



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 11:43 AM UTC

PDB ID : 9V27 / pdb_00009v27
EMDB ID : EMD-64719
Title : Cryo- EM structure of small subunit (body) of 75S ribosome with A/P- & P/E- tRNAs from *Entamoeba histolytica*
Authors : Sharma, S.; Mishra, S.; Gourinath, S.; Kaushal, P.S.
Deposited on : 2025-05-19
Resolution : 3.21 Å(reported)
Based on initial model : .

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:

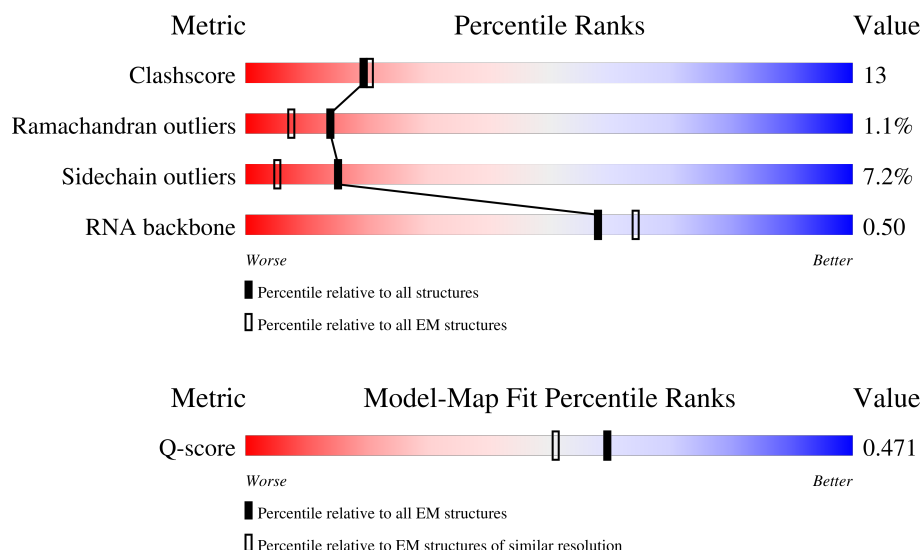
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.21 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.



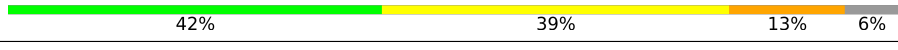
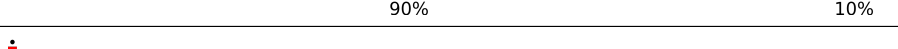
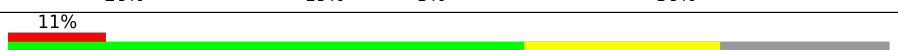
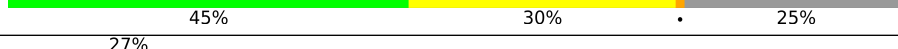
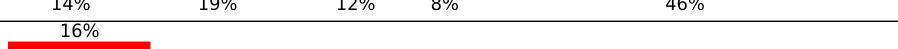
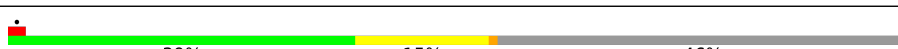
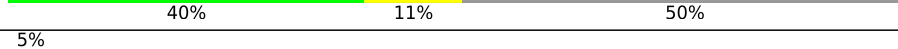
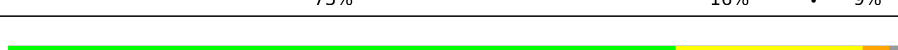
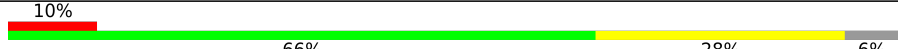
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14613 (2.71 - 3.71)

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	sB	144	
2	sC	84	
3	sH	6	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	sI	76	
5	sJ	77	
6	sK	10	
7	sa	1947	
8	sb	254	
9	sc	255	
10	se	256	
11	sf	326	
12	sh	266	
13	si	201	
14	sj	237	
15	sk	185	
16	sm	156	
17	so	151	
18	sp	146	
19	sr	130	
20	sx	86	
21	sy	141	
22	sz	140	

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 41199 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 protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	sB	98	Total	C	N	O	S	0	0
			787	478	169	134	6		

- Molecule 2 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	sC	31	Total	C	N	O	S	0	0
			238	152	41	44	1		

- Molecule 3 is a protein called Unknown peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	sH	2	Total	C	N	O	0	0
			9	6	2	1		

- Molecule 4 is a RNA chain called A/P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	sI	73	Total	C	N	O	P	0	0
			1556	695	283	506	72		

- Molecule 5 is a RNA chain called P/E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	sJ	72	Total	C	N	O	P	0	0
			1530	683	269	506	72		

- Molecule 6 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	sK	10	Total	C	N	O	P	0	0
			215	97	41	67	10		

- Molecule 7 is a RNA chain called 17S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	sa	975	Total	C	N	O	P	0	0
			20871	9343	3807	6746	975		

- Molecule 8 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	sb	205	Total	C	N	O	S	0	0
			1626	1029	286	296	15		

- Molecule 9 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	sc	215	Total	C	N	O	S	0	0
			1642	1052	291	291	8		

- Molecule 10 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	se	129	Total	C	N	O	S	0	0
			1042	669	186	181	6		

- Molecule 11 is a protein called 40S ribosomal protein S4, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	sf	246	Total	C	N	O	S	0	0
			1949	1245	364	329	11		

- Molecule 12 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	sh	143	Total	C	N	O	S	0	0
			1132	709	233	185	5		

- Molecule 13 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	si	72	Total	C	N	O	S	0	0
			568	367	105	95	1		

- Molecule 14 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	sj	129	Total	C	N	O	S	0	0
			1012	628	201	179	4		

- Molecule 15 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	sk	157	Total	C	N	O	S	0	0
			1288	825	245	212	6		

- Molecule 16 is a protein called 40S ribosomal protein S11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	sm	141	Total	C	N	O	S	0	0
			1161	735	224	196	6		

- Molecule 17 is a protein called 40S ribosomal protein S13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	so	76	Total	C	N	O	S	0	0
			644	410	123	108	3		

- Molecule 18 is a protein called Ribosomal protein S14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	sp	133	Total	C	N	O	S	0	0
			999	615	192	186	6		

- Molecule 19 is a protein called 40S ribosomal protein S15a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	sr	129	Total	C	N	O	S	0	0
			1022	650	186	181	5		

- Molecule 20 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	sx	81	Total	C	N	O	S	0	0
			634	402	113	116	3		

- Molecule 21 is a protein called 40S ribosomal protein S23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	sy	106	Total	C	N	O	S	0	0
			836	522	169	142	3		

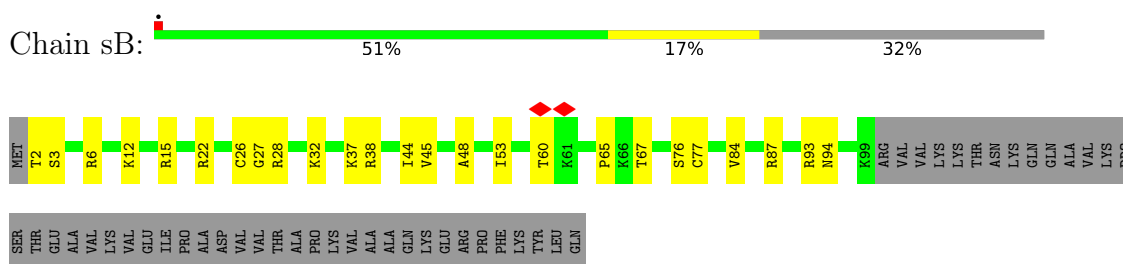
- Molecule 22 is a protein called 40S ribosomal protein S24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	sz	56	Total	C	N	O	S	0	0
			438	288	74	75	1		

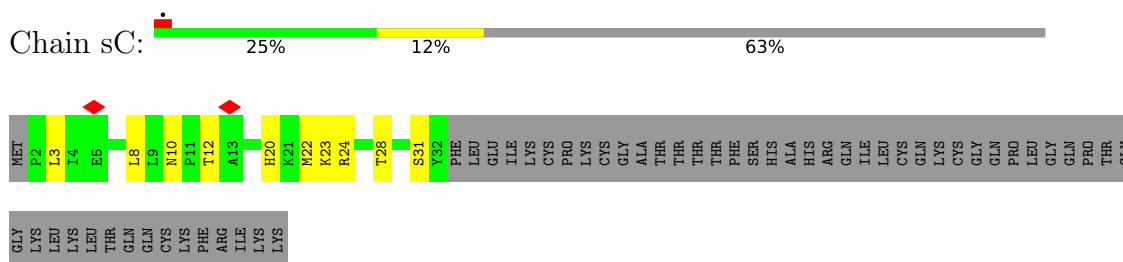
3 Residue-property plots [i](#)

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

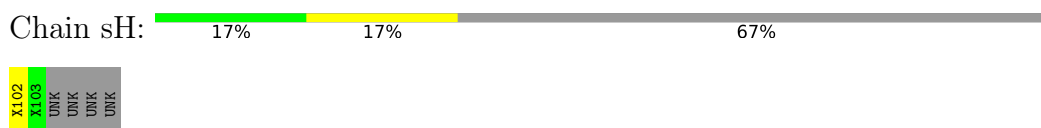
- Molecule 1: 40S ribosomal protein S26



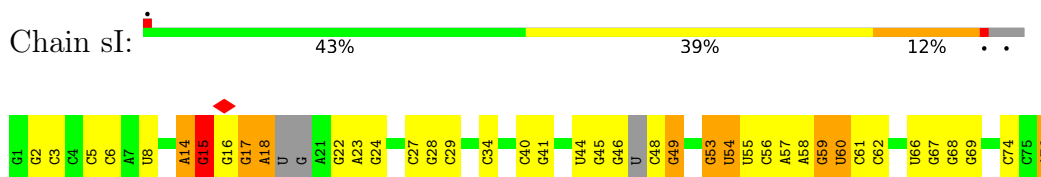
- Molecule 2: Small ribosomal subunit protein eS27



- Molecule 3: Unknown peptide

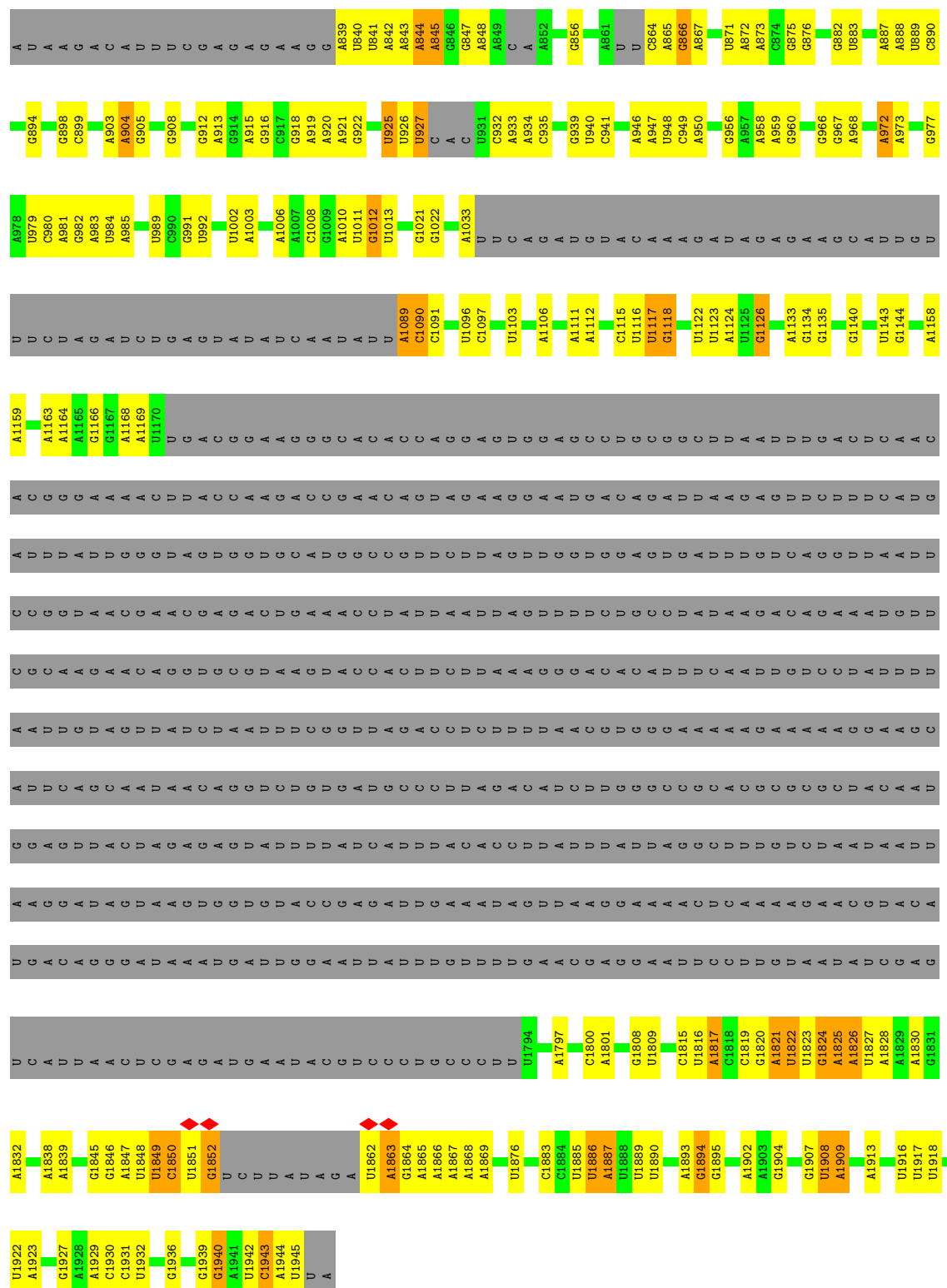


- Molecule 4: A/P-tRNA



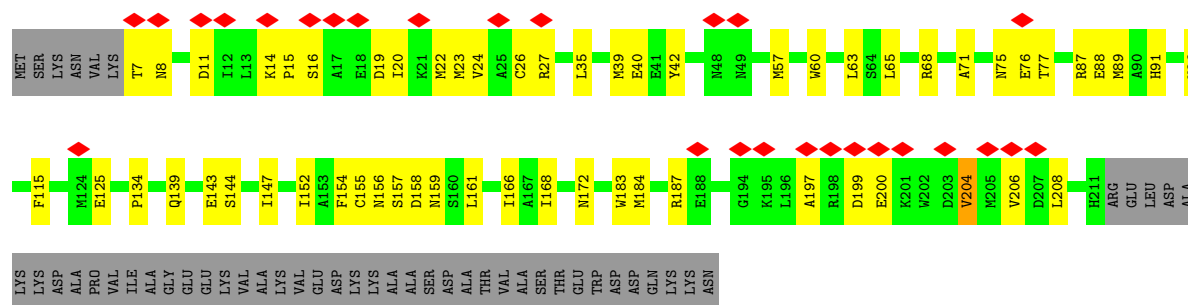
- Molecule 5: P/E-tRNA



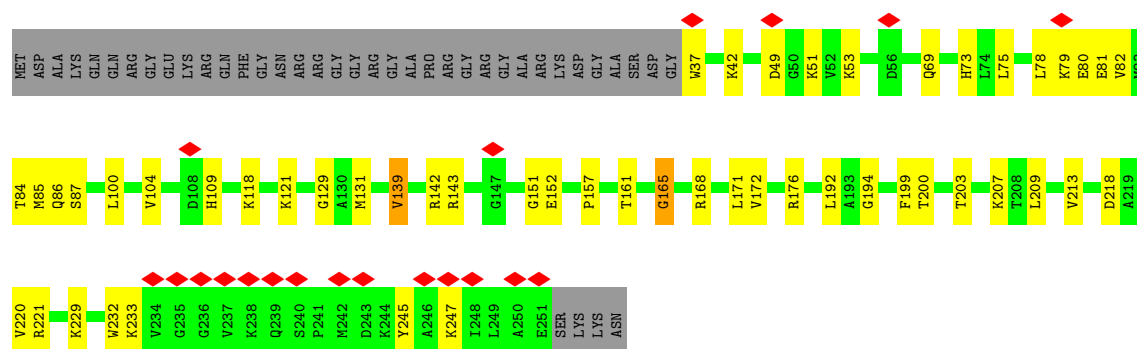


• Molecule 8: Small ribosomal subunit protein uS2

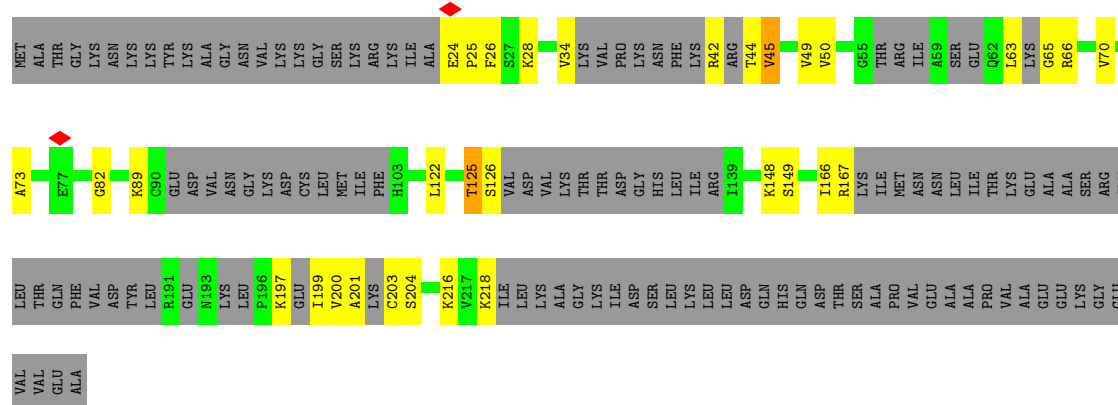
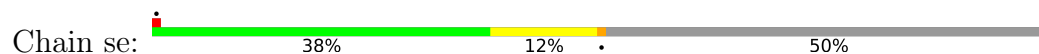




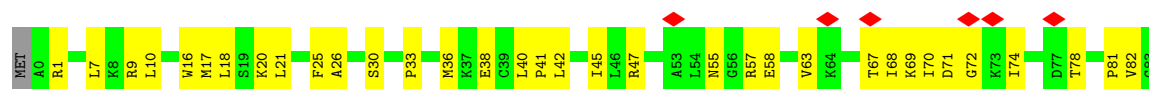
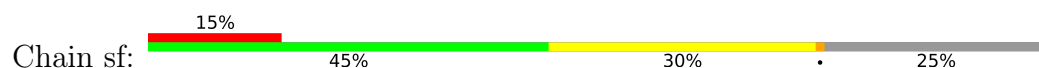
• Molecule 9: Small ribosomal subunit protein uS5

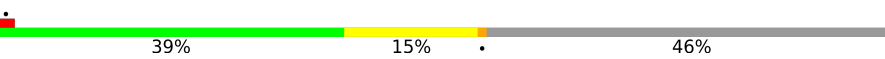


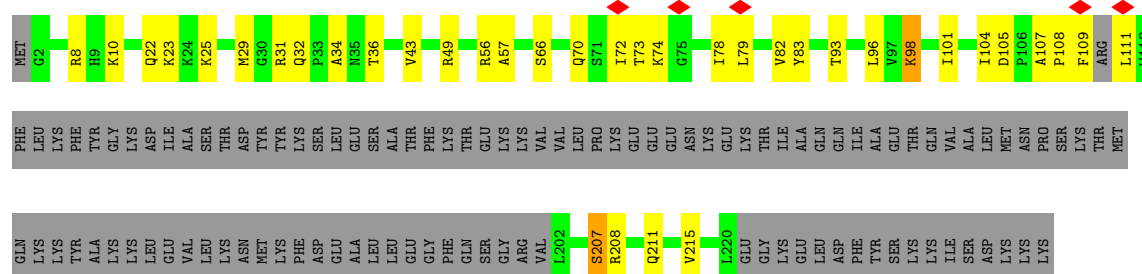
• Molecule 10: Small ribosomal subunit protein eS1



• Molecule 11: 40S ribosomal protein S4, putative

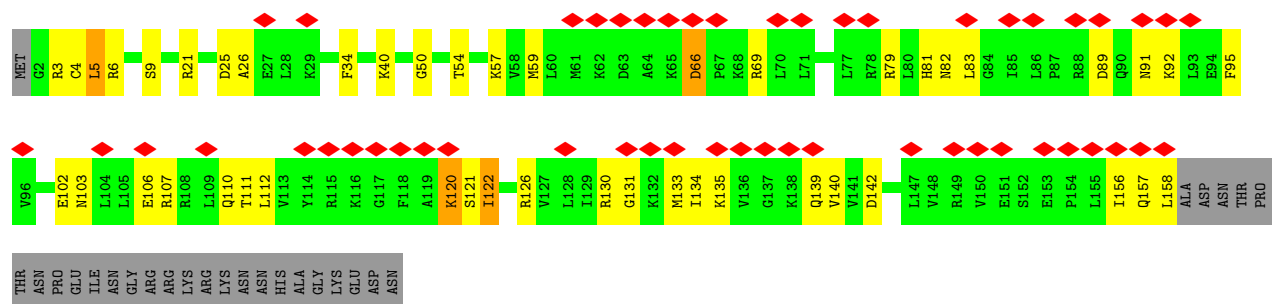


Chain sj: 



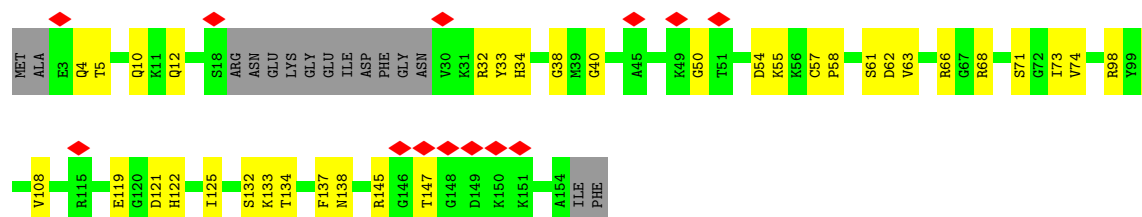
• Molecule 15: Small ribosomal subunit protein uS4

Chain sk: 



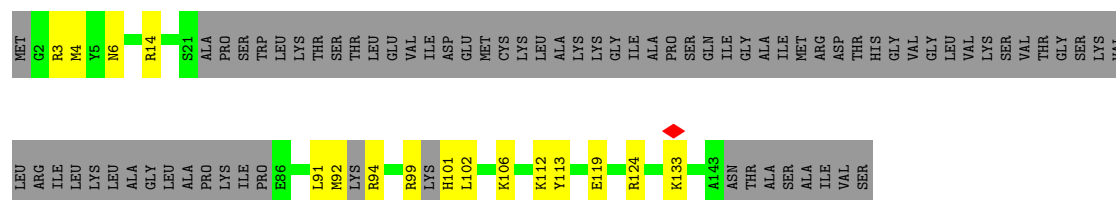
• Molecule 16: 40S ribosomal protein S11, putative

Chain sm: 



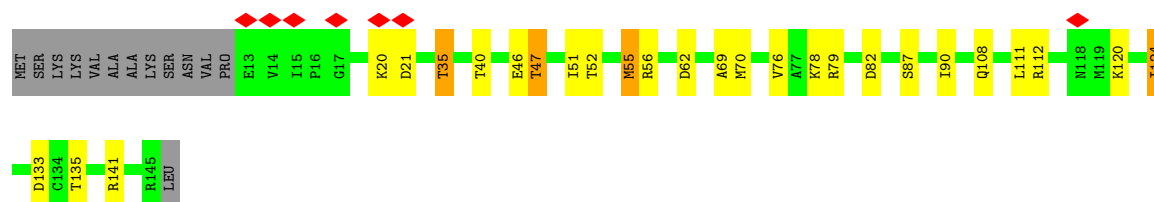
• Molecule 17: 40S ribosomal protein S13, putative

Chain so: 



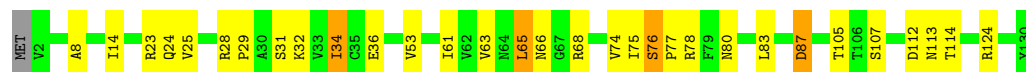
• Molecule 18: Ribosomal protein S14, putative

Chain sp: 



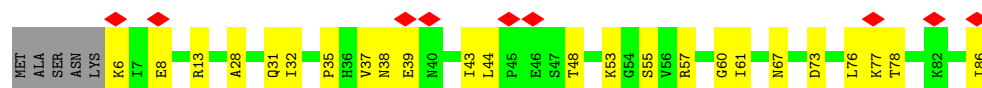
- Molecule 19: 40S ribosomal protein S15a, putative

Chain sr: 75% 21% . .



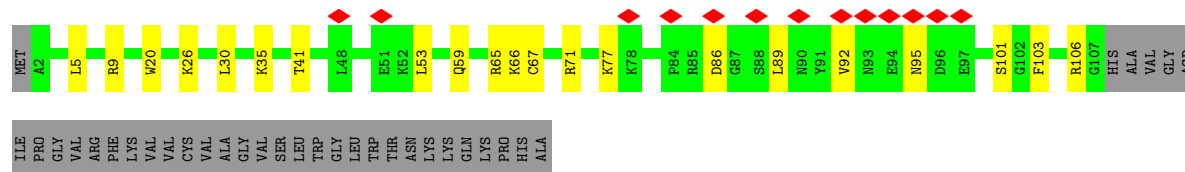
- Molecule 20: 40S ribosomal protein S21

Chain sx: 10% 66% 28% 6%



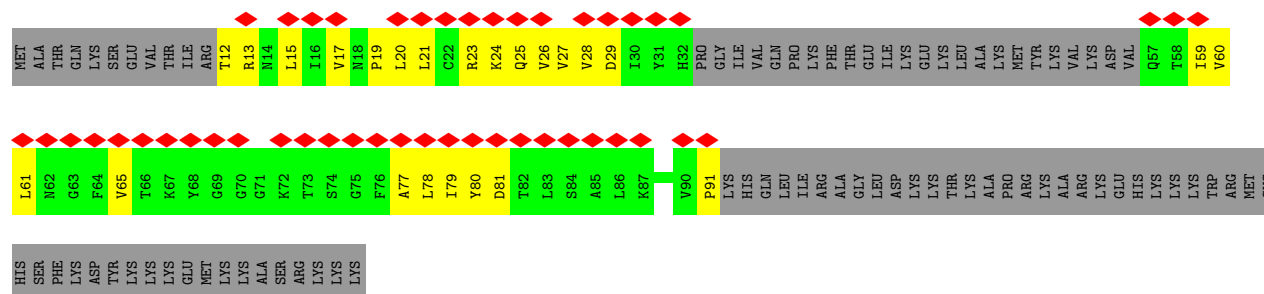
- Molecule 21: 40S ribosomal protein S23, putative

Chain sy: 9% 60% 15% 25%



- Molecule 22: 40S ribosomal protein S24, putative

Chain sz: 34% 23% 17% 60%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	39958	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.106	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	15.101	Depositor
Minimum map value	-5.678	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.2	Depositor
Map size (Å)	288.90002, 288.90002, 288.90002	wwPDB
Map dimensions	270, 270, 270	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	sB	0.22	0/797	0.27	0/1062
2	sC	0.16	0/243	0.28	0/330
4	sI	0.18	0/1737	0.39	1/2702 (0.0%)
5	sJ	0.16	0/1706	0.27	0/2649
6	sK	0.19	0/241	0.24	0/373
7	sa	0.25	5/23375 (0.0%)	0.33	3/36404 (0.0%)
8	sb	0.17	0/1659	0.26	0/2243
9	sc	0.20	0/1673	0.31	0/2257
10	se	0.18	0/1047	0.25	0/1380
11	sf	0.16	0/1990	0.30	0/2681
12	sh	1.65	36/1141 (3.2%)	1.46	24/1510 (1.6%)
13	si	0.15	0/578	0.29	0/777
14	sj	0.17	0/1025	0.26	0/1372
15	sk	0.14	0/1308	0.25	0/1749
16	sm	0.18	0/1187	0.27	0/1586
17	so	0.18	0/654	0.22	0/866
18	sp	0.19	0/1013	0.28	0/1361
19	sr	0.21	0/1040	0.33	0/1404
20	sx	0.20	0/646	0.30	0/876
21	sy	0.15	0/848	0.28	0/1131
22	sz	0.13	0/445	0.25	0/601
All	All	0.34	41/44353 (0.1%)	0.38	28/65314 (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
12	sh	0	2
19	sr	0	1
All	All	0	3

All (41) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	sh	106	ILE	CA-C	-16.05	1.31	1.52
12	sh	121	ILE	CA-C	-11.29	1.38	1.52
12	sh	106	ILE	C-O	-11.23	1.11	1.24
12	sh	106	ILE	CA-CB	-10.89	1.39	1.53
12	sh	142	ARG	N-CA	-10.24	1.34	1.46
12	sh	108	VAL	CA-C	-9.05	1.41	1.52
12	sh	109	LEU	CA-C	-8.70	1.42	1.52
12	sh	120	GLU	CA-C	-8.02	1.42	1.52
12	sh	143	LYS	CA-C	-7.87	1.42	1.52
12	sh	107	SER	CA-C	-7.74	1.42	1.52
12	sh	108	VAL	N-CA	-7.69	1.36	1.46
12	sh	117	GLY	CA-C	-7.41	1.41	1.51
12	sh	122	GLU	N-CA	-7.10	1.37	1.46
12	sh	139	SER	CA-C	-7.04	1.42	1.52
12	sh	106	ILE	N-CA	-7.04	1.36	1.46
12	sh	140	HIS	CA-C	-7.03	1.42	1.52
12	sh	108	VAL	CA-CB	-6.78	1.45	1.54
12	sh	113	VAL	CA-C	6.55	1.61	1.52
12	sh	110	ASN	C-O	-6.33	1.16	1.24
12	sh	142	ARG	CA-C	-6.30	1.45	1.52
12	sh	108	VAL	C-O	-6.28	1.16	1.24
12	sh	107	SER	C-N	-6.20	1.25	1.33
12	sh	109	LEU	N-CA	-6.18	1.38	1.45
12	sh	111	THR	N-CA	6.11	1.54	1.46
12	sh	103	ALA	CA-C	-5.78	1.45	1.52
7	sa	291	A	O3'-P	-5.65	1.52	1.61
12	sh	110	ASN	CA-C	-5.58	1.45	1.52
7	sa	293	U	O3'-P	-5.49	1.52	1.61
7	sa	295	A	O3'-P	-5.43	1.53	1.61
12	sh	141	ILE	C-N	-5.37	1.27	1.33
12	sh	117	GLY	C-O	-5.32	1.16	1.23
7	sa	1089	A	C1'-N9	-5.30	1.40	1.48
12	sh	136	LYS	C-N	-5.29	1.28	1.33
7	sa	1090	C	C1'-N1	5.29	1.56	1.48
12	sh	138	ALA	CA-C	-5.27	1.45	1.52
12	sh	137	ARG	C-O	-5.16	1.18	1.24
12	sh	119	GLY	CA-C	-5.12	1.45	1.51
12	sh	142	ARG	C-O	-5.12	1.18	1.24
12	sh	112	ILE	CA-C	-5.04	1.47	1.52
12	sh	138	ALA	C-O	-5.03	1.17	1.24
12	sh	113	VAL	N-CA	-5.03	1.40	1.46

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	sh	102	VAL	O-C-N	-18.00	103.31	122.57
12	sh	139	SER	N-CA-C	-14.95	94.33	113.17
12	sh	113	VAL	CB-CA-C	12.21	131.32	111.29
12	sh	111	THR	CB-CA-C	-9.87	90.78	110.42
12	sh	137	ARG	N-CA-C	-9.79	95.48	109.29
12	sh	134	GLY	N-CA-C	9.48	131.68	112.34
12	sh	106	ILE	N-CA-CB	-8.79	100.82	111.90
12	sh	114	VAL	N-CA-C	8.59	127.20	109.34
12	sh	109	LEU	N-CA-C	-8.54	96.05	109.72
12	sh	111	THR	N-CA-CB	8.09	124.17	110.49
12	sh	106	ILE	CB-CA-C	-7.98	100.62	110.99
7	sa	294	G	C1'-C2'-O2'	-7.90	99.95	111.80
12	sh	140	HIS	N-CA-C	-7.69	103.23	114.39
12	sh	110	ASN	CB-CA-C	-7.13	96.22	110.42
12	sh	114	VAL	N-CA-CB	-7.05	99.60	111.23
12	sh	121	ILE	CB-CA-C	-7.04	99.74	111.29
12	sh	142	ARG	N-CA-C	-7.02	103.23	111.03
12	sh	110	ASN	O-C-N	-6.53	113.90	122.59
12	sh	105	ASP	CB-CA-C	-5.92	103.86	111.50
12	sh	115	LYS	CA-C-O	-5.77	114.99	121.05
7	sa	293	U	C2'-C3'-O3'	-5.76	105.06	113.70
12	sh	141	ILE	N-CA-C	-5.57	104.85	113.16
12	sh	113	VAL	N-CA-CB	-5.52	102.12	111.23
7	sa	295	A	C2'-C3'-O3'	-5.41	101.38	109.50
12	sh	108	VAL	N-CA-C	5.12	119.99	109.34
4	sI	15	G	C4'-C3'-O3'	5.11	117.06	109.40
12	sh	104	GLY	N-CA-C	5.07	125.19	113.18
12	sh	105	ASP	N-CA-C	5.00	119.01	111.81

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	sh	102	VAL	Mainchain
12	sh	183	LEU	Peptide
19	sr	76	SER	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	sB	787	0	833	17	0
2	sC	238	0	250	5	0
3	sH	9	0	4	1	0
4	sI	1556	0	795	41	0
5	sJ	1530	0	778	27	0
6	sK	215	0	108	2	0
7	sa	20871	0	10485	335	0
8	sb	1626	0	1627	37	0
9	sc	1642	0	1721	32	0
10	se	1042	0	1094	21	0
11	sf	1949	0	2055	81	0
12	sh	1132	0	1245	211	0
13	si	568	0	599	14	0
14	sj	1012	0	1051	27	0
15	sk	1288	0	1391	30	0
16	sm	1161	0	1181	22	0
17	so	644	0	664	14	0
18	sp	999	0	1024	19	0
19	sr	1022	0	1051	24	0
20	sx	634	0	649	14	0
21	sy	836	0	885	12	0
22	sz	438	0	465	18	0
All	All	41199	0	29955	877	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 13.

All (877) 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)
12:sh:80:ARG:HH12	12:sh:81:ASN:ND2	1.31	1.26
12:sh:58:LYS:HG2	12:sh:105:ASP:HB2	1.43	1.01
7:sa:69:G:N2	7:sa:80:A:H62	1.58	1.00
12:sh:80:ARG:NH1	12:sh:81:ASN:ND2	2.13	0.96
7:sa:69:G:H21	7:sa:80:A:N6	1.64	0.95

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:sa:956:G:H1	7:sa:1003:A:HO2'	1.12	0.91
4:sI:14:A:H3'	4:sI:15:G:H8	1.33	0.91
7:sa:751:A:H61	7:sa:784:U:H3	1.18	0.89
7:sa:69:G:H21	7:sa:80:A:H62	1.16	0.89
7:sa:389:U:H3	7:sa:396:A:H62	1.21	0.88
12:sh:138:ALA:HB3	12:sh:182:ARG:C	1.98	0.88
12:sh:103:ALA:H	12:sh:106:ILE:HG13	1.39	0.87
7:sa:103:U:OP2	7:sa:305:A:N6	2.09	0.86
12:sh:74:ARG:HA	12:sh:96:THR:HA	1.56	0.86
4:sI:18:A:H5'	4:sI:57:A:H2	1.40	0.85
12:sh:64:MET:HE2	12:sh:80:ARG:HH22	1.42	0.84
12:sh:64:MET:CE	12:sh:80:ARG:HH22	1.91	0.83
12:sh:135:PRO:HB2	12:sh:141:ILE:HG12	1.61	0.83
7:sa:772:U:H3	22:sz:12:THR:HA	1.43	0.83
12:sh:111:THR:HA	12:sh:114:VAL:HB	1.61	0.82
12:sh:58:LYS:NZ	12:sh:106:ILE:C	2.37	0.82
12:sh:194:GLN:HG3	12:sh:195:LYS:HG2	1.60	0.82
12:sh:76:LEU:HA	12:sh:94:ARG:HA	1.62	0.81
7:sa:262:G:H1	7:sa:282:C:H42	1.30	0.80
11:sf:86:ASP:HA	11:sf:120:LYS:HD2	1.64	0.79
7:sa:401:U:H4'	12:sh:94:ARG:HH21	1.48	0.78
12:sh:80:ARG:HH12	12:sh:81:ASN:CG	1.90	0.78
12:sh:106:ILE:HG22	12:sh:107:SER:O	1.85	0.77
7:sa:262:G:N2	12:sh:194:GLN:OE1	2.17	0.77
12:sh:138:ALA:HA	12:sh:141:ILE:HB	1.65	0.76
12:sh:80:ARG:NH1	12:sh:81:ASN:CG	2.44	0.76
17:so:99:ARG:O	17:so:101:HIS:N	2.19	0.76
12:sh:58:LYS:HZ3	12:sh:107:SER:N	1.82	0.76
7:sa:1852:G:O6	7:sa:1863:A:N6	2.18	0.76
7:sa:601:G:H4'	7:sa:604:G:H21	1.50	0.76
12:sh:58:LYS:HZ3	12:sh:106:ILE:C	1.95	0.75
12:sh:112:ILE:O	12:sh:114:VAL:HG23	1.86	0.75
5:sJ:55:U:O2	5:sJ:59:A:N7	2.20	0.75
12:sh:121:ILE:O	12:sh:122:GLU:C	2.24	0.74
12:sh:138:ALA:N	12:sh:181:GLN:O	2.20	0.74
12:sh:98:ARG:NH2	12:sh:106:ILE:HD11	2.03	0.74
12:sh:209:GLU:N	12:sh:209:GLU:OE1	2.21	0.74
12:sh:70:ASN:HB3	12:sh:101:ILE:HB	1.69	0.73
7:sa:866:G:N2	18:sp:133:ASP:O	2.21	0.73
12:sh:117:GLY:O	12:sh:118:GLU:C	2.29	0.73
10:se:66:ARG:NH1	18:sp:46:GLU:OE2	2.21	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:sI:34:C:H42	6:sK:10:A:H61	1.37	0.72
12:sh:217:LEU:HG	12:sh:220:TYR:HB2	1.71	0.72
12:sh:107:SER:O	12:sh:108:VAL:C	2.25	0.71
12:sh:138:ALA:HB1	12:sh:183:LEU:HB2	1.71	0.71
12:sh:114:VAL:HG12	12:sh:115:LYS:N	2.05	0.71
15:sk:130:ARG:NH1	15:sk:142:ASP:O	2.22	0.71
1:sB:15:ARG:NH2	7:sa:916:G:N7	2.38	0.71
7:sa:783:A:H3'	7:sa:784:U:H4'	1.72	0.71
7:sa:845:A:OP1	19:sr:28:ARG:NH2	2.24	0.70
12:sh:112:ILE:C	12:sh:114:VAL:H	1.99	0.70
12:sh:102:VAL:HG11	12:sh:109:LEU:HD11	1.73	0.70
22:sz:59:ILE:HG22	22:sz:79:ILE:HG22	1.74	0.70
1:sB:2:THR:OG1	1:sB:3:SER:N	2.15	0.70
3:sH:102:UNK:N	4:sI:76:A:O3'	2.24	0.70
12:sh:58:LYS:NZ	12:sh:107:SER:N	2.38	0.70
7:sa:394:A:OP1	14:sj:49:ARG:NH2	2.24	0.70
9:sc:85:MET:HE1	9:sc:100:LEU:HB3	1.73	0.70
9:sc:152:GLU:N	9:sc:152:GLU:OE2	2.25	0.70
10:se:201:ALA:O	10:se:203:CYS:N	2.25	0.70
7:sa:332:G:O2'	14:sj:10:LYS:NZ	2.25	0.69
11:sf:127:ARG:NH2	12:sh:220:TYR:OH	2.25	0.69
7:sa:125:U:O2'	7:sa:203:C:O2	2.10	0.69
15:sk:25:ASP:OD1	15:sk:26:ALA:N	2.26	0.69
12:sh:54:GLY:N	12:sh:111:THR:HG1	1.90	0.68
12:sh:98:ARG:CZ	12:sh:106:ILE:HD11	2.23	0.68
7:sa:209:A:N6	7:sa:250:G:O6	2.26	0.68
12:sh:64:MET:CE	12:sh:80:ARG:NH2	2.55	0.68
7:sa:558:G:N2	7:sa:571:G:OP1	2.24	0.68
7:sa:865:A:OP1	10:se:218:LYS:NZ	2.22	0.68
12:sh:98:ARG:HD2	12:sh:99:GLY:H	1.57	0.68
12:sh:108:VAL:HA	12:sh:121:ILE:HA	1.75	0.68
4:sI:66:U:H2'	4:sI:67:G:H8	1.58	0.68
7:sa:941:C:OP2	17:so:14:ARG:NH1	2.18	0.68
4:sI:18:A:H5'	4:sI:57:A:C2	2.28	0.67
8:sb:197:ALA:HB3	8:sb:200:GLU:HG2	1.76	0.67
4:sI:17:G:C6	4:sI:58:A:C6	2.82	0.67
22:sz:60:VAL:HB	22:sz:78:LEU:HB2	1.76	0.67
5:sJ:15:G:N2	5:sJ:49:C:O2	2.26	0.67
7:sa:467:C:O2'	7:sa:760:A:N3	2.28	0.67
12:sh:63:MET:HA	12:sh:98:ARG:HB3	1.76	0.67
7:sa:623:U:OP2	7:sa:949:C:N4	2.27	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:sh:204:ILE:HA	12:sh:207:LEU:HD12	1.76	0.67
12:sh:114:VAL:CG1	12:sh:115:LYS:H	2.07	0.67
12:sh:121:ILE:O	12:sh:123:GLY:N	2.28	0.67
11:sf:105:ARG:HD3	11:sf:187:MET:HB3	1.77	0.67
10:se:42:ARG:O	10:se:44:THR:N	2.28	0.66
7:sa:115:U:O2'	7:sa:328:C:O2	2.11	0.66
12:sh:58:LYS:NZ	12:sh:106:ILE:N	2.44	0.66
12:sh:184:VAL:O	12:sh:188:ARG:NE	2.25	0.66
5:sJ:23:G:N7	5:sJ:47:G:O6	2.28	0.66
8:sb:154:PHE:O	8:sb:172:ASN:ND2	2.24	0.66
17:so:92:MET:O	17:so:94:ARG:N	2.28	0.66
7:sa:243:U:OP1	16:sm:33:TYR:OH	2.12	0.66
8:sb:8:ASN:ND2	20:sx:73:ASP:O	2.28	0.66
11:sf:169:ASP:OD1	11:sf:170:PHE:N	2.29	0.66
18:sp:55:MET:O	18:sp:56:ARG:NH1	2.29	0.66
4:sI:15:G:N2	4:sI:48:C:H42	1.94	0.66
14:sj:109:PHE:O	14:sj:111:LEU:N	2.29	0.65
12:sh:111:THR:CA	12:sh:114:VAL:HB	2.24	0.65
12:sh:187:ARG:HE	12:sh:190:GLN:HB2	1.61	0.65
17:so:102:LEU:HD21	17:so:112:LYS:HG2	1.79	0.65
9:sc:152:GLU:O	9:sc:176:ARG:NH2	2.30	0.65
1:sB:2:THR:HG21	7:sa:612:U:H1'	1.79	0.65
8:sb:139:GLN:NE2	8:sb:143:GLU:OE1	2.26	0.65
12:sh:142:ARG:HG3	12:sh:183:LEU:CD1	2.27	0.65
7:sa:794:U:H2'	7:sa:795:G:H8	1.61	0.64
22:sz:23:ARG:HH11	22:sz:25:GLN:HE21	1.45	0.64
7:sa:558:G:C5	7:sa:572:U:H1'	2.32	0.64
12:sh:116:LYS:C	12:sh:118:GLU:N	2.47	0.64
14:sj:83:TYR:HB3	14:sj:101:ILE:HB	1.79	0.64
16:sm:4:GLN:NE2	16:sm:10:GLN:O	2.31	0.64
4:sI:14:A:H2'	4:sI:15:G:O4'	1.98	0.64
16:sm:147:THR:HG1	17:so:133:LYS:HZ3	1.45	0.64
18:sp:90:ILE:HB	18:sp:124:ILE:HG23	1.78	0.64
7:sa:157:A:H5'	12:sh:62:PRO:HB3	1.79	0.63
7:sa:395:G:H5''	14:sj:25:LYS:HA	1.79	0.63
12:sh:67:VAL:HG11	12:sh:73:VAL:HG11	1.79	0.63
12:sh:114:VAL:CG1	12:sh:115:LYS:N	2.61	0.63
7:sa:389:U:O4	7:sa:396:A:N7	2.32	0.63
12:sh:116:LYS:O	12:sh:118:GLU:N	2.31	0.63
7:sa:250:G:H21	14:sj:73:THR:HG21	1.62	0.63
7:sa:783:A:N7	7:sa:784:U:O2'	2.32	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:sh:74:ARG:HA	12:sh:96:THR:CA	2.27	0.63
7:sa:960:G:H4'	7:sa:1923:A:H4'	1.80	0.63
7:sa:389:U:H1'	12:sh:92:ARG:HH12	1.64	0.63
9:sc:218:ASP:OD1	9:sc:221:ARG:NH1	2.32	0.63
12:sh:114:VAL:HG12	12:sh:115:LYS:H	1.63	0.63
12:sh:138:ALA:HB3	12:sh:182:ARG:O	1.99	0.63
15:sk:81:HIS:NE2	15:sk:91:ASN:OD1	2.28	0.63
8:sb:19:ASP:OD2	8:sb:187:ARG:NH2	2.30	0.63
12:sh:64:MET:HE2	12:sh:80:ARG:NH2	2.14	0.63
11:sf:58:GLU:HB3	22:sz:21:LEU:HD11	1.80	0.62
11:sf:153:GLN:N	11:sf:156:ASP:OD2	2.30	0.62
7:sa:972:A:O2'	7:sa:1932:U:O2	2.17	0.62
7:sa:148:G:N2	12:sh:56:CYS:SG	2.70	0.62
7:sa:866:G:H2'	7:sa:867:A:C8	2.35	0.62
8:sb:76:GLU:HG2	8:sb:77:THR:HG23	1.80	0.62
4:sI:18:A:N1	4:sI:56:C:N3	2.48	0.62
7:sa:263:U:O4	7:sa:281:A:N6	2.33	0.62
7:sa:875:G:H21	18:sp:47:THR:HG21	1.64	0.62
8:sb:16:SER:OG	8:sb:19:ASP:OD1	2.16	0.62
7:sa:562:G:N7	21:sy:65:ARG:NH2	2.46	0.62
1:sB:32:LYS:O	1:sB:37:LYS:NZ	2.33	0.62
11:sf:98:ARG:HB2	11:sf:112:LEU:HD11	1.81	0.62
7:sa:366:G:N2	7:sa:606:U:O2	2.33	0.61
7:sa:414:G:H4'	12:sh:72:ARG:HH12	1.65	0.61
7:sa:746:A:H2'	7:sa:747:A:C8	2.35	0.61
11:sf:93:THR:HG22	22:sz:19:PRO:HG2	1.80	0.61
7:sa:345:A:H5''	7:sa:346:U:H3'	1.81	0.61
12:sh:57:ASP:H	12:sh:61:PHE:H	1.47	0.61
12:sh:188:ARG:HD3	12:sh:191:HIS:HB2	1.81	0.61
11:sf:69:LYS:NZ	11:sf:72:GLY:O	2.33	0.61
7:sa:844:A:OP1	19:sr:28:ARG:NH1	2.33	0.61
12:sh:74:ARG:HD2	12:sh:96:THR:HB	1.83	0.61
1:sB:37:LYS:O	1:sB:38:ARG:NH1	2.34	0.61
4:sI:17:G:H4'	4:sI:18:A:OP1	2.00	0.61
7:sa:841:U:O2'	7:sa:842:A:O4'	2.19	0.61
8:sb:39:MET:HE2	8:sb:155:CYS:HB3	1.80	0.61
7:sa:1089:A:C5	7:sa:1090:C:C4	2.90	0.60
12:sh:181:GLN:HA	12:sh:185:THR:HG23	1.82	0.60
7:sa:51:U:H2'	7:sa:52:G:H8	1.67	0.60
9:sc:165:GLY:O	9:sc:168:ARG:NH1	2.31	0.60
7:sa:746:A:H2'	7:sa:747:A:H8	1.63	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:sf:127:ARG:HB2	11:sf:137:ILE:HG22	1.83	0.60
12:sh:144:LEU:CD2	12:sh:158:ILE:HD11	2.32	0.60
16:sm:74:VAL:HG12	16:sm:119:GLU:HA	1.83	0.60
7:sa:172:G:N7	7:sa:173:A:N6	2.49	0.60
7:sa:442:U:OP1	11:sf:47:ARG:NH1	2.35	0.60
7:sa:772:U:O2	22:sz:13:ARG:N	2.35	0.60
21:sy:26:LYS:HG2	21:sy:30:LEU:HD23	1.83	0.60
7:sa:784:U:OP1	11:sf:105:ARG:NH1	2.35	0.60
7:sa:327:U:OP1	14:sj:31:ARG:NH1	2.33	0.60
7:sa:865:A:H2'	7:sa:866:G:C8	2.37	0.60
7:sa:1124:A:OP1	9:sc:161:THR:OG1	2.17	0.60
22:sz:13:ARG:HB3	22:sz:27:VAL:HB	1.83	0.60
7:sa:111:A:O2'	16:sm:66:ARG:NH1	2.35	0.59
11:sf:57:ARG:HG2	22:sz:91:PRO:HG3	1.82	0.59
7:sa:77:A:N1	12:sh:187:ARG:HB2	2.18	0.59
7:sa:1838:A:H2'	7:sa:1839:A:C8	2.37	0.59
7:sa:208:C:H2'	7:sa:209:A:H8	1.68	0.59
11:sf:120:LYS:NZ	11:sf:141:ASP:OD2	2.34	0.59
4:sI:15:G:N2	4:sI:59:G:N7	2.50	0.59
7:sa:414:G:H4'	12:sh:72:ARG:NH1	2.18	0.59
7:sa:1868:A:H4'	12:sh:80:ARG:HE	1.68	0.59
11:sf:105:ARG:NH2	11:sf:185:ASN:O	2.36	0.59
18:sp:51:ILE:HG23	18:sp:55:MET:HE2	1.83	0.59
7:sa:947:A:OP2	17:so:124:ARG:NH2	2.36	0.59
7:sa:1816:U:H2'	7:sa:1817:A:C8	2.37	0.59
10:se:197:LYS:O	10:se:199:ILE:N	2.35	0.59
7:sa:584:C:H2'	7:sa:585:A:H8	1.68	0.58
7:sa:769:C:H2'	7:sa:770:A:C8	2.38	0.58
9:sc:84:THR:HB	9:sc:209:LEU:HD13	1.85	0.58
16:sm:108:VAL:HG12	16:sm:137:PHE:HB2	1.83	0.58
7:sa:601:G:H4'	7:sa:604:G:N2	2.17	0.58
7:sa:887:A:H2'	7:sa:888:A:C8	2.38	0.58
7:sa:1868:A:O2'	12:sh:66:GLY:HA3	2.04	0.58
13:si:136:LEU:HD11	13:si:195:PHE:HE2	1.68	0.58
7:sa:574:A:O2'	7:sa:576:U:OP1	2.20	0.58
12:sh:58:LYS:HZ1	12:sh:106:ILE:N	2.00	0.58
7:sa:78:G:OP2	12:sh:159:ARG:NH1	2.36	0.58
7:sa:301:U:O2	16:sm:68:ARG:NH2	2.34	0.58
7:sa:335:U:H2'	7:sa:336:A:H8	1.68	0.58
7:sa:763:G:H21	7:sa:765:A:H1'	1.68	0.58
14:sj:72:ILE:HD11	14:sj:74:LYS:HE2	1.83	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:sJ:23:G:O2'	5:sJ:24:C:OP1	2.22	0.58
7:sa:319:U:OP1	16:sm:133:LYS:NZ	2.35	0.58
12:sh:138:ALA:C	12:sh:182:ARG:O	2.46	0.58
12:sh:74:ARG:CA	12:sh:96:THR:HA	2.29	0.58
4:sI:58:A:O2'	4:sI:60:U:OP2	2.13	0.58
9:sc:143:ARG:NH1	9:sc:194:GLY:O	2.37	0.58
10:se:63:LEU:O	10:se:65:GLY:N	2.37	0.58
7:sa:77:A:H61	12:sh:187:ARG:HD2	1.68	0.57
7:sa:1845:G:H21	7:sa:1869:A:H62	1.50	0.57
21:sy:35:LYS:O	21:sy:77:LYS:NZ	2.37	0.57
5:sJ:42:C:H2'	5:sJ:43:G:C8	2.38	0.57
7:sa:242:G:O2'	7:sa:243:U:OP1	2.20	0.57
12:sh:103:ALA:N	12:sh:106:ILE:HG13	2.16	0.57
15:sk:59:MET:HE1	15:sk:69:ARG:HA	1.86	0.57
19:sr:87:ASP:OD1	19:sr:87:ASP:N	2.36	0.57
5:sJ:42:C:H2'	5:sJ:43:G:H8	1.69	0.57
7:sa:51:U:H2'	7:sa:52:G:C8	2.40	0.57
7:sa:562:G:OP2	21:sy:66:LYS:NZ	2.37	0.57
11:sf:33:PRO:HD2	11:sf:81:PRO:HG2	1.85	0.57
15:sk:83:LEU:O	15:sk:107:ARG:NE	2.37	0.57
15:sk:157:GLN:OE1	15:sk:157:GLN:N	2.37	0.57
22:sz:23:ARG:NH2	22:sz:80:TYR:OH	2.36	0.57
7:sa:872:A:H2'	7:sa:873:A:C8	2.39	0.57
11:sf:9:ARG:HD2	11:sf:26:ALA:HB2	1.87	0.57
12:sh:159:ARG:HD3	12:sh:177:ALA:HB2	1.86	0.57
15:sk:34:PHE:HA	15:sk:122:ILE:HD13	1.85	0.57
16:sm:132:SER:OG	16:sm:133:LYS:N	2.38	0.57
7:sa:173:A:H62	7:sa:257:C:H41	1.53	0.57
10:se:73:ALA:HB2	10:se:82:GLY:HA2	1.87	0.57
13:si:128:HIS:ND1	13:si:191:GLU:OE2	2.37	0.57
7:sa:366:G:H1	7:sa:607:G:H1	1.52	0.56
7:sa:367:G:O2'	7:sa:605:C:N3	2.37	0.56
7:sa:1821:A:H3'	7:sa:1822:U:O4'	2.05	0.56
8:sb:115:PHE:HB3	8:sb:147:ILE:HD13	1.87	0.56
13:si:163:VAL:HG22	13:si:198:PRO:HG3	1.86	0.56
12:sh:73:VAL:HG23	12:sh:97:VAL:HG23	1.86	0.56
7:sa:400:C:H5''	12:sh:93:ARG:NE	2.20	0.56
7:sa:1893:A:H3'	7:sa:1894:G:H5'	1.87	0.56
11:sf:67:THR:HG22	11:sf:92:ARG:HH21	1.70	0.56
12:sh:76:LEU:CA	12:sh:94:ARG:HA	2.35	0.56
12:sh:108:VAL:HG12	12:sh:110:ASN:ND2	2.20	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:sk:106:GLU:HA	15:sk:111:THR:HG21	1.87	0.56
7:sa:1824:G:N3	7:sa:1824:G:H2'	2.19	0.56
7:sa:1850:C:H2'	7:sa:1851:U:C6	2.40	0.56
4:sI:15:G:H22	4:sI:48:C:N4	2.03	0.56
7:sa:788:C:N4	7:sa:789:A:H62	2.04	0.56
7:sa:1089:A:C5	7:sa:1090:C:C5	2.94	0.56
8:sb:65:LEU:HD22	20:sx:76:LEU:HD21	1.87	0.56
1:sB:2:THR:HG22	7:sa:1168:A:OP1	2.06	0.56
7:sa:934:A:H2'	7:sa:935:C:C6	2.40	0.56
9:sc:139:VAL:HG11	9:sc:221:ARG:HA	1.87	0.56
7:sa:1847:A:N6	7:sa:1867:A:O2'	2.38	0.56
15:sk:139:GLN:NE2	15:sk:140:VAL:O	2.37	0.56
1:sB:48:ALA:O	18:sp:112:ARG:NH2	2.38	0.56
8:sb:125:GLU:O	9:sc:42:LYS:NZ	2.38	0.56
11:sf:20:LYS:NZ	15:sk:5:LEU:O	2.29	0.56
12:sh:190:GLN:O	12:sh:194:GLN:HG2	2.06	0.56
12:sh:108:VAL:HG12	12:sh:110:ASN:HD21	1.72	0.55
7:sa:91:G:H2'	12:sh:88:ARG:HH22	1.71	0.55
10:se:34:VAL:HG21	10:se:45:VAL:HG22	1.88	0.55
14:sj:78:ILE:HA	14:sj:104:ILE:HG22	1.86	0.55
7:sa:69:G:N2	7:sa:80:A:N6	2.31	0.55
7:sa:399:G:H21	12:sh:92:ARG:HH21	1.53	0.55
7:sa:866:G:H2'	7:sa:867:A:H8	1.70	0.55
10:se:24:GLU:O	10:se:28:LYS:NZ	2.39	0.55
7:sa:443:U:H2'	7:sa:444:U:C6	2.42	0.55
7:sa:619:C:H2'	7:sa:620:U:C6	2.42	0.55
7:sa:773:A:H5'	7:sa:774:U:C5	2.42	0.55
16:sm:61:SER:OG	16:sm:62:ASP:N	2.37	0.55
7:sa:247:G:OP1	11:sf:132:GLY:N	2.33	0.55
7:sa:261:U:H3	7:sa:283:A:H62	1.54	0.55
16:sm:58:PRO:HA	16:sm:63:VAL:HG23	1.89	0.55
12:sh:137:ARG:C	12:sh:181:GLN:O	2.50	0.55
5:sJ:50:U:O2'	5:sJ:51:U:OP1	2.24	0.55
7:sa:956:G:N1	7:sa:1003:A:O2'	2.33	0.55
15:sk:92:LYS:HD3	15:sk:95:PHE:HE2	1.72	0.55
10:se:200:VAL:O	10:se:204:SER:N	2.40	0.55
11:sf:158:ILE:HD12	11:sf:167:ILE:HD12	1.88	0.55
16:sm:34:HIS:O	16:sm:34:HIS:ND1	2.40	0.55
7:sa:622:G:N1	7:sa:950:A:OP2	2.36	0.55
20:sx:53:LYS:NZ	20:sx:55:SER:OG	2.30	0.55
4:sI:17:G:C6	4:sI:55:U:O2	2.61	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:sa:584:C:H2'	7:sa:585:A:C8	2.42	0.54
12:sh:64:MET:HE1	12:sh:80:ARG:NH2	2.22	0.54
18:sp:78:LYS:NZ	18:sp:82:ASP:OD1	2.40	0.54
4:sI:14:A:H3'	4:sI:15:G:C8	2.25	0.54
10:se:42:ARG:NH1	10:se:44:THR:O	2.40	0.54
7:sa:1866:A:H2'	7:sa:1867:A:O4'	2.07	0.54
7:sa:1824:G:H22	7:sa:1890:U:H3	1.56	0.54
7:sa:1862:U:H2'	7:sa:1863:A:H8	1.73	0.54
12:sh:106:ILE:C	12:sh:107:SER:O	2.49	0.54
1:sB:44:ILE:O	18:sp:108:GLN:NE2	2.25	0.54
7:sa:948:U:OP1	7:sa:1013:U:O2'	2.25	0.54
9:sc:49:ASP:O	9:sc:51:LYS:NZ	2.37	0.54
7:sa:333:A:H5''	14:sj:10:LYS:HD2	1.87	0.54
16:sm:32:ARG:NH2	16:sm:50:GLY:O	2.41	0.54
7:sa:864:C:H2'	7:sa:865:A:C8	2.42	0.54
15:sk:134:ILE:HD11	15:sk:156:ILE:HG22	1.89	0.54
7:sa:63:U:O2'	7:sa:163:A:N3	2.39	0.54
12:sh:63:MET:O	12:sh:64:MET:C	2.51	0.54
12:sh:183:LEU:H	12:sh:185:THR:H	1.54	0.54
20:sx:28:ALA:O	20:sx:57:ARG:NH1	2.37	0.54
12:sh:58:LYS:NZ	12:sh:105:ASP:C	2.66	0.54
19:sr:112:ASP:OD1	19:sr:114:THR:N	2.41	0.53
7:sa:991:G:N2	7:sa:992:U:O4	2.41	0.53
5:sJ:68:G:O2'	5:sJ:69:A:O5'	2.27	0.53
7:sa:934:A:H2'	7:sa:935:C:H6	1.72	0.53
8:sb:35:LEU:HD21	8:sb:40:GLU:HG2	1.89	0.53
12:sh:209:GLU:HG3	12:sh:212:ARG:HH12	1.73	0.53
4:sI:66:U:H2'	4:sI:67:G:C8	2.41	0.53
7:sa:443:U:H2'	7:sa:444:U:H6	1.73	0.53
7:sa:788:C:H2'	7:sa:789:A:H8	1.73	0.53
8:sb:87:ARG:HG2	8:sb:89:MET:H	1.74	0.53
12:sh:116:LYS:O	12:sh:117:GLY:C	2.51	0.53
12:sh:62:PRO:HG2	12:sh:97:VAL:HG12	1.90	0.53
12:sh:98:ARG:HD2	12:sh:99:GLY:N	2.23	0.53
7:sa:7:G:O6	9:sc:207:LYS:NZ	2.40	0.53
7:sa:442:U:O2'	11:sf:25:PHE:O	2.27	0.53
7:sa:1115:C:N4	7:sa:1116:U:O4	2.42	0.53
7:sa:1936:G:OP2	18:sp:141:ARG:NH2	2.41	0.53
7:sa:77:A:H5''	12:sh:159:ARG:HH12	1.73	0.53
7:sa:261:U:OP2	12:sh:195:LYS:NZ	2.31	0.53
7:sa:149:U:H2'	7:sa:150:G:H8	1.73	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:sJ:62:C:H2'	5:sJ:63:C:C6	2.44	0.53
12:sh:108:VAL:HG13	12:sh:121:ILE:HG23	1.91	0.53
11:sf:152:LEU:HD21	11:sf:170:PHE:HB2	1.91	0.52
7:sa:28:U:H2'	7:sa:29:G:H8	1.75	0.52
7:sa:327:U:OP2	14:sj:211:GLN:NE2	2.36	0.52
12:sh:77:LEU:H	12:sh:94:ARG:HA	1.74	0.52
5:sJ:24:C:H2'	5:sJ:25:U:C6	2.44	0.52
7:sa:67:A:OP1	12:sh:160:ARG:NH2	2.43	0.52
7:sa:401:U:H4'	12:sh:94:ARG:NH2	2.21	0.52
12:sh:83:CYS:SG	12:sh:97:VAL:HG11	2.49	0.52
7:sa:264:A:O2'	7:sa:265:G:O4'	2.26	0.52
12:sh:219:ARG:HA	12:sh:222:VAL:HG12	1.89	0.52
7:sa:620:U:HO2'	17:so:113:TYR:HH	1.49	0.52
12:sh:121:ILE:C	12:sh:123:GLY:N	2.62	0.52
7:sa:107:A:H2'	7:sa:108:G:C8	2.45	0.52
7:sa:463:A:N1	7:sa:588:A:O2'	2.42	0.52
12:sh:54:GLY:HA2	12:sh:63:MET:SD	2.49	0.52
1:sB:93:ARG:NH2	7:sa:1103:U:OP1	2.42	0.52
7:sa:328:C:C5	14:sj:49:ARG:HD2	2.44	0.52
7:sa:797:G:OP2	7:sa:797:G:N2	2.24	0.52
10:se:25:PRO:HG2	18:sp:79:ARG:HH22	1.74	0.52
12:sh:58:LYS:HG2	12:sh:105:ASP:O	2.10	0.52
7:sa:801:A:H2'	7:sa:802:U:C6	2.45	0.52
7:sa:867:A:H2	18:sp:135:THR:HG23	1.75	0.52
17:so:106:LYS:O	17:so:112:LYS:NZ	2.34	0.52
2:sC:3:LEU:HG	20:sx:61:ILE:HD11	1.92	0.51
5:sJ:49:C:H5''	5:sJ:50:U:H5''	1.91	0.51
7:sa:73:A:O2'	7:sa:74:A:OP2	2.25	0.51
7:sa:847:G:OP2	17:so:3:ARG:NH2	2.29	0.51
12:sh:77:LEU:HD11	12:sh:97:VAL:HG13	1.92	0.51
7:sa:864:C:H2'	7:sa:865:A:H8	1.75	0.51
7:sa:875:G:H2'	7:sa:876:G:C8	2.45	0.51
11:sf:98:ARG:HB3	11:sf:110:VAL:HG23	1.92	0.51
22:sz:26:VAL:HG13	22:sz:77:ALA:HB3	1.93	0.51
12:sh:57:ASP:HB2	12:sh:61:PHE:HB2	1.92	0.51
19:sr:31:SER:HB3	19:sr:34:ILE:HG13	1.91	0.51
11:sf:120:LYS:HZ3	11:sf:143:ARG:HH21	1.56	0.51
7:sa:213:A:N6	7:sa:243:U:O4'	2.44	0.51
7:sa:399:G:H21	12:sh:92:ARG:NH2	2.09	0.51
7:sa:903:A:H2'	7:sa:904:A:C8	2.45	0.51
7:sa:1089:A:N7	7:sa:1090:C:N4	2.59	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:sh:112:ILE:C	12:sh:114:VAL:N	2.64	0.51
1:sB:44:ILE:HD11	1:sB:65:PRO:HD2	1.92	0.51
7:sa:397:U:OP1	11:sf:1:ARG:NH2	2.44	0.51
7:sa:441:C:H5''	11:sf:55:ASN:HD22	1.76	0.51
7:sa:1863:A:H2'	7:sa:1864:G:C8	2.46	0.51
11:sf:85:MET:SD	11:sf:121:LEU:HB2	2.50	0.51
4:sI:23:A:H2'	4:sI:24:G:C8	2.46	0.51
11:sf:102:ASN:ND2	11:sf:106:ARG:O	2.43	0.51
12:sh:65:THR:O	12:sh:66:GLY:C	2.54	0.51
12:sh:107:SER:O	12:sh:108:VAL:O	2.27	0.51
12:sh:115:LYS:O	12:sh:116:LYS:C	2.53	0.51
12:sh:120:GLU:O	12:sh:121:ILE:C	2.53	0.51
13:si:101:ARG:HD2	13:si:122:ARG:HE	1.76	0.51
7:sa:772:U:N3	22:sz:12:THR:HA	2.21	0.51
9:sc:75:LEU:HD13	9:sc:78:LEU:HD21	1.93	0.50
9:sc:80:GLU:CG	9:sc:131:MET:HE1	2.42	0.50
2:sC:8:LEU:HD13	19:sr:24:GLN:HG3	1.93	0.50
7:sa:264:A:H2'	7:sa:265:G:C8	2.46	0.50
7:sa:919:A:H2'	7:sa:920:A:C8	2.46	0.50
7:sa:926:U:HO2'	7:sa:927:U:H6	1.59	0.50
7:sa:549:A:N3	7:sa:584:C:O2'	2.41	0.50
12:sh:142:ARG:O	12:sh:143:LYS:C	2.54	0.50
12:sh:185:THR:O	12:sh:187:ARG:N	2.45	0.50
12:sh:77:LEU:HB2	12:sh:95:LYS:HB2	1.92	0.50
12:sh:114:VAL:C	12:sh:115:LYS:HG2	2.35	0.50
14:sj:36:THR:OG1	14:sj:57:ALA:O	2.21	0.50
1:sB:87:ARG:NH2	1:sB:94:ASN:O	2.33	0.50
5:sJ:27:G:H22	5:sJ:45:A:H2	1.60	0.50
7:sa:400:C:H5''	12:sh:93:ARG:CZ	2.42	0.50
7:sa:400:C:H5'	12:sh:91:GLU:CD	2.36	0.50
11:sf:21:LEU:HD11	15:sk:6:ARG:HG3	1.94	0.50
15:sk:66:ASP:OD2	15:sk:69:ARG:N	2.44	0.50
7:sa:152:A:H2'	7:sa:153:U:H6	1.76	0.50
10:se:50:VAL:HG21	10:se:63:LEU:HD11	1.92	0.50
12:sh:137:ARG:HD3	12:sh:182:ARG:HD2	1.92	0.50
14:sj:70:GLN:HB2	14:sj:72:ILE:HG22	1.93	0.50
5:sJ:25:U:H2'	5:sJ:26:C:C6	2.47	0.50
15:sk:120:LYS:NZ	15:sk:121:SER:OG	2.45	0.50
1:sB:26:CYS:HB2	1:sB:77:CYS:SG	2.52	0.49
5:sJ:19:G:N2	5:sJ:59:A:O5'	2.45	0.49
7:sa:620:U:O2'	17:so:113:TYR:OH	2.18	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:sa:934:A:OP1	17:so:6:ASN:ND2	2.45	0.49
12:sh:61:PHE:CD2	12:sh:72:ARG:HD3	2.47	0.49
4:sI:23:A:H2'	4:sI:24:G:H8	1.77	0.49
7:sa:412:A:H4'	7:sa:413:G:O5'	2.11	0.49
7:sa:540:U:H2'	7:sa:541:U:C6	2.47	0.49
7:sa:630:A:H5''	19:sr:31:SER:HB2	1.94	0.49
8:sb:156:ASN:HB2	8:sb:172:ASN:HD21	1.77	0.49
11:sf:112:LEU:HD23	11:sf:235:ASN:HD21	1.77	0.49
12:sh:189:LEU:HD22	12:sh:189:LEU:H	1.77	0.49
7:sa:1133:A:O2'	7:sa:1134:G:H5'	2.11	0.49
7:sa:1825:A:H1'	7:sa:1826:A:OP2	2.12	0.49
9:sc:82:VAL:HG22	9:sc:104:VAL:HG12	1.93	0.49
11:sf:189:ARG:HD2	11:sf:243:LYS:HD2	1.94	0.49
12:sh:112:ILE:O	12:sh:113:VAL:HB	2.12	0.49
9:sc:80:GLU:HG2	9:sc:131:MET:HE1	1.94	0.49
7:sa:150:G:N2	7:sa:152:A:H3'	2.27	0.49
11:sf:102:ASN:HD21	11:sf:106:ARG:HD2	1.78	0.49
7:sa:151:A:H2'	7:sa:152:A:O4'	2.13	0.49
7:sa:261:U:H3	7:sa:283:A:N6	2.11	0.49
7:sa:416:A:HO2'	7:sa:417:G:C5'	2.26	0.49
7:sa:565:G:N2	7:sa:592:U:OP1	2.45	0.49
22:sz:17:VAL:HG13	22:sz:24:LYS:HD3	1.93	0.49
1:sB:76:SER:OG	7:sa:1940:G:N2	2.40	0.49
7:sa:208:C:H2'	7:sa:209:A:C8	2.46	0.49
7:sa:966:G:H2'	7:sa:967:G:O4'	2.13	0.49
7:sa:1021:G:H2'	7:sa:1022:G:C8	2.48	0.49
8:sb:134:PRO:HG3	8:sb:155:CYS:SG	2.52	0.49
20:sx:38:ASN:HB3	20:sx:44:LEU:HD11	1.95	0.49
7:sa:444:U:H2'	7:sa:445:C:H6	1.78	0.49
12:sh:57:ASP:N	12:sh:61:PHE:H	2.10	0.49
19:sr:78:ARG:HB3	19:sr:124:ARG:HB3	1.93	0.49
21:sy:101:SER:O	21:sy:101:SER:OG	2.22	0.49
7:sa:359:G:H1	7:sa:375:A:H2	1.59	0.49
11:sf:159:LYS:HB3	11:sf:169:ASP:H	1.77	0.49
7:sa:1827:U:H2'	7:sa:1828:A:C8	2.47	0.48
8:sb:156:ASN:OD1	8:sb:157:SER:N	2.37	0.48
10:se:125:THR:OG1	10:se:126:SER:N	2.44	0.48
11:sf:42:LEU:HD21	11:sf:68:ILE:HD13	1.95	0.48
11:sf:121:LEU:HD11	11:sf:233:LEU:HB2	1.94	0.48
7:sa:1862:U:H2'	7:sa:1863:A:C8	2.48	0.48
7:sa:1908:U:O2'	7:sa:1909:A:OP2	2.23	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:sb:11:ASP:HA	8:sb:14:LYS:NZ	2.28	0.48
8:sb:161:LEU:O	20:sx:60:GLY:HA2	2.13	0.48
12:sh:142:ARG:HG3	12:sh:183:LEU:HD11	1.95	0.48
14:sj:208:ARG:HD3	14:sj:211:GLN:HG3	1.94	0.48
5:sJ:63:C:H2'	5:sJ:64:G:H8	1.77	0.48
8:sb:15:PRO:HB3	8:sb:60:TRP:CD2	2.48	0.48
11:sf:58:GLU:OE2	22:sz:23:ARG:NH2	2.25	0.48
11:sf:212:LYS:HE2	11:sf:242:ILE:HG12	1.95	0.48
13:si:123:THR:HG23	13:si:126:ALA:H	1.78	0.48
13:si:163:VAL:HA	13:si:198:PRO:HD3	1.95	0.48
4:sI:27:C:H2'	4:sI:28:G:C8	2.48	0.48
7:sa:1824:G:H1	7:sa:1890:U:H3	1.61	0.48
12:sh:111:THR:HA	12:sh:114:VAL:CB	2.39	0.48
7:sa:444:U:H2'	7:sa:445:C:C6	2.48	0.48
12:sh:58:LYS:HZ3	12:sh:106:ILE:N	2.11	0.48
12:sh:76:LEU:HD11	12:sh:92:ARG:HB2	1.95	0.48
22:sz:12:THR:HG21	22:sz:29:ASP:H	1.78	0.48
11:sf:145:ILE:HG21	11:sf:167:ILE:HD11	1.95	0.48
12:sh:102:VAL:HG13	12:sh:106:ILE:HG21	1.95	0.48
18:sp:20:LYS:HG3	18:sp:21:ASP:H	1.79	0.48
21:sy:20:TRP:CE3	21:sy:26:LYS:HG3	2.49	0.48
7:sa:932:C:H2'	7:sa:933:A:C8	2.48	0.48
11:sf:103:THR:OG1	11:sf:239:ASP:OD2	2.21	0.48
11:sf:105:ARG:HA	11:sf:187:MET:HG2	1.96	0.48
12:sh:63:MET:HB2	12:sh:100:ALA:HA	1.94	0.48
1:sB:84:VAL:HB	7:sa:1944:A:N6	2.29	0.48
5:sJ:48:U:H5'	5:sJ:49:C:OP1	2.14	0.48
7:sa:65:U:O2	12:sh:160:ARG:NE	2.47	0.48
7:sa:389:U:H1'	12:sh:92:ARG:HH22	1.79	0.48
7:sa:1886:U:H2'	7:sa:1887:A:C8	2.48	0.48
11:sf:9:ARG:HE	11:sf:18:LEU:HD22	1.79	0.48
12:sh:136:LYS:O	12:sh:136:LYS:HG3	2.14	0.48
7:sa:458:U:H2'	7:sa:459:A:H8	1.79	0.47
7:sa:561:A:H5''	7:sa:562:G:OP2	2.14	0.47
12:sh:138:ALA:CB	12:sh:181:GLN:O	2.62	0.47
16:sm:100:GLU:OE1	21:sy:9:ARG:NH2	2.47	0.47
19:sr:8:ALA:HB2	19:sr:74:VAL:HG11	1.95	0.47
21:sy:20:TRP:HE3	21:sy:26:LYS:HG3	1.78	0.47
21:sy:59:GLN:O	21:sy:59:GLN:NE2	2.47	0.47
7:sa:153:U:H2'	7:sa:155:A:H5'	1.96	0.47
7:sa:740:U:H2'	7:sa:741:U:C6	2.49	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:sh:135:PRO:HB2	12:sh:141:ILE:CG1	2.38	0.47
12:sh:209:GLU:HG3	12:sh:212:ARG:HH22	1.78	0.47
14:sj:107:ALA:HB3	14:sj:108:PRO:HD3	1.95	0.47
7:sa:170:G:C5	7:sa:171:A:H2	2.31	0.47
7:sa:579:A:H2'	7:sa:580:G:H8	1.79	0.47
7:sa:782:A:C8	7:sa:784:U:H1'	2.49	0.47
11:sf:159:LYS:HB2	11:sf:159:LYS:HE2	1.66	0.47
12:sh:84:TYR:HE2	12:sh:91:GLU:O	1.97	0.47
12:sh:144:LEU:HD21	12:sh:158:ILE:HD11	1.96	0.47
4:sI:14:A:C3'	4:sI:15:G:H8	2.17	0.47
12:sh:99:GLY:O	12:sh:100:ALA:C	2.57	0.47
12:sh:102:VAL:CG1	12:sh:109:LEU:HD11	2.42	0.47
7:sa:395:G:O6	14:sj:29:MET:HG3	2.14	0.47
14:sj:79:LEU:HD11	14:sj:105:ASP:HB3	1.97	0.47
14:sj:207:SER:OG	14:sj:208:ARG:N	2.48	0.47
5:sJ:24:C:H2'	5:sJ:25:U:H6	1.80	0.47
7:sa:77:A:H5'	12:sh:159:ARG:HH22	1.80	0.47
7:sa:150:G:H4'	12:sh:59:ASP:HA	1.96	0.47
7:sa:581:C:H2'	7:sa:582:U:C6	2.49	0.47
7:sa:887:A:H2'	7:sa:888:A:H8	1.79	0.47
7:sa:1158:A:H2'	7:sa:1159:A:H8	1.79	0.47
10:se:42:ARG:NH1	10:se:45:VAL:HA	2.29	0.47
11:sf:70:ILE:HG22	11:sf:71:ASP:OD1	2.15	0.47
12:sh:120:GLU:C	12:sh:121:ILE:HG13	2.39	0.47
16:sm:38:GLY:O	16:sm:40:GLY:N	2.47	0.47
5:sJ:5:U:H2'	5:sJ:6:C:C6	2.49	0.47
7:sa:149:U:H2'	7:sa:150:G:C8	2.48	0.47
7:sa:602:U:C5'	7:sa:604:G:H22	2.27	0.47
7:sa:1111:A:H2'	7:sa:1112:A:C8	2.50	0.47
8:sb:68:ARG:HD3	20:sx:35:PRO:O	2.15	0.47
11:sf:85:MET:HE1	11:sf:234:VAL:HG21	1.96	0.47
12:sh:200:LYS:HE3	12:sh:204:ILE:HB	1.97	0.47
7:sa:5:U:H2'	7:sa:6:G:H8	1.80	0.47
7:sa:69:G:H4'	7:sa:70:A:OP2	2.15	0.47
7:sa:295:A:N6	11:sf:38:GLU:CD	2.72	0.47
7:sa:389:U:H2'	7:sa:390:U:C6	2.49	0.47
7:sa:1117:U:H5'	7:sa:1118:G:C2	2.49	0.47
8:sb:7:THR:OG1	8:sb:8:ASN:N	2.48	0.47
8:sb:144:SER:OG	20:sx:57:ARG:NH2	2.46	0.47
12:sh:116:LYS:H	12:sh:116:LYS:HG2	1.34	0.47
2:sC:22:MET:HE2	7:sa:844:A:H5''	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:sf:217:THR:OG1	11:sf:218:THR:N	2.48	0.47
7:sa:785:A:H2'	7:sa:786:U:O4'	2.14	0.46
7:sa:959:A:N3	7:sa:1922:U:O2'	2.47	0.46
19:sr:28:ARG:HB3	19:sr:29:PRO:HD3	1.95	0.46
7:sa:580:G:H2'	7:sa:581:C:C6	2.50	0.46
7:sa:927:U:OP1	10:se:167:ARG:HD2	2.14	0.46
7:sa:1808:G:H2'	7:sa:1809:U:H6	1.81	0.46
8:sb:11:ASP:OD1	8:sb:11:ASP:N	2.49	0.46
9:sc:51:LYS:HD2	9:sc:245:TYR:HE2	1.80	0.46
17:so:99:ARG:NH2	17:so:119:GLU:OE2	2.47	0.46
11:sf:106:ARG:HG2	11:sf:107:PHE:N	2.30	0.46
20:sx:13:ARG:HE	20:sx:31:GLN:HE21	1.64	0.46
5:sJ:54:G:O2'	5:sJ:55:U:OP1	2.29	0.46
7:sa:292:A:C2'	7:sa:293:U:H5'	2.45	0.46
7:sa:866:G:OP1	10:se:216:LYS:NZ	2.45	0.46
11:sf:159:LYS:HZ1	11:sf:233:LEU:HD13	1.81	0.46
12:sh:138:ALA:HA	12:sh:141:ILE:CB	2.41	0.46
13:si:135:MET:HE1	13:si:185:TYR:HB2	1.97	0.46
21:sy:53:LEU:O	21:sy:67:CYS:N	2.43	0.46
7:sa:322:U:H2'	7:sa:323:A:H8	1.80	0.46
7:sa:328:C:H2'	7:sa:329:G:C8	2.51	0.46
12:sh:72:ARG:HA	12:sh:97:VAL:O	2.15	0.46
14:sj:66:SER:HA	14:sj:73:THR:HA	1.97	0.46
4:sI:34:C:H42	6:sK:10:A:N6	2.09	0.46
5:sJ:63:C:H2'	5:sJ:64:G:C8	2.51	0.46
7:sa:387:G:OP1	7:sa:1876:U:O2'	2.28	0.46
7:sa:585:A:H2'	7:sa:586:A:C8	2.50	0.46
11:sf:190:VAL:HG13	11:sf:241:GLY:HA3	1.97	0.46
12:sh:68:ALA:HA	12:sh:100:ALA:HB3	1.98	0.46
12:sh:109:LEU:O	12:sh:110:ASN:ND2	2.49	0.46
15:sk:57:LYS:HE3	15:sk:57:LYS:HB2	1.53	0.46
16:sm:108:VAL:HG11	16:sm:125:ILE:HD12	1.96	0.46
7:sa:324:G:H5''	14:sj:98:LYS:HB3	1.97	0.46
11:sf:190:VAL:HG11	11:sf:236:LEU:HD13	1.98	0.46
12:sh:138:ALA:CB	12:sh:182:ARG:O	2.64	0.46
7:sa:774:U:O2'	7:sa:775:G:H2'	2.15	0.46
9:sc:37:TRP:N	9:sc:69:GLN:OE1	2.49	0.46
11:sf:146:ARG:HE	11:sf:146:ARG:HA	1.79	0.46
13:si:159:LYS:HB3	13:si:193:VAL:HG22	1.97	0.46
18:sp:90:ILE:HG21	18:sp:111:LEU:HD13	1.97	0.46
1:sB:45:VAL:HG11	1:sB:53:ILE:HG13	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:sa:442:U:H2'	7:sa:443:U:O4'	2.15	0.46
7:sa:1863:A:H2'	7:sa:1864:G:H8	1.81	0.46
7:sa:1893:A:H3'	7:sa:1894:G:C5'	2.45	0.46
9:sc:118:LYS:HG2	9:sc:129:GLY:HA3	1.98	0.46
12:sh:97:VAL:HB	12:sh:98:ARG:H	1.45	0.46
9:sc:121:LYS:HB2	9:sc:121:LYS:HE2	1.77	0.46
9:sc:171:LEU:HD23	9:sc:200:THR:HG22	1.98	0.46
12:sh:75:LEU:O	12:sh:76:LEU:C	2.59	0.46
12:sh:138:ALA:HB3	12:sh:181:GLN:O	2.16	0.46
4:sI:15:G:N1	4:sI:48:C:N3	2.63	0.45
7:sa:66:A:O2'	7:sa:68:A:OP1	2.34	0.45
11:sf:16:TRP:HE3	11:sf:18:LEU:HD11	1.81	0.45
12:sh:58:LYS:HZ3	12:sh:106:ILE:CA	2.28	0.45
12:sh:208:LYS:O	12:sh:212:ARG:N	2.39	0.45
7:sa:587:U:H5''	15:sk:40:LYS:HE2	1.98	0.45
7:sa:958:A:H2'	7:sa:959:A:O4'	2.16	0.45
11:sf:235:ASN:OD1	11:sf:235:ASN:N	2.49	0.45
19:sr:112:ASP:OD1	19:sr:112:ASP:C	2.59	0.45
22:sz:61:LEU:HD23	22:sz:61:LEU:HA	1.83	0.45
7:sa:157:A:H2'	7:sa:158:A:N3	2.32	0.45
7:sa:335:U:H2'	7:sa:336:A:C8	2.49	0.45
7:sa:794:U:H2'	7:sa:795:G:C8	2.47	0.45
8:sb:88:GLU:HA	8:sb:91:HIS:CE1	2.52	0.45
11:sf:112:LEU:HB3	11:sf:116:GLN:HG3	1.98	0.45
12:sh:74:ARG:HE	12:sh:74:ARG:HB3	1.53	0.45
12:sh:84:TYR:CE2	12:sh:93:ARG:HB2	2.51	0.45
7:sa:1011:U:H4'	7:sa:1012:G:OP2	2.16	0.45
11:sf:40:LEU:HD12	11:sf:41:PRO:HD2	1.98	0.45
12:sh:58:LYS:HG2	12:sh:105:ASP:CB	2.31	0.45
8:sb:14:LYS:N	8:sb:14:LYS:HD3	2.32	0.45
7:sa:594:U:H2'	7:sa:595:A:H8	1.81	0.45
7:sa:908:G:O2'	7:sa:925:U:H5'	2.17	0.45
12:sh:77:LEU:HD23	12:sh:77:LEU:HA	1.66	0.45
18:sp:56:ARG:HA	18:sp:56:ARG:HD3	1.67	0.45
7:sa:68:A:H2'	7:sa:69:G:O4'	2.17	0.45
7:sa:111:A:H4'	16:sm:66:ARG:HB3	1.98	0.45
19:sr:23:ARG:HA	19:sr:23:ARG:HD3	1.77	0.45
19:sr:25:VAL:HG12	19:sr:63:VAL:HB	1.98	0.45
7:sa:138:G:H2'	7:sa:139:G:C8	2.52	0.45
8:sb:22:MET:HE1	8:sb:183:TRP:CZ3	2.52	0.45
8:sb:71:ALA:O	8:sb:75:ASN:HB3	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:sk:4:CYS:SG	15:sk:5:LEU:N	2.90	0.45
7:sa:203:C:N4	7:sa:255:G:O2'	2.50	0.44
7:sa:1848:U:C2'	7:sa:1849:U:H5'	2.47	0.44
12:sh:142:ARG:HG3	12:sh:183:LEU:HD12	1.97	0.44
7:sa:77:A:O2'	7:sa:78:G:OP1	2.32	0.44
7:sa:164:A:C4	7:sa:166:A:C8	3.05	0.44
7:sa:1126:G:H1'	19:sr:76:SER:OG	2.17	0.44
11:sf:7:LEU:HD22	11:sf:36:MET:HE1	1.99	0.44
4:sI:5:C:H2'	4:sI:6:C:C6	2.52	0.44
7:sa:26:U:H2'	7:sa:27:A:C8	2.53	0.44
7:sa:898:G:H2'	7:sa:899:C:C6	2.53	0.44
12:sh:70:ASN:N	12:sh:99:GLY:HA3	2.32	0.44
7:sa:243:U:H4'	7:sa:244:U:OP2	2.16	0.44
7:sa:327:U:P	14:sj:56:ARG:HH22	2.40	0.44
8:sb:23:MET:HG3	8:sb:184:MET:HE1	1.98	0.44
9:sc:172:VAL:HB	9:sc:199:PHE:HB2	1.99	0.44
11:sf:129:LEU:HD12	11:sf:135:PRO:HB3	1.99	0.44
11:sf:152:LEU:HD23	11:sf:152:LEU:HA	1.76	0.44
13:si:186:LYS:NZ	13:si:190:GLY:HA2	2.32	0.44
19:sr:77:PRO:HB2	21:sy:5:LEU:HB2	1.98	0.44
21:sy:66:LYS:HB3	21:sy:89:LEU:HD13	1.98	0.44
7:sa:609:G:O2'	7:sa:615:A:N1	2.47	0.44
7:sa:1002:U:O4	7:sa:1003:A:N6	2.50	0.44
7:sa:1089:A:C6	7:sa:1090:C:C4	3.06	0.44
11:sf:45:ILE:HD11	11:sf:99:LEU:HD11	1.98	0.44
12:sh:118:GLU:O	12:sh:119:GLY:C	2.59	0.44
12:sh:136:LYS:O	12:sh:136:LYS:CG	2.66	0.44
16:sm:57:CYS:O	16:sm:61:SER:HB3	2.17	0.44
4:sI:27:C:H2'	4:sI:28:G:H8	1.82	0.44
9:sc:79:LYS:HD3	9:sc:109:HIS:CE1	2.53	0.44
11:sf:102:ASN:OD1	11:sf:106:ARG:NH1	2.50	0.44
22:sz:23:ARG:NE	22:sz:78:LEU:HD13	2.32	0.44
4:sI:17:G:O2'	4:sI:18:A:O5'	2.35	0.44
11:sf:84:PHE:O	11:sf:86:ASP:N	2.50	0.44
12:sh:58:LYS:HZ2	12:sh:107:SER:HA	1.83	0.44
10:se:42:ARG:HH11	10:se:45:VAL:HA	1.83	0.44
12:sh:69:THR:C	12:sh:99:GLY:HA3	2.43	0.44
12:sh:95:LYS:HB2	12:sh:95:LYS:HE3	1.79	0.44
11:sf:102:ASN:O	11:sf:188:GLY:HA3	2.18	0.44
18:sp:51:ILE:HD12	18:sp:76:VAL:HG23	2.00	0.44
7:sa:771:U:O5'	7:sa:772:U:H5'	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:sh:72:ARG:HA	12:sh:98:ARG:HA	1.99	0.43
7:sa:158:A:H4'	12:sh:111:THR:OG1	2.17	0.43
7:sa:322:U:H2'	7:sa:323:A:C8	2.52	0.43
9:sc:229:LYS:HA	9:sc:232:TRP:NE1	2.32	0.43
12:sh:58:LYS:HE2	12:sh:105:ASP:HA	1.99	0.43
12:sh:71:ASN:O	12:sh:72:ARG:C	2.61	0.43
4:sI:15:G:C2	4:sI:59:G:C6	3.06	0.43
7:sa:324:G:H2'	7:sa:325:U:H6	1.82	0.43
7:sa:765:A:N6	7:sa:780:U:O2	2.50	0.43
12:sh:65:THR:O	12:sh:100:ALA:HB2	2.18	0.43
12:sh:85:LYS:HA	12:sh:85:LYS:HD3	1.58	0.43
19:sr:75:ILE:HG22	19:sr:76:SER:O	2.18	0.43
19:sr:113:ASN:OD1	19:sr:113:ASN:N	2.51	0.43
1:sB:6:ARG:HB3	7:sa:1943:C:H5	1.83	0.43
7:sa:587:U:H4'	7:sa:589:G:H4'	2.00	0.43
7:sa:632:U:OP2	19:sr:32:LYS:NZ	2.50	0.43
7:sa:778:A:N1	11:sf:110:VAL:HG12	2.32	0.43
7:sa:784:U:H2'	7:sa:785:A:N7	2.34	0.43
10:se:34:VAL:HG23	10:se:45:VAL:H	1.84	0.43
12:sh:77:LEU:HB2	12:sh:93:ARG:O	2.17	0.43
12:sh:183:LEU:O	12:sh:184:VAL:HB	2.18	0.43
4:sI:15:G:N2	4:sI:59:G:C5	2.87	0.43
7:sa:365:G:H2'	7:sa:366:G:C8	2.53	0.43
11:sf:147:TYR:HB3	12:sh:217:LEU:HD13	2.00	0.43
11:sf:239:ASP:C	11:sf:239:ASP:OD1	2.62	0.43
12:sh:144:LEU:HD22	12:sh:158:ILE:HD11	2.01	0.43
7:sa:753:G:P	15:sk:79:ARG:HH22	2.41	0.43
8:sb:152:ILE:HG12	8:sb:166:ILE:HB	1.99	0.43
12:sh:138:ALA:HA	12:sh:141:ILE:H	1.84	0.43
14:sj:208:ARG:HH11	14:sj:211:GLN:HG3	1.84	0.43
2:sC:20:HIS:HB3	2:sC:23:LYS:HG3	1.99	0.43
4:sI:28:G:H2'	4:sI:29:C:C6	2.54	0.43
5:sJ:1:C:H2'	5:sJ:2:U:C6	2.54	0.43
11:sf:227:GLY:HA3	11:sf:231:GLU:O	2.18	0.43
12:sh:76:LEU:HA	12:sh:94:ARG:CA	2.40	0.43
12:sh:191:HIS:CD2	12:sh:191:HIS:N	2.87	0.43
14:sj:96:LEU:HD13	14:sj:215:VAL:HG21	2.01	0.43
20:sx:6:LYS:HE3	20:sx:8:GLU:O	2.19	0.43
7:sa:839:A:N3	7:sa:839:A:H2'	2.34	0.43
9:sc:233:LYS:HD3	9:sc:233:LYS:HA	1.79	0.43
12:sh:75:LEU:O	12:sh:77:LEU:N	2.51	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:sh:93:ARG:O	12:sh:94:ARG:C	2.60	0.43
12:sh:100:ALA:O	12:sh:101:ILE:C	2.60	0.43
13:si:140:GLU:O	13:si:165:VAL:N	2.52	0.43
16:sm:71:SER:OG	16:sm:122:HIS:NE2	2.45	0.43
18:sp:35:THR:HG21	18:sp:69:ALA:HB2	2.00	0.43
4:sI:14:A:C8	4:sI:15:G:C8	3.06	0.43
7:sa:602:U:H5'	7:sa:604:G:H22	1.83	0.43
7:sa:619:C:H2'	7:sa:620:U:H6	1.82	0.43
9:sc:142:ARG:HG2	9:sc:157:PRO:HG3	2.01	0.43
12:sh:74:ARG:NH1	12:sh:95:LYS:HA	2.34	0.43
12:sh:155:LYS:HA	12:sh:155:LYS:HD3	1.76	0.43
15:sk:110:GLN:HE22	15:sk:126:ARG:HD2	1.84	0.43
16:sm:122:HIS:HB2	16:sm:145:ARG:HH21	1.84	0.43
20:sx:39:GLU:CD	20:sx:39:GLU:H	2.27	0.43
7:sa:213:A:O2'	7:sa:214:A:H5'	2.19	0.43
7:sa:470:A:OP1	15:sk:126:ARG:NE	2.49	0.43
7:sa:948:U:H2'	7:sa:949:C:O4'	2.19	0.43
7:sa:979:U:H2'	7:sa:980:C:O4'	2.18	0.43
7:sa:1824:G:H3'	7:sa:1825:A:H3'	2.01	0.43
9:sc:53:LYS:HB3	9:sc:53:LYS:HE3	1.76	0.43
12:sh:64:MET:N	12:sh:98:ARG:O	2.52	0.43
7:sa:212:C:H2'	7:sa:213:A:O4'	2.19	0.42
7:sa:459:A:C2	7:sa:460:G:C8	3.07	0.42
7:sa:747:A:H1'	11:sf:10:LEU:O	2.19	0.42
11:sf:134:ILE:HG23	11:sf:147:TYR:CZ	2.54	0.42
11:sf:181:MET:HE1	11:sf:218:THR:HG21	2.01	0.42
12:sh:188:ARG:HD3	12:sh:188:ARG:HA	1.70	0.42
19:sr:66:ASN:OD1	19:sr:66:ASN:N	2.51	0.42
5:sJ:2:U:H2'	5:sJ:3:C:C6	2.54	0.42
7:sa:439:C:O2	7:sa:455:A:N6	2.52	0.42
7:sa:1869:A:O2'	12:sh:67:VAL:HA	2.18	0.42
14:sj:8:ARG:HD3	14:sj:22:GLN:HE22	1.85	0.42
7:sa:601:G:N1	7:sa:607:G:H5'	2.34	0.42
7:sa:748:A:C5	7:sa:749:A:C8	3.07	0.42
7:sa:980:C:N4	7:sa:983:A:OP2	2.52	0.42
7:sa:1089:A:C2	10:se:204:SER:O	2.72	0.42
8:sb:26:CYS:C	8:sb:27:ARG:HG2	2.45	0.42
8:sb:158:ASP:OD1	8:sb:159:ASN:ND2	2.53	0.42
9:sc:232:TRP:CE2	19:sr:68:ARG:HG2	2.54	0.42
12:sh:58:LYS:HD3	12:sh:58:LYS:HA	1.58	0.42
14:sj:34:ALA:HB3	14:sj:56:ARG:HD2	2.00	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:sk:21:ARG:HA	15:sk:21:ARG:HD3	1.96	0.42
4:sI:40:C:H2'	4:sI:41:G:H8	1.83	0.42
7:sa:104:A:H62	7:sa:305:A:H2	1.68	0.42
7:sa:876:G:H8	7:sa:876:G:O5'	2.02	0.42
7:sa:1096:U:H2'	7:sa:1097:C:C6	2.54	0.42
7:sa:1917:U:H2'	7:sa:1918:U:C6	2.54	0.42
4:sI:53:G:H2'	4:sI:54:U:C6	2.55	0.42
7:sa:1864:G:H2'	7:sa:1865:A:C8	2.54	0.42
8:sb:96:LYS:HZ3	8:sb:208:LEU:HB3	1.83	0.42
12:sh:54:GLY:N	12:sh:111:THR:OG1	2.51	0.42
12:sh:64:MET:HE3	12:sh:67:VAL:H	1.85	0.42
7:sa:1931:C:H2'	7:sa:1932:U:C6	2.55	0.42
19:sr:76:SER:HB2	19:sr:77:PRO:CD	2.49	0.42
7:sa:594:U:H2'	7:sa:595:A:C8	2.54	0.42
7:sa:905:G:N2	7:sa:968:A:H1'	2.35	0.42
11:sf:147:TYR:CD1	12:sh:217:LEU:HD22	2.55	0.42
15:sk:50:GLY:O	15:sk:54:THR:OG1	2.34	0.42
15:sk:59:MET:CE	15:sk:69:ARG:HA	2.50	0.42
7:sa:286:U:H2'	7:sa:287:A:H8	1.85	0.42
8:sb:42:TYR:OH	20:sx:67:ASN:ND2	2.51	0.42
11:sf:17:MET:HE3	11:sf:106:ARG:HG3	2.02	0.42
11:sf:159:LYS:HZ1	11:sf:233:LEU:HD22	1.85	0.42
11:sf:172:LYS:HD2	11:sf:172:LYS:HA	1.78	0.42
7:sa:69:G:N7	12:sh:176:LYS:NZ	2.59	0.42
12:sh:110:ASN:O	12:sh:111:THR:OG1	2.38	0.42
12:sh:185:THR:OG1	12:sh:188:ARG:NH2	2.52	0.42
4:sI:17:G:O2'	4:sI:57:A:N1	2.44	0.42
4:sI:40:C:H2'	4:sI:41:G:C8	2.55	0.42
7:sa:775:G:H1'	7:sa:776:U:OP2	2.20	0.42
8:sb:204:VAL:HG23	8:sb:208:LEU:HD12	2.02	0.42
9:sc:209:LEU:O	9:sc:213:VAL:HG22	2.20	0.42
16:sm:55:LYS:O	16:sm:61:SER:OG	2.32	0.42
4:sI:44:U:H2'	4:sI:45:G:O4'	2.20	0.41
5:sJ:55:U:C2	5:sJ:59:A:N7	2.87	0.41
7:sa:250:G:H2'	7:sa:251:C:C6	2.54	0.41
7:sa:287:A:H2'	7:sa:288:A:C8	2.55	0.41
7:sa:416:A:OP1	12:sh:95:LYS:HD3	2.20	0.41
7:sa:604:G:O2'	7:sa:607:G:O2'	2.27	0.41
7:sa:736:U:C2	7:sa:737:A:C8	3.08	0.41
7:sa:1819:C:H2'	7:sa:1820:G:O4'	2.20	0.41
11:sf:63:VAL:HG11	11:sf:78:THR:HA	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:sh:74:ARG:HG2	12:sh:96:THR:HB	2.01	0.41
12:sh:117:GLY:O	12:sh:119:GLY:O	2.38	0.41
7:sa:84:A:H2'	7:sa:85:A:H8	1.85	0.41
7:sa:388:C:H2'	7:sa:389:U:C6	2.55	0.41
7:sa:90:G:OP1	7:sa:392:A:N6	2.54	0.41
7:sa:561:A:H8	7:sa:561:A:OP2	2.02	0.41
7:sa:871:U:H2'	7:sa:872:A:H8	1.86	0.41
11:sf:94:LYS:HD2	11:sf:94:LYS:HA	1.78	0.41
11:sf:147:TYR:CE1	12:sh:217:LEU:HD22	2.56	0.41
11:sf:149:HIS:CG	11:sf:150:PRO:HD2	2.56	0.41
15:sk:92:LYS:HB2	15:sk:95:PHE:CD2	2.55	0.41
19:sr:14:ILE:HG23	19:sr:65:LEU:HD21	2.02	0.41
4:sI:67:G:H2'	4:sI:68:G:H8	1.86	0.41
5:sJ:1:C:H2'	5:sJ:2:U:H6	1.86	0.41
5:sJ:39:A:O2'	7:sa:981:A:OP1	2.22	0.41
7:sa:796:G:H21	19:sr:107:SER:HB2	1.85	0.41
8:sb:156:ASN:HB2	8:sb:172:ASN:ND2	2.36	0.41
13:si:163:VAL:HG13	13:si:198:PRO:HG3	2.01	0.41
15:sk:102:GLU:OE1	15:sk:102:GLU:N	2.53	0.41
16:sm:121:ASP:OD1	16:sm:121:ASP:N	2.51	0.41
20:sx:77:LYS:HD2	20:sx:77:LYS:HA	1.60	0.41
1:sB:22:ARG:NH1	1:sB:27:GLY:O	2.51	0.41
4:sI:14:A:C4	4:sI:15:G:C8	3.08	0.41
7:sa:5:U:O2'	7:sa:547:G:H4'	2.21	0.41
7:sa:1822:U:C5	7:sa:1824:G:H1'	2.55	0.41
12:sh:87:LEU:HD22	12:sh:87:LEU:HA	1.76	0.41
18:sp:21:ASP:OD1	18:sp:21:ASP:C	2.63	0.41
4:sI:2:G:H2'	4:sI:3:C:C6	2.55	0.41
7:sa:1158:A:H2'	7:sa:1159:A:C8	2.55	0.41
7:sa:1816:U:H2'	7:sa:1817:A:H8	1.83	0.41
12:sh:107:SER:HB2	12:sh:108:VAL:H	1.34	0.41
17:so:4:MET:HE3	17:so:124:ARG:CZ	2.51	0.41
18:sp:87:SER:HB3	18:sp:120:LYS:HB2	2.02	0.41
4:sI:8:U:H5'	4:sI:49:G:H5'	2.03	0.41
7:sa:373:A:O5'	7:sa:373:A:H8	2.04	0.41
7:sa:918:G:N2	7:sa:921:A:OP2	2.48	0.41
7:sa:1864:G:H2'	7:sa:1865:A:H8	1.86	0.41
9:sc:51:LYS:HD3	9:sc:51:LYS:HA	1.76	0.41
11:sf:210:ASP:OD1	11:sf:211:ALA:N	2.54	0.41
12:sh:93:ARG:N	12:sh:93:ARG:HD2	2.36	0.41
12:sh:206:MET:O	12:sh:206:MET:HE3	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:sJ:25:U:H2'	5:sJ:26:C:H6	1.85	0.41
7:sa:912:G:H8	7:sa:912:G:OP1	2.04	0.41
7:sa:154:G:C5	12:sh:87:LEU:HD21	2.56	0.41
7:sa:209:A:C6	7:sa:250:G:C6	3.09	0.41
7:sa:286:U:O2'	7:sa:287:A:H5'	2.21	0.41
7:sa:338:C:C2	7:sa:339:A:C8	3.09	0.41
7:sa:840:U:C4	7:sa:841:U:O4	2.74	0.41
7:sa:872:A:H2'	7:sa:873:A:H8	1.83	0.41
7:sa:889:U:H2'	7:sa:890:C:H6	1.86	0.41
8:sb:20:ILE:O	8:sb:24:VAL:HG12	2.20	0.41
8:sb:63:LEU:HD21	8:sb:184:MET:HB3	2.03	0.41
9:sc:151:GLY:HA2	9:sc:152:GLU:HA	1.67	0.41
10:se:148:LYS:HE3	10:se:148:LYS:HB3	1.82	0.41
11:sf:99:LEU:HD23	11:sf:99:LEU:HA	1.82	0.41
12:sh:58:LYS:CG	12:sh:105:ASP:HB2	2.31	0.41
13:si:143:GLY:O	13:si:162:PHE:N	2.50	0.41
15:sk:131:GLY:HA3	15:sk:133:MET:HE2	2.03	0.41
22:sz:15:LEU:HG	22:sz:26:VAL:HB	2.03	0.41
7:sa:17:C:O2'	7:sa:1163:A:N1	2.49	0.41
7:sa:74:A:O2'	7:sa:75:G:O4'	2.34	0.41
7:sa:752:A:H2'	7:sa:753:G:H8	1.86	0.41
7:sa:888:A:H2	7:sa:989:U:H1'	1.86	0.41
7:sa:1089:A:C5	7:sa:1090:C:N4	2.89	0.41
7:sa:1143:U:N3	7:sa:1144:G:N7	2.69	0.41
12:sh:64:MET:SD	12:sh:81:ASN:HB3	2.61	0.41
12:sh:191:HIS:O	12:sh:195:LYS:HB2	2.20	0.41
14:sj:22:GLN:HG2	14:sj:23:LYS:O	2.20	0.41
5:sJ:9:G:O2'	5:sJ:10:G:N7	2.41	0.40
7:sa:152:A:H2'	7:sa:153:U:C6	2.55	0.40
7:sa:353:U:H2'	7:sa:355:A:H5'	2.03	0.40
7:sa:424:G:C2	7:sa:425:G:C8	3.10	0.40
9:sc:81:GLU:HG3	9:sc:192:LEU:HD21	2.03	0.40
11:sf:85:MET:HE3	11:sf:100:MET:HE3	2.02	0.40
15:sk:135:LYS:HZ2	15:sk:135:LYS:HG3	1.75	0.40
7:sa:848:A:H5''	17:so:91:LEU:HD13	2.03	0.40
7:sa:882:G:H2'	7:sa:883:U:C6	2.56	0.40
12:sh:57:ASP:CB	12:sh:61:PHE:HB2	2.51	0.40
4:sI:28:G:H2'	4:sI:29:C:H6	1.86	0.40
4:sI:61:C:H2'	4:sI:62:C:H6	1.87	0.40
7:sa:15:U:H2'	7:sa:16:G:O4'	2.22	0.40
7:sa:1815:C:H2'	7:sa:1816:U:C6	2.56	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:sh:86:PRO:HA	12:sh:91:GLU:O	2.21	0.40
13:si:188:ILE:HG13	13:si:189:THR:HG23	2.02	0.40
13:si:189:THR:OG1	13:si:190:GLY:N	2.53	0.40
7:sa:369:U:O2	7:sa:597:U:H4'	2.21	0.40
7:sa:618:G:H2'	7:sa:619:C:C6	2.56	0.40
12:sh:112:ILE:O	12:sh:112:ILE:HG22	2.21	0.40
2:sC:24:ARG:NH1	2:sC:28:THR:O	2.54	0.40
7:sa:362:A:H2'	7:sa:363:U:O4'	2.22	0.40
7:sa:466:A:O2'	15:sk:9:SER:O	2.35	0.40
15:sk:130:ARG:HA	15:sk:130:ARG:HD2	1.93	0.40
19:sr:80:ASN:OD1	19:sr:80:ASN:N	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	sB	96/144 (67%)	91 (95%)	5 (5%)	0	100	100
2	sC	29/84 (34%)	29 (100%)	0	0	100	100
8	sb	203/254 (80%)	195 (96%)	8 (4%)	0	100	100
9	sc	213/255 (84%)	199 (93%)	13 (6%)	1 (0%)	24	58
10	se	107/256 (42%)	101 (94%)	6 (6%)	0	100	100
11	sf	244/326 (75%)	223 (91%)	21 (9%)	0	100	100
12	sh	135/266 (51%)	84 (62%)	30 (22%)	21 (16%)	0	0
13	si	66/201 (33%)	62 (94%)	4 (6%)	0	100	100
14	sj	123/237 (52%)	117 (95%)	6 (5%)	0	100	100
15	sk	155/185 (84%)	149 (96%)	6 (4%)	0	100	100
16	sm	137/156 (88%)	127 (93%)	10 (7%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	so	68/151 (45%)	66 (97%)	2 (3%)	0	100	100
18	sp	131/146 (90%)	121 (92%)	10 (8%)	0	100	100
19	sr	127/130 (98%)	114 (90%)	13 (10%)	0	100	100
20	sx	79/86 (92%)	77 (98%)	2 (2%)	0	100	100
21	sy	104/141 (74%)	96 (92%)	8 (8%)	0	100	100
22	sz	52/140 (37%)	47 (90%)	4 (8%)	1 (2%)	6	31
All	All	2069/3158 (66%)	1898 (92%)	148 (7%)	23 (1%)	14	42

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	sh	108	VAL
12	sh	111	THR
12	sh	114	VAL
12	sh	120	GLU
12	sh	184	VAL
12	sh	76	LEU
12	sh	97	VAL
12	sh	107	SER
12	sh	117	GLY
12	sh	118	GLU
12	sh	121	ILE
12	sh	122	GLU
12	sh	143	LYS
22	sz	81	ASP
12	sh	64	MET
12	sh	104	GLY
12	sh	86	PRO
12	sh	103	ALA
12	sh	113	VAL
12	sh	68	ALA
12	sh	74	ARG
12	sh	67	VAL
9	sc	165	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	
1	sB	87/127 (68%)	83 (95%)	4 (5%)	24	56
2	sC	27/73 (37%)	24 (89%)	3 (11%)	6	25
8	sb	178/218 (82%)	173 (97%)	5 (3%)	38	65
9	sc	172/199 (86%)	165 (96%)	7 (4%)	27	58
10	se	116/225 (52%)	107 (92%)	9 (8%)	11	39
11	sf	213/283 (75%)	203 (95%)	10 (5%)	23	55
12	sh	117/220 (53%)	81 (69%)	36 (31%)	0	1
13	si	61/167 (36%)	57 (93%)	4 (7%)	15	45
14	sj	108/205 (53%)	102 (94%)	6 (6%)	19	50
15	sk	140/164 (85%)	130 (93%)	10 (7%)	13	43
16	sm	126/138 (91%)	119 (94%)	7 (6%)	19	50
17	so	68/129 (53%)	68 (100%)	0	100	100
18	sp	103/114 (90%)	95 (92%)	8 (8%)	11	39
19	sr	112/113 (99%)	104 (93%)	8 (7%)	13	43
20	sx	73/77 (95%)	67 (92%)	6 (8%)	10	37
21	sy	86/114 (75%)	79 (92%)	7 (8%)	11	38
22	sz	49/125 (39%)	46 (94%)	3 (6%)	17	47
All	All	1836/2691 (68%)	1703 (93%)	133 (7%)	15	42

All (133) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	sB	12	LYS
1	sB	28	ARG
1	sB	60	THR
1	sB	67	THR
2	sC	10	ASN
2	sC	12	THR
2	sC	31	SER
8	sb	57	MET
8	sb	168	ILE
8	sb	199	ASP
8	sb	204	VAL
8	sb	206	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	sc	73	HIS
9	sc	86	GLN
9	sc	87	SER
9	sc	139	VAL
9	sc	203	THR
9	sc	220	VAL
9	sc	247	LYS
10	se	26	PHE
10	se	45	VAL
10	se	49	VAL
10	se	70	VAL
10	se	89	LYS
10	se	122	LEU
10	se	125	THR
10	se	149	SER
10	se	166	ILE
11	sf	30	SER
11	sf	74	ILE
11	sf	82	VAL
11	sf	85	MET
11	sf	106	ARG
11	sf	128	VAL
11	sf	180	MET
11	sf	198	VAL
11	sf	217	THR
11	sf	232	THR
12	sh	58	LYS
12	sh	59	ASP
12	sh	63	MET
12	sh	64	MET
12	sh	70	ASN
12	sh	71	ASN
12	sh	73	VAL
12	sh	74	ARG
12	sh	75	LEU
12	sh	77	LEU
12	sh	80	ARG
12	sh	83	CYS
12	sh	85	LYS
12	sh	87	LEU
12	sh	88	ARG
12	sh	92	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
12	sh	93	ARG
12	sh	94	ARG
12	sh	97	VAL
12	sh	108	VAL
12	sh	109	LEU
12	sh	111	THR
12	sh	112	ILE
12	sh	115	LYS
12	sh	116	LYS
12	sh	118	GLU
12	sh	121	ILE
12	sh	136	LYS
12	sh	141	ILE
12	sh	143	LYS
12	sh	157	VAL
12	sh	176	LYS
12	sh	184	VAL
12	sh	185	THR
12	sh	209	GLU
12	sh	216	ILE
13	si	102	VAL
13	si	135	MET
13	si	162	PHE
13	si	199	VAL
14	sj	32	GLN
14	sj	43	VAL
14	sj	82	VAL
14	sj	93	THR
14	sj	98	LYS
14	sj	207	SER
15	sk	3	ARG
15	sk	5	LEU
15	sk	66	ASP
15	sk	82	ASN
15	sk	89	ASP
15	sk	103	ASN
15	sk	112	LEU
15	sk	120	LYS
15	sk	122	ILE
15	sk	158	LEU
16	sm	5	THR
16	sm	12	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
16	sm	54	ASP
16	sm	73	ILE
16	sm	98	ARG
16	sm	134	THR
16	sm	138	ASN
18	sp	35	THR
18	sp	40	THR
18	sp	47	THR
18	sp	52	THR
18	sp	55	MET
18	sp	62	ASP
18	sp	70	MET
18	sp	124	ILE
19	sr	34	ILE
19	sr	36	GLU
19	sr	53	VAL
19	sr	61	ILE
19	sr	65	LEU
19	sr	83	LEU
19	sr	87	ASP
19	sr	105	THR
20	sx	32	ILE
20	sx	37	VAL
20	sx	43	ILE
20	sx	48	THR
20	sx	78	THR
20	sx	86	ILE
21	sy	41	THR
21	sy	71	ARG
21	sy	86	ASP
21	sy	92	VAL
21	sy	95	ASN
21	sy	103	PHE
21	sy	106	ARG
22	sz	20	LEU
22	sz	28	VAL
22	sz	65	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	sB	94	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	sC	10	ASN
11	sf	161	ASN
12	sh	70	ASN
12	sh	71	ASN
12	sh	110	ASN
14	sj	80	ASN
15	sk	43	GLN
20	sx	31	GLN
21	sy	37	ASN
21	sy	50	GLN
22	sz	14	ASN
22	sz	25	GLN
22	sz	32	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	sI	70/76 (92%)	15 (21%)	0
5	sJ	69/77 (89%)	19 (27%)	0
6	sK	9/10 (90%)	0	0
7	sa	961/1947 (49%)	207 (21%)	0
All	All	1109/2110 (52%)	241 (21%)	0

All (241) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	sI	14	A
4	sI	15	G
4	sI	16	G
4	sI	17	G
4	sI	18	A
4	sI	22	G
4	sI	46	G
4	sI	49	G
4	sI	53	G
4	sI	54	U
4	sI	59	G
4	sI	60	U
4	sI	69	G
4	sI	74	C
4	sI	76	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	sJ	23	G
5	sJ	24	C
5	sJ	47	G
5	sJ	48	U
5	sJ	50	U
5	sJ	51	U
5	sJ	53	G
5	sJ	55	U
5	sJ	56	U
5	sJ	57	C
5	sJ	58	A
5	sJ	61	U
5	sJ	64	G
5	sJ	65	G
5	sJ	66	C
5	sJ	67	C
5	sJ	68	G
5	sJ	69	A
5	sJ	77	A
7	sa	4	C
7	sa	17	C
7	sa	24	U
7	sa	26	U
7	sa	33	A
7	sa	41	G
7	sa	42	A
7	sa	46	A
7	sa	53	C
7	sa	56	G
7	sa	61	A
7	sa	62	G
7	sa	64	A
7	sa	65	U
7	sa	67	A
7	sa	68	A
7	sa	69	G
7	sa	70	A
7	sa	74	A
7	sa	75	G
7	sa	76	U
7	sa	77	A
7	sa	78	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	sa	80	A
7	sa	103	U
7	sa	113	A
7	sa	114	G
7	sa	115	U
7	sa	135	C
7	sa	136	A
7	sa	139	G
7	sa	141	U
7	sa	148	G
7	sa	153	U
7	sa	154	G
7	sa	171	A
7	sa	173	A
7	sa	204	A
7	sa	243	U
7	sa	244	U
7	sa	246	G
7	sa	253	A
7	sa	262	G
7	sa	263	U
7	sa	264	A
7	sa	287	A
7	sa	288	A
7	sa	292	A
7	sa	294	G
7	sa	295	A
7	sa	296	G
7	sa	299	U
7	sa	310	U
7	sa	311	C
7	sa	313	A
7	sa	317	G
7	sa	332	G
7	sa	333	A
7	sa	345	A
7	sa	347	A
7	sa	354	A
7	sa	355	A
7	sa	356	C
7	sa	385	G
7	sa	394	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	sa	395	G
7	sa	397	U
7	sa	399	G
7	sa	411	A
7	sa	412	A
7	sa	413	G
7	sa	417	G
7	sa	418	G
7	sa	419	C
7	sa	420	A
7	sa	421	G
7	sa	430	U
7	sa	434	U
7	sa	440	A
7	sa	455	A
7	sa	463	A
7	sa	470	A
7	sa	545	G
7	sa	549	A
7	sa	551	G
7	sa	553	C
7	sa	555	G
7	sa	559	C
7	sa	561	A
7	sa	562	G
7	sa	568	G
7	sa	572	U
7	sa	573	A
7	sa	576	U
7	sa	579	A
7	sa	584	C
7	sa	588	A
7	sa	589	G
7	sa	600	A
7	sa	602	U
7	sa	604	G
7	sa	605	C
7	sa	613	A
7	sa	614	A
7	sa	616	A
7	sa	617	C
7	sa	618	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	sa	628	G
7	sa	741	U
7	sa	742	G
7	sa	746	A
7	sa	756	G
7	sa	757	U
7	sa	762	A
7	sa	765	A
7	sa	769	C
7	sa	771	U
7	sa	773	A
7	sa	774	U
7	sa	775	G
7	sa	776	U
7	sa	777	U
7	sa	782	A
7	sa	783	A
7	sa	784	U
7	sa	785	A
7	sa	787	U
7	sa	789	A
7	sa	803	G
7	sa	804	C
7	sa	843	A
7	sa	844	A
7	sa	845	A
7	sa	856	G
7	sa	866	G
7	sa	894	G
7	sa	904	A
7	sa	913	A
7	sa	915	A
7	sa	922	G
7	sa	925	U
7	sa	927	U
7	sa	939	G
7	sa	940	U
7	sa	946	A
7	sa	972	A
7	sa	973	A
7	sa	977	G
7	sa	982	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	sa	984	U
7	sa	985	A
7	sa	1006	A
7	sa	1008	C
7	sa	1010	A
7	sa	1012	G
7	sa	1033	A
7	sa	1091	C
7	sa	1106	A
7	sa	1117	U
7	sa	1118	G
7	sa	1122	U
7	sa	1123	U
7	sa	1126	G
7	sa	1135	G
7	sa	1140	G
7	sa	1164	A
7	sa	1166	G
7	sa	1169	A
7	sa	1797	A
7	sa	1800	C
7	sa	1801	A
7	sa	1817	A
7	sa	1821	A
7	sa	1822	U
7	sa	1823	U
7	sa	1824	G
7	sa	1825	A
7	sa	1826	A
7	sa	1830	A
7	sa	1832	A
7	sa	1846	G
7	sa	1849	U
7	sa	1850	C
7	sa	1852	G
7	sa	1863	A
7	sa	1883	C
7	sa	1885	U
7	sa	1886	U
7	sa	1887	A
7	sa	1889	U
7	sa	1894	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	sa	1895	G
7	sa	1902	A
7	sa	1904	G
7	sa	1907	G
7	sa	1908	U
7	sa	1909	A
7	sa	1913	A
7	sa	1916	U
7	sa	1927	G
7	sa	1929	A
7	sa	1930	C
7	sa	1939	G
7	sa	1940	G
7	sa	1942	U
7	sa	1943	C
7	sa	1945	U

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

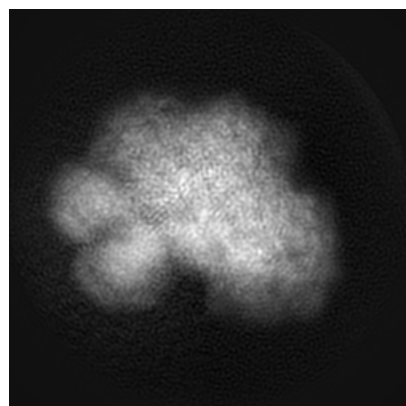
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64719. These allow visual inspection of the internal detail of the map and identification of artifacts.

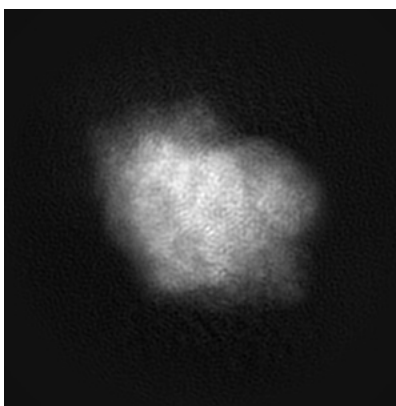
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

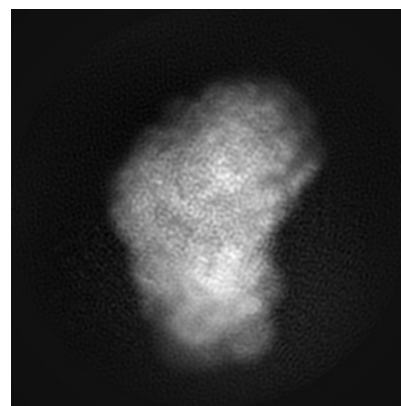
6.1.1 Primary map



X

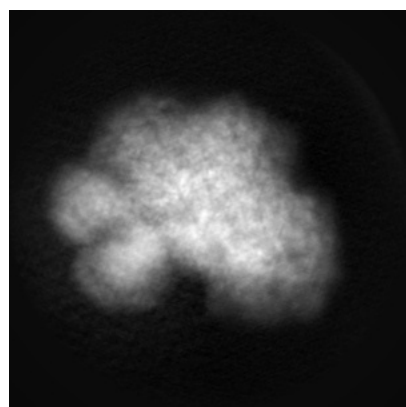


Y

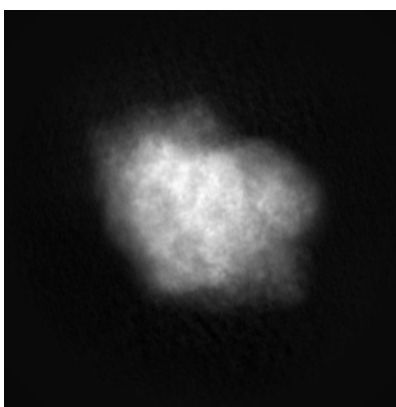


Z

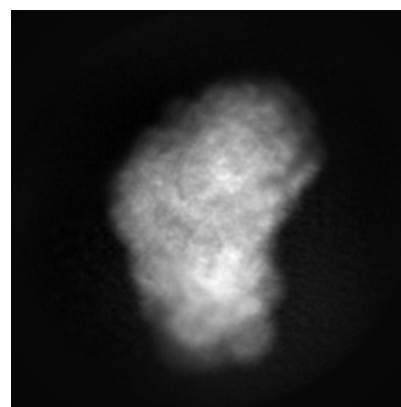
6.1.2 Raw map



X



Y

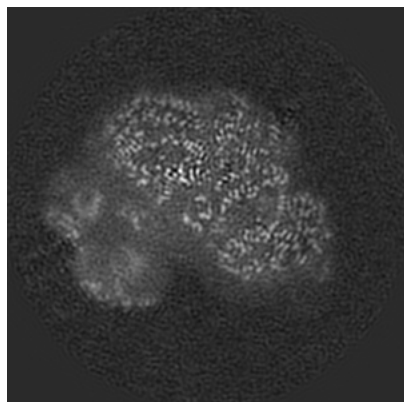


Z

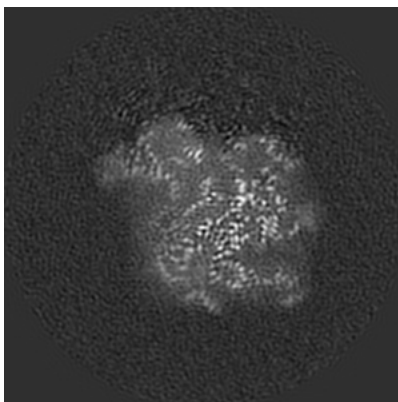
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

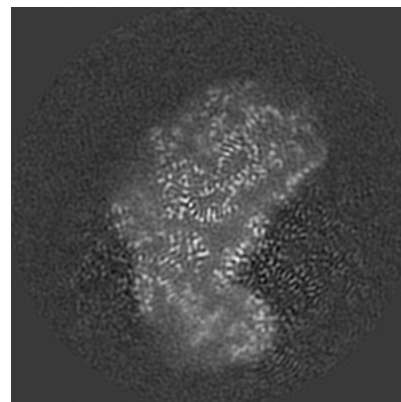
6.2.1 Primary map



X Index: 135

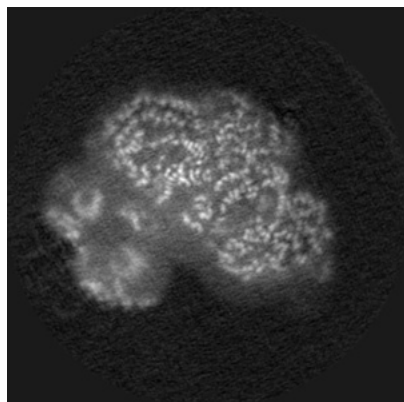


Y Index: 135

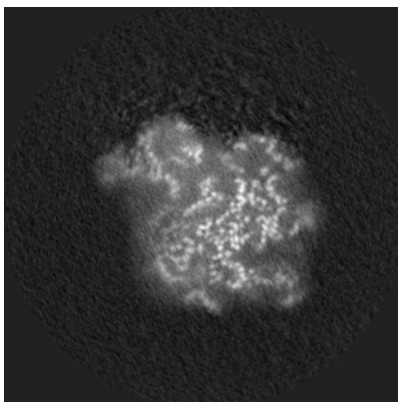


Z Index: 135

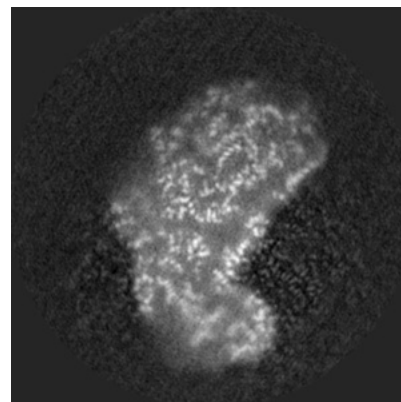
6.2.2 Raw map



X Index: 135



Y Index: 135

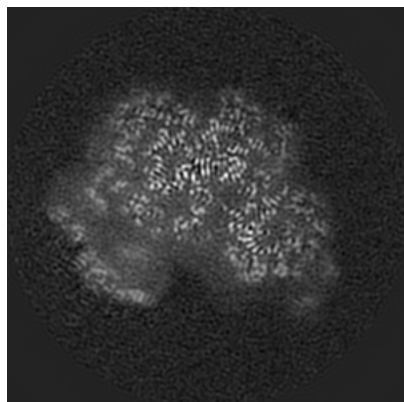


Z Index: 135

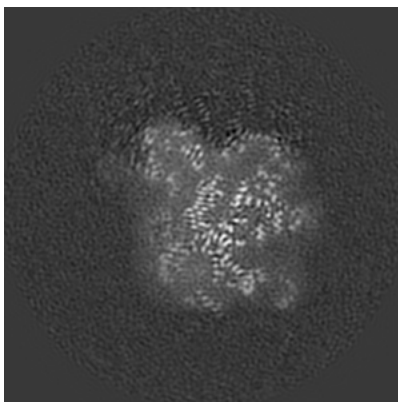
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

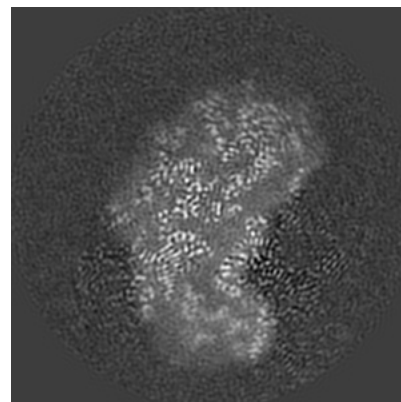
6.3.1 Primary map



X Index: 141

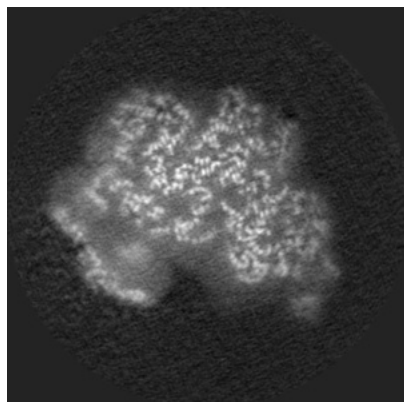


Y Index: 132

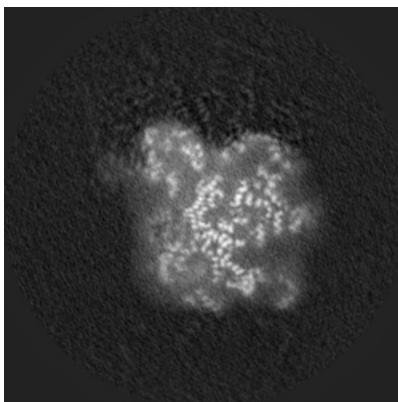


Z Index: 138

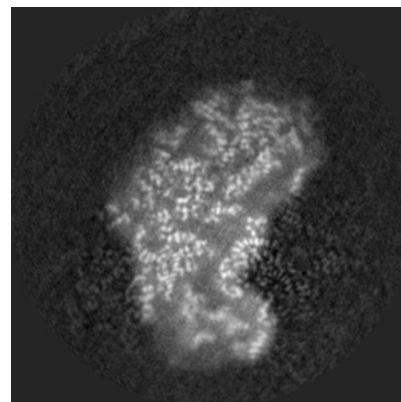
6.3.2 Raw map



X Index: 142



Y Index: 132

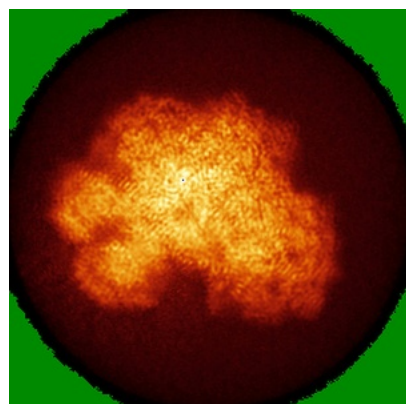


Z Index: 139

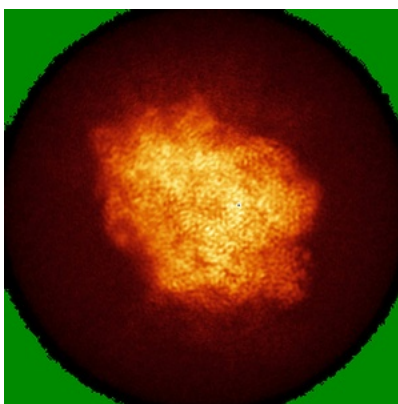
The images above show the largest variance slices of the map in three orthogonal directions.

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

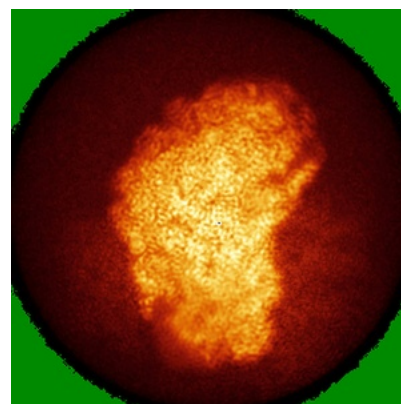
6.4.1 Primary map



X

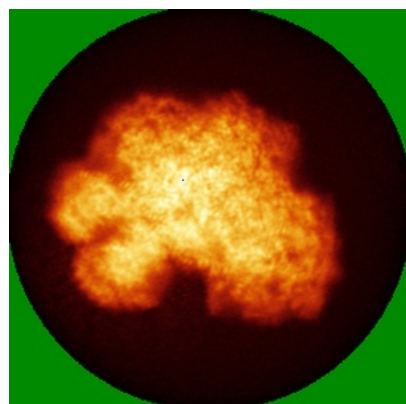


Y

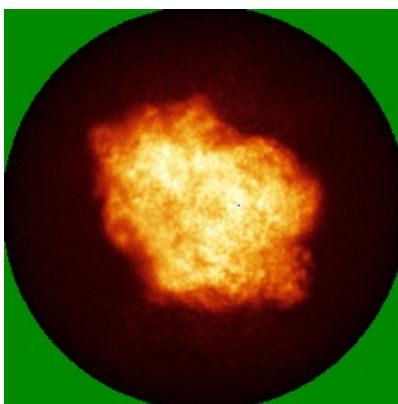


Z

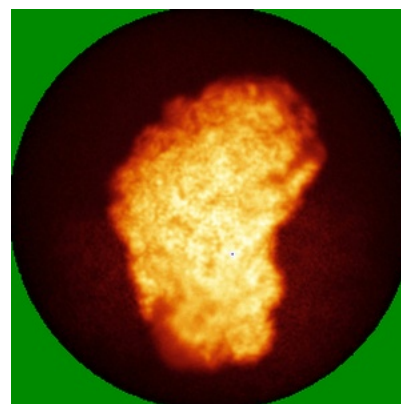
6.4.2 Raw map



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 3.2. 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.

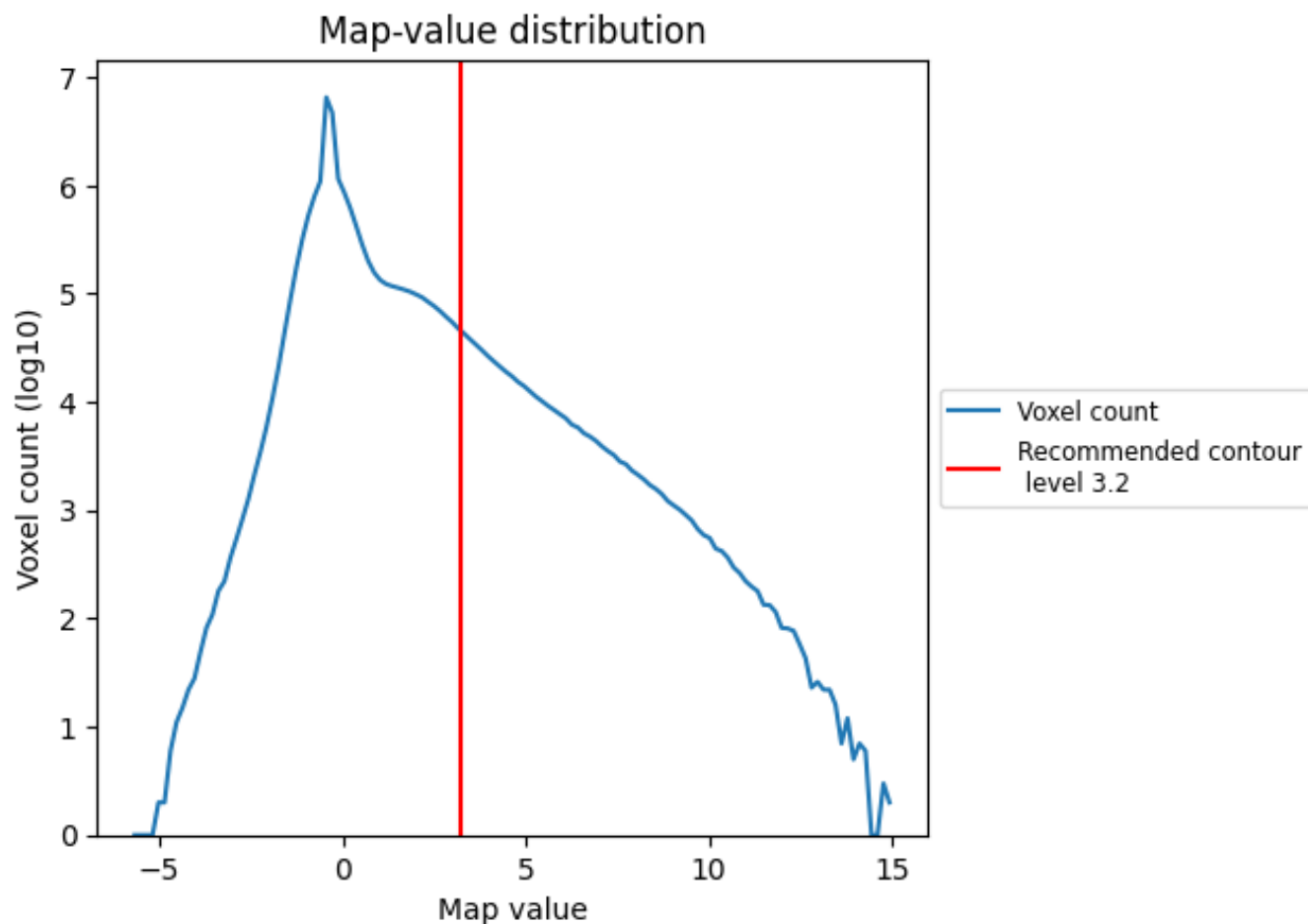
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

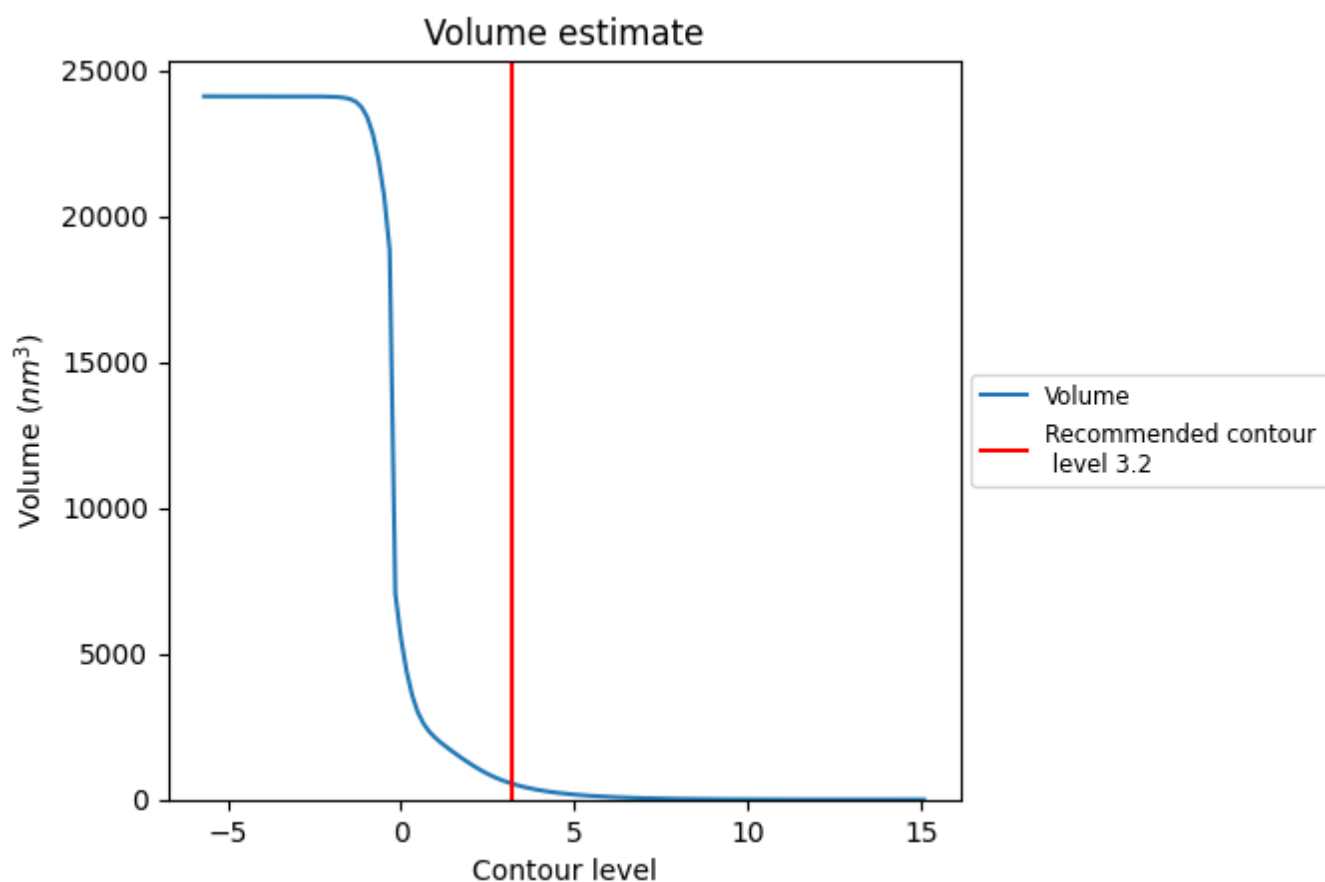
This section contains the results of statistical analysis of the map.

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.

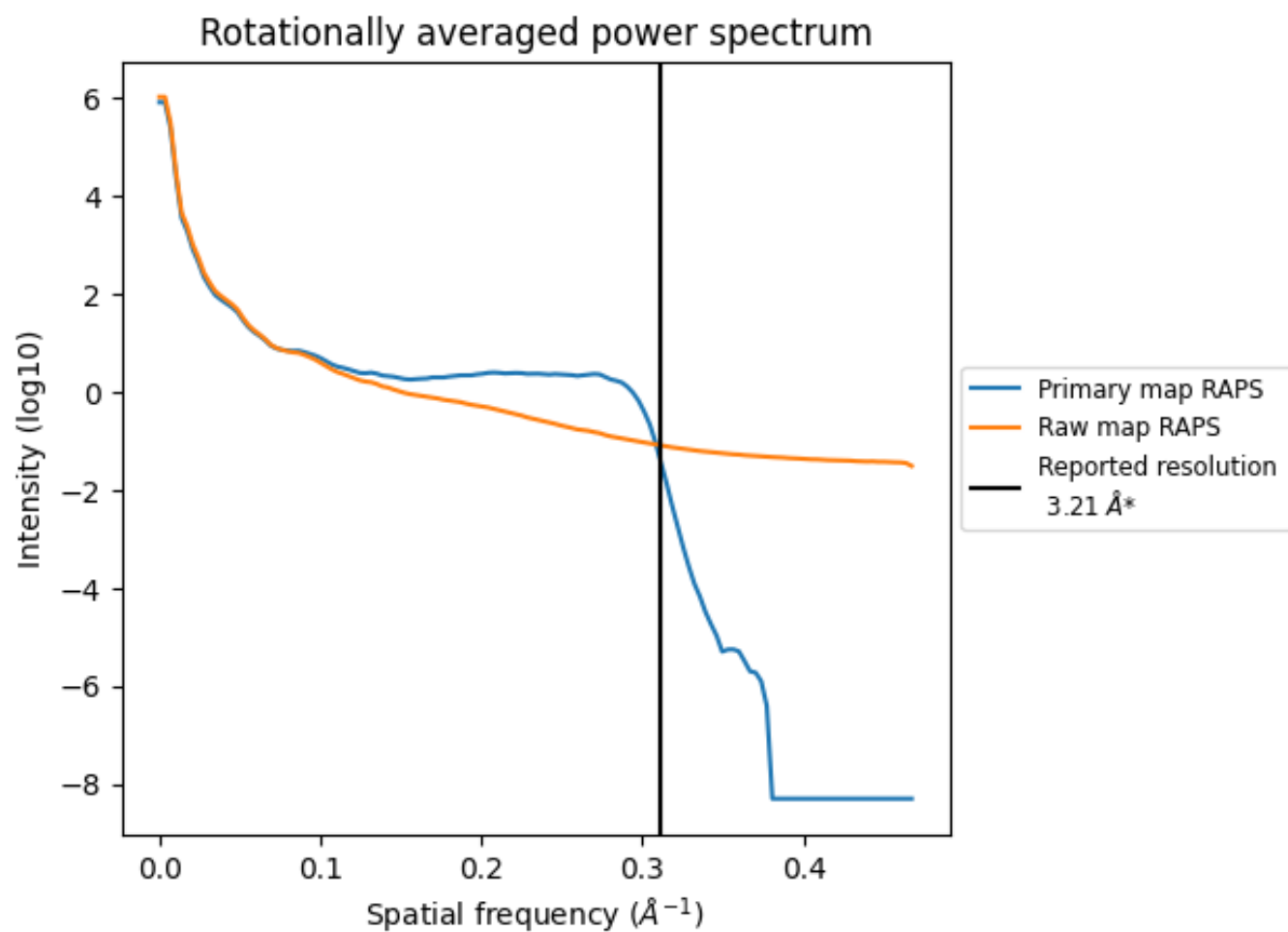
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 548 nm³; this corresponds to an approximate mass of 495 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

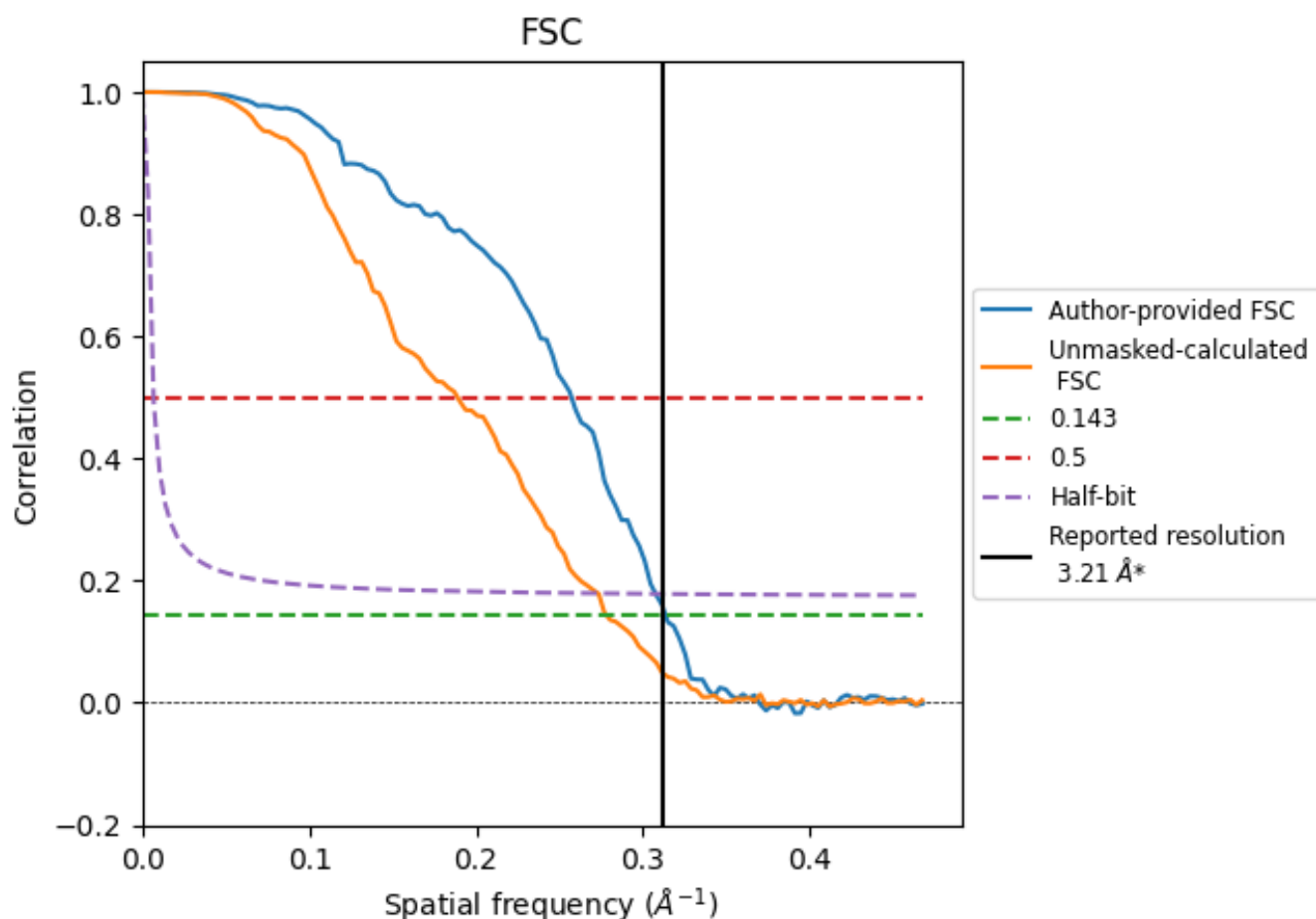


*Reported resolution corresponds to spatial frequency of 0.312 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

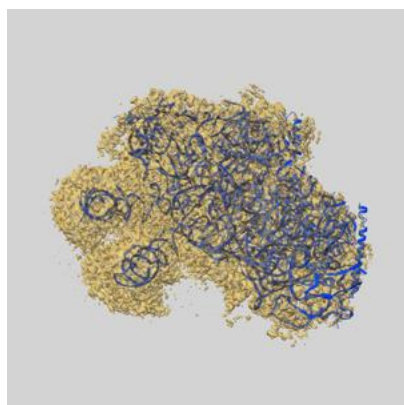
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.21	-	-
Author-provided FSC curve	3.19	3.89	3.25
Unmasked-calculated*	3.59	5.29	3.66

*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 3.59 differs from the reported value 3.21 by more than 10 %

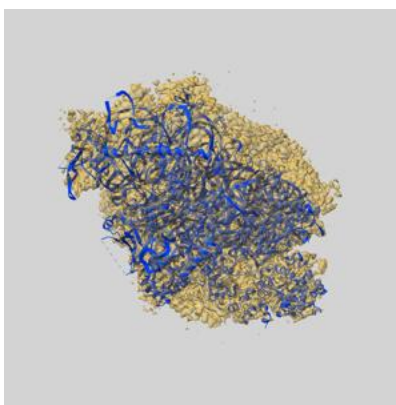
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-64719 and PDB model 9V27. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

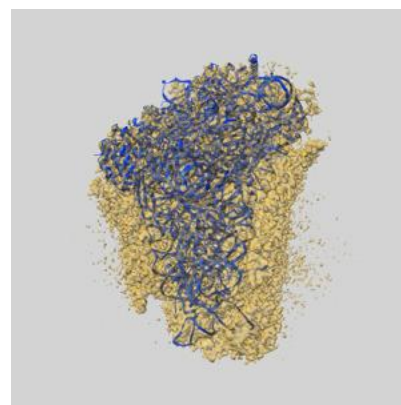
9.1 Map-model overlay [i](#)



X



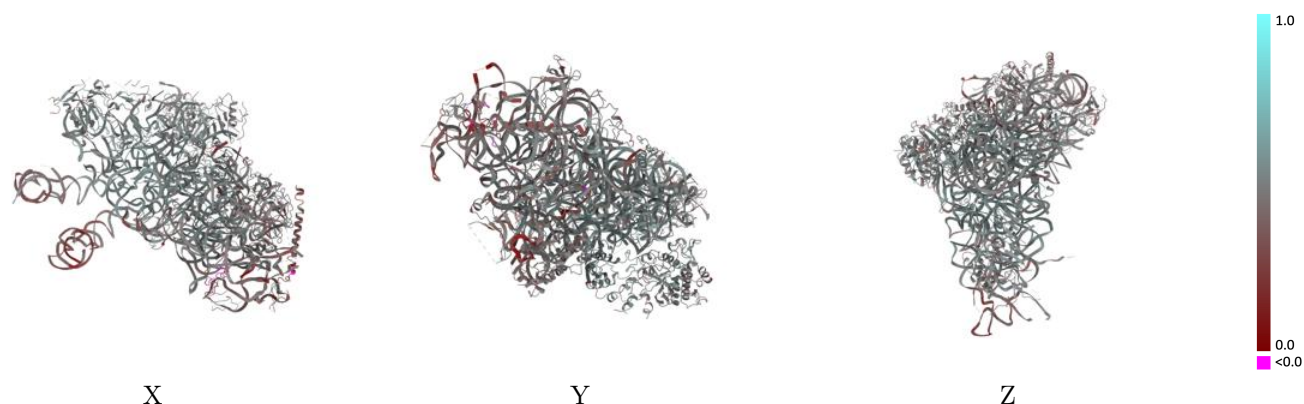
Y



Z

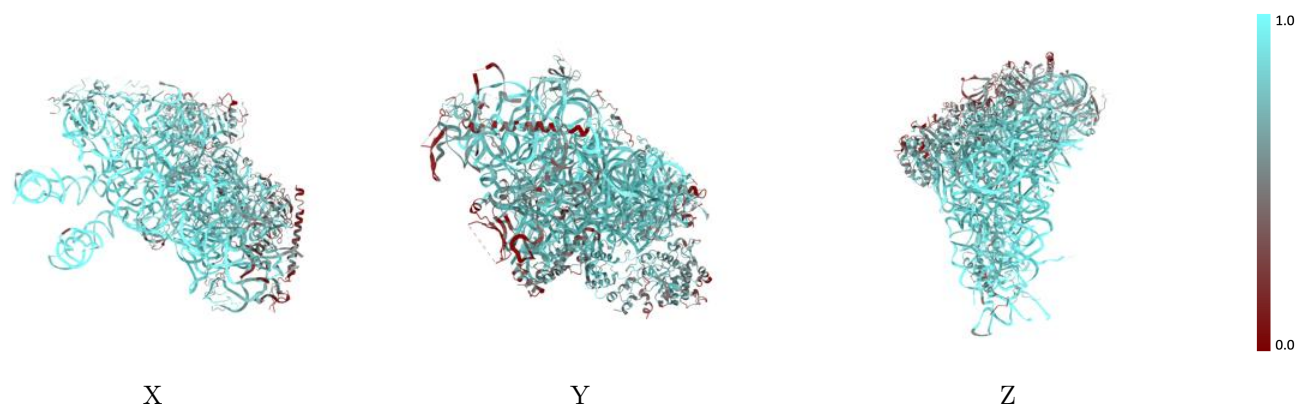
The images above show the 3D surface view of the map at the recommended contour level 3.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



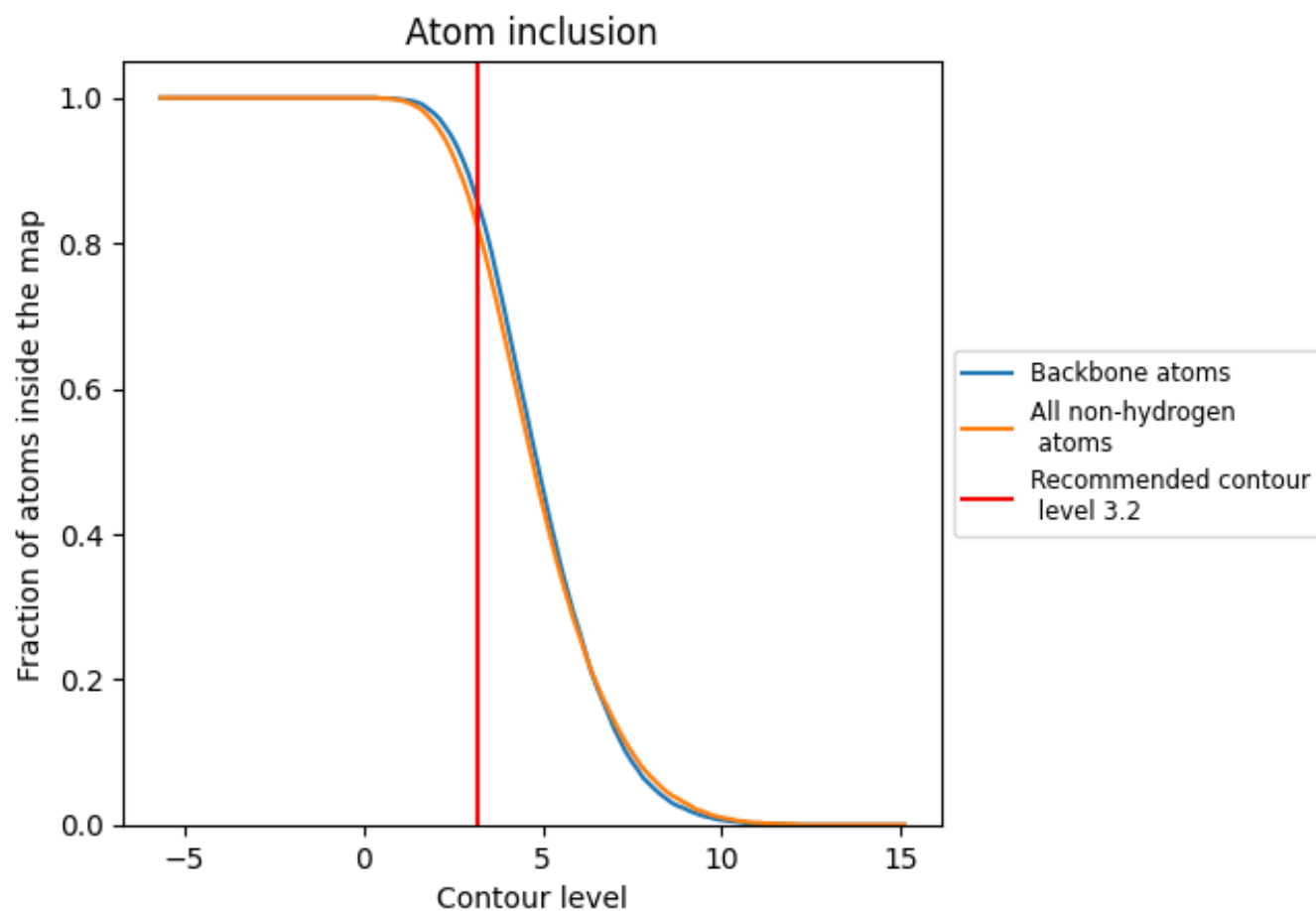
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 82% 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 (3.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8180	 0.4710
sB	 0.8780	 0.5250
sC	 0.6890	 0.5040
sH	 1.0000	 0.5540
sI	 0.9260	 0.3470
sJ	 0.9410	 0.4120
sK	 0.9950	 0.5330
sa	 0.9070	 0.4800
sb	 0.6640	 0.4850
sc	 0.7600	 0.5130
se	 0.7980	 0.5070
sf	 0.6130	 0.4640
sh	 0.4340	 0.3080
si	 0.4070	 0.4590
sj	 0.7680	 0.4810
sk	 0.5360	 0.4590
sm	 0.7590	 0.4780
so	 0.8560	 0.4980
sp	 0.8370	 0.5030
sr	 0.8360	 0.5140
sx	 0.6840	 0.5030
sy	 0.7170	 0.4770
sz	 0.1650	 0.4160

