LYS:NZ	12:H:40:ALA:O	2.44	0.51
3:B:36:GLN:O	3:B:53:ARG:NH1	2.44	0.50
18:N:87:GLU:OE1	18:N:96:ARG:NH2	2.43	0.50
19:Q:96:VAL:HB	19:Q:116:LEU:HD12	1.93	0.50
1:A:1236:G:O2'	19:Q:131:PRO:O	2.23	0.50
1:A:1355:C:O3'	6:D:238:LYS:NZ	2.44	0.50
1:A:1555:U:H4'	1:A:1556:A:H5'	1.93	0.50
6:D:176:LYS:O	6:D:200:ARG:NH1	2.40	0.50
14:I:69:LEU:HD22	14:I:96:ALA:HB2	1.92	0.50
1:A:507:G:O6	26:Z:105:LYS:NZ	2.43	0.50
1:A:924:G:OP2	30:P:3:ARG:NH1	2.45	0.50
15:J:73:THR:O	15:J:74:ARG:NH1	2.43	0.50
17:L:95:ARG:HH11	17:L:96:ARG:HG2	1.76	0.50
28:M:130:PHE:HB2	28:M:138:HIS:HB2	1.91	0.50
32:Y:42:MET:HE2	32:Y:49:GLU:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1259:A:O2'	1:A:1263:U:N3	2.44	0.50
1:A:1622:U:OP1	22:T:120:HIS:ND1	2.33	0.50
4:b:44:ILE:HD12	4:b:65:PRO:HG2	1.94	0.50
15:J:11:ARG:NH1	15:J:15:GLY:O	2.44	0.50
22:T:103:LEU:HA	22:T:106:LYS:HB2	1.93	0.50
8:E:31:GLU:HA	8:E:107:TYR:HE2	1.76	0.50
10:G:14:THR:HG1	10:G:48:TYR:HH	1.58	0.50
10:G:123:GLU:OE1	10:G:204:ARG:NH1	2.45	0.50
12:H:43:GLU:OE2	12:H:119:LYS:NZ	2.45	0.50
18:N:113:ASP:OD1	18:N:121:LYS:NZ	2.40	0.50
1:A:687:C:OP2	32:Y:32:LYS:NZ	2.41	0.50
1:A:1665:G:OP1	23:U:91:HIS:NE2	2.40	0.50
12:H:19:ASP:OD1	12:H:19:ASP:N	2.38	0.50
13:h:42:MET:HB3	13:h:57:ARG:HB3	1.94	0.50
8:E:51:LEU:HB3	8:E:91:VAL:HG12	1.94	0.50
10:G:51:HIS:O	20:R:82:TYR:OH	2.30	0.50
22:T:65:GLU:HA	22:T:68:ILE:HG12	1.93	0.50
28:M:176:ASP:OD1	28:M:176:ASP:N	2.45	0.50
10:G:18:LYS:HB2	10:G:24:SER:HA	1.93	0.50
24:V:49:LYS:NZ	24:V:92:HIS:O	2.44	0.50
25:W:71:ARG:HH12	32:Y:23:ARG:HH21	1.58	0.50
22:T:46:ARG:HB3	23:U:35:ASP:HB2	1.93	0.49
28:M:104:ASP:HB3	28:M:110:ALA:HB2	1.93	0.49
30:P:56:ASP:OD2	34:e:52:THR:OG1	2.30	0.49
13:h:133:ASN:OD1	13:h:139:LYS:NZ	2.44	0.49
18:N:116:LYS:HA	18:N:121:LYS:HE3	1.94	0.49
31:X:131:ASP:OD2	31:X:131:ASP:N	2.45	0.49
1:A:1283:C:O2'	1:A:1313:A:N1	2.39	0.49
22:T:109:GLU:HG3	22:T:113:ARG:HH21	1.78	0.49
31:X:20:GLN:NE2	31:X:21:VAL:O	2.45	0.49
1:A:446:G:OP2	15:J:47:ARG:NH1	2.41	0.49
1:A:1444:U:OP1	20:R:15:ARG:NH2	2.46	0.49
2:a:64:ASN:O	2:a:111:ARG:NH2	2.45	0.49
15:J:113:TYR:OH	15:J:156:ALA:O	2.30	0.49
16:K:136:ARG:NH1	16:K:159:PHE:O	2.44	0.49
30:P:31:ASP:OD1	30:P:31:ASP:N	2.40	0.49
2:a:62:VAL:HG22	2:a:68:ILE:HD12	1.95	0.49
1:A:1232:U:H2'	1:A:1233:G:H8	1.78	0.49
8:E:42:THR:HG23	8:E:45:ARG:HB3	1.95	0.49
12:H:30:LYS:HG2	12:H:34:THR:HG21	1.94	0.49
13:h:131:LEU:HD12	13:h:140:TYR:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:h:217:MET:HE3	13:h:219:TRP:HE1	1.77	0.49
1:A:945:U:H1'	31:X:140:THR:HG21	1.94	0.49
1:A:1060:A:O2'	1:A:1062:A:N7	2.43	0.49
3:B:63:ARG:NH1	25:W:37:ALA:O	2.46	0.49
5:C:52:THR:HG23	5:C:57:ILE:HA	1.93	0.49
6:D:72:ASP:O	6:D:74:LYS:NZ	2.46	0.49
20:R:45:ARG:NH2	23:U:10:ASN:OD1	2.45	0.49
1:A:496:C:H5'	28:M:29:PRO:HA	1.94	0.49
1:A:994:C:N4	4:b:14:GLY:O	2.42	0.49
7:d:10:LYS:HE3	7:d:61:SER:HB2	1.95	0.49
13:h:156:PHE:HE1	13:h:179:LEU:HD21	1.77	0.49
14:I:82:GLU:HA	14:I:85:LYS:HG2	1.94	0.49
18:N:52:LEU:HD13	18:N:65:VAL:HG11	1.95	0.49
22:T:34:LYS:HB3	22:T:100:ALA:HA	1.95	0.49
1:A:560:A:H5'	16:K:174:LYS:HB2	1.95	0.49
1:A:570:C:O2'	26:Z:34:THR:O	2.27	0.49
4:b:23:CYS:SG	4:b:24:THR:N	2.86	0.49
11:g:119:ARG:HB3	11:g:132:MET:HB3	1.95	0.49
12:H:74:ARG:NH1	12:H:96:SER:OG	2.45	0.49
30:P:75:LEU:HD12	30:P:80:LEU:HB2	1.94	0.49
1:A:1488:C:O2'	1:A:1490:G:OP2	2.28	0.49
5:C:63:LYS:HE2	5:C:90:ASP:HA	1.95	0.49
6:D:106:VAL:H	27:F:178:ASN:HD21	1.61	0.49
22:T:26:ILE:HD12	22:T:29:ALA:HB3	1.95	0.49
29:O:19:ASN:OD1	29:O:22:ARG:NH2	2.41	0.49
1:A:495:U:H4'	28:M:25:SER:HB2	1.93	0.48
1:A:1013:U:OP1	1:A:1129:G:O2'	2.31	0.48
2:a:67:LEU:HD12	10:G:102:LEU:HD22	1.95	0.48
7:d:44:ARG:HH12	7:d:60:GLU:HG3	1.78	0.48
32:Y:66:THR:OG1	32:Y:67:GLY:N	2.46	0.48
1:A:1550:G:H3'	1:A:1579:A:H61	1.77	0.48
1:A:1628:C:O2'	22:T:82:TRP:O	2.26	0.48
2:a:79:ILE:HB	2:a:83:LEU:HD23	1.95	0.48
17:L:37:ASP:N	17:L:37:ASP:OD1	2.44	0.48
19:Q:50:ARG:O	19:Q:54:HIS:ND1	2.44	0.48
28:M:46:ILE:HA	28:M:50:ASN:HD22	1.78	0.48
1:A:183:G:O2'	1:A:184:G:O4'	2.31	0.48
1:A:1553:C:O2'	1:A:1554:C:O4'	2.30	0.48
1:A:1623:A:H5''	22:T:133:GLY:HA3	1.95	0.48
2:a:73:VAL:HG21	2:a:88:LEU:HD21	1.93	0.48
5:C:33:VAL:HG22	5:C:44:ILE:HD12	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:129:THR:OG1	5:C:131:ASP:O	2.30	0.48
13:h:28:PRO:HB3	13:h:293:ALA:HB3	1.94	0.48
24:V:26:SER:HB2	24:V:110:VAL:HA	1.95	0.48
6:D:144:SER:OG	6:D:145:LYS:N	2.45	0.48
13:h:84:ASP:OD1	13:h:86:THR:OG1	2.31	0.48
1:A:142:C:N4	1:A:329:G:OP2	2.47	0.48
1:A:1616:U:OP2	19:Q:43:ARG:NH2	2.46	0.48
5:C:129:THR:OG1	5:C:131:ASP:OD1	2.29	0.48
13:h:72:SER:OG	13:h:73:SER:N	2.47	0.48
15:J:6:ASP:OD1	15:J:6:ASP:N	2.44	0.48
20:R:113:ILE:HD11	20:R:120:LEU:HD12	1.95	0.48
1:A:1580:A:OP1	24:V:86:LYS:NZ	2.40	0.48
8:E:69:LEU:HA	8:E:72:VAL:HG22	1.95	0.48
29:O:1:MET:HE3	29:O:3:ASP:H	1.79	0.48
1:A:1275:G:O2'	1:A:1321:G:N2	2.46	0.48
6:D:271:ASP:OD2	6:D:271:ASP:N	2.44	0.48
8:E:66:ILE:O	8:E:70:THR:OG1	2.25	0.48
15:J:158:ILE:HD11	15:J:163:GLU:HB3	1.95	0.48
1:A:1542:C:H4'	23:U:11:GLN:HB2	1.95	0.48
3:B:126:ASP:OD1	3:B:165:ASN:ND2	2.47	0.48
30:P:99:ARG:HH12	30:P:143:SER:HB3	1.79	0.48
31:X:75:MET:HE3	31:X:75:MET:HB3	1.82	0.48
1:A:377:G:H5'	15:J:98:LYS:HB3	1.96	0.48
1:A:1533:A:OP2	10:G:164:ARG:NH2	2.40	0.48
29:O:101:ARG:HH12	33:c:5:ARG:HA	1.78	0.48
32:Y:86:LEU:HD21	32:Y:113:HIS:HB2	1.96	0.48
1:A:661:U:OP2	33:c:3:LYS:NZ	2.41	0.47
1:A:1524:G:OP2	22:T:141:ARG:NH1	2.45	0.47
13:h:99:ARG:NH2	13:h:135:LEU:O	2.47	0.47
33:c:95:GLU:OE1	33:c:140:ARG:NH1	2.42	0.47
1:A:441:C:OP2	15:J:2:GLY:N	2.47	0.47
1:A:744:G:N2	1:A:797:C:O2	2.42	0.47
1:A:1139:C:H5	1:A:1149:A:H62	1.61	0.47
1:A:1171:G:O2'	1:A:1187:G:O6	2.31	0.47
10:G:74:ASN:HA	10:G:77:MET:HE3	1.95	0.47
13:h:51:ASN:ND2	13:h:53:GLY:O	2.46	0.47
1:A:1563:G:O3'	23:U:115:LYS:NZ	2.46	0.47
13:h:58:ALA:HB3	20:R:97:GLN:HE21	1.79	0.47
19:Q:136:THR:OG1	19:Q:139:SER:N	2.48	0.47
29:O:152:LYS:HG2	29:O:154:GLN:HE21	1.78	0.47
1:A:1401:A:H4'	24:V:52:GLY:HA3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1617:G:N1	1:A:1620:A:OP2	2.47	0.47
8:E:211:VAL:H	21:S:39:ALA:HA	1.80	0.47
15:J:57:ALA:HB2	15:J:183:GLY:HA2	1.96	0.47
18:N:41:ALA:O	18:N:46:GLN:NE2	2.48	0.47
20:R:106:LYS:HA	20:R:109:LYS:HB3	1.96	0.47
28:M:124:CYS:HB3	28:M:141:THR:HB	1.96	0.47
1:A:1507:G:N2	11:g:87:THR:OG1	2.48	0.47
7:d:49:PRO:HG2	10:G:144:LEU:HD23	1.96	0.47
10:G:14:THR:HB	10:G:17:ILE:HG23	1.97	0.47
1:A:1560:U:O2'	1:A:1583:C:O2'	2.32	0.47
1:A:1617:G:N7	19:Q:47:ARG:NH1	2.58	0.47
4:b:94:ASP:OD1	4:b:94:ASP:N	2.39	0.47
6:D:113:GLN:NE2	6:D:120:GLN:OE1	2.48	0.47
6:D:220:ASP:OD1	6:D:220:ASP:N	2.44	0.47
12:H:162:LEU:HD21	12:H:172:LYS:HD2	1.97	0.47
1:A:156:G:OP1	12:H:2:LYS:NZ	2.40	0.47
1:A:1649:U:OP1	20:R:128:GLU:N	2.47	0.47
5:C:34:LYS:O	5:C:98:THR:OG1	2.31	0.47
10:G:45:TYR:HB3	10:G:67:PRO:HD3	1.95	0.47
17:L:93:THR:HG23	17:L:94:LEU:HG	1.97	0.47
19:Q:29:SER:HB3	19:Q:32:GLN:HG2	1.95	0.47
1:A:317:C:OP2	12:H:183:ARG:NH2	2.47	0.47
1:A:1324:G:O2'	1:A:1510:G:O2'	2.22	0.47
1:A:1477:U:H5'	21:S:3:ARG:HH21	1.79	0.47
1:A:1596:U:OP2	2:a:85:ARG:NE	2.48	0.47
2:a:91:LEU:HA	2:a:94:LYS:HB2	1.97	0.47
1:A:1237:C:O2'	19:Q:128:HIS:ND1	2.36	0.47
21:S:47:ARG:HA	21:S:50:ILE:HB	1.97	0.47
1:A:1255:G:OP1	1:A:1256:G:O2'	2.32	0.46
7:d:44:ARG:NH2	7:d:63:ARG:O	2.48	0.46
12:H:31:ARG:HB3	12:H:101:ILE:HD13	1.97	0.46
13:h:19:THR:O	13:h:288:SER:OG	2.29	0.46
13:h:192:THR:OG1	13:h:213:ASP:OD2	2.34	0.46
13:h:235:ILE:HG23	13:h:253:GLY:HA2	1.97	0.46
17:L:14:LEU:HA	17:L:17:LYS:HB3	1.97	0.46
23:U:49:ASP:HB3	23:U:52:TRP:HB3	1.96	0.46
25:W:15:ARG:NH1	25:W:33:GLN:OE1	2.46	0.46
1:A:53:C:O2'	1:A:507:G:N7	2.41	0.46
1:A:75:G:O2'	1:A:77:A:OP1	2.34	0.46
1:A:983:A:H2	31:X:139:SER:HB2	1.80	0.46
14:I:154:ILE:HB	14:I:185:VAL:HG23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:J:162:LEU:HD11	15:J:191:GLU:HG2	1.96	0.46
18:N:77:ILE:HD13	18:N:127:TYR:HE2	1.78	0.46
23:U:22:LEU:HD22	23:U:28:LEU:HD11	1.97	0.46
24:V:20:ILE:HB	24:V:91:LEU:HB2	1.98	0.46
26:Z:55:ILE:HG23	26:Z:75:ILE:HG22	1.97	0.46
28:M:174:LYS:O	28:M:179:ASN:ND2	2.48	0.46
34:e:55:LEU:HD13	34:e:60:SER:HB3	1.96	0.46
8:E:211:VAL:O	21:S:20:TYR:OH	2.33	0.46
14:I:159:ASP:OD1	14:I:159:ASP:N	2.45	0.46
20:R:58:LEU:HD21	20:R:112:LEU:HG	1.97	0.46
25:W:73:ALA:HB1	25:W:78:ILE:HB	1.97	0.46
1:A:1519:U:O2	22:T:135:HIS:NE2	2.46	0.46
18:N:81:ASP:HB3	18:N:84:LYS:HG2	1.97	0.46
20:R:112:LEU:HD13	20:R:119:LEU:HD13	1.96	0.46
1:A:635:G:OP1	9:f:94:LYS:NZ	2.46	0.46
13:h:147:HIS:HB3	13:h:149:GLU:H	1.79	0.46
1:A:1562:C:H4'	23:U:120:GLY:H	1.80	0.46
1:A:1707:U:O2	1:A:1849:G:N2	2.47	0.46
2:a:87:ALA:HA	22:T:3:LEU:HD21	1.97	0.46
9:f:104:ARG:HH21	16:K:124:HIS:HD2	1.63	0.46
15:J:132:GLU:O	15:J:136:ILE:N	2.44	0.46
1:A:1649:U:H2'	1:A:1650:A:C8	2.51	0.46
6:D:169:TYR:OH	6:D:175:GLY:O	2.31	0.46
20:R:44:PRO:HB2	20:R:46:THR:HG22	1.97	0.46
21:S:101:ASP:OD2	21:S:101:ASP:N	2.47	0.46
1:A:168:C:OP1	12:H:131:ARG:NE	2.43	0.46
1:A:616:A:OP1	33:c:68:LYS:NZ	2.49	0.46
5:C:146:ARG:HH11	5:C:206:PRO:HG3	1.81	0.46
13:h:35:SER:OG	13:h:36:ARG:N	2.49	0.46
13:h:177:TRP:CD1	13:h:185:LYS:H	2.34	0.46
28:M:38:LEU:HD23	28:M:39:ARG:HD3	1.98	0.46
31:X:86:LYS:NZ	31:X:122:SER:O	2.47	0.46
1:A:1465:A:OP1	21:S:60:ARG:NH1	2.49	0.46
2:a:63:PRO:HG3	2:a:96:LEU:HB3	1.98	0.46
17:L:52:LEU:HG	17:L:57:TYR:HB2	1.98	0.46
1:A:642:U:OP2	9:f:107:ARG:NH2	2.49	0.45
1:A:753:C:O2'	1:A:754:G:O4'	2.34	0.45
16:K:121:LYS:H	16:K:125:HIS:CD2	2.32	0.45
21:S:43:SER:HB3	21:S:46:LEU:HB2	1.97	0.45
32:Y:27:ILE:HG12	32:Y:61:ILE:HB	1.98	0.45
1:A:1529:C:H1'	1:A:1665:G:H21	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:d:60:GLU:OE2	7:d:63:ARG:NH1	2.50	0.45
10:G:35:LEU:HD12	10:G:117:ILE:HG12	1.99	0.45
28:M:9:LEU:HB3	28:M:28:ALA:HB3	1.98	0.45
1:A:1645:C:H5'	20:R:139:ALA:HA	1.98	0.45
6:D:121:ARG:HH12	6:D:123:ARG:HD3	1.82	0.45
10:G:154:LEU:HD13	10:G:177:LEU:HD21	1.98	0.45
31:X:23:GLU:H	31:X:23:GLU:HG3	1.63	0.45
31:X:36:SER:OG	31:X:37:PHE:N	2.49	0.45
1:A:1115:U:O2	1:A:1116:C:O2'	2.34	0.45
3:B:37:TYR:OH	3:B:57:LYS:NZ	2.44	0.45
5:C:123:ALA:HB2	5:C:165:ARG:HG3	1.98	0.45
6:D:204:ILE:O	6:D:211:LYS:NZ	2.46	0.45
20:R:7:LEU:O	20:R:99:TYR:OH	2.28	0.45
10:G:14:THR:O	10:G:18:LYS:NZ	2.48	0.45
13:h:64:HIS:ND1	13:h:83:TRP:O	2.44	0.45
22:T:20:ILE:HB	22:T:24:ARG:HH22	1.81	0.45
23:U:9:VAL:HG22	23:U:139:ALA:HB2	1.98	0.45
24:V:38:ASP:O	24:V:42:GLY:N	2.47	0.45
30:P:56:ASP:OD1	30:P:57:SER:N	2.50	0.45
32:Y:35:VAL:O	32:Y:39:THR:OG1	2.32	0.45
33:c:50:ILE:HG23	33:c:97:ASN:HA	1.98	0.45
33:c:54:LYS:NZ	33:c:91:LEU:O	2.50	0.45
13:h:173:LEU:HD12	13:h:175:LYS:HZ1	1.81	0.45
1:A:1298:G:H4'	19:Q:78:THR:HA	1.98	0.45
12:H:64:LYS:HZ3	12:H:82:SER:HB3	1.82	0.45
16:K:107:GLU:O	16:K:113:GLN:NE2	2.49	0.45
1:A:104:A:H62	1:A:356:C:H5	1.65	0.45
1:A:581:U:H4'	26:Z:66:GLY:HA3	1.98	0.45
1:A:934:G:H22	1:A:1008:A:H2	1.64	0.45
2:a:73:VAL:HG12	2:a:79:ILE:HD11	1.98	0.45
4:b:7:ASN:ND2	4:b:10:ARG:O	2.39	0.45
12:H:20:ASP:OD2	12:H:23:LYS:N	2.45	0.45
13:h:121:VAL:HG21	13:h:165:ILE:HG21	1.98	0.45
22:T:21:ASP:O	22:T:24:ARG:NH2	2.49	0.45
1:A:1566:G:H1	23:U:97:LYS:HE3	1.82	0.45
1:A:1585:U:O2'	1:A:1587:G:OP2	2.34	0.45
8:E:141:LYS:NZ	8:E:179:GLN:O	2.50	0.45
9:f:115:PHE:HZ	16:K:26:ASP:HB2	1.81	0.45
13:h:129:ILE:HD12	13:h:177:TRP:HZ3	1.81	0.45
13:h:158:PRO:HG2	13:h:202:PRO:HA	1.98	0.45
16:K:179:LYS:O	16:K:183:GLY:N	2.40	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:122:ARG:N	10:G:197:GLU:OE2	2.48	0.45
32:Y:112:ASP:OD1	32:Y:112:ASP:N	2.50	0.45
1:A:198:U:O2'	1:A:201:C:N4	2.51	0.44
2:a:106:GLN:NE2	10:G:171:GLU:OE2	2.50	0.44
5:C:107:ARG:NH1	31:X:133:THR:O	2.50	0.44
13:h:23:THR:HB	13:h:31:ILE:HG22	1.98	0.44
16:K:67:ASP:OD2	16:K:70:ARG:N	2.45	0.44
26:Z:27:VAL:HG11	26:Z:35:VAL:HG11	2.00	0.44
33:c:28:LYS:HE2	33:c:32:LEU:HD22	1.98	0.44
1:A:816:A:OP2	16:K:10:ARG:NH2	2.51	0.44
2:a:74:SER:HA	2:a:79:ILE:HG13	1.99	0.44
1:A:495:U:O2'	28:M:25:SER:OG	2.30	0.44
1:A:1786:U:H2'	1:A:1787:G:H8	1.82	0.44
2:a:102:LYS:HG2	2:a:107:VAL:HG12	1.99	0.44
5:C:139:CYS:SG	5:C:140:VAL:N	2.90	0.44
18:N:86:GLY:HA2	18:N:106:CYS:H	1.83	0.44
31:X:63:LYS:HA	31:X:63:LYS:HD3	1.81	0.44
1:A:72:C:O2'	1:A:74:G:OP2	2.35	0.44
5:C:128:LYS:HE2	5:C:132:GLY:HA2	2.00	0.44
6:D:149:THR:HG22	6:D:152:ARG:HH12	1.83	0.44
13:h:197:THR:OG1	13:h:237:ASN:O	2.33	0.44
18:N:45:ARG:HA	18:N:45:ARG:HD3	1.88	0.44
10:G:71:ARG:HH11	10:G:151:ILE:HD12	1.83	0.44
23:U:38:LYS:HE3	23:U:38:LYS:HB2	1.77	0.44
29:O:151:THR:HG23	29:O:153:LYS:HE2	1.98	0.44
33:c:93:PHE:O	33:c:140:ARG:NH1	2.51	0.44
1:A:115:U:O2'	1:A:381:C:O2	2.30	0.44
1:A:1808:U:H2'	1:A:1809:A:C8	2.50	0.44
21:S:24:LEU:HD12	21:S:24:LEU:HA	1.88	0.44
1:A:67:C:H41	12:H:163:ASN:HA	1.83	0.44
1:A:792:C:H2'	1:A:793:G:C8	2.53	0.44
1:A:1565:C:H2'	1:A:1566:G:H8	1.82	0.44
10:G:14:THR:O	10:G:48:TYR:OH	2.36	0.44
20:R:83:ALA:O	20:R:87:SER:OG	2.29	0.44
22:T:14:ARG:HH21	22:T:19:ASN:HD21	1.66	0.44
1:A:380:G:P	15:J:56:ARG:HH22	2.41	0.43
1:A:1734:G:O2'	1:A:1800:A:N6	2.50	0.43
20:R:86:GLN:HE22	20:R:122:ALA:HB2	1.82	0.43
1:A:874:G:H2'	1:A:875:A:C8	2.53	0.43
1:A:1114:U:H3	1:A:1119:A:H61	1.66	0.43
1:A:1289:U:H3'	11:g:95:ARG:HH21	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1513:C:H2'	1:A:1514:G:H8	1.83	0.43
13:h:176:VAL:O	13:h:186:THR:OG1	2.37	0.43
13:h:177:TRP:HA	13:h:185:LYS:HE2	1.99	0.43
18:N:54:SER:HB2	18:N:80:ASP:HA	2.00	0.43
21:S:31:ASN:ND2	21:S:55:THR:OG1	2.51	0.43
28:M:258:ALA:O	28:M:262:SER:OG	2.37	0.43
1:A:943:U:OP1	5:C:214:LYS:NZ	2.39	0.43
1:A:1294:G:H2'	1:A:1295:A:H8	1.84	0.43
1:A:1719:A:N6	1:A:1720:U:O2	2.50	0.43
2:a:49:LEU:HD23	22:T:5:ILE:HA	1.99	0.43
3:B:205:ARG:NH2	21:S:81:ARG:O	2.51	0.43
8:E:214:LYS:HD2	8:E:214:LYS:HA	1.81	0.43
13:h:220:ASP:OD1	13:h:220:ASP:N	2.51	0.43
28:M:44:LEU:HD13	28:M:72:ILE:HD11	2.01	0.43
1:A:996:A:OP1	30:P:114:ARG:NH1	2.51	0.43
1:A:1549:U:OP2	8:E:8:LYS:NZ	2.50	0.43
13:h:140:TYR:OH	13:h:143:GLN:NE2	2.50	0.43
15:J:103:LEU:HD23	15:J:103:LEU:HA	1.90	0.43
17:L:14:LEU:HD22	17:L:35:LEU:HD21	2.01	0.43
19:Q:15:PHE:HB3	19:Q:22:LEU:HD21	1.99	0.43
1:A:552:G:H4'	9:f:117:ASN:HD22	1.84	0.43
1:A:1016:U:OP1	34:e:30:SER:OG	2.30	0.43
8:E:226:GLN:HE21	13:h:224:GLY:HA3	1.83	0.43
26:Z:103:SER:H	26:Z:106:GLN:HE21	1.67	0.43
1:A:560:A:OP1	16:K:174:LYS:NZ	2.52	0.43
1:A:1590:C:H42	20:R:77:HIS:HE1	1.67	0.43
10:G:184:SER:OG	10:G:186:ASN:OD1	2.34	0.43
13:h:294:ASP:OD1	13:h:294:ASP:N	2.52	0.43
1:A:1624:U:H3	19:Q:40:ARG:HH22	1.66	0.43
1:A:1649:U:H2'	1:A:1650:A:H8	1.84	0.43
7:d:46:VAL:HG22	10:G:140:ASP:HB2	2.01	0.43
25:W:14:PRO:HG2	25:W:23:ILE:HD12	2.01	0.43
11:g:124:ASP:N	11:g:124:ASP:OD1	2.49	0.43
18:N:68:LEU:HB2	18:N:71:GLU:HG2	2.00	0.43
22:T:20:ILE:HG22	22:T:32:ALA:HB3	2.00	0.43
24:V:51:LYS:HA	24:V:51:LYS:HD3	1.74	0.43
31:X:85:CYS:SG	31:X:86:LYS:N	2.92	0.43
1:A:448:A:H5''	15:J:25:ARG:HA	2.01	0.43
1:A:1525:C:H2'	1:A:1526:G:H8	1.84	0.43
5:C:144:LYS:HD3	5:C:208:HIS:HB3	2.00	0.43
10:G:49:LEU:HD13	20:R:47:LEU:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:h:196:ASN:H	13:h:211:GLY:HA2	1.84	0.43
16:K:82:VAL:HG21	16:K:92:MET:HE2	2.01	0.43
22:T:111:LEU:O	22:T:115:LYS:N	2.52	0.43
30:P:5:HIS:HB3	30:P:117:LEU:HD13	2.00	0.43
1:A:793:G:H2'	1:A:794:A:H8	1.83	0.43
1:A:1033:G:N1	1:A:1080:A:O2'	2.43	0.43
2:a:67:LEU:HD21	2:a:108:ILE:HG23	2.01	0.43
13:h:5:MET:HB2	13:h:270:LEU:HD11	2.00	0.43
13:h:140:TYR:OH	13:h:145:GLU:OE2	2.37	0.43
28:M:143:ASP:OD1	28:M:143:ASP:N	2.45	0.43
1:A:756:C:O2	1:A:788:G:N2	2.51	0.42
8:E:14:ASP:OD2	8:E:14:ASP:N	2.52	0.42
13:h:239:LEU:HB3	13:h:248:LEU:HD11	2.01	0.42
14:I:101:LEU:O	14:I:116:ARG:NH1	2.52	0.42
23:U:134:ILE:HD13	23:U:134:ILE:HA	1.88	0.42
26:Z:53:ASP:OD1	26:Z:53:ASP:N	2.51	0.42
30:P:140:LYS:NZ	30:P:142:GLU:OE1	2.45	0.42
1:A:1514:G:H2'	1:A:1515:G:H8	1.84	0.42
7:d:21:THR:OG1	7:d:66:ARG:NH1	2.51	0.42
10:G:72:LEU:HD12	10:G:151:ILE:HG23	2.01	0.42
13:h:22:ALA:HB3	13:h:32:LEU:HB2	2.00	0.42
14:I:133:LEU:HD23	14:I:133:LEU:HA	1.85	0.42
30:P:101:HIS:CE1	30:P:105:ASN:HD22	2.36	0.42
1:A:1302:G:H1	1:A:1307:U:H3	1.66	0.42
3:B:109:THR:O	6:D:89:LYS:NZ	2.50	0.42
5:C:57:ILE:HG22	5:C:59:SER:H	1.84	0.42
6:D:172:ASN:ND2	16:K:95:ASP:OD1	2.52	0.42
9:f:81:ARG:HH12	33:c:66:ILE:HD12	1.84	0.42
21:S:36:GLU:HG3	21:S:47:ARG:HG2	2.01	0.42
26:Z:12:PHE:HZ	26:Z:21:LYS:HD3	1.85	0.42
28:M:68:ARG:HD2	28:M:76:VAL:HG11	2.01	0.42
29:O:56:ILE:HG23	29:O:57:ASP:H	1.83	0.42
1:A:68:A:OP2	12:H:164:LYS:NZ	2.53	0.42
3:B:102:ARG:HD2	3:B:102:ARG:HA	1.80	0.42
8:E:193:ASP:N	8:E:193:ASP:OD1	2.51	0.42
10:G:125:SER:HA	10:G:138:ALA:HA	2.02	0.42
13:h:79:LEU:HD13	13:h:89:LEU:HG	2.01	0.42
20:R:103:ALA:HA	20:R:106:LYS:HG2	2.01	0.42
28:M:155:LYS:HA	28:M:155:LYS:HD3	1.72	0.42
1:A:1578:U:H2'	8:E:4:GLN:HB3	2.02	0.42
5:C:40:ASN:ND2	5:C:75:GLN:OE1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:H:67:VAL:HG23	12:H:99:GLY:HA2	2.00	0.42
13:h:129:ILE:HG12	13:h:151:VAL:HG11	2.01	0.42
23:U:51:ASN:HB2	23:U:54:TYR:HD2	1.84	0.42
1:A:35:C:H5''	1:A:579:C:H5''	2.02	0.42
1:A:345:U:OP1	28:M:37:LYS:NZ	2.50	0.42
1:A:1299:A:H5'	19:Q:52:LYS:HE3	2.02	0.42
13:h:57:ARG:NH1	20:R:97:GLN:O	2.52	0.42
13:h:89:LEU:HB2	13:h:99:ARG:HB2	2.01	0.42
1:A:1598:G:N2	1:A:1599:U:O4	2.45	0.42
1:A:1630:A:H5''	22:T:37:GLY:H	1.84	0.42
13:h:174:VAL:HB	13:h:188:HIS:HB2	2.01	0.42
14:I:9:VAL:HB	14:I:44:ASN:HD21	1.83	0.42
19:Q:121:ILE:HD12	19:Q:121:ILE:HA	1.89	0.42
20:R:126:ARG:HD3	20:R:126:ARG:HA	1.87	0.42
22:T:106:LYS:HD2	22:T:106:LYS:HA	1.76	0.42
22:T:142:ARG:HD3	22:T:142:ARG:HA	1.76	0.42
1:A:1294:G:H1	1:A:1305:C:H42	1.68	0.42
16:K:180:LYS:HD2	16:K:180:LYS:HA	1.80	0.42
1:A:1627:C:H5''	23:U:41:LYS:HZ3	1.85	0.42
13:h:116:ASP:OD1	13:h:116:ASP:N	2.50	0.42
13:h:200:VAL:HG23	13:h:207:CYS:HB3	2.02	0.42
15:J:10:LYS:O	15:J:18:ARG:NH1	2.53	0.42
21:S:16:ILE:O	21:S:20:TYR:N	2.50	0.42
23:U:110:LEU:HB3	23:U:112:MET:HG2	2.02	0.42
30:P:16:LEU:HD23	30:P:16:LEU:HA	1.93	0.42
1:A:163:U:OP2	12:H:87:ARG:NH1	2.36	0.42
1:A:912:C:C2	1:A:914:U:H1'	2.55	0.42
29:O:68:ILE:HD13	29:O:131:CYS:HB3	2.01	0.42
32:Y:85:ASP:OD2	32:Y:85:ASP:N	2.46	0.42
1:A:201:C:H3'	1:A:202:G:H8	1.84	0.41
1:A:969:U:OP1	1:A:970:G:O2'	2.29	0.41
12:H:1:MET:HE2	12:H:106:LEU:HB2	2.02	0.41
14:I:51:ILE:HG12	14:I:61:ILE:HD11	2.00	0.41
31:X:101:GLY:HA2	31:X:106:LYS:HB3	2.02	0.41
3:B:89:LYS:HZ1	21:S:82:ASP:HB2	1.84	0.41
5:C:77:ASP:OD1	5:C:77:ASP:N	2.52	0.41
13:h:111:VAL:HG23	13:h:122:SER:HB3	2.02	0.41
21:S:77:GLU:HB3	21:S:81:ARG:HH22	1.85	0.41
29:O:21:LYS:HD2	29:O:21:LYS:HA	1.76	0.41
1:A:857:U:H2'	1:A:858:A:C8	2.56	0.41
1:A:882:U:H3	1:A:904:A:H61	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1101:U:H2'	1:A:1102:G:C8	2.56	0.41
13:h:23:THR:HG21	13:h:292:SER:HA	2.02	0.41
16:K:151:LEU:HD23	16:K:151:LEU:HA	1.89	0.41
19:Q:52:LYS:HG3	19:Q:80:LEU:HD11	2.01	0.41
20:R:73:LYS:HB2	20:R:73:LYS:HE2	1.88	0.41
27:F:162:ASN:OD1	27:F:162:ASN:N	2.51	0.41
1:A:981:A:H2'	1:A:982:G:C8	2.55	0.41
1:A:1226:G:N1	1:A:1639:G:OP2	2.40	0.41
1:A:1392:U:H2'	1:A:1393:G:C8	2.55	0.41
1:A:1823:A:H3'	1:A:1824:A:H8	1.85	0.41
5:C:29:ASP:N	5:C:49:VAL:O	2.53	0.41
6:D:76:LYS:HA	6:D:76:LYS:HD3	1.87	0.41
8:E:222:PRO:HD2	13:h:226:HIS:CE1	2.55	0.41
10:G:55:ARG:HG3	20:R:125:ARG:HD3	2.02	0.41
16:K:50:LEU:HD13	16:K:105:PHE:HE2	1.85	0.41
19:Q:81:ARG:NH1	19:Q:120:SER:OG	2.54	0.41
19:Q:85:ILE:HD11	19:Q:116:LEU:HB3	2.01	0.41
25:W:27:LYS:HD3	25:W:27:LYS:HA	1.89	0.41
26:Z:74:MET:HB2	26:Z:74:MET:HE3	1.79	0.41
1:A:49:C:N4	1:A:473:A:OP2	2.43	0.41
1:A:64:A:OP1	12:H:177:GLN:NE2	2.53	0.41
1:A:871:U:H2'	1:A:873:G:H22	1.85	0.41
1:A:1010:G:H2'	1:A:1011:A:C8	2.55	0.41
7:d:13:ARG:HG2	7:d:55:VAL:HG22	2.03	0.41
11:g:100:LEU:HD23	11:g:100:LEU:HA	1.83	0.41
11:g:132:MET:HG3	11:g:141:CYS:HA	2.01	0.41
12:H:79:LYS:HE3	12:H:79:LYS:HB2	1.87	0.41
19:Q:81:ARG:HB3	19:Q:117:GLY:HA3	2.02	0.41
22:T:54:LYS:HE3	22:T:54:LYS:HB3	1.96	0.41
28:M:115:THR:OG1	28:M:117:GLU:O	2.25	0.41
1:A:1270:G:O2'	1:A:1299:A:N6	2.54	0.41
1:A:1541:G:H4'	23:U:15:VAL:HG21	2.02	0.41
5:C:103:MET:HG3	5:C:215:VAL:HB	2.02	0.41
16:K:19:PRO:O	16:K:24:ARG:NH2	2.53	0.41
19:Q:29:SER:H	19:Q:32:GLN:HE21	1.67	0.41
19:Q:90:VAL:HG11	19:Q:109:PRO:HG3	2.02	0.41
25:W:4:ASP:OD2	25:W:4:ASP:N	2.54	0.41
28:M:180:LEU:HD23	28:M:180:LEU:HA	1.93	0.41
5:C:33:VAL:HA	5:C:96:CYS:HB2	2.02	0.41
8:E:71:ALA:HA	8:E:74:GLN:HE21	1.86	0.41
10:G:14:THR:OG1	10:G:48:TYR:OH	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:119:SER:HB2	10:G:150:ALA:HB1	2.02	0.41
18:N:121:LYS:HB2	18:N:121:LYS:HE2	1.84	0.41
20:R:50:LYS:HB3	20:R:50:LYS:HE3	1.84	0.41
22:T:62:ASP:N	22:T:62:ASP:OD1	2.52	0.41
23:U:130:ASP:O	23:U:134:ILE:N	2.47	0.41
28:M:51:LYS:HD3	28:M:51:LYS:HA	1.81	0.41
30:P:99:ARG:NH2	30:P:119:GLU:OE2	2.54	0.41
1:A:1205:C:O2'	1:A:1834:A:N6	2.53	0.41
5:C:137:LEU:HG	5:C:215:VAL:HG22	2.01	0.41
6:D:254:ASP:N	6:D:254:ASP:OD1	2.51	0.41
1:A:28:U:H2'	1:A:29:G:H8	1.85	0.41
1:A:166:A:H1'	12:H:13:GLN:HE21	1.85	0.41
1:A:522:A:H5''	16:K:145:PRO:HD2	2.02	0.41
1:A:831:G:N7	26:Z:11:LYS:NZ	2.50	0.41
1:A:982:G:H2'	1:A:983:A:H8	1.86	0.41
1:A:1453:C:H2'	1:A:1454:A:H4'	2.02	0.41
10:G:101:HIS:O	10:G:105:GLY:N	2.51	0.41
12:H:70:HIS:HA	12:H:98:ARG:HH12	1.85	0.41
13:h:32:LEU:HD12	13:h:71:ILE:HG12	2.02	0.41
13:h:199:THR:HG21	13:h:240:CYS:HA	2.02	0.41
13:h:249:CYS:HA	13:h:258:ILE:HA	2.02	0.41
18:N:71:GLU:OE1	18:N:72:HIS:ND1	2.44	0.41
19:Q:86:LEU:HB3	19:Q:88:GLU:HG2	2.03	0.41
25:W:22:ARG:HE	25:W:22:ARG:HB3	1.60	0.41
27:F:156:ASP:OD1	27:F:156:ASP:N	2.53	0.41
28:M:25:SER:OG	28:M:26:VAL:N	2.54	0.41
28:M:132:GLY:N	28:M:136:ILE:O	2.43	0.41
32:Y:31:SER:H	32:Y:34:ILE:HD12	1.85	0.41
1:A:744:G:H22	1:A:797:C:H1'	1.86	0.41
1:A:1643:U:H2'	1:A:1644:C:C6	2.56	0.41
8:E:219:PRO:HG2	13:h:190:GLY:HA2	2.02	0.41
17:L:48:ALA:O	17:L:51:SER:OG	2.37	0.41
20:R:32:ILE:HG21	20:R:39:LEU:HD22	2.02	0.41
23:U:30:VAL:HA	23:U:31:PRO:HD3	1.96	0.41
1:A:171:A:OP2	12:H:137:ARG:NH2	2.46	0.40
1:A:846:G:OP2	28:M:108:ARG:NH2	2.44	0.40
1:A:1480:A:O2'	24:V:79:ARG:NH2	2.55	0.40
1:A:1513:C:H2'	1:A:1514:G:C8	2.56	0.40
12:H:61:PHE:HA	12:H:62:PRO:HD3	1.93	0.40
14:I:105:THR:HG23	14:I:107:LYS:H	1.86	0.40
19:Q:78:THR:N	19:Q:95:GLY:O	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:83:MET:HB3	19:Q:116:LEU:HD21	2.03	0.40
22:T:44:VAL:HG23	22:T:45:LEU:HD12	2.03	0.40
23:U:67:ARG:HE	23:U:67:ARG:HB3	1.58	0.40
1:A:903:A:H1'	1:A:904:A:C8	2.56	0.40
1:A:1474:A:H4'	20:R:121:VAL:HG11	2.03	0.40
1:A:1647:A:N1	1:A:1675:A:H5''	2.36	0.40
4:b:46:GLU:H	4:b:46:GLU:HG3	1.72	0.40
12:H:103:ASP:OD1	12:H:103:ASP:N	2.54	0.40
13:h:46:THR:OG1	13:h:48:ASP:OD1	2.31	0.40
13:h:54:ILE:HD13	13:h:54:ILE:HA	1.97	0.40
15:J:192:GLY:HA2	29:O:20:LYS:HD2	2.03	0.40
19:Q:57:LEU:HD22	19:Q:89:MET:HE3	2.04	0.40
23:U:27:LYS:HG3	23:U:110:LEU:HG	2.04	0.40
28:M:212:ASP:OD1	28:M:216:ASN:N	2.54	0.40
33:c:25:LYS:HD3	33:c:25:LYS:HA	1.81	0.40
5:C:131:ASP:OD1	5:C:131:ASP:N	2.55	0.40
5:C:147:ASN:OD1	5:C:147:ASN:N	2.46	0.40
7:d:45:ASN:HB3	10:G:139:VAL:HG12	2.03	0.40
12:H:201:LYS:HE3	12:H:201:LYS:HB3	1.90	0.40
22:T:5:ILE:HD12	22:T:6:PRO:HD2	2.03	0.40
26:Z:103:SER:HB3	26:Z:106:GLN:HG2	2.02	0.40
28:M:93:ASP:N	28:M:93:ASP:OD1	2.51	0.40
28:M:188:ASN:HB3	28:M:191:ARG:HD3	2.04	0.40
33:c:6:GLY:O	33:c:9:THR:OG1	2.38	0.40
1:A:429:C:O2'	1:A:811:A:N1	2.46	0.40
1:A:1221:G:O2'	1:A:1676:U:O2	2.28	0.40
1:A:1550:G:O2'	1:A:1558:C:O2	2.32	0.40
1:A:166:A:N3	12:H:13:GLN:NE2	2.68	0.40
1:A:1351:G:O2'	1:A:1378:A:N1	2.50	0.40
1:A:1692:U:H2'	1:A:1693:G:C8	2.57	0.40
2:a:81:GLY:O	2:a:85:ARG:N	2.52	0.40
7:d:51:ARG:NE	10:G:38:TYR:OH	2.55	0.40
10:G:96:ALA:HA	10:G:174:ALA:HB2	2.02	0.40
13:h:120:ILE:H	13:h:120:ILE:HG12	1.65	0.40
31:X:85:CYS:HB2	31:X:90:ILE:HB	2.03	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	
2	a	73/125 (58%)	66 (90%)	7 (10%)	0	100	100
3	B	215/295 (73%)	209 (97%)	6 (3%)	0	100	100
4	b	99/115 (86%)	93 (94%)	6 (6%)	0	100	100
5	C	211/264 (80%)	200 (95%)	11 (5%)	0	100	100
6	D	219/293 (75%)	216 (99%)	3 (1%)	0	100	100
7	d	60/69 (87%)	58 (97%)	2 (3%)	0	100	100
8	E	226/243 (93%)	212 (94%)	14 (6%)	0	100	100
9	f	55/133 (41%)	53 (96%)	2 (4%)	0	100	100
10	G	181/204 (89%)	170 (94%)	11 (6%)	0	100	100
11	g	66/156 (42%)	56 (85%)	10 (15%)	0	100	100
12	H	235/249 (94%)	226 (96%)	9 (4%)	0	100	100
13	h	311/317 (98%)	281 (90%)	30 (10%)	0	100	100
14	I	181/194 (93%)	172 (95%)	9 (5%)	0	100	100
15	J	204/208 (98%)	191 (94%)	13 (6%)	0	100	100
16	K	183/194 (94%)	180 (98%)	3 (2%)	0	100	100
17	L	94/165 (57%)	89 (95%)	5 (5%)	0	100	100
18	N	115/132 (87%)	101 (88%)	14 (12%)	0	100	100
19	Q	127/145 (88%)	115 (91%)	12 (9%)	0	100	100
20	R	140/146 (96%)	130 (93%)	10 (7%)	0	100	100
21	S	130/135 (96%)	117 (90%)	13 (10%)	0	100	100
22	T	142/152 (93%)	127 (89%)	15 (11%)	0	100	100
23	U	139/145 (96%)	130 (94%)	9 (6%)	0	100	100
24	V	98/119 (82%)	91 (93%)	7 (7%)	0	100	100
25	W	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
26	Z	122/130 (94%)	121 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	F	34/36 (94%)	32 (94%)	2 (6%)	0	100	100
28	M	261/263 (99%)	237 (91%)	24 (9%)	0	100	100
29	O	156/158 (99%)	137 (88%)	18 (12%)	1 (1%)	21	44
30	P	148/151 (98%)	137 (93%)	11 (7%)	0	100	100
31	X	134/168 (80%)	108 (81%)	26 (19%)	0	100	100
32	Y	127/130 (98%)	119 (94%)	7 (6%)	1 (1%)	16	37
33	c	140/143 (98%)	128 (91%)	11 (8%)	1 (1%)	18	41
34	e	82/84 (98%)	73 (89%)	9 (11%)	0	100	100
All	All	4789/5544 (86%)	4455 (93%)	331 (7%)	3 (0%)	49	73

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
29	O	5	GLN
33	c	130	LEU
32	Y	67	GLY

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	
2	a	66/103 (64%)	65 (98%)	1 (2%)	57	81
3	B	180/245 (74%)	179 (99%)	1 (1%)	78	91
4	b	88/98 (90%)	88 (100%)	0	100	100
5	C	194/231 (84%)	194 (100%)	0	100	100
6	D	187/225 (83%)	185 (99%)	2 (1%)	65	85
7	d	55/62 (89%)	55 (100%)	0	100	100
8	E	190/202 (94%)	189 (100%)	1 (0%)	81	92
9	f	47/106 (44%)	47 (100%)	0	100	100
10	G	158/170 (93%)	158 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	g	61/140 (44%)	60 (98%)	1 (2%)	55	80
12	H	207/218 (95%)	206 (100%)	1 (0%)	81	92
13	h	272/275 (99%)	272 (100%)	0	100	100
14	I	165/174 (95%)	165 (100%)	0	100	100
15	J	178/180 (99%)	178 (100%)	0	100	100
16	K	161/168 (96%)	161 (100%)	0	100	100
17	L	87/136 (64%)	87 (100%)	0	100	100
18	N	99/108 (92%)	99 (100%)	0	100	100
19	Q	115/130 (88%)	115 (100%)	0	100	100
20	R	117/121 (97%)	116 (99%)	1 (1%)	70	87
21	S	119/121 (98%)	118 (99%)	1 (1%)	73	88
22	T	125/132 (95%)	125 (100%)	0	100	100
23	U	111/115 (96%)	111 (100%)	0	100	100
24	V	92/107 (86%)	92 (100%)	0	100	100
25	W	67/67 (100%)	66 (98%)	1 (2%)	57	81
26	Z	107/112 (96%)	106 (99%)	1 (1%)	70	87
27	F	29/31 (94%)	29 (100%)	0	100	100
28	M	225/225 (100%)	225 (100%)	0	100	100
29	O	142/142 (100%)	142 (100%)	0	100	100
30	P	130/131 (99%)	129 (99%)	1 (1%)	73	88
31	X	106/130 (82%)	105 (99%)	1 (1%)	70	87
32	Y	112/113 (99%)	111 (99%)	1 (1%)	70	87
33	c	114/115 (99%)	113 (99%)	1 (1%)	70	87
34	e	76/76 (100%)	76 (100%)	0	100	100
All	All	4182/4709 (89%)	4167 (100%)	15 (0%)	81	93

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

Mol	Chain	Res	Type
2	a	113	THR
3	B	104	THR
6	D	209	VAL
6	D	262	THR
8	E	168	VAL

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Mol	Chain	Res	Type
11	g	98	VAL
12	H	133	LEU
20	R	100	VAL
21	S	31	ASN
25	W	13	VAL
26	Z	35	VAL
30	P	75	LEU
31	X	62	VAL
32	Y	104	LEU
33	c	125	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (62) such sidechains are listed below:

Mol	Chain	Res	Type
2	a	64	ASN
2	a	112	ASN
3	B	141	ASN
5	C	92	GLN
5	C	149	GLN
5	C	158	HIS
6	D	136	HIS
6	D	178	HIS
6	D	272	HIS
7	d	29	GLN
8	E	74	GLN
8	E	179	GLN
9	f	88	GLN
9	f	117	ASN
10	G	31	ASN
10	G	110	GLN
12	H	146	ASN
12	H	177	GLN
13	h	143	GLN
13	h	187	ASN
13	h	215	GLN
13	h	226	HIS
14	I	44	ASN
14	I	73	GLN
14	I	162	GLN
14	I	165	ASN
14	I	193	GLN
15	J	35	ASN

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Mol	Chain	Res	Type
15	J	64	ASN
15	J	165	GLN
15	J	181	GLN
16	K	124	HIS
16	K	125	HIS
17	L	7	ASN
17	L	39	ASN
17	L	84	HIS
18	N	15	ASN
18	N	48	HIS
19	Q	32	GLN
19	Q	35	GLN
19	Q	53	GLN
20	R	97	GLN
20	R	142	GLN
21	S	83	ASN
21	S	118	GLN
22	T	17	ASN
22	T	19	ASN
23	U	85	ASN
26	Z	106	GLN
27	F	178	ASN
28	M	179	ASN
29	O	83	GLN
29	O	154	GLN
30	P	5	HIS
30	P	69	ASN
30	P	105	ASN
31	X	32	HIS
32	Y	24	GLN
32	Y	64	ASN
33	c	16	HIS
33	c	97	ASN
34	e	83	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1685/1869 (90%)	354 (21%)	15 (0%)

All (354) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	A
1	A	3	C
1	A	17	C
1	A	25	A
1	A	33	G
1	A	41	G
1	A	44	U
1	A	45	A
1	A	46	A
1	A	56	G
1	A	58	C
1	A	62	G
1	A	65	C
1	A	67	C
1	A	68	A
1	A	71	G
1	A	73	C
1	A	74	G
1	A	76	U
1	A	77	A
1	A	79	A
1	A	103	A
1	A	111	A
1	A	113	G
1	A	115	U
1	A	126	G
1	A	129	C
1	A	130	G
1	A	143	U
1	A	146	G
1	A	147	A
1	A	155	G
1	A	162	C
1	A	163	U
1	A	175	A
1	A	180	G
1	A	183	G
1	A	184	G
1	A	187	G
1	A	188	C
1	A	190	G
1	A	192	C
1	A	206	G

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Mol	Chain	Res	Type
1	A	209	A
1	A	294	U
1	A	302	A
1	A	307	G
1	A	308	G
1	A	309	G
1	A	312	G
1	A	319	C
1	A	320	G
1	A	323	C
1	A	347	G
1	A	351	G
1	A	362	C
1	A	364	A
1	A	368	U
1	A	369	C
1	A	370	G
1	A	381	C
1	A	382	C
1	A	385	G
1	A	386	C
1	A	398	A
1	A	400	C
1	A	407	G
1	A	408	A
1	A	409	C
1	A	418	A
1	A	438	G
1	A	441	C
1	A	447	A
1	A	448	A
1	A	449	A
1	A	450	C
1	A	465	A
1	A	466	G
1	A	467	G
1	A	470	G
1	A	471	G
1	A	472	C
1	A	473	A
1	A	474	G
1	A	482	G

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Mol	Chain	Res	Type
1	A	487	U
1	A	492	C
1	A	508	A
1	A	509	G
1	A	516	A
1	A	531	A
1	A	532	C
1	A	533	A
1	A	541	U
1	A	544	G
1	A	547	G
1	A	548	C
1	A	549	C
1	A	551	U
1	A	554	A
1	A	556	U
1	A	559	G
1	A	561	A
1	A	562	U
1	A	568	C
1	A	576	A
1	A	583	A
1	A	587	A
1	A	588	G
1	A	589	G
1	A	590	A
1	A	591	U
1	A	604	A
1	A	605	A
1	A	606	G
1	A	607	U
1	A	608	C
1	A	614	C
1	A	627	U
1	A	628	A
1	A	629	A
1	A	631	U
1	A	643	A
1	A	644	G
1	A	655	A
1	A	660	C
1	A	662	G

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Mol	Chain	Res	Type
1	A	663	C
1	A	664	A
1	A	668	A
1	A	669	A
1	A	671	A
1	A	672	A
1	A	673	G
1	A	678	U
1	A	684	G
1	A	689	U
1	A	690	G
1	A	734	C
1	A	752	G
1	A	753	C
1	A	754	G
1	A	798	G
1	A	799	U
1	A	801	U
1	A	808	A
1	A	810	A
1	A	811	A
1	A	821	G
1	A	822	U
1	A	830	A
1	A	845	G
1	A	847	A
1	A	859	G
1	A	868	G
1	A	870	A
1	A	871	U
1	A	872	A
1	A	873	G
1	A	874	G
1	A	875	A
1	A	878	G
1	A	884	C
1	A	885	U
1	A	887	U
1	A	888	U
1	A	889	U
1	A	891	G
1	A	892	U

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Mol	Chain	Res	Type
1	A	894	G
1	A	895	G
1	A	898	U
1	A	901	G
1	A	903	A
1	A	909	G
1	A	913	A
1	A	914	U
1	A	920	A
1	A	933	G
1	A	934	G
1	A	938	A
1	A	943	U
1	A	955	A
1	A	963	A
1	A	971	G
1	A	978	G
1	A	990	A
1	A	992	A
1	A	999	G
1	A	1017	U
1	A	1023	A
1	A	1050	A
1	A	1060	A
1	A	1062	A
1	A	1080	A
1	A	1083	A
1	A	1085	C
1	A	1115	U
1	A	1116	C
1	A	1117	C
1	A	1118	C
1	A	1121	G
1	A	1133	A
1	A	1138	C
1	A	1143	A
1	A	1148	A
1	A	1149	A
1	A	1153	C
1	A	1154	U
1	A	1168	G
1	A	1195	A

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Mol	Chain	Res	Type
1	A	1203	G
1	A	1207	G
1	A	1208	A
1	A	1215	C
1	A	1221	G
1	A	1224	G
1	A	1242	U
1	A	1248	U
1	A	1251	A
1	A	1253	A
1	A	1256	G
1	A	1257	G
1	A	1258	A
1	A	1264	C
1	A	1273	C
1	A	1274	G
1	A	1275	G
1	A	1282	A
1	A	1284	A
1	A	1285	G
1	A	1286	G
1	A	1287	A
1	A	1295	A
1	A	1298	G
1	A	1301	A
1	A	1302	G
1	A	1303	C
1	A	1308	U
1	A	1309	C
1	A	1311	C
1	A	1320	G
1	A	1330	G
1	A	1332	A
1	A	1333	U
1	A	1341	C
1	A	1342	U
1	A	1343	U
1	A	1348	G
1	A	1354	G
1	A	1371	U
1	A	1372	U
1	A	1378	A

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Mol	Chain	Res	Type
1	A	1382	A
1	A	1396	A
1	A	1397	U
1	A	1398	G
1	A	1401	A
1	A	1402	A
1	A	1404	U
1	A	1424	G
1	A	1428	G
1	A	1431	G
1	A	1432	U
1	A	1449	G
1	A	1452	A
1	A	1454	A
1	A	1455	A
1	A	1463	U
1	A	1464	C
1	A	1466	G
1	A	1480	A
1	A	1484	A
1	A	1489	A
1	A	1490	G
1	A	1494	U
1	A	1498	A
1	A	1506	A
1	A	1507	G
1	A	1508	A
1	A	1510	G
1	A	1519	U
1	A	1520	G
1	A	1521	C
1	A	1522	A
1	A	1523	C
1	A	1533	A
1	A	1536	G
1	A	1547	C
1	A	1548	G
1	A	1552	G
1	A	1553	C
1	A	1554	C
1	A	1555	U
1	A	1556	A

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Mol	Chain	Res	Type
1	A	1557	C
1	A	1560	U
1	A	1570	G
1	A	1574	C
1	A	1578	U
1	A	1580	A
1	A	1582	C
1	A	1584	G
1	A	1585	U
1	A	1587	G
1	A	1588	A
1	A	1601	A
1	A	1602	U
1	A	1605	G
1	A	1606	G
1	A	1621	U
1	A	1622	U
1	A	1623	A
1	A	1637	A
1	A	1638	G
1	A	1646	C
1	A	1647	A
1	A	1648	G
1	A	1654	G
1	A	1663	A
1	A	1665	G
1	A	1671	G
1	A	1686	G
1	A	1698	C
1	A	1699	A
1	A	1701	C
1	A	1702	G
1	A	1715	A
1	A	1721	U
1	A	1722	G
1	A	1726	G
1	A	1744	G
1	A	1753	C
1	A	1757	G
1	A	1779	G
1	A	1780	G
1	A	1783	C

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Mol	Chain	Res	Type
1	A	1784	G
1	A	1785	C
1	A	1800	A
1	A	1801	A
1	A	1823	A
1	A	1825	A
1	A	1835	A
1	A	1836	G
1	A	1838	U
1	A	1849	G
1	A	1851	A
1	A	1861	G
1	A	1862	G
1	A	1863	A
1	A	1865	C
1	A	1867	U
1	A	1869	A

All (15) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	24	C
1	A	110	U
1	A	369	C
1	A	465	A
1	A	532	C
1	A	553	U
1	A	561	A
1	A	627	U
1	A	688	U
1	A	752	G
1	A	870	A
1	A	874	G
1	A	1137	U
1	A	1395	C
1	A	1646	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

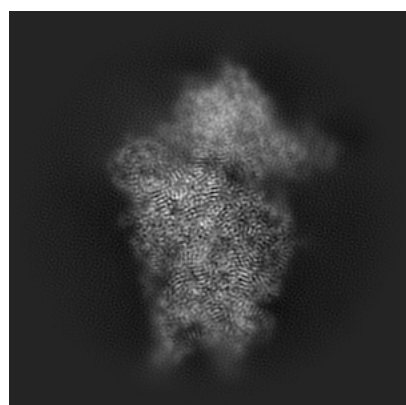
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22432. These allow visual inspection of the internal detail of the map and identification of artifacts.

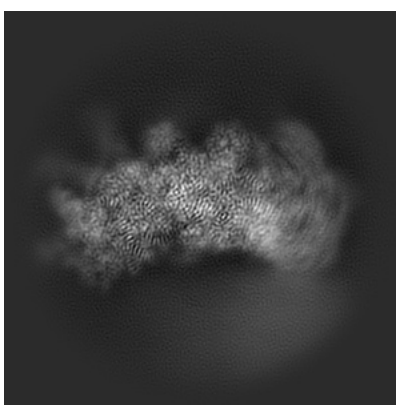
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

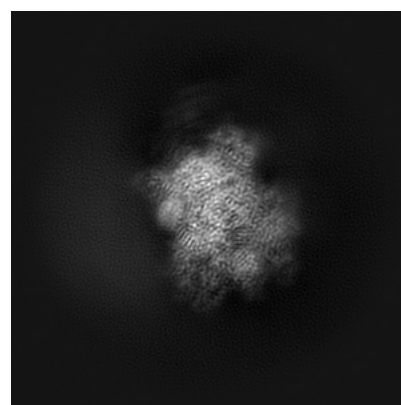
6.1.1 Primary map



X



Y

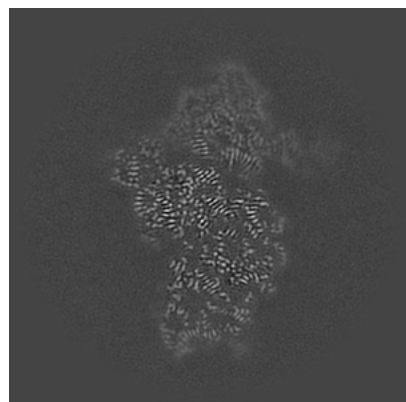


Z

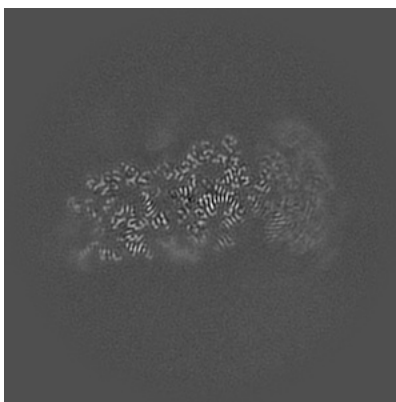
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

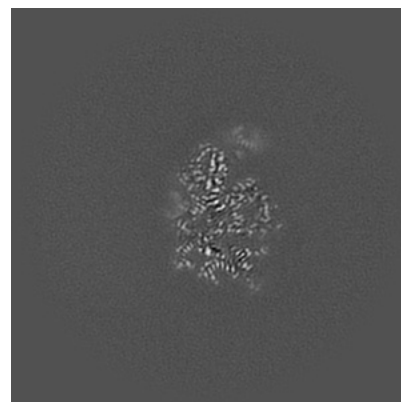
6.2.1 Primary map



X Index: 160



Y Index: 160

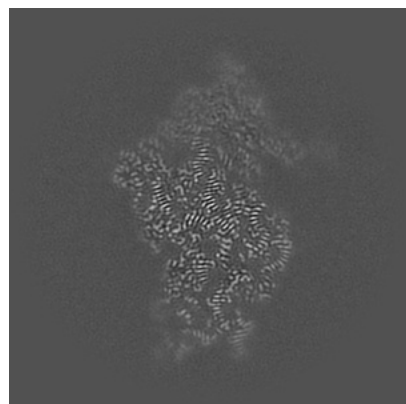


Z Index: 160

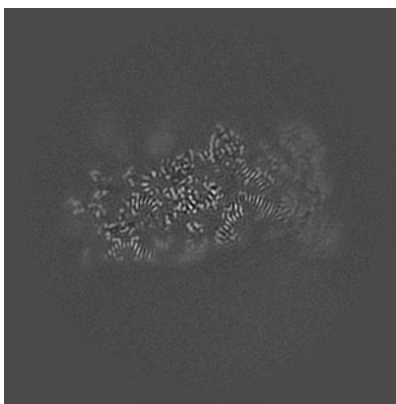
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

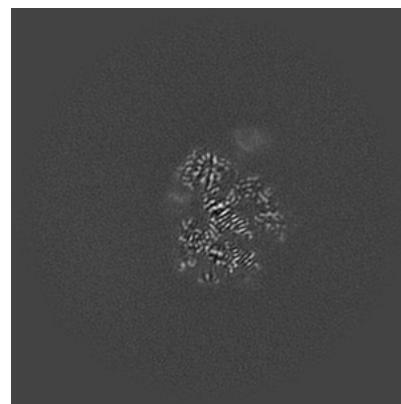
6.3.1 Primary map



X Index: 165



Y Index: 154

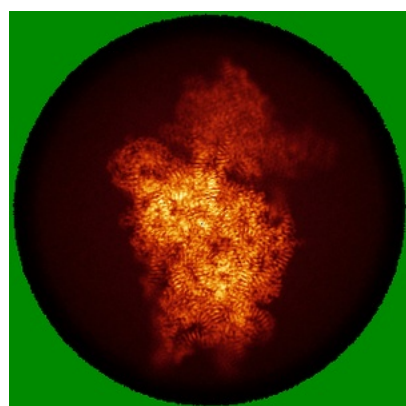


Z Index: 165

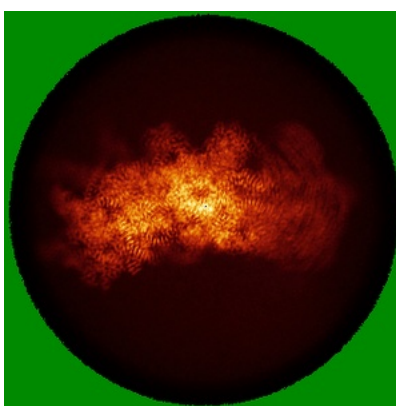
The images above show the largest variance slices of the map in three orthogonal directions.

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

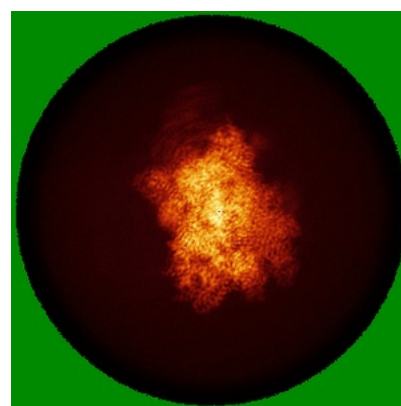
6.4.1 Primary map



X



Y

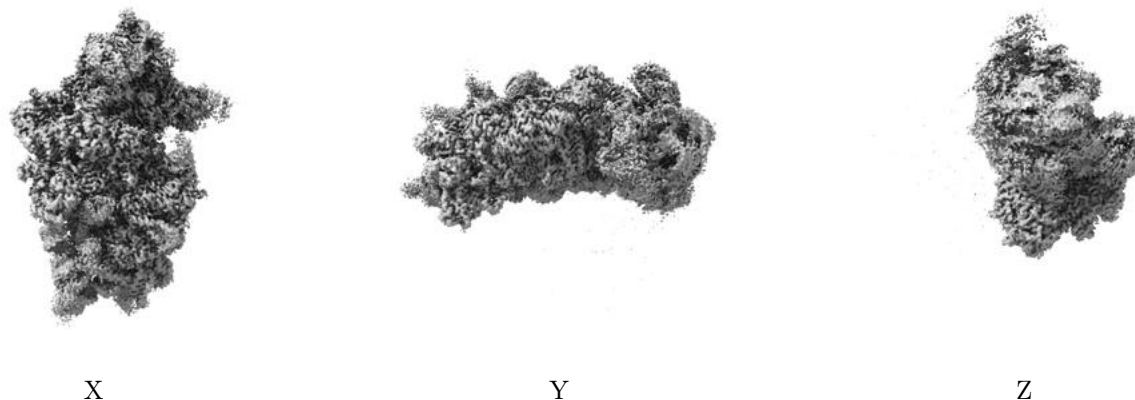


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.35. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

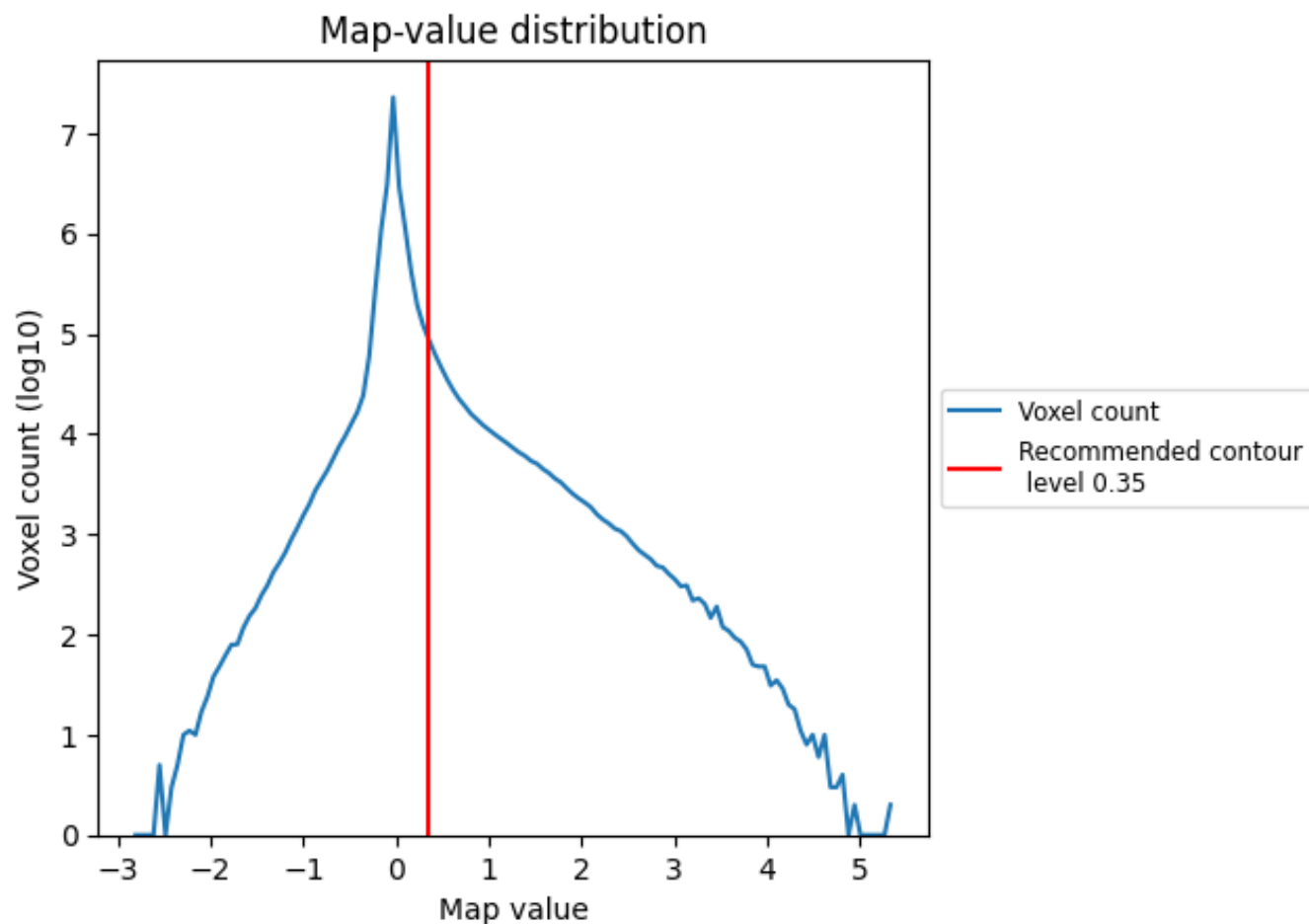
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

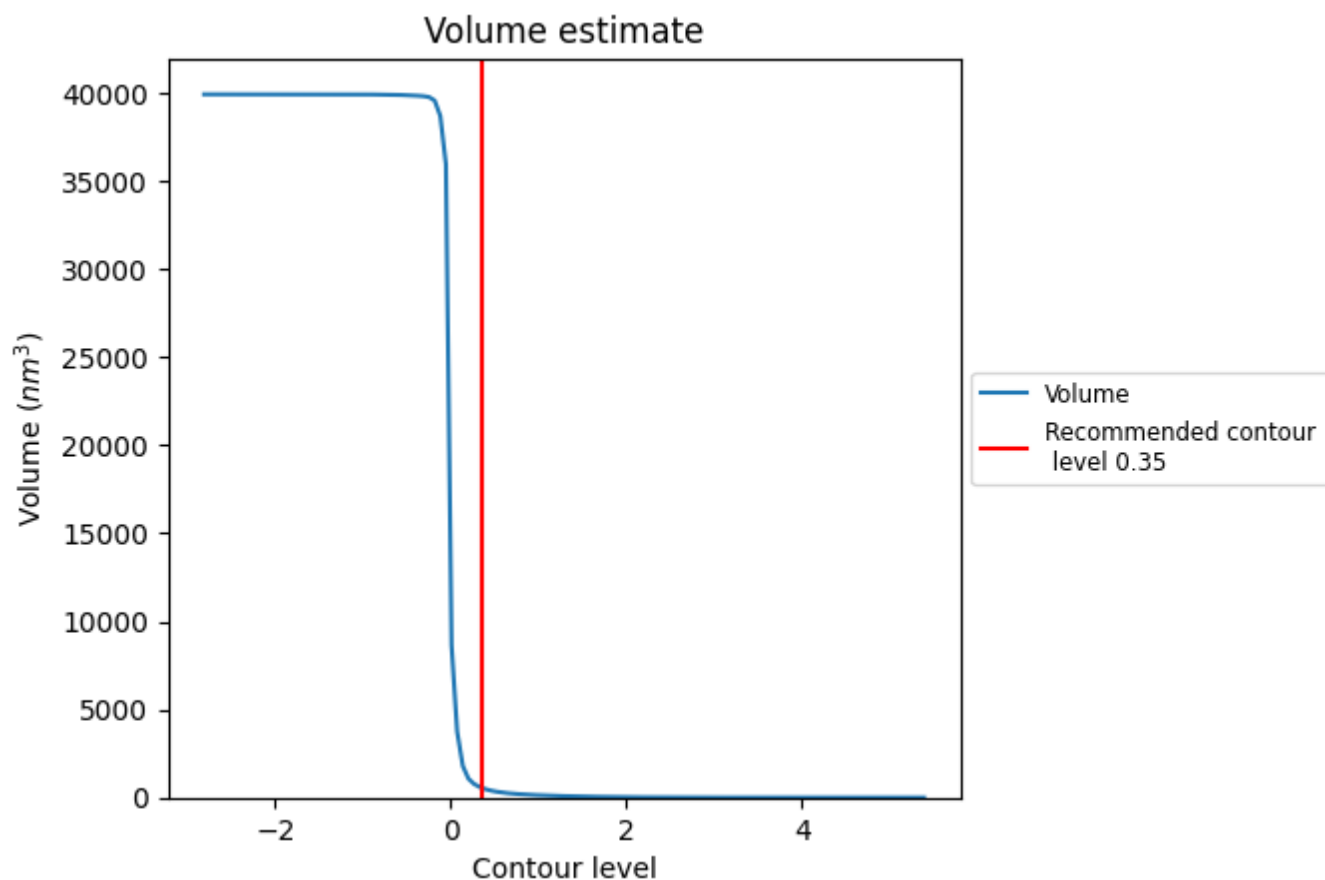
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

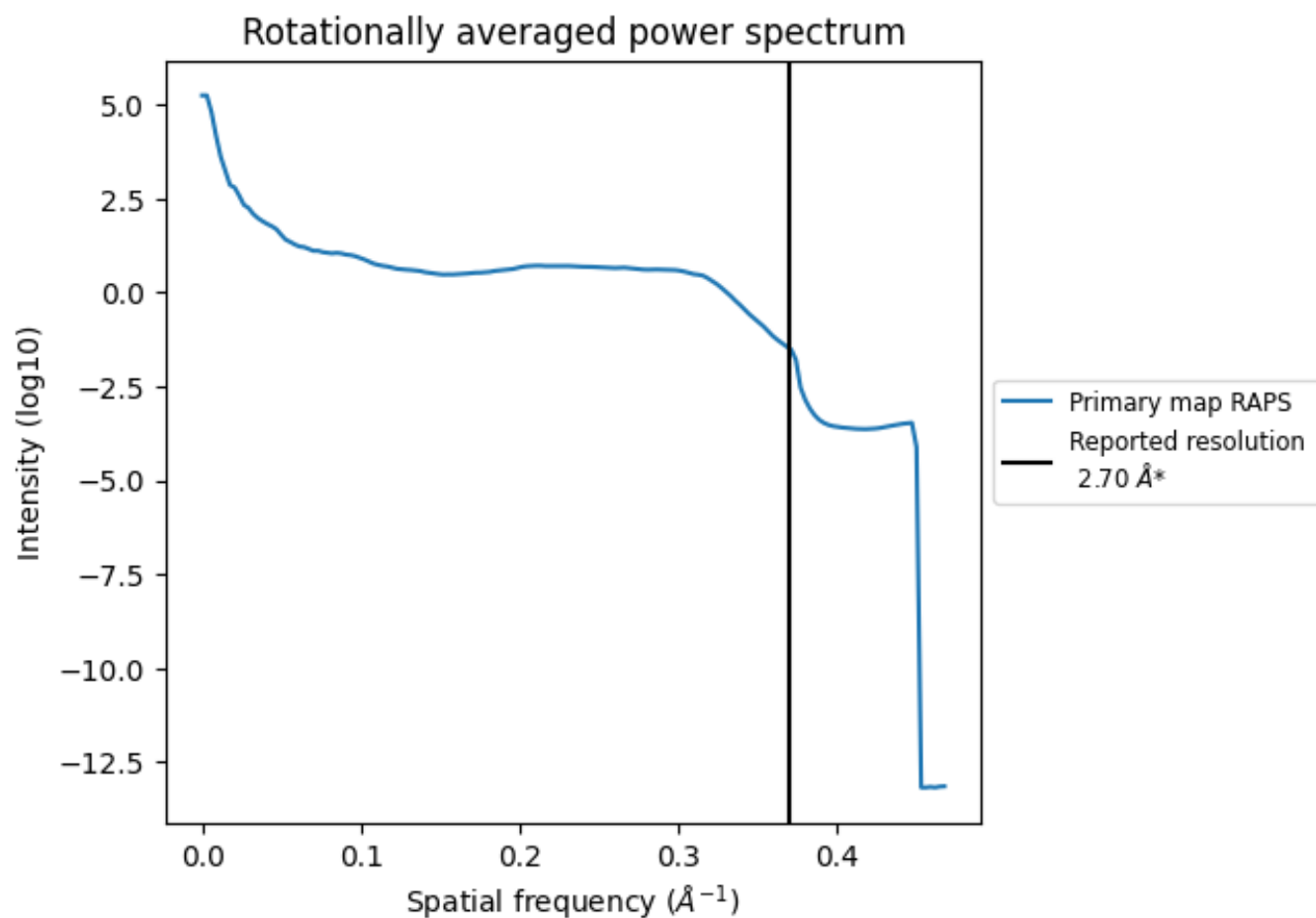
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 567 nm^3 ; this corresponds to an approximate mass of 512 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

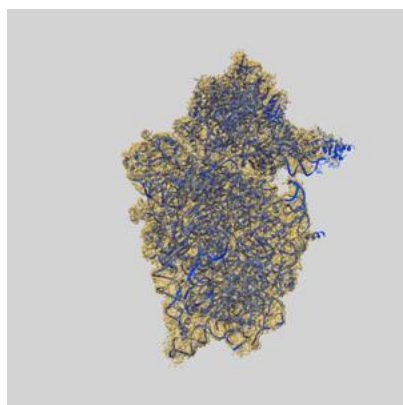
8 Fourier-Shell correlation ⓘ

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

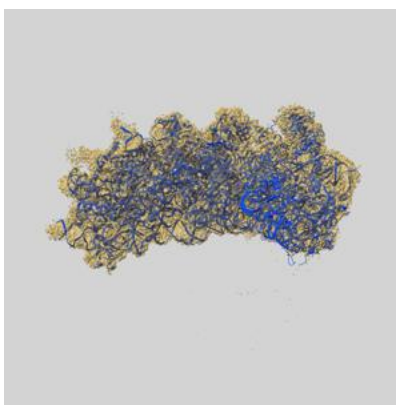
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22432 and PDB model 7JQB. Per-residue inclusion information can be found in section [3](#) on page [11](#).

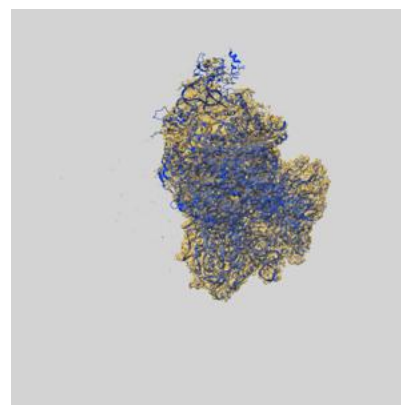
9.1 Map-model overlay [i](#)



X



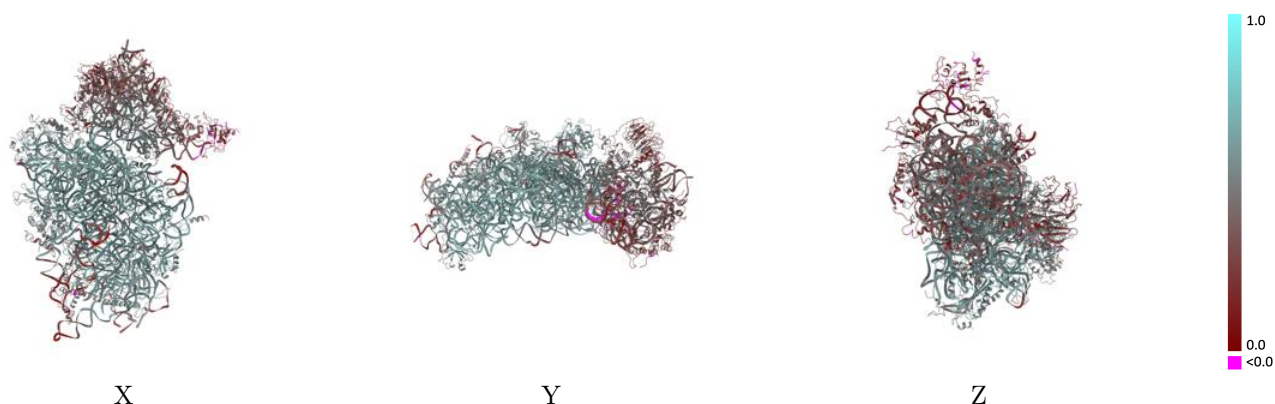
Y



Z

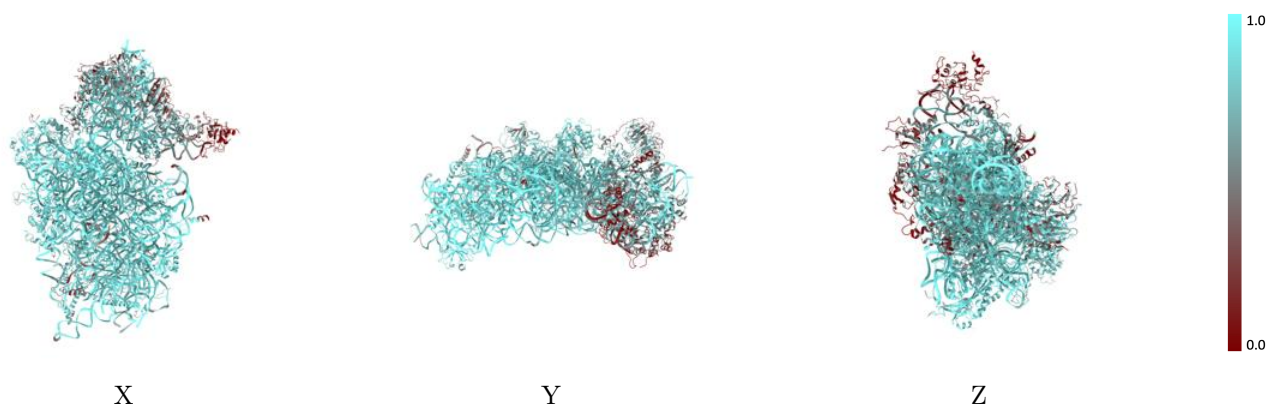
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



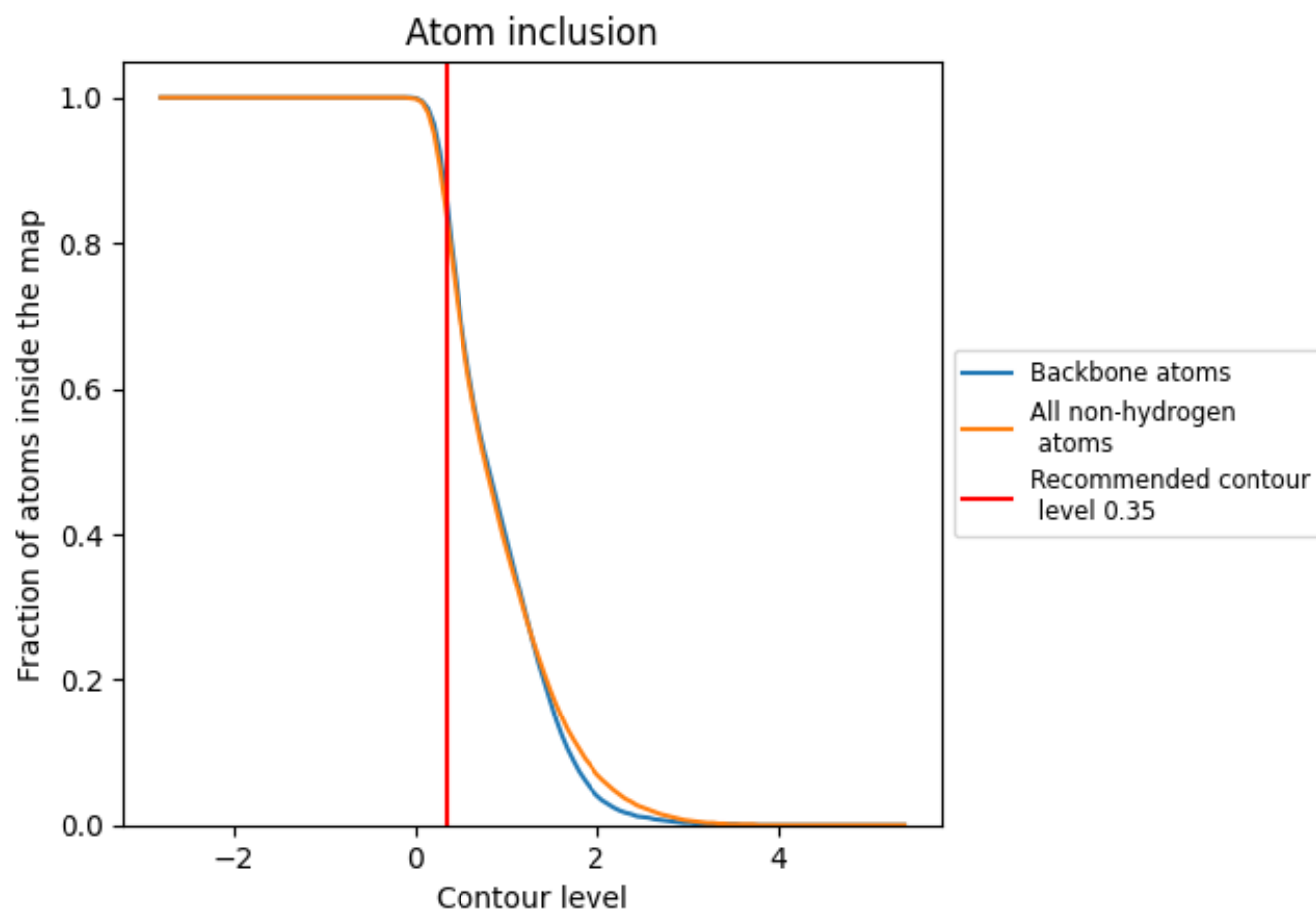
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.35).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 83% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8310	 0.4980
A	 0.9220	 0.5290
B	 0.9140	 0.5770
C	 0.9110	 0.5630
D	 0.9200	 0.5920
E	 0.6710	 0.4240
F	 0.8320	 0.5460
G	 0.5910	 0.3590
H	 0.8750	 0.5270
I	 0.8250	 0.5130
J	 0.8890	 0.5500
K	 0.9040	 0.5820
L	 0.6110	 0.3500
M	 0.9050	 0.5650
N	 0.0430	 0.1560
O	 0.7970	 0.5210
P	 0.8980	 0.5590
Q	 0.3630	 0.2950
R	 0.6890	 0.3670
S	 0.7600	 0.4560
T	 0.4040	 0.3280
U	 0.6510	 0.3590
V	 0.4780	 0.3560
W	 0.9240	 0.5800
X	 0.8580	 0.5090
Y	 0.9470	 0.6010
Z	 0.9310	 0.5800
a	 0.3670	 0.2860
b	 0.8960	 0.5660
c	 0.9180	 0.5810
d	 0.6090	 0.3920
e	 0.8500	 0.5320
f	 0.8160	 0.5310
g	 0.1020	 0.1760
h	 0.5390	 0.2980

