



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 08:03 PM UTC

PDB ID : 2WYY / pdb_00002wyy
EMDB ID : EMD-1663
Title : CRYOEM MODEL OF THE VESICULAR STOMATITIS VIRUS
Authors : Ge, P.; Tsao, J.; Green, T.J.; Luo, M.; Zhou, Z.H.
Deposited on : 2009-11-20
Resolution : 10.60 Å(reported)
Based on initial model : 2WYY

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:

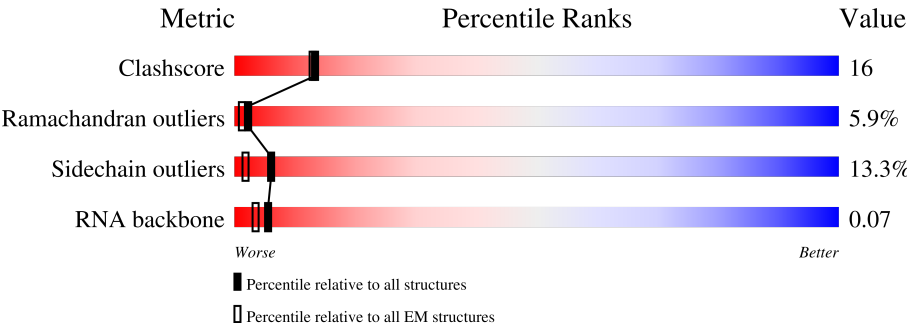
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson 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 10.60 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)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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	422	98% 64% 28% 5% .
1	C	422	98% 64% 28% 5% .
1	D	422	98% 65% 27% 5% .
1	F	422	98% 65% 27% 5% .
1	H	422	98% 65% 27% 6% .
1	I	422	98% 65% 27% 6% .
1	J	422	98% 65% 27% 6% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	K	422	98% 66% 27% 5%
1	L	422	98% 65% 27% 6%
1	M	422	98% 65% 27% 6%
2	R	45	100% 38% 53% 9%
2	S	45	100% 33% 56% 9%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 34620 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 NUCLEOPROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	C	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	D	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	F	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	H	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	I	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	J	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	K	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	L	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	M	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		

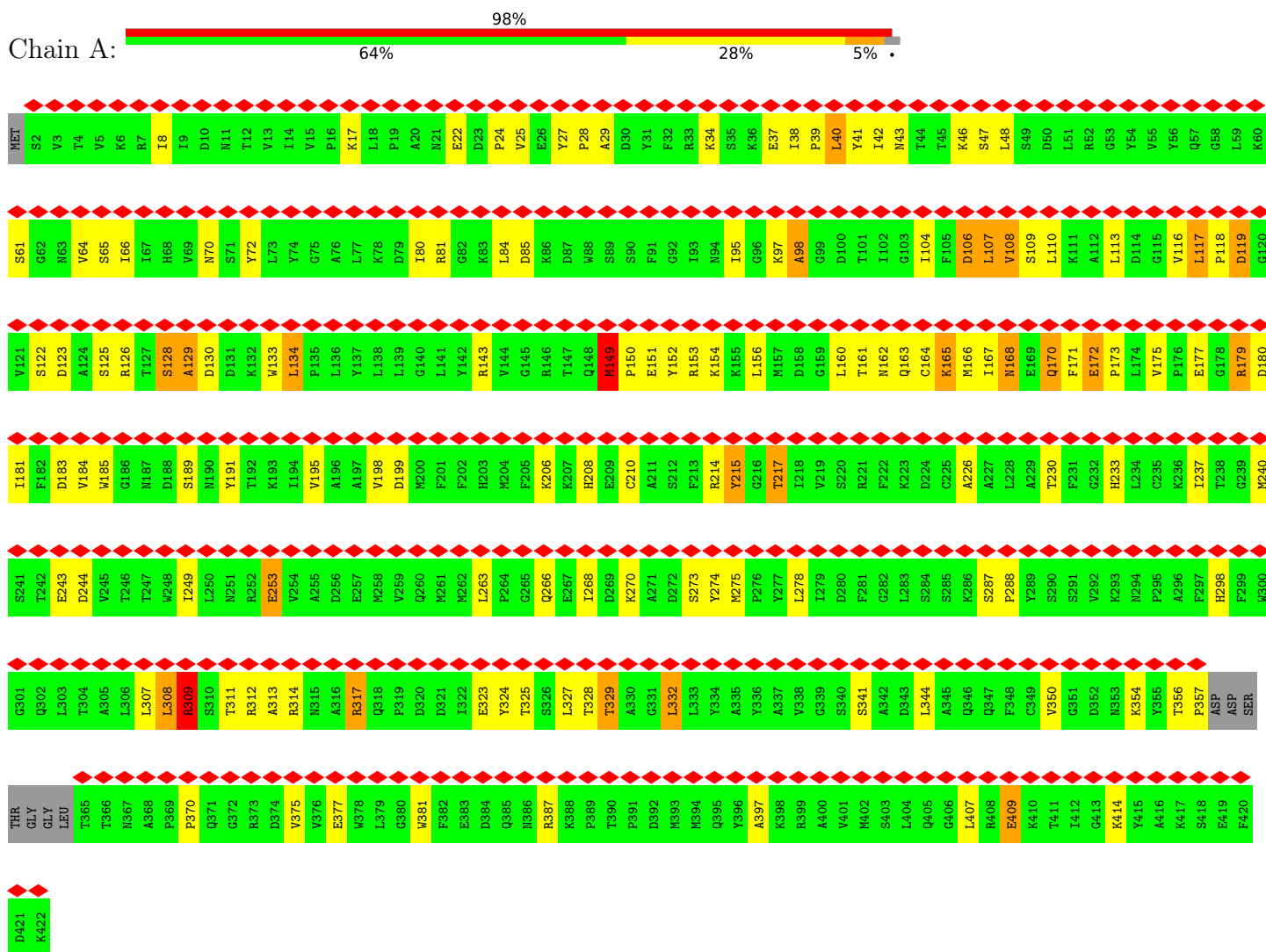
- Molecule 2 is a RNA chain called POLY-URIDINE.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	R	45	Total	C	N	O	P	0	0
			900	405	90	360	45		
2	S	45	Total	C	N	O	P	0	0
			900	405	90	360	45		

3 Residue-property plots

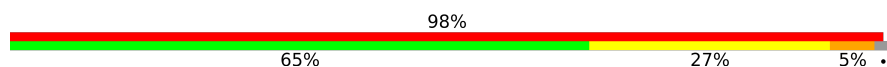
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: NUCLEOPROTEIN

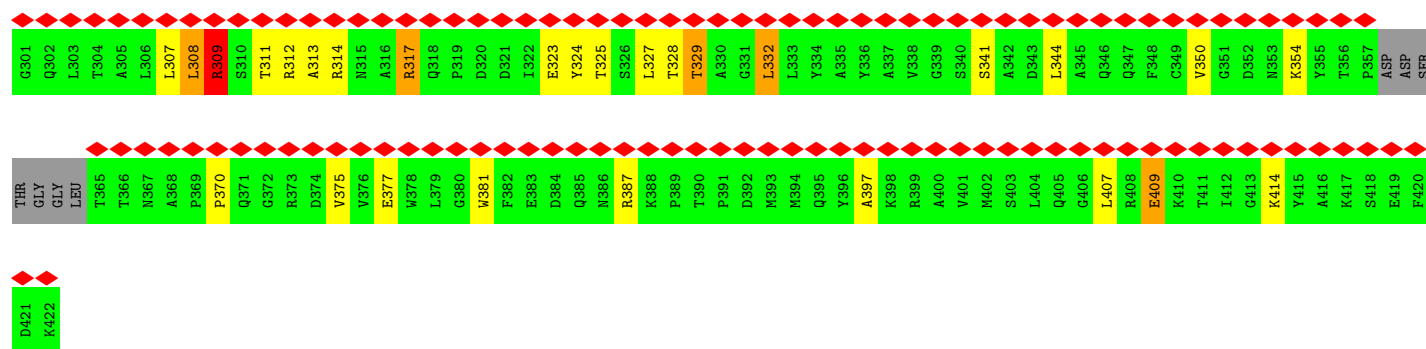


D421
K422

Chain D:

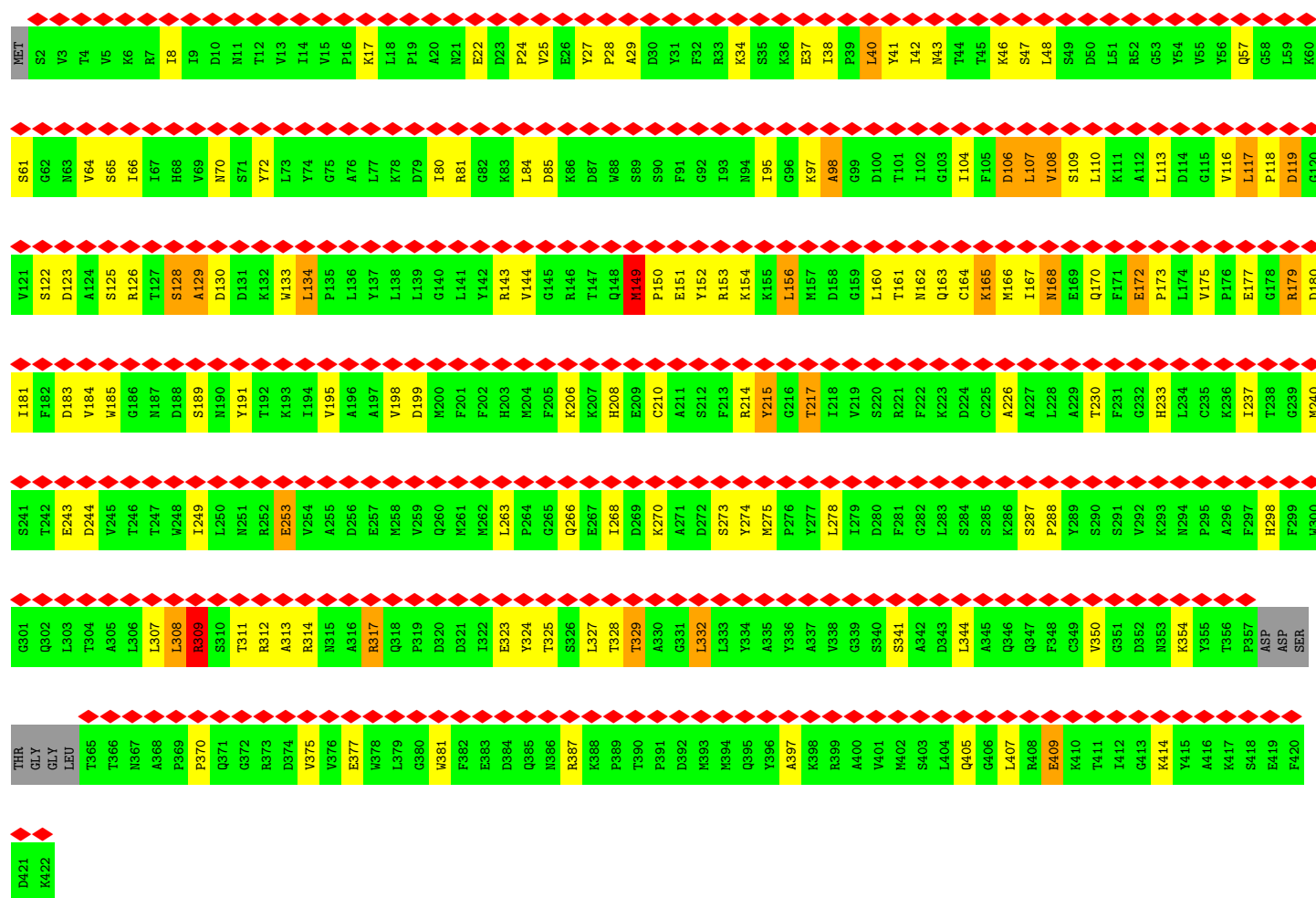


S241	S242	S243	S244	S245	S246	S247	S248	S249	S250	S251	S252	S253	S254	S255	S256	S257	S258	S259	S260	S261	S262	S263	S264	S265	S266	S267	S268	S269	S270	S271	S272	S273	S274	S275	S276	S277	S278	S279	S280	S281	S282	S283	S284	S285	S286	S287	S288	S289	S290	S291	S292	S293	S294	S295	S296	S297	S298	S299	S300
I181	F182	D183	V184	W185	G186	N187	D188	S189	N190	Y191	T192	K193	I194	V195	A196	A197	V198	D199	M200	F201	F202	H203	M204	G205	K206	K207	H208	E209	C210	A211	S212	F213	R214	Y215	G216	T217	I218	V219	S220	R221	F222	K223	D224	C225	A226	A227	L228	A229	T230	F231	G232	H233	L234	C235	K236	I237	T238	G239	M240
V121	S122	D123	A124	S125	R126	T127	S128	A129	D130	K131	K132	W133	L134	P135	L136	Y137	L138	L139	G140	L141	Y142	R143	V144	G145	R146	T147	Q148	M149	P150	E151	Y152	R153	K154	L155	L156	M157	D158	G159	L160	T161	N162	Q163	C164	K165	M166	L167	N168	E169	Q170	F171	E172	P173	L174	V175	P176	E177	G178	D179	L180
S61	G62	N63	V64	S65	T66	L67	H68	V69	N70	S71	Y72	L73	Y74	G75	A76	L77	K78	D79	T80	R81	G82	K83	L84	D85	K86	D87	N88	S89	S90	F91	G92	R93	N94	P95	G96	K97	A98	G99	D100	T101	I102	G103	I104	F105	D106	L107	V108	S109	L110	K111	A112	L113	D114	G115	V116	L117	P118	R119	G120
MET	S2	V3	T4	W5	K6	L7	R8	I9	D10	M11	T12	V13	I14	V15	P16	K17	L18	P19	A20	N21	E22	D23	P24	V25	E26	Y27	P28	A29	D30	F31	F32	R33	K34	S35	K36	E37	I38	P39	L40	Y41	I42	M43	T44	T45	K46	S47	L48	S49	D50	L51	R52	G53	Y54	V55	V56	Q57	G58	L59	K60



• Molecule 1: NUCLEOPROTEIN

Chain F: 98% 65% 27% 5% .

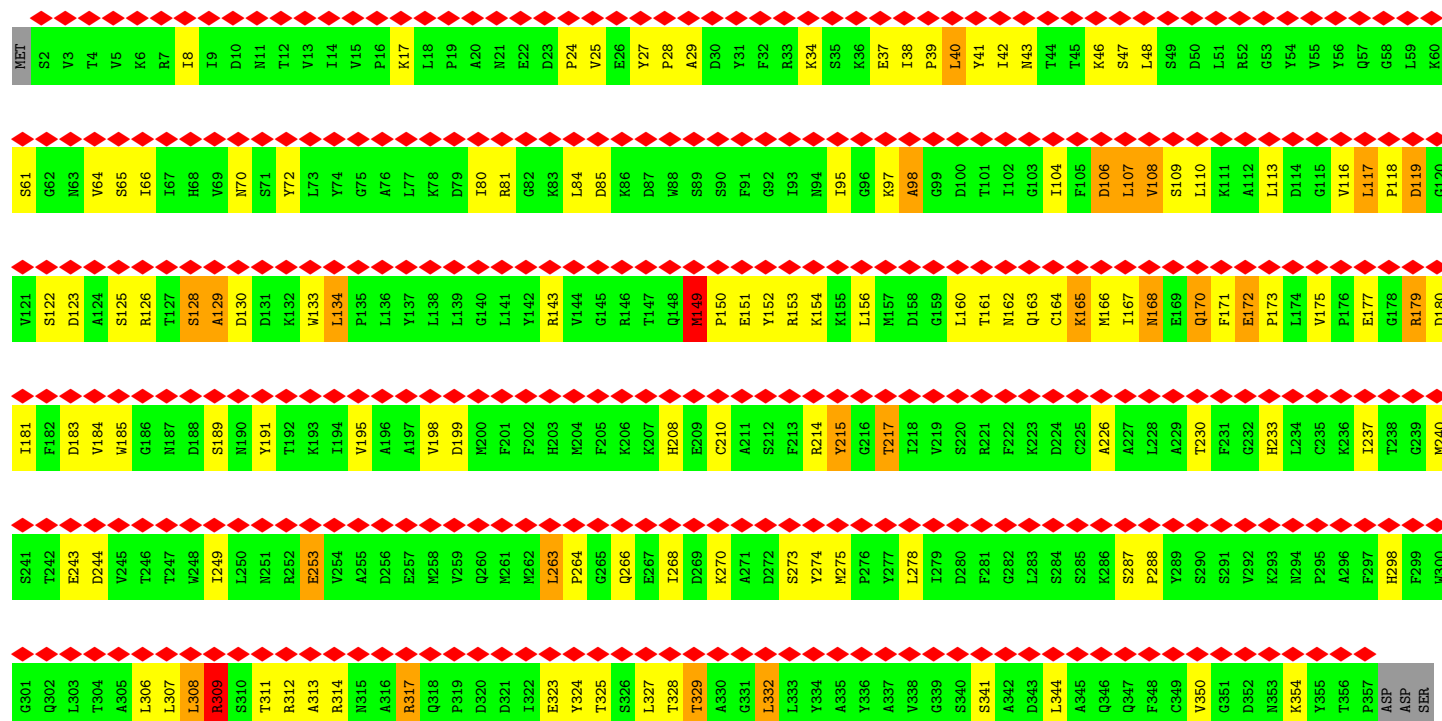


• Molecule 1: NUCLEOPROTEIN

Chain H: 98% 65% 27% 6% .

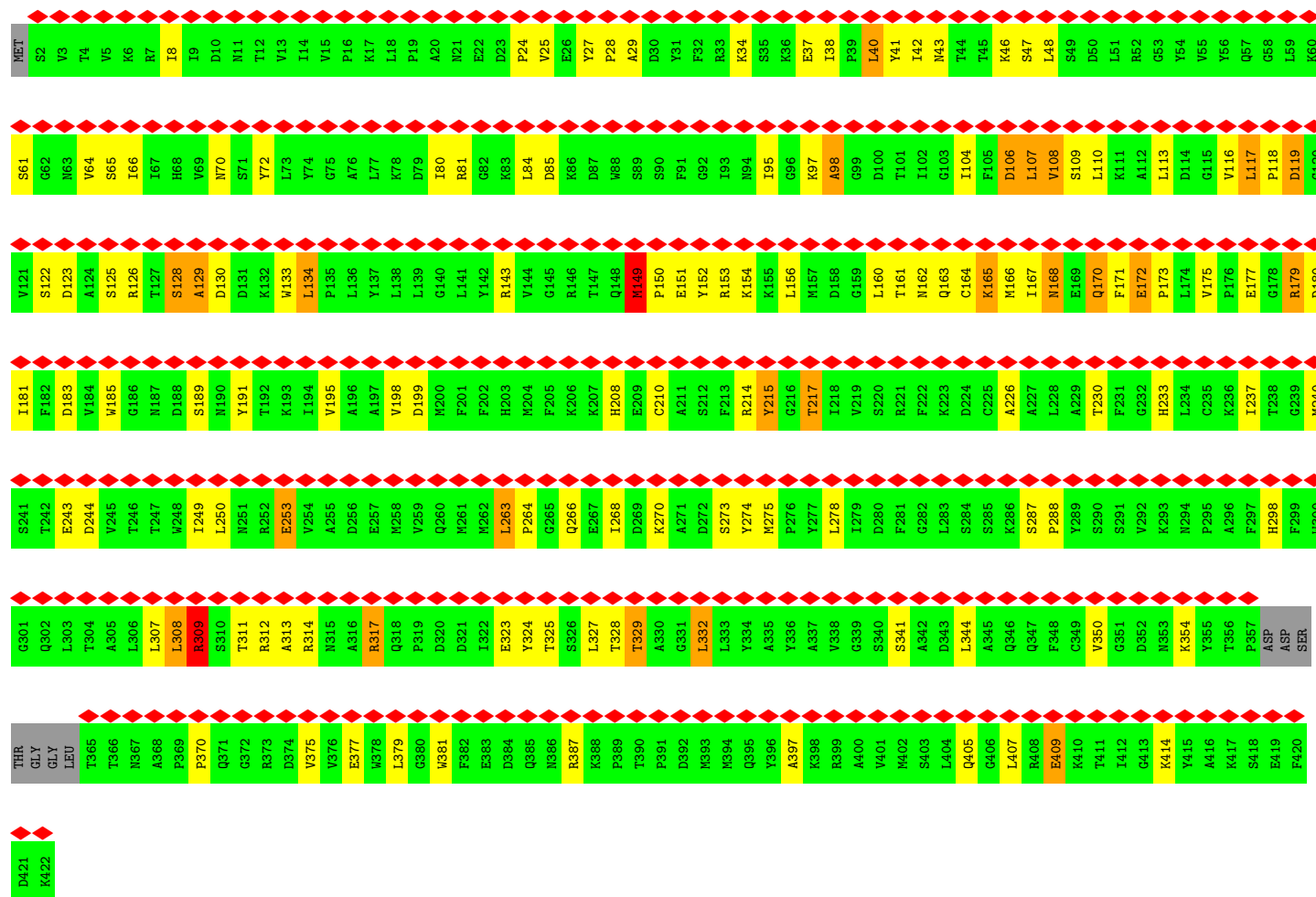


- Molecule 1: NUCLEOPROTEIN





• Molecule 1: NUCLEOPROTEIN

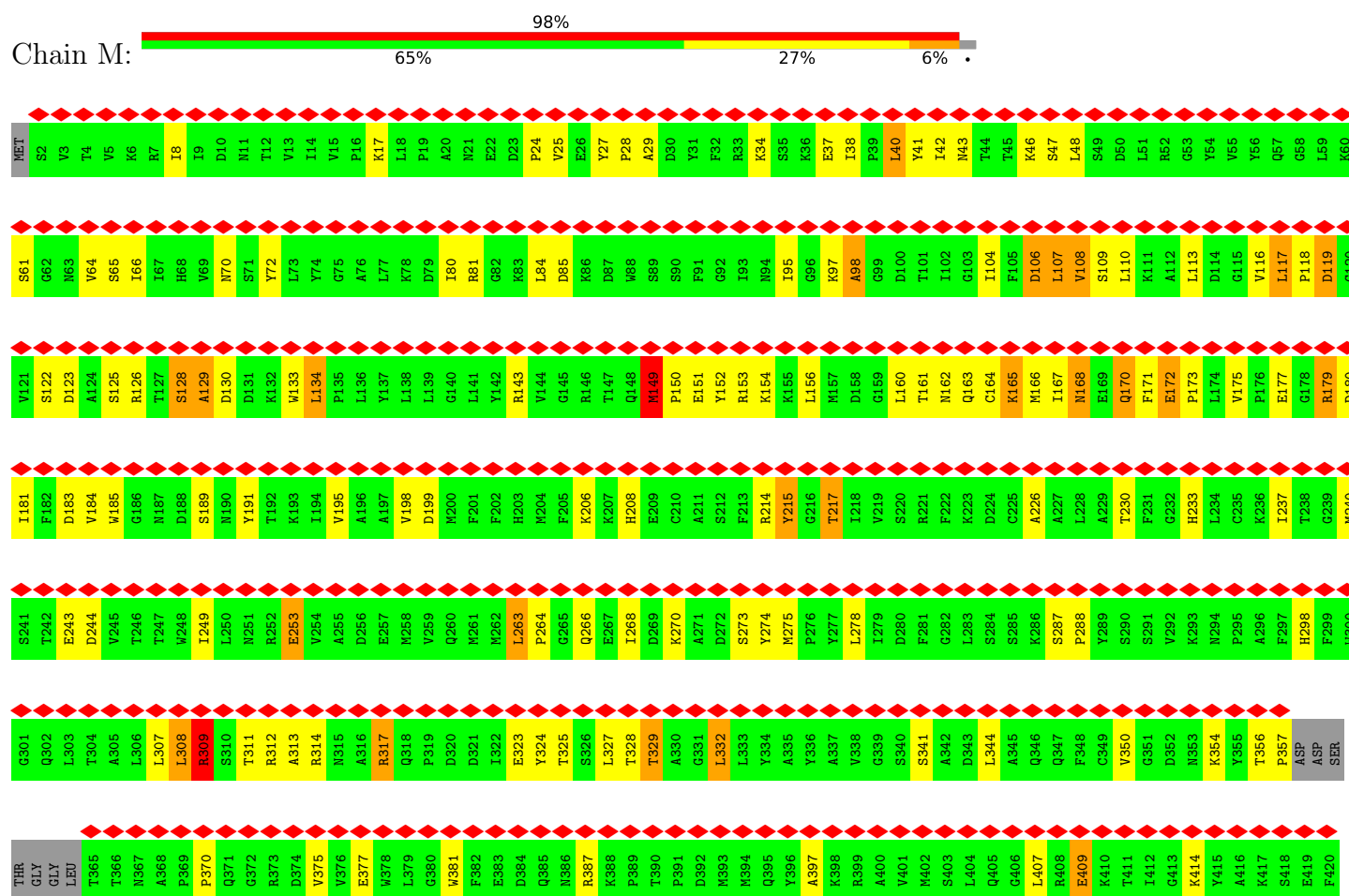


• Molecule 1: NUCLEOPROTEIN

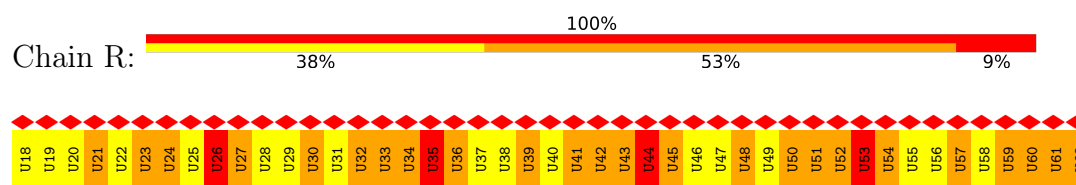




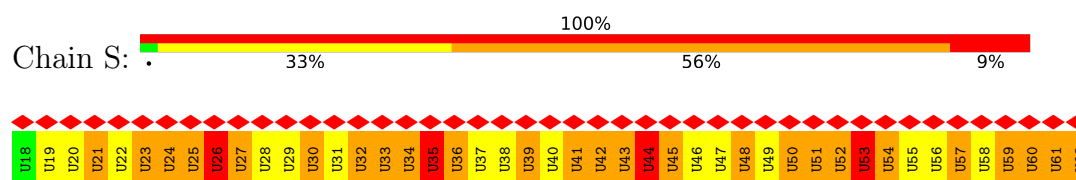
• Molecule 1: NUCLEOPROTEIN



• Molecule 2: POLY-URIDINE



• Molecule 2: POLY-URIDINE



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of segments used	Not provided	
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	98000	Depositor
Image detector	GENERIC TVIPS	Depositor
Maximum map value	5.997	Depositor
Minimum map value	-6.598	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.999	Depositor
Recommended contour level	1	Depositor
Map size (Å)	490.24, 490.24, 490.24	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90, 90, 90	wwPDB
Pixel spacing (Å)	1.532, 1.532, 1.532	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	0.69	1/3357 (0.0%)	0.94	4/4543 (0.1%)
1	C	0.70	1/3357 (0.0%)	0.94	4/4543 (0.1%)
1	D	0.65	1/3357 (0.0%)	0.92	4/4543 (0.1%)
1	F	0.70	1/3357 (0.0%)	0.93	4/4543 (0.1%)
1	H	0.70	1/3357 (0.0%)	0.94	4/4543 (0.1%)
1	I	0.70	1/3357 (0.0%)	0.94	4/4543 (0.1%)
1	J	0.70	1/3357 (0.0%)	0.94	4/4543 (0.1%)
1	K	0.65	1/3357 (0.0%)	0.92	4/4543 (0.1%)
1	L	0.70	1/3357 (0.0%)	0.93	4/4543 (0.1%)
1	M	0.70	1/3357 (0.0%)	0.94	4/4543 (0.1%)
2	R	0.70	0/989	0.97	4/1526 (0.3%)
2	S	0.70	0/989	0.97	4/1526 (0.3%)
All	All	0.69	10/35548 (0.0%)	0.94	48/48482 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
1	D	0	1
1	F	0	1
1	H	0	1
1	I	0	1
1	J	0	1
1	K	0	1
1	L	0	1
1	M	0	1
All	All	0	10

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	64	VAL	C-N	-6.18	1.25	1.33
1	I	64	VAL	C-N	-6.14	1.25	1.33
1	D	64	VAL	C-N	-5.95	1.25	1.33
1	H	64	VAL	C-N	-5.92	1.25	1.33
1	K	64	VAL	C-N	-5.92	1.25	1.33
1	M	64	VAL	C-N	-5.87	1.25	1.33
1	C	64	VAL	C-N	-5.82	1.25	1.33
1	J	64	VAL	C-N	-5.77	1.25	1.33
1	F	64	VAL	C-N	-5.75	1.25	1.33
1	L	64	VAL	C-N	-5.73	1.25	1.33

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	263	LEU	CA-C-N	7.07	127.38	119.32
1	M	263	LEU	C-N-CA	7.07	127.38	119.32
1	H	263	LEU	CA-C-N	7.05	127.35	119.32
1	H	263	LEU	C-N-CA	7.05	127.35	119.32
1	D	263	LEU	CA-C-N	6.86	127.14	119.32
1	D	263	LEU	C-N-CA	6.86	127.14	119.32
1	K	263	LEU	CA-C-N	6.85	127.13	119.32
1	K	263	LEU	C-N-CA	6.85	127.13	119.32
1	A	263	LEU	CA-C-N	6.72	126.98	119.32
1	A	263	LEU	C-N-CA	6.72	126.98	119.32
1	I	263	LEU	CA-C-N	6.70	126.96	119.32
1	I	263	LEU	C-N-CA	6.70	126.96	119.32
1	L	263	LEU	CA-C-N	6.63	126.88	119.32
1	L	263	LEU	C-N-CA	6.63	126.88	119.32
1	F	263	LEU	CA-C-N	6.60	126.84	119.32
1	F	263	LEU	C-N-CA	6.60	126.84	119.32
1	J	263	LEU	CA-C-N	6.58	126.82	119.32
1	J	263	LEU	C-N-CA	6.58	126.82	119.32
1	C	263	LEU	CA-C-N	6.57	126.81	119.32
1	C	263	LEU	C-N-CA	6.57	126.81	119.32
1	L	149	MET	CA-C-N	5.54	126.77	119.84
1	L	149	MET	C-N-CA	5.54	126.77	119.84
1	F	149	MET	CA-C-N	5.52	126.74	119.84
1	F	149	MET	C-N-CA	5.52	126.74	119.84
2	R	26	U	C4'-C3'-O3'	-5.47	104.79	113.00
2	S	35	U	C4'-C3'-O3'	-5.47	104.80	113.00
2	S	26	U	C4'-C3'-O3'	-5.46	104.81	113.00
2	R	35	U	C4'-C3'-O3'	-5.46	104.81	113.00
1	H	149	MET	CA-C-N	5.34	126.52	119.84

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	149	MET	C-N-CA	5.34	126.52	119.84
1	M	149	MET	CA-C-N	5.34	126.52	119.84
1	M	149	MET	C-N-CA	5.34	126.52	119.84
2	R	53	U	C4'-C3'-O3'	-5.25	105.12	113.00
2	R	44	U	C4'-C3'-O3'	-5.24	105.14	113.00
2	S	53	U	C4'-C3'-O3'	-5.24	105.15	113.00
1	D	149	MET	CA-C-N	5.23	126.38	119.84
1	D	149	MET	C-N-CA	5.23	126.38	119.84
2	S	44	U	C4'-C3'-O3'	-5.23	105.16	113.00
1	K	149	MET	CA-C-N	5.21	126.35	119.84
1	K	149	MET	C-N-CA	5.21	126.35	119.84
1	A	149	MET	CA-C-N	5.13	126.25	119.84
1	A	149	MET	C-N-CA	5.13	126.25	119.84
1	J	149	MET	CA-C-N	5.11	126.23	119.84
1	J	149	MET	C-N-CA	5.11	126.23	119.84
1	I	149	MET	CA-C-N	5.10	126.22	119.84
1	I	149	MET	C-N-CA	5.10	126.22	119.84
1	C	149	MET	CA-C-N	5.09	126.21	119.84
1	C	149	MET	C-N-CA	5.09	126.21	119.84

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	106	ASP	Peptide
1	C	106	ASP	Peptide
1	D	106	ASP	Peptide
1	F	106	ASP	Peptide
1	H	106	ASP	Peptide
1	I	106	ASP	Peptide
1	J	106	ASP	Peptide
1	K	106	ASP	Peptide
1	L	106	ASP	Peptide
1	M	106	ASP	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3282	0	3249	112	0
1	C	3282	0	3249	115	0
1	D	3282	0	3249	114	0
1	F	3282	0	3249	113	0
1	H	3282	0	3249	107	0
1	I	3282	0	3249	114	0
1	J	3282	0	3249	103	0
1	K	3282	0	3249	112	0
1	L	3282	0	3249	114	0
1	M	3282	0	3249	115	0
2	R	900	0	451	70	0
2	S	900	0	450	70	0
All	All	34620	0	33391	1101	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 16.

All (1101) 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:C:184:VAL:HG21	1:M:166:MET:CE	1.39	1.51
1:L:166:MET:CE	1:M:184:VAL:HG21	1.40	1.51
1:I:184:VAL:HG21	1:J:166:MET:CE	1.40	1.51
1:D:166:MET:CE	1:F:184:VAL:HG21	1.40	1.50
1:F:166:MET:CE	1:H:184:VAL:HG21	1.40	1.50
1:A:166:MET:CE	1:D:184:VAL:HG21	1.39	1.49
1:I:166:MET:CE	1:K:184:VAL:HG21	1.39	1.49
1:K:166:MET:CE	1:L:184:VAL:HG21	1.40	1.49
1:A:184:VAL:HG21	1:C:166:MET:CE	1.40	1.48
1:I:109:SER:O	1:I:110:LEU:HD23	1.31	1.30
1:D:109:SER:O	1:D:110:LEU:HD23	1.31	1.30
1:M:109:SER:O	1:M:110:LEU:HD23	1.32	1.30
1:K:109:SER:O	1:K:110:LEU:HD23	1.31	1.29
1:C:109:SER:O	1:C:110:LEU:HD23	1.32	1.27
1:F:109:SER:O	1:F:110:LEU:HD23	1.31	1.27
1:H:109:SER:O	1:H:110:LEU:HD23	1.32	1.25
1:L:109:SER:O	1:L:110:LEU:HD23	1.31	1.25
1:A:109:SER:O	1:A:110:LEU:HD23	1.31	1.25
1:J:109:SER:O	1:J:110:LEU:HD23	1.32	1.24
1:H:107:LEU:HD23	1:H:107:LEU:N	1.58	1.16
1:J:117:LEU:HB2	1:J:118:PRO:HD3	1.27	1.16
1:K:37:GLU:HB2	1:K:108:VAL:CG2	1.76	1.16

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:107:LEU:HD23	1:C:107:LEU:N	1.58	1.15
1:I:107:LEU:N	1:I:107:LEU:HD23	1.57	1.15
1:I:117:LEU:HB2	1:I:118:PRO:HD3	1.27	1.15
1:A:107:LEU:HD23	1:A:107:LEU:N	1.57	1.15
1:H:37:GLU:HB2	1:H:108:VAL:CG2	1.76	1.15
1:J:107:LEU:N	1:J:107:LEU:HD23	1.58	1.15
1:C:37:GLU:HB2	1:C:108:VAL:CG2	1.76	1.15
1:C:117:LEU:HB2	1:C:118:PRO:HD3	1.27	1.14
1:I:37:GLU:HB2	1:I:108:VAL:CG2	1.76	1.14
1:K:107:LEU:HD23	1:K:107:LEU:N	1.57	1.14
1:L:117:LEU:HB2	1:L:118:PRO:HD3	1.28	1.14
1:A:37:GLU:HB2	1:A:108:VAL:CG2	1.76	1.14
1:D:107:LEU:N	1:D:107:LEU:HD23	1.57	1.14
1:M:37:GLU:HB2	1:M:108:VAL:CG2	1.76	1.14
1:F:37:GLU:HB2	1:F:108:VAL:CG2	1.77	1.13
1:J:37:GLU:HB2	1:J:108:VAL:CG2	1.76	1.13
1:L:107:LEU:N	1:L:107:LEU:HD23	1.57	1.13
1:D:37:GLU:HB2	1:D:108:VAL:CG2	1.76	1.13
1:K:117:LEU:HB2	1:K:118:PRO:HD3	1.28	1.12
1:L:37:GLU:HB2	1:L:108:VAL:CG2	1.77	1.12
1:A:184:VAL:HG21	1:C:166:MET:HE1	1.30	1.12
1:F:107:LEU:HD23	1:F:107:LEU:N	1.56	1.11
1:A:117:LEU:HB2	1:A:118:PRO:HD3	1.27	1.11
1:M:117:LEU:HB2	1:M:118:PRO:HD3	1.28	1.11
1:D:117:LEU:HB2	1:D:118:PRO:HD3	1.28	1.11
1:D:166:MET:HE1	1:F:184:VAL:HG21	1.32	1.11
1:F:166:MET:HE1	1:H:184:VAL:HG21	1.31	1.10
1:I:184:VAL:HG21	1:J:166:MET:HE1	1.30	1.10
1:F:117:LEU:HB2	1:F:118:PRO:HD3	1.28	1.09
1:C:184:VAL:CG2	1:M:166:MET:HE2	1.81	1.09
1:H:117:LEU:HB2	1:H:118:PRO:HD3	1.28	1.09
1:K:166:MET:HE1	1:L:184:VAL:HG21	1.32	1.09
1:I:166:MET:HE2	1:K:184:VAL:CG2	1.81	1.09
1:L:166:MET:HE2	1:M:184:VAL:CG2	1.81	1.09
1:F:166:MET:HE2	1:H:184:VAL:CG2	1.81	1.09
1:M:107:LEU:HD23	1:M:107:LEU:N	1.58	1.09
1:A:184:VAL:CG2	1:C:166:MET:HE2	1.81	1.08
1:D:166:MET:HE2	1:F:184:VAL:CG2	1.81	1.08
1:L:166:MET:HE1	1:M:184:VAL:HG21	1.31	1.08
1:A:166:MET:HE2	1:D:184:VAL:CG2	1.81	1.08
1:I:184:VAL:CG2	1:J:166:MET:HE2	1.81	1.08

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:166:MET:HE2	1:L:184:VAL:CG2	1.81	1.08
1:C:37:GLU:HB2	1:C:108:VAL:HG21	1.34	1.08
1:C:184:VAL:HG21	1:M:166:MET:HE1	1.31	1.08
1:A:37:GLU:HB2	1:A:108:VAL:HG21	1.35	1.07
1:I:106:ASP:C	1:I:107:LEU:HD23	1.80	1.06
1:M:37:GLU:HB2	1:M:108:VAL:HG21	1.34	1.06
1:I:166:MET:CE	1:K:184:VAL:CG2	2.34	1.06
1:I:184:VAL:CG2	1:J:166:MET:CE	2.34	1.06
1:A:166:MET:HE1	1:D:184:VAL:HG21	1.31	1.06
1:C:184:VAL:CG2	1:M:166:MET:CE	2.34	1.06
1:J:106:ASP:C	1:J:107:LEU:HD23	1.80	1.06
1:L:166:MET:CE	1:M:184:VAL:CG2	2.34	1.06
1:M:106:ASP:C	1:M:107:LEU:HD23	1.80	1.06
1:A:184:VAL:CG2	1:C:166:MET:CE	2.34	1.06
1:H:37:GLU:HB2	1:H:108:VAL:HG21	1.34	1.06
1:K:166:MET:CE	1:L:184:VAL:CG2	2.34	1.06
1:A:166:MET:CE	1:D:184:VAL:CG2	2.34	1.05
1:C:106:ASP:C	1:C:107:LEU:HD23	1.80	1.05
1:D:37:GLU:HB2	1:D:108:VAL:HG21	1.34	1.05
1:F:106:ASP:C	1:F:107:LEU:HD23	1.80	1.05
1:D:106:ASP:C	1:D:107:LEU:HD23	1.80	1.05
1:L:106:ASP:C	1:L:107:LEU:HD23	1.80	1.05
2:R:38:U:H3'	2:R:39:U:H5''	1.38	1.05
2:R:47:U:H3'	2:R:48:U:H5''	1.38	1.05
1:D:166:MET:CE	1:F:184:VAL:CG2	2.34	1.05
1:F:166:MET:CE	1:H:184:VAL:CG2	2.34	1.05
2:R:56:U:H3'	2:R:57:U:H5''	1.38	1.05
1:A:106:ASP:C	1:A:107:LEU:HD23	1.80	1.05
1:H:106:ASP:C	1:H:107:LEU:HD23	1.80	1.05
1:K:106:ASP:C	1:K:107:LEU:HD23	1.80	1.05
2:S:47:U:H3'	2:S:48:U:H5''	1.38	1.04
1:I:166:MET:HE1	1:K:184:VAL:HG21	1.31	1.04
2:R:20:U:H3'	2:R:21:U:H5''	1.39	1.04
2:R:29:U:H3'	2:R:30:U:H5''	1.38	1.04
1:A:184:VAL:HG21	1:C:166:MET:HE2	1.05	1.04
1:F:317:ARG:HE	2:R:49:U:H2'	1.20	1.04
1:J:37:GLU:HB2	1:J:108:VAL:HG21	1.34	1.04
2:S:56:U:H3'	2:S:57:U:H5''	1.38	1.04
1:C:184:VAL:HG21	1:M:166:MET:HE2	1.04	1.04
2:S:29:U:H3'	2:S:30:U:H5''	1.38	1.04
1:I:184:VAL:HG21	1:J:166:MET:HE2	1.05	1.03

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:166:MET:HE2	1:H:184:VAL:HG21	1.04	1.03
2:S:38:U:H3'	2:S:39:U:H5''	1.38	1.03
1:L:317:ARG:HE	2:S:49:U:H2'	1.20	1.03
1:I:166:MET:HE2	1:K:184:VAL:HG21	1.04	1.02
1:M:317:ARG:HE	2:S:58:U:H2'	1.21	1.02
1:L:37:GLU:HB2	1:L:108:VAL:HG21	1.36	1.02
1:C:317:ARG:HE	2:R:22:U:H2'	1.21	1.02
1:F:37:GLU:HB2	1:F:108:VAL:HG21	1.36	1.02
2:S:20:U:H3'	2:S:21:U:H5''	1.39	1.02
1:A:166:MET:HE2	1:D:184:VAL:HG21	1.04	1.02
1:A:317:ARG:HE	2:R:31:U:H2'	1.21	1.01
1:I:317:ARG:HE	2:S:31:U:H2'	1.21	1.01
1:K:37:GLU:HB2	1:K:108:VAL:HG21	1.34	1.01
1:I:37:GLU:HB2	1:I:108:VAL:HG21	1.35	1.01
1:K:166:MET:HE2	1:L:184:VAL:HG21	1.04	1.01
1:L:166:MET:HE2	1:M:184:VAL:HG21	1.04	1.01
1:D:166:MET:HE2	1:F:184:VAL:HG21	1.04	1.01
1:D:317:ARG:HE	2:R:40:U:H2'	1.21	1.01
1:J:317:ARG:HE	2:S:22:U:H2'	1.21	1.01
1:H:317:ARG:HE	2:R:58:U:H2'	1.21	1.00
1:K:317:ARG:HE	2:S:40:U:H2'	1.21	0.98
1:H:172:GLU:HB3	1:H:173:PRO:HD3	1.48	0.95
1:A:172:GLU:HB3	1:A:173:PRO:HD3	1.48	0.94
1:F:172:GLU:HB3	1:F:173:PRO:HD3	1.48	0.94
1:C:172:GLU:HB3	1:C:173:PRO:HD3	1.48	0.94
1:D:172:GLU:HB3	1:D:173:PRO:HD3	1.48	0.94
1:M:172:GLU:HB3	1:M:173:PRO:HD3	1.48	0.94
1:J:172:GLU:HB3	1:J:173:PRO:HD3	1.48	0.93
1:I:172:GLU:HB3	1:I:173:PRO:HD3	1.48	0.93
1:K:172:GLU:HB3	1:K:173:PRO:HD3	1.48	0.93
1:L:172:GLU:HB3	1:L:173:PRO:HD3	1.48	0.93
1:L:107:LEU:N	1:L:107:LEU:CD2	2.32	0.93
1:K:107:LEU:N	1:K:107:LEU:CD2	2.32	0.92
1:I:107:LEU:N	1:I:107:LEU:CD2	2.33	0.92
1:J:107:LEU:N	1:J:107:LEU:CD2	2.33	0.91
1:K:37:GLU:HB2	1:K:108:VAL:HG22	1.55	0.88
1:M:37:GLU:HB2	1:M:108:VAL:HG22	1.55	0.88
1:I:37:GLU:HB2	1:I:108:VAL:HG22	1.55	0.88
1:L:109:SER:O	1:L:110:LEU:CD2	2.21	0.88
1:H:107:LEU:N	1:H:107:LEU:CD2	2.32	0.88
1:A:37:GLU:HB2	1:A:108:VAL:HG22	1.55	0.88

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:107:LEU:N	1:F:107:LEU:CD2	2.32	0.87
1:D:107:LEU:N	1:D:107:LEU:CD2	2.32	0.87
1:H:37:GLU:HB2	1:H:108:VAL:HG22	1.55	0.87
1:D:37:GLU:HB2	1:D:108:VAL:HG22	1.55	0.87
1:J:37:GLU:HB2	1:J:108:VAL:HG22	1.56	0.87
1:A:109:SER:O	1:A:110:LEU:CD2	2.22	0.86
1:A:117:LEU:HB2	1:A:118:PRO:CD	2.05	0.86
1:K:109:SER:O	1:K:110:LEU:CD2	2.22	0.86
1:M:107:LEU:N	1:M:107:LEU:CD2	2.32	0.86
1:A:107:LEU:N	1:A:107:LEU:CD2	2.33	0.86
1:C:37:GLU:HB2	1:C:108:VAL:HG22	1.56	0.86
1:K:117:LEU:HB2	1:K:118:PRO:CD	2.06	0.86
1:L:117:LEU:HB2	1:L:118:PRO:CD	2.06	0.86
1:C:117:LEU:HB2	1:C:118:PRO:CD	2.05	0.86
1:C:107:LEU:N	1:C:107:LEU:CD2	2.33	0.86
1:F:37:GLU:HB2	1:F:108:VAL:HG22	1.56	0.86
1:I:117:LEU:HB2	1:I:118:PRO:CD	2.06	0.86
1:J:117:LEU:HB2	1:J:118:PRO:CD	2.05	0.86
1:D:117:LEU:HB2	1:D:118:PRO:CD	2.06	0.85
1:H:109:SER:O	1:H:110:LEU:CD2	2.22	0.85
1:L:37:GLU:HB2	1:L:108:VAL:HG22	1.56	0.85
1:K:107:LEU:HD13	1:K:274:TYR:OH	1.77	0.85
1:C:107:LEU:HD13	1:C:274:TYR:OH	1.77	0.85
1:M:117:LEU:HB2	1:M:118:PRO:CD	2.06	0.85
1:F:107:LEU:HD13	1:F:274:TYR:OH	1.77	0.85
1:H:117:LEU:HB2	1:H:118:PRO:CD	2.06	0.85
1:D:107:LEU:HD13	1:D:274:TYR:OH	1.77	0.85
1:F:117:LEU:HB2	1:F:118:PRO:CD	2.06	0.85
1:C:109:SER:O	1:C:110:LEU:CD2	2.22	0.84
1:I:109:SER:O	1:I:110:LEU:CD2	2.22	0.84
1:D:109:SER:O	1:D:110:LEU:CD2	2.22	0.84
1:I:107:LEU:HD13	1:I:274:TYR:OH	1.77	0.84
1:M:107:LEU:HD13	1:M:274:TYR:OH	1.77	0.84
1:F:109:SER:O	1:F:110:LEU:CD2	2.21	0.84
1:J:107:LEU:HD13	1:J:274:TYR:OH	1.77	0.84
1:L:107:LEU:HD13	1:L:274:TYR:OH	1.77	0.84
1:A:107:LEU:HD13	1:A:274:TYR:OH	1.77	0.84
1:H:107:LEU:HD13	1:H:274:TYR:OH	1.77	0.83
1:H:37:GLU:CB	1:H:108:VAL:HG21	2.09	0.82
2:S:38:U:C3'	2:S:39:U:H5''	2.08	0.82
1:J:37:GLU:CB	1:J:108:VAL:HG21	2.08	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:37:GLU:CB	1:D:108:VAL:HG21	2.09	0.82
1:M:109:SER:O	1:M:110:LEU:CD2	2.22	0.82
2:S:20:U:C3'	2:S:21:U:H5''	2.09	0.82
2:S:47:U:C3'	2:S:48:U:H5''	2.08	0.82
1:C:37:GLU:CB	1:C:108:VAL:HG21	2.08	0.82
2:R:38:U:C3'	2:R:39:U:H5''	2.08	0.82
2:R:47:U:C3'	2:R:48:U:H5''	2.08	0.82
2:S:56:U:C3'	2:S:57:U:H5''	2.08	0.82
1:A:37:GLU:CB	1:A:108:VAL:HG21	2.09	0.82
2:R:56:U:C3'	2:R:57:U:H5''	2.08	0.82
1:F:37:GLU:CB	1:F:108:VAL:HG21	2.09	0.82
2:R:29:U:C3'	2:R:30:U:H5''	2.09	0.82
1:F:164:CYS:HA	1:F:168:ASN:H	1.45	0.81
1:I:37:GLU:CB	1:I:108:VAL:HG21	2.09	0.81
1:K:37:GLU:CB	1:K:108:VAL:HG21	2.09	0.81
1:M:37:GLU:CB	1:M:108:VAL:HG21	2.09	0.81
2:R:20:U:C3'	2:R:21:U:H5''	2.09	0.81
1:J:109:SER:O	1:J:110:LEU:CD2	2.22	0.81
2:S:29:U:C3'	2:S:30:U:H5''	2.09	0.81
1:F:106:ASP:C	1:F:107:LEU:CD2	2.54	0.81
1:H:106:ASP:C	1:H:107:LEU:CD2	2.53	0.81
1:L:37:GLU:CB	1:L:108:VAL:HG21	2.09	0.81
1:C:106:ASP:C	1:C:107:LEU:CD2	2.54	0.80
1:A:106:ASP:C	1:A:107:LEU:CD2	2.54	0.80
1:D:106:ASP:C	1:D:107:LEU:CD2	2.54	0.80
1:L:164:CYS:HA	1:L:168:ASN:H	1.45	0.80
1:M:164:CYS:HA	1:M:168:ASN:H	1.46	0.80
1:H:164:CYS:HA	1:H:168:ASN:H	1.46	0.80
1:A:164:CYS:HA	1:A:168:ASN:H	1.47	0.80
1:K:164:CYS:HA	1:K:168:ASN:H	1.46	0.80
1:M:106:ASP:C	1:M:107:LEU:CD2	2.53	0.80
1:L:106:ASP:C	1:L:107:LEU:CD2	2.54	0.80
1:I:164:CYS:HA	1:I:168:ASN:H	1.47	0.79
1:K:106:ASP:C	1:K:107:LEU:CD2	2.54	0.79
1:D:164:CYS:HA	1:D:168:ASN:H	1.46	0.79
1:I:106:ASP:C	1:I:107:LEU:CD2	2.54	0.79
1:J:164:CYS:HA	1:J:168:ASN:H	1.46	0.79
1:J:106:ASP:C	1:J:107:LEU:CD2	2.54	0.79
1:C:164:CYS:HA	1:C:168:ASN:H	1.46	0.78
1:M:317:ARG:HH21	2:S:59:U:H5'	1.56	0.71
1:H:317:ARG:HH21	2:R:59:U:H5'	1.56	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:179:ARG:HA	1:F:183:ASP:CG	2.17	0.70
1:H:179:ARG:HA	1:H:183:ASP:CG	2.17	0.70
1:M:179:ARG:HA	1:M:183:ASP:CG	2.17	0.70
1:D:214:ARG:HA	1:D:217:THR:HG22	1.73	0.70
1:F:214:ARG:HA	1:F:217:THR:HG22	1.73	0.70
1:H:214:ARG:HA	1:H:217:THR:HG22	1.74	0.70
1:C:214:ARG:HA	1:C:217:THR:HG22	1.73	0.70
1:C:179:ARG:HA	1:C:183:ASP:CG	2.17	0.70
1:F:317:ARG:HH21	2:R:50:U:H5'	1.56	0.70
1:K:317:ARG:HH21	2:S:41:U:H5'	1.57	0.70
1:L:179:ARG:HA	1:L:183:ASP:CG	2.16	0.69
1:I:179:ARG:HA	1:I:183:ASP:CG	2.17	0.69
1:J:179:ARG:HA	1:J:183:ASP:CG	2.17	0.69
1:L:214:ARG:HA	1:L:217:THR:HG22	1.73	0.69
1:A:317:ARG:HH21	2:R:32:U:H5'	1.58	0.69
1:D:179:ARG:HA	1:D:183:ASP:CG	2.17	0.69
1:D:317:ARG:HH21	2:R:41:U:H5'	1.57	0.69
1:J:317:ARG:HH21	2:S:23:U:H5'	1.57	0.69
1:M:214:ARG:HA	1:M:217:THR:HG22	1.74	0.69
1:A:179:ARG:HA	1:A:183:ASP:CG	2.17	0.69
1:A:214:ARG:HA	1:A:217:THR:HG22	1.74	0.69
1:K:179:ARG:HA	1:K:183:ASP:CG	2.17	0.69
1:K:214:ARG:HA	1:K:217:THR:HG22	1.74	0.69
1:J:214:ARG:HA	1:J:217:THR:HG22	1.73	0.69
1:C:317:ARG:HH21	2:R:23:U:H5'	1.57	0.68
1:I:214:ARG:HA	1:I:217:THR:HG22	1.74	0.68
2:R:48:U:H2'	2:R:49:U:O4'	1.94	0.68
1:L:317:ARG:HH21	2:S:50:U:H5'	1.56	0.68
1:M:317:ARG:NH2	2:S:59:U:H5'	2.09	0.68
2:S:30:U:H2'	2:S:31:U:O4'	1.94	0.68
1:I:317:ARG:HH21	2:S:32:U:H5'	1.58	0.68
2:S:57:U:H2'	2:S:58:U:O4'	1.94	0.67
2:R:30:U:H2'	2:R:31:U:O4'	1.94	0.67
2:R:57:U:H2'	2:R:58:U:O4'	1.94	0.67
1:F:317:ARG:NH2	2:R:50:U:H5'	2.10	0.67
1:J:317:ARG:NH2	2:S:23:U:H5'	2.10	0.67
2:R:21:U:H2'	2:R:22:U:O4'	1.95	0.67
1:H:317:ARG:NH2	2:R:59:U:H5'	2.09	0.67
2:S:39:U:H2'	2:S:40:U:O4'	1.94	0.67
1:L:317:ARG:NH2	2:S:50:U:H5'	2.10	0.67
1:A:317:ARG:NH2	2:R:32:U:H5'	2.10	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:21:U:H2'	2:S:22:U:O4'	1.95	0.67
2:S:48:U:H2'	2:S:49:U:O4'	1.94	0.67
2:R:39:U:H2'	2:R:40:U:O4'	1.94	0.67
1:K:317:ARG:NH2	2:S:41:U:H5'	2.10	0.66
1:C:317:ARG:NH2	2:R:23:U:H5'	2.10	0.66
1:I:317:ARG:NH2	2:S:32:U:H5'	2.10	0.66
1:D:317:ARG:NH2	2:R:41:U:H5'	2.10	0.66
1:M:240:MET:HE2	1:M:244:ASP:HB3	1.77	0.65
1:C:240:MET:HE2	1:C:244:ASP:HB3	1.78	0.65
1:F:240:MET:HE2	1:F:244:ASP:HB3	1.77	0.65
1:H:240:MET:HE2	1:H:244:ASP:HB3	1.77	0.65
1:L:240:MET:HE2	1:L:244:ASP:HB3	1.77	0.64
1:I:240:MET:HE2	1:I:244:ASP:HB3	1.78	0.64
1:K:240:MET:HE2	1:K:244:ASP:HB3	1.78	0.64
1:J:240:MET:HE2	1:J:244:ASP:HB3	1.78	0.64
1:A:240:MET:HE2	1:A:244:ASP:HB3	1.78	0.64
1:D:240:MET:HE2	1:D:244:ASP:HB3	1.78	0.64
1:I:184:VAL:CG2	1:J:166:MET:HE1	2.18	0.63
1:F:29:ALA:H	1:F:266:GLN:HE22	1.47	0.63
1:K:29:ALA:H	1:K:266:GLN:HE22	1.47	0.63
1:H:325:THR:O	1:H:329:THR:HG22	1.99	0.63
1:I:29:ALA:H	1:I:266:GLN:HE22	1.46	0.63
1:H:28:PRO:HG2	1:H:266:GLN:HE21	1.64	0.62
1:M:325:THR:O	1:M:329:THR:HG22	1.99	0.62
1:C:29:ALA:H	1:C:266:GLN:HE22	1.47	0.62
1:L:166:MET:HE1	1:M:184:VAL:CG2	2.19	0.62
1:M:29:ALA:H	1:M:266:GLN:HE22	1.46	0.62
1:D:29:ALA:H	1:D:266:GLN:HE22	1.47	0.62
1:A:28:PRO:HG2	1:A:266:GLN:HE21	1.64	0.62
1:A:29:ALA:H	1:A:266:GLN:HE22	1.46	0.62
1:I:325:THR:O	1:I:329:THR:HG22	1.99	0.62
1:J:28:PRO:HG2	1:J:266:GLN:HE21	1.64	0.62
1:L:28:PRO:HG2	1:L:266:GLN:HE21	1.64	0.62
1:F:325:THR:O	1:F:329:THR:HG22	1.99	0.62
1:J:325:THR:O	1:J:329:THR:HG22	2.00	0.62
1:L:29:ALA:H	1:L:266:GLN:HE22	1.47	0.62
1:M:149:MET:O	1:M:151:GLU:N	2.33	0.62
1:C:149:MET:O	1:C:151:GLU:N	2.33	0.62
1:J:29:ALA:H	1:J:266:GLN:HE22	1.47	0.62
1:A:166:MET:HE1	1:D:184:VAL:CG2	2.19	0.62
1:C:325:THR:O	1:C:329:THR:HG22	2.00	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:MET:O	1:A:151:GLU:N	2.33	0.62
1:D:28:PRO:HG2	1:D:266:GLN:HE21	1.64	0.62
1:K:28:PRO:HG2	1:K:266:GLN:HE21	1.64	0.62
1:D:149:MET:O	1:D:151:GLU:N	2.33	0.61
1:L:149:MET:O	1:L:151:GLU:N	2.33	0.61
1:A:325:THR:O	1:A:329:THR:HG22	1.99	0.61
1:C:28:PRO:HG2	1:C:266:GLN:HE21	1.64	0.61
1:H:29:ALA:H	1:H:266:GLN:HE22	1.46	0.61
1:L:325:THR:O	1:L:329:THR:HG22	1.99	0.61
1:I:28:PRO:HG2	1:I:266:GLN:HE21	1.64	0.61
1:K:325:THR:O	1:K:329:THR:HG22	2.00	0.61
1:M:28:PRO:HG2	1:M:266:GLN:HE21	1.64	0.61
1:I:172:GLU:HB3	1:I:173:PRO:CD	2.27	0.61
1:F:28:PRO:HG2	1:F:266:GLN:HE21	1.64	0.61
1:F:149:MET:O	1:F:151:GLU:N	2.33	0.61
1:H:149:MET:O	1:H:151:GLU:N	2.33	0.61
1:K:149:MET:O	1:K:151:GLU:N	2.33	0.61
1:D:325:THR:O	1:D:329:THR:HG22	2.00	0.61
1:J:149:MET:O	1:J:151:GLU:N	2.33	0.61
1:I:117:LEU:CB	1:I:118:PRO:HD3	2.17	0.60
1:I:149:MET:O	1:I:151:GLU:N	2.33	0.60
1:K:253:GLU:CD	1:K:253:GLU:H	2.10	0.60
1:F:253:GLU:CD	1:F:253:GLU:H	2.10	0.59
1:D:253:GLU:H	1:D:253:GLU:CD	2.10	0.59
1:L:253:GLU:CD	1:L:253:GLU:H	2.10	0.59
1:A:298:HIS:NE2	1:A:317:ARG:NH1	2.50	0.59
1:K:268:ILE:HD11	1:L:17:LYS:HG3	1.84	0.59
1:I:230:THR:HG21	1:I:298:HIS:CE1	2.38	0.59
1:K:230:THR:HG21	1:K:298:HIS:CE1	2.38	0.59
1:D:268:ILE:HD11	1:F:17:LYS:HG3	1.84	0.59
1:D:298:HIS:NE2	1:D:317:ARG:NH1	2.51	0.59
1:H:172:GLU:HB3	1:H:173:PRO:CD	2.28	0.59
1:L:230:THR:HG21	1:L:298:HIS:CE1	2.38	0.59
1:A:253:GLU:CD	1:A:253:GLU:H	2.10	0.59
1:C:253:GLU:CD	1:C:253:GLU:H	2.11	0.59
1:H:253:GLU:CD	1:H:253:GLU:H	2.10	0.59
1:J:253:GLU:CD	1:J:253:GLU:H	2.11	0.59
1:A:184:VAL:CG2	1:C:166:MET:HE1	2.18	0.59
1:I:17:LYS:HG3	1:J:268:ILE:HD11	1.85	0.59
1:F:298:HIS:NE2	1:F:317:ARG:NH1	2.50	0.58
1:I:268:ILE:HD11	1:K:17:LYS:HG3	1.84	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:253:GLU:CD	1:M:253:GLU:H	2.10	0.58
1:M:298:HIS:NE2	1:M:317:ARG:NH1	2.51	0.58
1:F:166:MET:HE1	1:H:184:VAL:CG2	2.19	0.58
1:F:230:THR:HG21	1:F:298:HIS:CE1	2.38	0.58
1:I:253:GLU:H	1:I:253:GLU:CD	2.10	0.58
1:J:230:THR:HG21	1:J:298:HIS:CE1	2.38	0.58
1:M:230:THR:HG21	1:M:298:HIS:CE1	2.38	0.58
1:C:17:LYS:HG3	1:M:268:ILE:HD11	1.85	0.58
1:C:298:HIS:NE2	1:C:317:ARG:NH1	2.51	0.58
1:H:298:HIS:NE2	1:H:317:ARG:NH1	2.51	0.58
1:M:117:LEU:CB	1:M:118:PRO:HD3	2.17	0.58
1:A:17:LYS:HG3	1:C:268:ILE:HD11	1.85	0.58
1:A:230:THR:HG21	1:A:298:HIS:CE1	2.37	0.58
1:A:268:ILE:HD11	1:D:17:LYS:HG3	1.84	0.58
1:D:230:THR:HG21	1:D:298:HIS:CE1	2.38	0.58
1:C:230:THR:HG21	1:C:298:HIS:CE1	2.38	0.58
1:K:166:MET:HE1	1:L:184:VAL:CG2	2.20	0.58
1:K:172:GLU:HB3	1:K:173:PRO:CD	2.28	0.58
1:L:268:ILE:HD11	1:M:17:LYS:HG3	1.85	0.58
1:I:298:HIS:NE2	1:I:317:ARG:NH1	2.50	0.58
1:L:298:HIS:NE2	1:L:317:ARG:NH1	2.50	0.58
2:R:18:U:H5'	2:S:62:U:O2'	2.04	0.58
2:R:35:U:O2'	2:R:36:U:H5'	2.04	0.58
1:F:268:ILE:HD11	1:H:17:LYS:HG3	1.85	0.58
2:R:44:U:O2'	2:R:45:U:H5'	2.04	0.58
2:S:35:U:O2'	2:S:36:U:H5'	2.04	0.58
1:H:230:THR:HG21	1:H:298:HIS:CE1	2.38	0.57
1:J:298:HIS:NE2	1:J:317:ARG:NH1	2.51	0.57
1:C:172:GLU:HB3	1:C:173:PRO:CD	2.28	0.57
1:H:106:ASP:O	1:H:107:LEU:HD22	2.04	0.57
2:R:60:U:H6	2:R:60:U:H5'	1.70	0.57
1:K:298:HIS:NE2	1:K:317:ARG:NH1	2.51	0.57
1:C:317:ARG:CZ	1:C:317:ARG:H	2.18	0.57
1:J:317:ARG:CZ	1:J:317:ARG:H	2.18	0.57
2:S:53:U:O2'	2:S:54:U:H5'	2.04	0.57
1:L:104:ILE:HD11	1:L:198:VAL:HG22	1.87	0.57
1:H:38:ILE:HD11	1:H:107:LEU:HD12	1.87	0.57
1:M:104:ILE:HD11	1:M:198:VAL:HG22	1.87	0.57
2:R:42:U:H5'	2:R:42:U:H6	1.70	0.57
2:R:53:U:O2'	2:R:54:U:H5'	2.04	0.57
1:C:104:ILE:HD11	1:C:198:VAL:HG22	1.87	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:104:ILE:HD11	1:K:198:VAL:HG22	1.87	0.57
1:A:109:SER:C	1:A:110:LEU:HD23	2.24	0.56
1:F:104:ILE:HD11	1:F:198:VAL:HG22	1.87	0.56
1:F:172:GLU:HB3	1:F:173:PRO:CD	2.28	0.56
1:H:104:ILE:HD11	1:H:198:VAL:HG22	1.87	0.56
1:J:104:ILE:HD11	1:J:198:VAL:HG22	1.87	0.56
1:L:233:HIS:CE1	1:L:312:ARG:HD2	2.40	0.56
1:M:38:ILE:HD11	1:M:107:LEU:HD12	1.87	0.56
1:M:106:ASP:O	1:M:107:LEU:HD22	2.04	0.56
1:C:233:HIS:CE1	1:C:312:ARG:HD2	2.40	0.56
1:D:117:LEU:CB	1:D:118:PRO:HD3	2.18	0.56
1:F:38:ILE:HD11	1:F:107:LEU:HD12	1.87	0.56
2:S:26:U:O2'	2:S:27:U:H5'	2.05	0.56
1:A:38:ILE:HD11	1:A:107:LEU:HD12	1.88	0.56
1:D:104:ILE:HD11	1:D:198:VAL:HG22	1.87	0.56
1:D:233:HIS:CE1	1:D:312:ARG:HD2	2.40	0.56
1:F:37:GLU:OE2	1:F:108:VAL:HG11	2.05	0.56
1:F:106:ASP:O	1:F:107:LEU:HD22	2.05	0.56
1:H:117:LEU:CB	1:H:118:PRO:HD3	2.17	0.56
1:I:37:GLU:OE2	1:I:108:VAL:HG11	2.06	0.56
1:I:104:ILE:HD11	1:I:198:VAL:HG22	1.88	0.56
1:K:233:HIS:CE1	1:K:312:ARG:HD2	2.40	0.56
1:L:37:GLU:OE2	1:L:108:VAL:HG11	2.05	0.56
2:S:33:U:H5'	2:S:33:U:H6	1.70	0.56
2:S:42:U:H6	2:S:42:U:H5'	1.70	0.56
2:S:44:U:O2'	2:S:45:U:H5'	2.04	0.56
2:S:60:U:H5'	2:S:60:U:H6	1.70	0.56
1:H:37:GLU:OE2	1:H:108:VAL:HG11	2.05	0.56
1:K:317:ARG:H	1:K:317:ARG:CZ	2.18	0.56
1:L:38:ILE:HD11	1:L:107:LEU:HD12	1.87	0.56
1:L:106:ASP:O	1:L:107:LEU:HD22	2.05	0.56
1:L:317:ARG:CZ	1:L:317:ARG:H	2.19	0.56
1:A:37:GLU:OE2	1:A:108:VAL:HG11	2.06	0.56
1:A:104:ILE:HD11	1:A:198:VAL:HG22	1.88	0.56
1:D:38:ILE:HD11	1:D:107:LEU:HD12	1.87	0.56
1:F:109:SER:C	1:F:110:LEU:HD23	2.24	0.56
1:F:317:ARG:H	1:F:317:ARG:CZ	2.19	0.56
1:M:37:GLU:OE2	1:M:108:VAL:HG11	2.05	0.56
1:M:317:ARG:NE	2:S:58:U:H2'	2.06	0.56
2:R:24:U:H6	2:R:24:U:H5'	1.71	0.56
2:R:26:U:O2'	2:R:27:U:H5'	2.05	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:324:TYR:O	1:J:328:THR:HG22	2.06	0.56
2:S:24:U:H6	2:S:24:U:H5'	1.71	0.56
2:S:51:U:H6	2:S:51:U:H5'	1.71	0.56
1:D:106:ASP:O	1:D:107:LEU:HD22	2.05	0.56
1:H:233:HIS:CE1	1:H:312:ARG:HD2	2.41	0.56
1:H:317:ARG:CZ	1:H:317:ARG:H	2.18	0.56
1:K:106:ASP:O	1:K:107:LEU:HD22	2.05	0.56
1:M:233:HIS:CE1	1:M:312:ARG:HD2	2.41	0.56
1:A:233:HIS:CE1	1:A:312:ARG:HD2	2.41	0.56
1:A:317:ARG:CZ	1:A:317:ARG:H	2.19	0.56
1:F:233:HIS:CE1	1:F:312:ARG:HD2	2.40	0.56
1:I:38:ILE:HD11	1:I:107:LEU:HD12	1.88	0.56
1:J:106:ASP:O	1:J:107:LEU:HD22	2.05	0.56
1:J:233:HIS:CE1	1:J:312:ARG:HD2	2.40	0.56
1:K:38:ILE:HD11	1:K:107:LEU:HD12	1.87	0.56
1:D:37:GLU:OE2	1:D:108:VAL:HG11	2.06	0.56
1:F:118:PRO:O	1:F:119:ASP:HB2	2.06	0.56
1:H:317:ARG:NE	2:R:58:U:H2'	2.06	0.56
1:I:109:SER:C	1:I:110:LEU:HD23	2.24	0.56
1:C:317:ARG:NE	2:R:22:U:H2'	2.06	0.55
1:C:324:TYR:O	1:C:328:THR:HG22	2.06	0.55
1:I:233:HIS:CE1	1:I:312:ARG:HD2	2.41	0.55
1:M:172:GLU:HB3	1:M:173:PRO:CD	2.28	0.55
1:M:317:ARG:CZ	1:M:317:ARG:H	2.18	0.55
1:D:317:ARG:H	1:D:317:ARG:CZ	2.18	0.55
2:R:33:U:H6	2:R:33:U:H5'	1.70	0.55
1:I:317:ARG:CZ	1:I:317:ARG:H	2.19	0.55
1:C:37:GLU:OE2	1:C:108:VAL:HG11	2.06	0.55
1:K:37:GLU:OE2	1:K:108:VAL:HG11	2.06	0.55
1:L:172:GLU:HB3	1:L:173:PRO:CD	2.28	0.55
1:L:317:ARG:NE	2:S:49:U:H2'	2.05	0.55
2:R:51:U:H6	2:R:51:U:H5'	1.71	0.55
1:H:118:PRO:O	1:H:119:ASP:HB2	2.06	0.55
1:J:106:ASP:O	1:J:107:LEU:CD2	2.55	0.55
1:L:118:PRO:O	1:L:119:ASP:HB2	2.06	0.55
1:J:37:GLU:OE2	1:J:108:VAL:HG11	2.06	0.55
1:K:106:ASP:O	1:K:107:LEU:CD2	2.54	0.55
1:F:324:TYR:O	1:F:328:THR:HG22	2.06	0.55
1:I:106:ASP:O	1:I:107:LEU:CD2	2.55	0.55
1:C:106:ASP:O	1:C:107:LEU:HD22	2.05	0.55
1:C:184:VAL:HG11	1:M:166:MET:CE	2.37	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:324:TYR:O	1:D:328:THR:HG22	2.06	0.55
1:F:166:MET:CE	1:H:184:VAL:HG11	2.37	0.55
1:I:324:TYR:O	1:I:328:THR:HG22	2.06	0.55
1:K:109:SER:C	1:K:110:LEU:HD23	2.24	0.55
1:A:324:TYR:O	1:A:328:THR:HG22	2.06	0.55
1:C:38:ILE:HD11	1:C:107:LEU:HD12	1.88	0.55
1:D:118:PRO:O	1:D:119:ASP:HB2	2.06	0.55
1:L:106:ASP:O	1:L:107:LEU:CD2	2.55	0.55
1:L:166:MET:CE	1:M:184:VAL:HG11	2.37	0.55
1:H:109:SER:C	1:H:110:LEU:HD23	2.24	0.54
1:H:324:TYR:O	1:H:328:THR:HG22	2.07	0.54
1:J:172:GLU:HB3	1:J:173:PRO:CD	2.28	0.54
1:I:106:ASP:O	1:I:107:LEU:HD22	2.06	0.54
1:L:109:SER:C	1:L:110:LEU:HD23	2.24	0.54
1:M:106:ASP:O	1:M:107:LEU:CD2	2.54	0.54
1:M:118:PRO:O	1:M:119:ASP:HB2	2.06	0.54
1:A:166:MET:CE	1:D:184:VAL:HG11	2.38	0.54
1:C:184:VAL:HG11	1:M:166:MET:HE3	1.89	0.54
1:I:166:MET:HE1	1:K:184:VAL:CG2	2.19	0.54
1:K:118:PRO:O	1:K:119:ASP:HB2	2.06	0.54
1:L:324:TYR:O	1:L:328:THR:HG22	2.06	0.54
1:A:106:ASP:O	1:A:107:LEU:HD22	2.06	0.54
1:A:184:VAL:HG11	1:C:166:MET:CE	2.38	0.54
1:D:172:GLU:HB3	1:D:173:PRO:CD	2.28	0.54
1:H:106:ASP:O	1:H:107:LEU:CD2	2.54	0.54
1:D:106:ASP:O	1:D:107:LEU:CD2	2.54	0.54
1:I:166:MET:CE	1:K:184:VAL:HG11	2.38	0.54
1:M:324:TYR:O	1:M:328:THR:HG22	2.07	0.54
1:F:106:ASP:O	1:F:107:LEU:CD2	2.55	0.54
1:F:226:ALA:O	1:F:230:THR:HG23	2.07	0.54
1:D:166:MET:CE	1:F:184:VAL:HG11	2.38	0.54
1:K:324:TYR:O	1:K:328:THR:HG22	2.06	0.54
1:A:106:ASP:O	1:A:107:LEU:CD2	2.55	0.54
1:C:106:ASP:O	1:C:107:LEU:CD2	2.55	0.54
1:I:184:VAL:HG11	1:J:166:MET:CE	2.38	0.54
1:J:38:ILE:HD11	1:J:107:LEU:HD12	1.88	0.54
1:C:184:VAL:CG2	1:M:166:MET:HE1	2.19	0.54
1:J:172:GLU:CB	1:J:173:PRO:HD3	2.32	0.54
1:K:166:MET:CE	1:L:184:VAL:HG11	2.38	0.54
1:K:226:ALA:O	1:K:230:THR:HG23	2.08	0.54
1:J:317:ARG:NH1	1:J:317:ARG:H	2.06	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:166:MET:HE3	1:F:184:VAL:HG11	1.90	0.53
1:H:317:ARG:NH1	1:H:317:ARG:H	2.06	0.53
1:A:166:MET:HE3	1:D:184:VAL:HG11	1.90	0.53
1:C:226:ALA:O	1:C:230:THR:HG23	2.08	0.53
1:L:226:ALA:O	1:L:230:THR:HG23	2.07	0.53
1:A:66:ILE:HD13	1:A:185:TRP:CD1	2.44	0.53
1:C:317:ARG:NH1	1:C:317:ARG:H	2.06	0.53
1:H:226:ALA:O	1:H:230:THR:HG23	2.08	0.53
1:C:118:PRO:O	1:C:119:ASP:HB2	2.07	0.53
1:I:166:MET:HE3	1:K:184:VAL:HG11	1.90	0.53
1:K:66:ILE:HD13	1:K:185:TRP:CD1	2.44	0.53
1:L:166:MET:HE3	1:M:184:VAL:HG11	1.90	0.53
1:F:166:MET:HE3	1:H:184:VAL:HG11	1.90	0.53
1:A:317:ARG:NH1	1:A:317:ARG:H	2.07	0.53
1:C:208:HIS:HD1	1:C:210:CYS:H	1.56	0.53
1:D:66:ILE:HD13	1:D:185:TRP:CD1	2.44	0.53
1:D:317:ARG:NH1	1:D:317:ARG:H	2.07	0.53
1:I:118:PRO:O	1:I:119:ASP:HB2	2.07	0.53
1:M:66:ILE:HD13	1:M:185:TRP:CD1	2.43	0.53
1:H:66:ILE:HD13	1:H:185:TRP:CD1	2.43	0.53
1:I:317:ARG:NE	2:S:31:U:H2'	2.06	0.53
1:L:66:ILE:HD13	1:L:185:TRP:CD1	2.44	0.53
1:L:317:ARG:NH1	1:L:317:ARG:H	2.07	0.53
1:M:226:ALA:O	1:M:230:THR:HG23	2.08	0.53
1:A:184:VAL:HG11	1:C:166:MET:HE3	1.90	0.53
1:C:66:ILE:HD13	1:C:185:TRP:CD1	2.44	0.53
1:D:166:MET:HE1	1:F:184:VAL:CG2	2.19	0.53
1:J:270:LYS:HE3	1:J:273:SER:HB2	1.91	0.53
1:M:317:ARG:NH1	1:M:317:ARG:H	2.06	0.53
1:A:118:PRO:O	1:A:119:ASP:HB2	2.07	0.53
1:I:226:ALA:O	1:I:230:THR:HG23	2.09	0.53
1:J:118:PRO:O	1:J:119:ASP:HB2	2.07	0.53
1:D:226:ALA:O	1:D:230:THR:HG23	2.08	0.52
1:F:317:ARG:NH1	1:F:317:ARG:H	2.07	0.52
1:J:226:ALA:O	1:J:230:THR:HG23	2.08	0.52
1:C:270:LYS:HE3	1:C:273:SER:HB2	1.91	0.52
1:D:109:SER:C	1:D:110:LEU:HD23	2.24	0.52
1:I:184:VAL:HG11	1:J:166:MET:HE3	1.90	0.52
1:I:66:ILE:HD13	1:I:185:TRP:CD1	2.44	0.52
1:J:104:ILE:HD11	1:J:198:VAL:HA	1.92	0.52
1:J:208:HIS:HD1	1:J:210:CYS:H	1.56	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:ALA:O	1:A:230:THR:HG23	2.09	0.52
1:J:66:ILE:HD13	1:J:185:TRP:CD1	2.44	0.52
1:A:208:HIS:HD1	1:A:210:CYS:H	1.56	0.52
1:H:149:MET:C	1:H:151:GLU:H	2.18	0.52
1:K:317:ARG:NH1	1:K:317:ARG:H	2.07	0.52
1:J:109:SER:C	1:J:110:LEU:HD23	2.25	0.52
1:K:208:HIS:HD1	1:K:210:CYS:H	1.55	0.52
1:A:317:ARG:NE	2:R:31:U:H2'	2.06	0.52
1:D:104:ILE:HD11	1:D:198:VAL:HA	1.92	0.52
1:I:317:ARG:NH1	1:I:317:ARG:H	2.07	0.52
1:K:166:MET:HE3	1:L:184:VAL:HG11	1.90	0.52
1:F:107:LEU:HD23	1:F:107:LEU:H	1.66	0.52
1:D:107:LEU:HD23	1:D:107:LEU:H	1.66	0.52
1:F:66:ILE:HD13	1:F:185:TRP:CD1	2.44	0.52
1:K:317:ARG:NE	2:S:40:U:H2'	2.06	0.52
1:L:104:ILE:HD11	1:L:198:VAL:HA	1.92	0.52
1:A:172:GLU:HB3	1:A:173:PRO:CD	2.27	0.52
1:F:66:ILE:HD13	1:F:185:TRP:CG	2.45	0.52
1:F:208:HIS:HD1	1:F:210:CYS:H	1.55	0.52
1:L:270:LYS:HE3	1:L:273:SER:HB2	1.92	0.52
1:F:270:LYS:HE3	1:F:273:SER:HB2	1.92	0.51
1:L:107:LEU:HD23	1:L:107:LEU:H	1.66	0.51
1:C:66:ILE:HD13	1:C:185:TRP:CG	2.45	0.51
1:D:270:LYS:HE3	1:D:273:SER:HB2	1.92	0.51
1:K:66:ILE:HD13	1:K:185:TRP:CG	2.46	0.51
1:K:270:LYS:HE3	1:K:273:SER:HB2	1.92	0.51
1:A:66:ILE:HD13	1:A:185:TRP:CG	2.45	0.51
1:A:268:ILE:HG22	1:A:275:MET:HE3	1.93	0.51
1:C:104:ILE:HD11	1:C:198:VAL:HA	1.92	0.51
1:D:66:ILE:HD13	1:D:185:TRP:CG	2.45	0.51
1:D:208:HIS:HD1	1:D:210:CYS:H	1.56	0.51
1:F:104:ILE:HD11	1:F:198:VAL:HA	1.92	0.51
1:I:268:ILE:HG22	1:I:275:MET:HE3	1.93	0.51
1:M:104:ILE:HD11	1:M:198:VAL:HA	1.93	0.51
1:A:143:ARG:HH21	2:R:35:U:H5''	1.76	0.51
1:H:66:ILE:HD13	1:H:185:TRP:CG	2.46	0.51
1:K:104:ILE:HD11	1:K:198:VAL:HA	1.92	0.51
1:L:66:ILE:HD13	1:L:185:TRP:CG	2.45	0.51
1:L:268:ILE:HG22	1:L:275:MET:HE3	1.93	0.51
1:M:149:MET:C	1:M:151:GLU:H	2.18	0.51
1:I:270:LYS:HE3	1:I:273:SER:HB2	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:107:LEU:HD23	1:K:107:LEU:H	1.66	0.51
1:F:317:ARG:NE	2:R:49:U:H2'	2.05	0.51
1:J:66:ILE:HD13	1:J:185:TRP:CG	2.45	0.51
1:L:149:MET:C	1:L:151:GLU:H	2.19	0.51
1:M:268:ILE:HG22	1:M:275:MET:HE3	1.93	0.51
1:A:270:LYS:HE3	1:A:273:SER:HB2	1.93	0.51
1:F:268:ILE:HG22	1:F:275:MET:HE3	1.93	0.51
1:I:66:ILE:HD13	1:I:185:TRP:CG	2.46	0.51
1:A:172:GLU:CB	1:A:173:PRO:HD3	2.31	0.51
1:K:149:MET:C	1:K:151:GLU:H	2.19	0.51
1:K:268:ILE:HG22	1:K:275:MET:HE3	1.93	0.51
1:M:66:ILE:HD13	1:M:185:TRP:CG	2.46	0.51
1:M:160:LEU:HD12	1:M:161:THR:HG23	1.93	0.51
1:C:109:SER:C	1:C:110:LEU:HD23	2.25	0.51
1:D:149:MET:C	1:D:151:GLU:H	2.19	0.51
1:H:143:ARG:HH21	2:R:62:U:H5''	1.76	0.51
1:D:268:ILE:HG22	1:D:275:MET:HE3	1.93	0.51
1:H:268:ILE:HG22	1:H:275:MET:HE3	1.93	0.51
1:M:270:LYS:HE3	1:M:273:SER:HB2	1.93	0.51
1:A:149:MET:C	1:A:151:GLU:H	2.20	0.50
1:F:149:MET:C	1:F:151:GLU:H	2.19	0.50
1:K:143:ARG:HH21	2:S:44:U:H5''	1.76	0.50
1:H:317:ARG:NH2	2:R:59:U:C5'	2.75	0.50
1:I:208:HIS:HD1	1:I:210:CYS:H	1.56	0.50
1:J:149:MET:C	1:J:151:GLU:H	2.19	0.50
1:L:143:ARG:HH21	2:S:53:U:H5''	1.76	0.50
1:M:143:ARG:HH21	2:S:62:U:H5''	1.76	0.50
1:F:143:ARG:HH21	2:R:53:U:H5''	1.76	0.50
1:H:160:LEU:HD12	1:H:161:THR:HG23	1.93	0.50
1:C:107:LEU:HD23	1:C:107:LEU:H	1.68	0.50
1:C:149:MET:C	1:C:151:GLU:H	2.19	0.50
1:C:268:ILE:HG22	1:C:275:MET:HE3	1.94	0.50
1:F:160:LEU:HD12	1:F:161:THR:HG23	1.94	0.50
1:H:104:ILE:HD11	1:H:198:VAL:HA	1.93	0.50
1:J:143:ARG:HH21	2:S:26:U:H5''	1.77	0.50
1:M:107:LEU:HD23	1:M:107:LEU:H	1.67	0.50
1:H:270:LYS:HE3	1:H:273:SER:HB2	1.93	0.50
1:A:104:ILE:HD11	1:A:198:VAL:HA	1.93	0.50
1:L:160:LEU:HD12	1:L:161:THR:HG23	1.94	0.50
1:D:160:LEU:HD12	1:D:161:THR:HG23	1.94	0.50
1:H:107:LEU:HD23	1:H:107:LEU:H	1.67	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:143:ARG:HH21	2:S:35:U:H5''	1.76	0.50
1:J:160:LEU:HD12	1:J:161:THR:HG23	1.94	0.50
1:K:172:GLU:CB	1:K:173:PRO:HD3	2.32	0.50
1:C:143:ARG:HH21	2:R:26:U:H5''	1.77	0.50
1:J:268:ILE:HG22	1:J:275:MET:HE3	1.94	0.50
1:H:65:SER:HB2	1:H:117:LEU:HD11	1.94	0.49
1:I:104:ILE:HD11	1:I:198:VAL:HA	1.93	0.49
1:C:317:ARG:NH2	2:R:23:U:C5'	2.75	0.49
1:I:149:MET:C	1:I:151:GLU:H	2.20	0.49
1:C:160:LEU:HD12	1:C:161:THR:HG23	1.94	0.49
1:D:143:ARG:HH21	2:R:44:U:H5''	1.76	0.49
1:I:65:SER:HB2	1:I:117:LEU:HD11	1.94	0.49
1:K:253:GLU:CD	1:K:253:GLU:N	2.70	0.49
1:M:65:SER:HB2	1:M:117:LEU:HD11	1.94	0.49
1:A:317:ARG:NH2	2:R:32:U:C5'	2.75	0.49
1:H:107:LEU:CD1	1:H:274:TYR:HE2	2.26	0.49
1:H:253:GLU:CD	1:H:253:GLU:N	2.70	0.49
1:M:317:ARG:NH2	2:S:59:U:C5'	2.75	0.49
1:C:123:ASP:C	1:C:125:SER:H	2.21	0.49
1:F:317:ARG:NH2	2:R:50:U:C5'	2.75	0.49
1:I:253:GLU:CD	1:I:253:GLU:N	2.70	0.49
1:J:107:LEU:CD1	1:J:274:TYR:HE2	2.26	0.49
1:M:107:LEU:CD1	1:M:274:TYR:HE2	2.26	0.49
1:A:65:SER:HB2	1:A:117:LEU:HD11	1.94	0.49
1:D:253:GLU:CD	1:D:253:GLU:N	2.70	0.49
1:D:65:SER:HB2	1:D:117:LEU:HD11	1.94	0.49
1:F:123:ASP:C	1:F:125:SER:H	2.21	0.49
1:J:123:ASP:C	1:J:125:SER:H	2.20	0.49
1:K:38:ILE:HG13	1:K:38:ILE:O	2.13	0.49
1:M:253:GLU:CD	1:M:253:GLU:N	2.70	0.49
1:A:253:GLU:CD	1:A:253:GLU:N	2.70	0.49
1:C:107:LEU:CD1	1:C:274:TYR:HE2	2.25	0.49
1:D:107:LEU:CD1	1:D:274:TYR:HE2	2.26	0.49
1:H:123:ASP:C	1:H:125:SER:H	2.21	0.49
1:I:38:ILE:HG13	1:I:38:ILE:O	2.13	0.49
1:I:128:SER:O	1:I:129:ALA:C	2.56	0.49
1:J:170:GLN:HB3	1:J:171:PHE:H	1.53	0.49
1:K:65:SER:HB2	1:K:117:LEU:HD11	1.94	0.49
1:M:38:ILE:HG13	1:M:38:ILE:O	2.13	0.49
1:M:123:ASP:C	1:M:125:SER:H	2.21	0.49
1:A:160:LEU:HD12	1:A:161:THR:HG23	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:128:SER:C	1:D:130:ASP:N	2.70	0.49
1:D:128:SER:O	1:D:129:ALA:C	2.56	0.49
1:F:128:SER:C	1:F:130:ASP:N	2.69	0.49
1:I:128:SER:C	1:I:130:ASP:N	2.69	0.49
1:J:38:ILE:HG13	1:J:38:ILE:O	2.13	0.49
1:J:128:SER:C	1:J:130:ASP:N	2.70	0.49
1:K:128:SER:O	1:K:129:ALA:C	2.56	0.49
1:K:317:ARG:NH2	2:S:41:U:C5'	2.75	0.49
1:A:128:SER:O	1:A:129:ALA:C	2.56	0.48
1:C:38:ILE:HG13	1:C:38:ILE:O	2.13	0.48
1:D:38:ILE:O	1:D:38:ILE:HG13	2.13	0.48
1:D:123:ASP:C	1:D:125:SER:H	2.21	0.48
1:H:128:SER:O	1:H:129:ALA:C	2.56	0.48
1:I:317:ARG:NH2	2:S:32:U:C5'	2.75	0.48
1:L:128:SER:C	1:L:130:ASP:N	2.69	0.48
1:A:107:LEU:CD1	1:A:274:TYR:HE2	2.27	0.48
1:F:128:SER:O	1:F:129:ALA:C	2.56	0.48
1:I:107:LEU:CD1	1:I:274:TYR:HE2	2.26	0.48
1:I:160:LEU:HD12	1:I:161:THR:HG23	1.94	0.48
1:J:107:LEU:HD23	1:J:107:LEU:H	1.68	0.48
1:K:160:LEU:HD12	1:K:161:THR:HG23	1.94	0.48
1:L:123:ASP:C	1:L:125:SER:H	2.21	0.48
1:C:128:SER:C	1:C:130:ASP:N	2.70	0.48
1:D:317:ARG:NH2	2:R:41:U:C5'	2.75	0.48
1:F:253:GLU:CD	1:F:253:GLU:N	2.71	0.48
1:I:107:LEU:HD23	1:I:107:LEU:H	1.68	0.48
1:J:253:GLU:CD	1:J:253:GLU:N	2.71	0.48
1:L:107:LEU:CD1	1:L:274:TYR:HE2	2.27	0.48
1:L:253:GLU:CD	1:L:253:GLU:N	2.71	0.48
1:H:38:ILE:HG13	1:H:38:ILE:O	2.13	0.48
1:L:65:SER:HB2	1:L:117:LEU:HD11	1.94	0.48
1:A:123:ASP:C	1:A:125:SER:H	2.21	0.48
1:K:128:SER:C	1:K:130:ASP:N	2.70	0.48
1:L:128:SER:O	1:L:129:ALA:C	2.56	0.48
1:A:128:SER:C	1:A:130:ASP:N	2.69	0.48
1:F:65:SER:HB2	1:F:117:LEU:HD11	1.94	0.48
1:F:107:LEU:CD1	1:F:274:TYR:HE2	2.27	0.48
1:H:107:LEU:HD13	1:H:274:TYR:CZ	2.48	0.48
1:J:128:SER:O	1:J:129:ALA:C	2.56	0.48
1:L:38:ILE:HG13	1:L:38:ILE:O	2.14	0.48
1:L:317:ARG:NH2	2:S:50:U:C5'	2.75	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:128:SER:C	1:M:130:ASP:N	2.70	0.48
1:M:128:SER:O	1:M:129:ALA:C	2.56	0.48
1:J:317:ARG:NH2	2:S:23:U:C5'	2.75	0.48
1:K:123:ASP:C	1:K:125:SER:H	2.21	0.48
1:A:38:ILE:HG13	1:A:38:ILE:O	2.13	0.48
1:C:253:GLU:CD	1:C:253:GLU:N	2.71	0.48
1:K:107:LEU:CD1	1:K:274:TYR:HE2	2.26	0.48
1:L:317:ARG:O	1:L:317:ARG:HG2	2.14	0.48
1:M:107:LEU:HD13	1:M:274:TYR:CZ	2.48	0.48
1:A:107:LEU:HD23	1:A:107:LEU:H	1.68	0.48
1:C:65:SER:HB2	1:C:117:LEU:HD11	1.95	0.47
1:C:128:SER:O	1:C:129:ALA:C	2.56	0.47
1:J:65:SER:HB2	1:J:117:LEU:HD11	1.95	0.47
1:J:313:ALA:O	1:J:314:ARG:C	2.57	0.47
1:D:107:LEU:HD13	1:D:274:TYR:CZ	2.49	0.47
1:H:409:GLU:OE2	1:H:409:GLU:N	2.48	0.47
1:H:107:LEU:CD1	1:H:274:TYR:CE2	2.97	0.47
1:L:317:ARG:HH21	2:S:50:U:C5'	2.27	0.47
1:M:41:TYR:HA	1:M:110:LEU:O	2.15	0.47
1:C:107:LEU:CD1	1:C:274:TYR:CE2	2.97	0.47
1:K:107:LEU:HD13	1:K:274:TYR:CZ	2.49	0.47
1:L:170:GLN:HB3	1:L:171:PHE:H	1.54	0.47
1:C:107:LEU:HD13	1:C:274:TYR:CZ	2.49	0.47
1:C:199:ASP:OD1	1:C:214:ARG:HD2	2.15	0.47
1:C:317:ARG:O	1:C:317:ARG:HG2	2.15	0.47
1:D:41:TYR:HA	1:D:110:LEU:O	2.15	0.47
1:F:38:ILE:O	1:F:38:ILE:HG13	2.14	0.47
1:F:317:ARG:O	1:F:317:ARG:HG2	2.14	0.47
1:F:409:GLU:OE2	1:F:409:GLU:N	2.48	0.47
1:I:123:ASP:C	1:I:125:SER:H	2.22	0.47
1:L:409:GLU:N	1:L:409:GLU:OE2	2.48	0.47
1:M:107:LEU:CD1	1:M:274:TYR:CE2	2.97	0.47
1:C:41:TYR:HA	1:C:110:LEU:O	2.15	0.47
1:C:317:ARG:HH21	2:R:23:U:C5'	2.27	0.47
1:K:313:ALA:O	1:K:314:ARG:C	2.58	0.47
1:M:409:GLU:OE2	1:M:409:GLU:N	2.48	0.47
1:H:199:ASP:OD1	1:H:214:ARG:HD2	2.15	0.47
1:J:107:LEU:HD13	1:J:274:TYR:CZ	2.49	0.47
1:J:107:LEU:CD1	1:J:274:TYR:CE2	2.97	0.47
1:K:41:TYR:HA	1:K:110:LEU:O	2.15	0.47
1:K:317:ARG:O	1:K:317:ARG:HG2	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:409:GLU:OE2	1:K:409:GLU:N	2.48	0.47
1:A:37:GLU:CG	1:A:108:VAL:HG21	2.45	0.47
1:C:409:GLU:N	1:C:409:GLU:OE2	2.48	0.47
1:D:107:LEU:CD1	1:D:274:TYR:CE2	2.97	0.47
1:H:66:ILE:O	1:H:70:ASN:ND2	2.48	0.47
1:I:313:ALA:O	1:I:314:ARG:C	2.58	0.47
1:I:409:GLU:OE2	1:I:409:GLU:N	2.48	0.47
1:L:41:TYR:HA	1:L:110:LEU:O	2.15	0.47
1:L:107:LEU:HD13	1:L:274:TYR:CZ	2.49	0.47
1:M:317:ARG:O	1:M:317:ARG:HG2	2.15	0.47
1:A:170:GLN:HB3	1:A:171:PHE:H	1.54	0.46
1:D:317:ARG:O	1:D:317:ARG:HG2	2.15	0.46
1:F:41:TYR:HA	1:F:110:LEU:O	2.15	0.46
1:F:107:LEU:HD13	1:F:274:TYR:CZ	2.49	0.46
1:F:107:LEU:CD1	1:F:274:TYR:CE2	2.97	0.46
1:H:133:TRP:HB3	1:H:167:ILE:HG21	1.97	0.46
1:F:199:ASP:OD1	1:F:214:ARG:HD2	2.15	0.46
1:H:41:TYR:HA	1:H:110:LEU:O	2.15	0.46
1:H:313:ALA:O	1:H:314:ARG:C	2.59	0.46
1:I:107:LEU:HD13	1:I:274:TYR:CZ	2.50	0.46
1:J:41:TYR:HA	1:J:110:LEU:O	2.15	0.46
1:J:199:ASP:OD1	1:J:214:ARG:HD2	2.15	0.46
1:A:41:TYR:HA	1:A:110:LEU:O	2.15	0.46
1:A:107:LEU:HD13	1:A:274:TYR:CZ	2.50	0.46
1:A:107:LEU:CD1	1:A:274:TYR:CE2	2.98	0.46
1:A:133:TRP:HB3	1:A:167:ILE:HG21	1.98	0.46
1:C:313:ALA:O	1:C:314:ARG:C	2.57	0.46
1:D:172:GLU:CB	1:D:173:PRO:HD3	2.32	0.46
1:F:313:ALA:O	1:F:314:ARG:C	2.59	0.46
1:I:317:ARG:HH21	2:S:32:U:C5'	2.28	0.46
1:J:409:GLU:N	1:J:409:GLU:OE2	2.48	0.46
1:L:172:GLU:CB	1:L:173:PRO:HD3	2.32	0.46
1:L:313:ALA:O	1:L:314:ARG:C	2.59	0.46
1:M:66:ILE:O	1:M:70:ASN:ND2	2.48	0.46
1:M:133:TRP:HB3	1:M:167:ILE:HG21	1.97	0.46
1:M:199:ASP:OD1	1:M:214:ARG:HD2	2.15	0.46
1:A:66:ILE:O	1:A:70:ASN:ND2	2.49	0.46
1:A:199:ASP:OD1	1:A:214:ARG:HD2	2.16	0.46
1:D:37:GLU:CG	1:D:108:VAL:HG21	2.46	0.46
1:D:199:ASP:OD1	1:D:214:ARG:HD2	2.16	0.46
1:D:313:ALA:O	1:D:314:ARG:C	2.58	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:317:ARG:HH21	2:R:41:U:C5'	2.28	0.46
1:H:37:GLU:CG	1:H:108:VAL:HG21	2.46	0.46
1:I:133:TRP:HB3	1:I:167:ILE:HG21	1.98	0.46
1:C:37:GLU:CG	1:C:108:VAL:HG21	2.45	0.46
1:D:66:ILE:O	1:D:70:ASN:ND2	2.48	0.46
1:D:409:GLU:OE2	1:D:409:GLU:N	2.48	0.46
1:H:128:SER:C	1:H:130:ASP:N	2.71	0.46
1:J:66:ILE:O	1:J:70:ASN:ND2	2.49	0.46
1:J:308:LEU:O	1:J:309:ARG:HB2	2.16	0.46
1:K:107:LEU:CD1	1:K:274:TYR:CE2	2.97	0.46
1:F:133:TRP:HB3	1:F:167:ILE:HG21	1.98	0.46
1:J:133:TRP:HB3	1:J:167:ILE:HG21	1.98	0.46
1:K:37:GLU:CG	1:K:108:VAL:HG21	2.46	0.46
1:K:308:LEU:O	1:K:309:ARG:HB2	2.16	0.46
1:L:107:LEU:CD1	1:L:274:TYR:CE2	2.97	0.46
1:D:133:TRP:HB3	1:D:167:ILE:HG21	1.98	0.46
1:I:199:ASP:OD1	1:I:214:ARG:HD2	2.16	0.46
1:J:317:ARG:O	1:J:317:ARG:HG2	2.15	0.46
1:K:133:TRP:HB3	1:K:167:ILE:HG21	1.98	0.46
1:M:37:GLU:CG	1:M:108:VAL:HG21	2.46	0.46
1:C:133:TRP:HB3	1:C:167:ILE:HG21	1.98	0.46
1:D:107:LEU:HD13	1:D:274:TYR:HH	1.79	0.46
1:I:107:LEU:CD1	1:I:274:TYR:CE2	2.98	0.46
1:J:37:GLU:CG	1:J:108:VAL:HG21	2.45	0.46
1:K:66:ILE:O	1:K:70:ASN:ND2	2.48	0.46
1:A:317:ARG:O	1:A:317:ARG:HG2	2.16	0.46
1:H:308:LEU:O	1:H:309:ARG:HB2	2.16	0.46
1:I:37:GLU:CG	1:I:108:VAL:HG21	2.45	0.46
1:I:66:ILE:O	1:I:70:ASN:ND2	2.49	0.46
1:L:66:ILE:O	1:L:70:ASN:ND2	2.49	0.46
1:L:133:TRP:HB3	1:L:167:ILE:HG21	1.98	0.46
1:M:313:ALA:O	1:M:314:ARG:C	2.59	0.46
1:D:308:LEU:O	1:D:309:ARG:HB2	2.16	0.46
1:M:308:LEU:O	1:M:309:ARG:HB2	2.16	0.46
1:A:409:GLU:OE2	1:A:409:GLU:N	2.48	0.45
1:F:308:LEU:O	1:F:309:ARG:HB2	2.16	0.45
1:H:170:GLN:HB3	1:H:171:PHE:H	1.54	0.45
1:I:317:ARG:O	1:I:317:ARG:HG2	2.16	0.45
1:J:317:ARG:HH21	2:S:23:U:C5'	2.27	0.45
1:A:313:ALA:O	1:A:314:ARG:C	2.58	0.45
1:F:66:ILE:O	1:F:70:ASN:ND2	2.49	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:41:TYR:HA	1:I:110:LEU:O	2.15	0.45
1:J:317:ARG:NE	2:S:22:U:H2'	2.06	0.45
1:C:66:ILE:O	1:C:70:ASN:ND2	2.49	0.45
1:L:199:ASP:OD1	1:L:214:ARG:HD2	2.15	0.45
1:C:72:TYR:CE1	1:C:134:LEU:HD12	2.52	0.45
1:C:308:LEU:O	1:C:309:ARG:HB2	2.16	0.45
1:I:72:TYR:CE1	1:I:134:LEU:HD12	2.52	0.45
1:K:199:ASP:OD1	1:K:214:ARG:HD2	2.16	0.45
1:M:72:TYR:CE1	1:M:134:LEU:HD12	2.52	0.45
1:A:308:LEU:O	1:A:309:ARG:HB2	2.16	0.45
1:D:128:SER:O	1:D:130:ASP:N	2.50	0.45
1:H:317:ARG:O	1:H:317:ARG:HG2	2.15	0.45
1:I:128:SER:O	1:I:130:ASP:N	2.50	0.45
1:I:215:TYR:CD2	1:I:215:TYR:N	2.85	0.45
1:M:128:SER:O	1:M:130:ASP:N	2.50	0.45
1:F:37:GLU:CG	1:F:108:VAL:HG21	2.46	0.45
1:M:109:SER:C	1:M:110:LEU:HD23	2.24	0.45
1:K:72:TYR:CE1	1:K:134:LEU:HD12	2.52	0.45
1:K:128:SER:O	1:K:130:ASP:N	2.50	0.45
1:L:308:LEU:O	1:L:309:ARG:HB2	2.16	0.45
1:C:332:LEU:HD21	1:C:397:ALA:HB2	1.99	0.45
1:J:72:TYR:CE1	1:J:134:LEU:HD12	2.52	0.45
1:M:38:ILE:H	1:M:108:VAL:HG23	1.82	0.45
1:D:72:TYR:CE1	1:D:134:LEU:HD12	2.52	0.45
1:F:128:SER:O	1:F:130:ASP:N	2.50	0.45
1:F:152:TYR:HD1	1:F:153:ARG:H	1.64	0.45
1:H:128:SER:O	1:H:130:ASP:N	2.50	0.45
1:K:107:LEU:HD13	1:K:274:TYR:HH	1.79	0.45
1:L:152:TYR:HD1	1:L:153:ARG:H	1.64	0.45
1:A:128:SER:O	1:A:130:ASP:N	2.50	0.45
1:C:66:ILE:HD11	1:C:191:TYR:HB2	1.99	0.45
1:D:317:ARG:NE	2:R:40:U:H2'	2.06	0.45
1:M:317:ARG:HH21	2:S:59:U:C5'	2.27	0.45
1:H:72:TYR:CE1	1:H:134:LEU:HD12	2.52	0.44
1:I:38:ILE:H	1:I:108:VAL:HG23	1.83	0.44
1:J:66:ILE:HD11	1:J:191:TYR:HB2	1.99	0.44
1:J:81:ARG:HD3	1:J:208:HIS:CE1	2.52	0.44
1:K:317:ARG:HH21	2:S:41:U:C5'	2.28	0.44
1:L:37:GLU:CG	1:L:108:VAL:HG21	2.46	0.44
1:M:215:TYR:N	1:M:215:TYR:CD2	2.85	0.44
1:F:72:TYR:CE1	1:F:134:LEU:HD12	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:152:TYR:HD1	1:J:153:ARG:N	2.16	0.44
1:L:81:ARG:HD3	1:L:208:HIS:HE2	1.82	0.44
1:L:332:LEU:HD21	1:L:397:ALA:HB2	1.99	0.44
1:A:66:ILE:HD11	1:A:191:TYR:HB2	2.00	0.44
1:A:72:TYR:CE1	1:A:134:LEU:HD12	2.52	0.44
1:F:287:SER:HA	1:F:288:PRO:HD3	1.88	0.44
1:K:215:TYR:N	1:K:215:TYR:CD2	2.86	0.44
1:C:81:ARG:HD3	1:C:208:HIS:CE1	2.52	0.44
1:C:128:SER:O	1:C:130:ASP:N	2.50	0.44
1:H:287:SER:HA	1:H:288:PRO:HD3	1.89	0.44
1:L:128:SER:O	1:L:130:ASP:N	2.50	0.44
1:L:215:TYR:N	1:L:215:TYR:CD2	2.86	0.44
1:A:215:TYR:CD2	1:A:215:TYR:N	2.85	0.44
1:I:308:LEU:O	1:I:309:ARG:HB2	2.16	0.44
1:L:152:TYR:HD1	1:L:153:ARG:N	2.16	0.44
1:D:38:ILE:H	1:D:108:VAL:HG23	1.83	0.44
1:H:215:TYR:N	1:H:215:TYR:CD2	2.85	0.44
1:J:128:SER:O	1:J:130:ASP:N	2.50	0.44
1:J:287:SER:HA	1:J:288:PRO:HD3	1.87	0.44
1:M:332:LEU:HD21	1:M:397:ALA:HB2	2.00	0.44
1:C:152:TYR:HD1	1:C:153:ARG:H	1.65	0.44
1:C:287:SER:HA	1:C:288:PRO:HD3	1.87	0.44
1:F:38:ILE:H	1:F:108:VAL:HG23	1.83	0.44
1:F:81:ARG:HD3	1:F:208:HIS:CE1	2.52	0.44
1:I:66:ILE:HD11	1:I:191:TYR:HB2	2.00	0.44
1:I:81:ARG:HD3	1:I:208:HIS:CE1	2.53	0.44
1:K:332:LEU:HD21	1:K:397:ALA:HB2	1.99	0.44
1:M:199:ASP:CG	1:M:214:ARG:HH11	2.26	0.44
1:A:97:LYS:O	1:A:98:ALA:C	2.61	0.44
1:J:215:TYR:CD2	1:J:215:TYR:N	2.86	0.44
1:K:81:ARG:HD3	1:K:208:HIS:CE1	2.53	0.44
1:M:97:LYS:O	1:M:98:ALA:C	2.61	0.44
1:F:152:TYR:HD1	1:F:153:ARG:N	2.16	0.44
1:H:152:TYR:HD1	1:H:153:ARG:H	1.65	0.44
1:K:152:TYR:HD1	1:K:153:ARG:N	2.16	0.44
1:L:66:ILE:HD11	1:L:191:TYR:HB2	1.99	0.44
1:L:72:TYR:CE1	1:L:134:LEU:HD12	2.52	0.44
1:C:152:TYR:HD1	1:C:153:ARG:N	2.16	0.43
1:D:66:ILE:HD11	1:D:191:TYR:HB2	2.00	0.43
1:D:81:ARG:HD3	1:D:208:HIS:CE1	2.53	0.43
1:D:287:SER:HA	1:D:288:PRO:HD3	1.89	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:38:ILE:H	1:H:108:VAL:HG23	1.82	0.43
1:H:332:LEU:HD21	1:H:397:ALA:HB2	2.00	0.43
1:J:152:TYR:HD1	1:J:153:ARG:H	1.65	0.43
1:K:38:ILE:H	1:K:108:VAL:HG23	1.83	0.43
1:L:81:ARG:HD3	1:L:208:HIS:CE1	2.52	0.43
2:R:29:U:O2'	2:R:30:U:OP1	2.34	0.43
1:C:215:TYR:N	1:C:215:TYR:CD2	2.86	0.43
1:D:97:LYS:O	1:D:98:ALA:C	2.61	0.43
1:D:199:ASP:CG	1:D:214:ARG:HH11	2.26	0.43
1:A:152:TYR:HD1	1:A:153:ARG:H	1.66	0.43
1:D:152:TYR:HD1	1:D:153:ARG:N	2.16	0.43
1:D:332:LEU:HD21	1:D:397:ALA:HB2	1.99	0.43
1:F:66:ILE:HD11	1:F:191:TYR:HB2	1.99	0.43
1:F:332:LEU:HD21	1:F:397:ALA:HB2	1.99	0.43
1:H:97:LYS:O	1:H:98:ALA:C	2.61	0.43
1:I:287:SER:HA	1:I:288:PRO:HD3	1.90	0.43
1:M:81:ARG:HD3	1:M:208:HIS:CE1	2.53	0.43
1:A:332:LEU:HD21	1:A:397:ALA:HB2	2.00	0.43
1:C:38:ILE:HA	1:C:39:PRO:HD3	1.86	0.43
1:C:97:LYS:O	1:C:98:ALA:C	2.61	0.43
1:F:97:LYS:O	1:F:98:ALA:C	2.61	0.43
1:I:97:LYS:O	1:I:98:ALA:C	2.61	0.43
1:I:152:TYR:HD1	1:I:153:ARG:N	2.17	0.43
1:L:97:LYS:O	1:L:98:ALA:C	2.61	0.43
1:M:66:ILE:HD11	1:M:191:TYR:HB2	2.01	0.43
1:A:81:ARG:HD3	1:A:208:HIS:CE1	2.53	0.43
1:A:287:SER:HA	1:A:288:PRO:HD3	1.90	0.43
1:C:38:ILE:H	1:C:108:VAL:HG23	1.84	0.43
1:F:215:TYR:CD2	1:F:215:TYR:N	2.86	0.43
1:H:38:ILE:HA	1:H:39:PRO:HD3	1.87	0.43
1:H:81:ARG:HD3	1:H:208:HIS:HE2	1.84	0.43
1:I:152:TYR:C	1:I:154:LYS:H	2.27	0.43
1:K:66:ILE:HD11	1:K:191:TYR:HB2	2.00	0.43
1:C:199:ASP:CG	1:C:214:ARG:HH11	2.27	0.43
1:D:152:TYR:C	1:D:154:LYS:H	2.27	0.43
1:F:199:ASP:CG	1:F:214:ARG:HH11	2.27	0.43
1:H:66:ILE:HD11	1:H:191:TYR:HB2	2.01	0.43
1:H:81:ARG:HD3	1:H:208:HIS:CE1	2.53	0.43
1:I:263:LEU:HA	1:I:264:PRO:HD3	1.81	0.43
1:J:97:LYS:O	1:J:98:ALA:C	2.61	0.43
1:J:332:LEU:HD21	1:J:397:ALA:HB2	1.99	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:97:LYS:O	1:K:98:ALA:C	2.61	0.43
1:K:199:ASP:CG	1:K:214:ARG:HH11	2.26	0.43
1:F:152:TYR:C	1:F:154:LYS:H	2.27	0.43
1:H:199:ASP:CG	1:H:214:ARG:HH11	2.26	0.43
1:I:38:ILE:HA	1:I:39:PRO:HD3	1.87	0.43
1:I:170:GLN:HB3	1:I:171:PHE:H	1.54	0.43
1:I:199:ASP:CG	1:I:214:ARG:HH11	2.27	0.43
1:L:38:ILE:H	1:L:108:VAL:HG23	1.83	0.43
1:L:81:ARG:HD3	1:L:208:HIS:NE2	2.34	0.43
1:M:152:TYR:C	1:M:154:LYS:H	2.27	0.43
1:D:152:TYR:HD1	1:D:153:ARG:H	1.65	0.43
1:D:215:TYR:N	1:D:215:TYR:CD2	2.86	0.43
1:F:28:PRO:HG2	1:F:266:GLN:NE2	2.33	0.43
1:F:370:PRO:HD3	1:F:381:TRP:CG	2.54	0.43
1:J:38:ILE:H	1:J:108:VAL:HG23	1.84	0.43
1:J:199:ASP:CG	1:J:214:ARG:HH11	2.27	0.43
1:K:152:TYR:HD1	1:K:153:ARG:H	1.65	0.43
1:K:152:TYR:C	1:K:154:LYS:H	2.27	0.43
1:M:152:TYR:HD1	1:M:153:ARG:N	2.17	0.43
1:L:370:PRO:HD3	1:L:381:TRP:CG	2.54	0.42
1:M:81:ARG:HD3	1:M:208:HIS:HE2	1.84	0.42
1:A:38:ILE:H	1:A:108:VAL:HG23	1.82	0.42
1:D:81:ARG:HD3	1:D:208:HIS:NE2	2.35	0.42
1:F:317:ARG:HH21	2:R:50:U:C5'	2.27	0.42
1:I:332:LEU:HD21	1:I:397:ALA:HB2	2.00	0.42
1:J:81:ARG:HD3	1:J:208:HIS:NE2	2.34	0.42
1:J:263:LEU:HA	1:J:264:PRO:HD3	1.82	0.42
1:K:263:LEU:HA	1:K:264:PRO:HD3	1.81	0.42
1:C:28:PRO:HG2	1:C:266:GLN:NE2	2.33	0.42
1:F:81:ARG:HD3	1:F:208:HIS:NE2	2.34	0.42
1:L:152:TYR:C	1:L:154:LYS:H	2.27	0.42
1:M:172:GLU:CB	1:M:173:PRO:HD3	2.32	0.42
2:R:56:U:C2'	2:R:57:U:OP1	2.67	0.42
1:A:152:TYR:HD1	1:A:153:ARG:N	2.17	0.42
1:A:317:ARG:HH21	2:R:32:U:C5'	2.28	0.42
1:K:370:PRO:HD3	1:K:381:TRP:CG	2.55	0.42
1:M:152:TYR:HD1	1:M:153:ARG:H	1.65	0.42
1:A:199:ASP:CG	1:A:214:ARG:HH11	2.27	0.42
1:A:370:PRO:HD3	1:A:381:TRP:CG	2.55	0.42
1:H:152:TYR:HD1	1:H:153:ARG:N	2.17	0.42
2:R:29:U:C2'	2:R:30:U:OP1	2.68	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:50:U:H2'	2:R:52:U:H5''	2.01	0.42
1:C:152:TYR:C	1:C:154:LYS:H	2.27	0.42
1:D:370:PRO:HD3	1:D:381:TRP:CG	2.55	0.42
1:F:172:GLU:CB	1:F:173:PRO:HD3	2.32	0.42
1:I:370:PRO:HD3	1:I:381:TRP:CG	2.55	0.42
1:L:199:ASP:CG	1:L:214:ARG:HH11	2.27	0.42
2:S:56:U:C2'	2:S:57:U:OP1	2.67	0.42
1:A:152:TYR:C	1:A:154:LYS:H	2.27	0.42
1:C:81:ARG:HD3	1:C:208:HIS:NE2	2.34	0.42
1:C:370:PRO:HD3	1:C:381:TRP:CG	2.55	0.42
1:I:81:ARG:HD3	1:I:208:HIS:NE2	2.35	0.42
1:I:152:TYR:HD1	1:I:153:ARG:H	1.66	0.42
1:L:287:SER:HA	1:L:288:PRO:HD3	1.88	0.42
1:H:152:TYR:C	1:H:154:LYS:H	2.27	0.42
1:J:370:PRO:HD3	1:J:381:TRP:CG	2.55	0.42
1:M:287:SER:HA	1:M:288:PRO:HD3	1.89	0.42
2:S:47:U:C2'	2:S:48:U:OP1	2.68	0.42
1:J:152:TYR:C	1:J:154:LYS:H	2.27	0.41
1:L:152:TYR:CD1	1:L:153:ARG:N	2.89	0.41
1:M:81:ARG:HD3	1:M:208:HIS:NE2	2.35	0.41
1:M:263:LEU:HA	1:M:264:PRO:HD3	1.80	0.41
2:R:47:U:C2'	2:R:48:U:OP1	2.68	0.41
2:S:29:U:C2'	2:S:30:U:OP1	2.68	0.41
2:S:59:U:H2'	2:S:61:U:H5''	2.02	0.41
1:A:81:ARG:HD3	1:A:208:HIS:NE2	2.35	0.41
1:H:370:PRO:HD3	1:H:381:TRP:CG	2.56	0.41
1:F:40:LEU:HD13	1:F:42:ILE:HD11	2.02	0.41
1:K:81:ARG:HD3	1:K:208:HIS:NE2	2.35	0.41
1:M:170:GLN:HB3	1:M:171:PHE:H	1.54	0.41
2:R:38:U:C2'	2:R:39:U:OP1	2.68	0.41
2:S:41:U:H2'	2:S:43:U:H5''	2.02	0.41
1:H:323:GLU:H	1:H:323:GLU:HG3	1.70	0.41
1:J:152:TYR:CD1	1:J:153:ARG:N	2.88	0.41
1:C:152:TYR:CD1	1:C:153:ARG:N	2.88	0.41
1:H:40:LEU:HD13	1:H:42:ILE:HD11	2.02	0.41
1:H:81:ARG:HD3	1:H:208:HIS:NE2	2.35	0.41
1:H:166:MET:C	1:H:167:ILE:HG13	2.45	0.41
1:L:40:LEU:HD13	1:L:42:ILE:HD11	2.03	0.41
2:R:20:U:C2'	2:R:21:U:OP1	2.68	0.41
2:S:32:U:H2'	2:S:34:U:H5''	2.02	0.41
1:K:152:TYR:CD1	1:K:153:ARG:N	2.89	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:59:U:H2'	2:R:61:U:H5''	2.02	0.41
1:K:287:SER:HA	1:K:288:PRO:HD3	1.89	0.41
1:L:144:VAL:HG11	1:L:156:LEU:HG	2.03	0.41
2:S:20:U:C2'	2:S:21:U:OP1	2.68	0.41
2:S:50:U:H2'	2:S:52:U:H5''	2.01	0.41
2:S:38:U:C2'	2:S:39:U:OP1	2.68	0.41
1:A:38:ILE:HA	1:A:39:PRO:HD3	1.87	0.41
1:A:40:LEU:HD13	1:A:42:ILE:HD11	2.03	0.41
1:C:22:GLU:HB3	1:M:206:LYS:NZ	2.36	0.41
1:I:306:LEU:HD22	1:I:412:ILE:HD12	2.03	0.41
1:J:28:PRO:HG2	1:J:266:GLN:NE2	2.33	0.41
1:J:40:LEU:HD13	1:J:42:ILE:HD11	2.03	0.41
1:L:81:ARG:HB3	1:L:208:HIS:HE2	1.86	0.41
1:L:263:LEU:HA	1:L:264:PRO:HD3	1.81	0.41
1:M:28:PRO:HG2	1:M:266:GLN:NE2	2.33	0.41
1:M:40:LEU:HD13	1:M:42:ILE:HD11	2.02	0.41
1:M:149:MET:C	1:M:151:GLU:N	2.79	0.41
1:M:370:PRO:HD3	1:M:381:TRP:CG	2.56	0.41
1:D:149:MET:C	1:D:151:GLU:N	2.79	0.41
1:I:40:LEU:HD13	1:I:42:ILE:HD11	2.03	0.41
2:R:32:U:H2'	2:R:34:U:H5''	2.02	0.41
1:C:40:LEU:HD13	1:C:42:ILE:HD11	2.03	0.40
1:C:356:THR:N	1:C:357:PRO:HD3	2.36	0.40
1:D:166:MET:C	1:D:167:ILE:HG13	2.46	0.40
1:H:81:ARG:HB3	1:H:208:HIS:HE2	1.86	0.40
1:H:149:MET:C	1:H:151:GLU:N	2.79	0.40
1:H:356:THR:N	1:H:357:PRO:HD3	2.37	0.40
1:I:28:PRO:HG2	1:I:266:GLN:NE2	2.33	0.40
2:R:41:U:H2'	2:R:43:U:H5''	2.02	0.40
2:S:23:U:H2'	2:S:25:U:H5''	2.02	0.40
1:A:22:GLU:HB3	1:C:206:LYS:NZ	2.36	0.40
1:D:206:LYS:NZ	1:F:22:GLU:HB3	2.37	0.40
1:F:149:MET:C	1:F:151:GLU:N	2.79	0.40
1:H:317:ARG:HH21	2:R:59:U:C5'	2.27	0.40
1:K:149:MET:C	1:K:151:GLU:N	2.79	0.40
1:L:149:MET:C	1:L:151:GLU:N	2.79	0.40
1:M:152:TYR:CD1	1:M:153:ARG:N	2.89	0.40
1:M:356:THR:N	1:M:357:PRO:HD3	2.37	0.40
1:A:206:LYS:NZ	1:D:22:GLU:HB3	2.37	0.40
1:C:323:GLU:H	1:C:323:GLU:HG3	1.71	0.40
1:F:166:MET:C	1:F:167:ILE:HG13	2.46	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:118:PRO:O	1:I:119:ASP:CB	2.69	0.40
1:I:152:TYR:CD1	1:I:153:ARG:N	2.90	0.40
1:K:166:MET:CE	1:L:184:VAL:CB	2.99	0.40
1:C:250:LEU:HD22	1:C:379:LEU:HD21	2.02	0.40
1:D:170:GLN:HB3	1:D:171:PHE:H	1.54	0.40
1:F:206:LYS:NZ	1:H:22:GLU:HB3	2.37	0.40
1:H:152:TYR:CD1	1:H:153:ARG:N	2.89	0.40
1:K:144:VAL:HG11	1:K:156:LEU:HG	2.03	0.40
1:A:356:THR:N	1:A:357:PRO:HD3	2.36	0.40
1:C:149:MET:C	1:C:151:GLU:N	2.79	0.40
1:D:28:PRO:HG2	1:D:266:GLN:NE2	2.34	0.40
1:F:144:VAL:HG11	1:F:156:LEU:HG	2.03	0.40
1:J:250:LEU:HD22	1:J:379:LEU:HD21	2.02	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	A	410/422 (97%)	341 (83%)	45 (11%)	24 (6%)	1	13
1	C	410/422 (97%)	341 (83%)	45 (11%)	24 (6%)	1	13
1	D	410/422 (97%)	341 (83%)	45 (11%)	24 (6%)	1	13
1	F	410/422 (97%)	341 (83%)	45 (11%)	24 (6%)	1	13
1	H	410/422 (97%)	340 (83%)	46 (11%)	24 (6%)	1	13
1	I	410/422 (97%)	341 (83%)	45 (11%)	24 (6%)	1	13
1	J	410/422 (97%)	341 (83%)	45 (11%)	24 (6%)	1	13
1	K	410/422 (97%)	341 (83%)	45 (11%)	24 (6%)	1	13
1	L	410/422 (97%)	341 (83%)	45 (11%)	24 (6%)	1	13
1	M	410/422 (97%)	340 (83%)	46 (11%)	24 (6%)	1	13

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	4100/4220 (97%)	3408 (83%)	452 (11%)	240 (6%)	2	13

All (240) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	24	PRO
1	A	98	ALA
1	A	128	SER
1	A	150	PRO
1	A	168	ASN
1	C	24	PRO
1	C	98	ALA
1	C	117	LEU
1	C	128	SER
1	C	150	PRO
1	C	168	ASN
1	D	24	PRO
1	D	98	ALA
1	D	117	LEU
1	D	122	SER
1	D	128	SER
1	D	150	PRO
1	D	168	ASN
1	F	24	PRO
1	F	98	ALA
1	F	128	SER
1	F	150	PRO
1	F	168	ASN
1	H	24	PRO
1	H	98	ALA
1	H	122	SER
1	H	128	SER
1	H	150	PRO
1	H	168	ASN
1	I	24	PRO
1	I	98	ALA
1	I	128	SER
1	I	150	PRO
1	I	168	ASN
1	J	24	PRO
1	J	98	ALA
1	J	117	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	J	128	SER
1	J	150	PRO
1	J	168	ASN
1	K	24	PRO
1	K	98	ALA
1	K	117	LEU
1	K	122	SER
1	K	128	SER
1	K	150	PRO
1	K	168	ASN
1	L	24	PRO
1	L	98	ALA
1	L	128	SER
1	L	150	PRO
1	L	168	ASN
1	M	24	PRO
1	M	98	ALA
1	M	122	SER
1	M	128	SER
1	M	150	PRO
1	M	168	ASN
1	A	47	SER
1	A	117	LEU
1	A	119	ASP
1	A	122	SER
1	A	129	ALA
1	A	172	GLU
1	A	177	GLU
1	A	341	SER
1	C	47	SER
1	C	119	ASP
1	C	122	SER
1	C	129	ALA
1	C	172	GLU
1	C	177	GLU
1	C	341	SER
1	D	47	SER
1	D	119	ASP
1	D	172	GLU
1	D	177	GLU
1	D	341	SER
1	F	47	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	117	LEU
1	F	119	ASP
1	F	122	SER
1	F	129	ALA
1	F	172	GLU
1	F	177	GLU
1	F	341	SER
1	H	47	SER
1	H	117	LEU
1	H	119	ASP
1	H	172	GLU
1	H	177	GLU
1	H	341	SER
1	I	47	SER
1	I	117	LEU
1	I	119	ASP
1	I	122	SER
1	I	129	ALA
1	I	172	GLU
1	I	177	GLU
1	I	341	SER
1	J	47	SER
1	J	119	ASP
1	J	122	SER
1	J	129	ALA
1	J	172	GLU
1	J	177	GLU
1	J	341	SER
1	K	47	SER
1	K	119	ASP
1	K	172	GLU
1	K	177	GLU
1	K	341	SER
1	L	47	SER
1	L	117	LEU
1	L	119	ASP
1	L	122	SER
1	L	129	ALA
1	L	172	GLU
1	L	177	GLU
1	L	341	SER
1	M	47	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	M	117	LEU
1	M	119	ASP
1	M	172	GLU
1	M	177	GLU
1	M	341	SER
1	A	43	ASN
1	A	61	SER
1	A	113	LEU
1	A	170	GLN
1	A	180	ASP
1	C	43	ASN
1	C	61	SER
1	C	113	LEU
1	C	170	GLN
1	C	180	ASP
1	D	43	ASN
1	D	61	SER
1	D	113	LEU
1	D	129	ALA
1	D	170	GLN
1	D	180	ASP
1	F	43	ASN
1	F	61	SER
1	F	113	LEU
1	F	170	GLN
1	F	180	ASP
1	H	43	ASN
1	H	61	SER
1	H	113	LEU
1	H	129	ALA
1	H	165	LYS
1	H	170	GLN
1	H	180	ASP
1	I	43	ASN
1	I	61	SER
1	I	113	LEU
1	I	170	GLN
1	I	180	ASP
1	J	43	ASN
1	J	61	SER
1	J	113	LEU
1	J	170	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	J	180	ASP
1	K	43	ASN
1	K	61	SER
1	K	113	LEU
1	K	129	ALA
1	K	170	GLN
1	K	180	ASP
1	L	43	ASN
1	L	61	SER
1	L	113	LEU
1	L	170	GLN
1	L	180	ASP
1	M	43	ASN
1	M	61	SER
1	M	113	LEU
1	M	129	ALA
1	M	165	LYS
1	M	170	GLN
1	M	180	ASP
1	A	165	LYS
1	A	344	LEU
1	C	165	LYS
1	C	344	LEU
1	D	165	LYS
1	D	344	LEU
1	F	344	LEU
1	H	344	LEU
1	I	165	LYS
1	I	344	LEU
1	J	165	LYS
1	J	344	LEU
1	K	165	LYS
1	K	344	LEU
1	L	344	LEU
1	M	344	LEU
1	A	309	ARG
1	C	179	ARG
1	C	309	ARG
1	D	309	ARG
1	F	165	LYS
1	F	179	ARG
1	F	309	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	H	179	ARG
1	H	309	ARG
1	I	309	ARG
1	J	179	ARG
1	J	309	ARG
1	K	309	ARG
1	L	165	LYS
1	L	179	ARG
1	L	309	ARG
1	M	179	ARG
1	M	309	ARG
1	A	179	ARG
1	D	179	ARG
1	I	179	ARG
1	K	179	ARG
1	A	27	TYR
1	A	80	ILE
1	C	27	TYR
1	C	80	ILE
1	D	27	TYR
1	F	27	TYR
1	F	80	ILE
1	H	27	TYR
1	I	27	TYR
1	I	80	ILE
1	J	27	TYR
1	J	80	ILE
1	K	27	TYR
1	L	27	TYR
1	L	80	ILE
1	M	27	TYR
1	D	80	ILE
1	H	80	ILE
1	K	80	ILE
1	M	80	ILE

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	A	357/363 (98%)	310 (87%)	47 (13%)	4	15
1	C	357/363 (98%)	309 (87%)	48 (13%)	4	14
1	D	357/363 (98%)	310 (87%)	47 (13%)	4	15
1	F	357/363 (98%)	308 (86%)	49 (14%)	3	14
1	H	357/363 (98%)	310 (87%)	47 (13%)	4	15
1	I	357/363 (98%)	310 (87%)	47 (13%)	4	15
1	J	357/363 (98%)	309 (87%)	48 (13%)	4	14
1	K	357/363 (98%)	310 (87%)	47 (13%)	4	15
1	L	357/363 (98%)	308 (86%)	49 (14%)	3	14
1	M	357/363 (98%)	310 (87%)	47 (13%)	4	15
All	All	3570/3630 (98%)	3094 (87%)	476 (13%)	6	14

All (476) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ILE
1	A	25	VAL
1	A	34	LYS
1	A	40	LEU
1	A	46	LYS
1	A	48	LEU
1	A	84	LEU
1	A	85	ASP
1	A	95	ILE
1	A	107	LEU
1	A	108	VAL
1	A	116	VAL
1	A	126	ARG
1	A	134	LEU
1	A	149	MET
1	A	156	LEU
1	A	162	ASN
1	A	163	GLN
1	A	165	LYS
1	A	175	VAL
1	A	181	ILE
1	A	189	SER
1	A	195	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	215	TYR
1	A	217	THR
1	A	237	ILE
1	A	243	GLU
1	A	249	ILE
1	A	253	GLU
1	A	278	LEU
1	A	307	LEU
1	A	308	LEU
1	A	309	ARG
1	A	311	THR
1	A	317	ARG
1	A	323	GLU
1	A	327	LEU
1	A	329	THR
1	A	332	LEU
1	A	350	VAL
1	A	354	LYS
1	A	375	VAL
1	A	377	GLU
1	A	387	ARG
1	A	407	LEU
1	A	409	GLU
1	A	414	LYS
1	C	8	ILE
1	C	25	VAL
1	C	34	LYS
1	C	40	LEU
1	C	46	LYS
1	C	48	LEU
1	C	84	LEU
1	C	85	ASP
1	C	95	ILE
1	C	107	LEU
1	C	108	VAL
1	C	116	VAL
1	C	126	ARG
1	C	134	LEU
1	C	149	MET
1	C	156	LEU
1	C	162	ASN
1	C	163	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	165	LYS
1	C	175	VAL
1	C	181	ILE
1	C	189	SER
1	C	195	VAL
1	C	215	TYR
1	C	217	THR
1	C	237	ILE
1	C	243	GLU
1	C	249	ILE
1	C	253	GLU
1	C	278	LEU
1	C	307	LEU
1	C	308	LEU
1	C	309	ARG
1	C	311	THR
1	C	317	ARG
1	C	323	GLU
1	C	327	LEU
1	C	329	THR
1	C	332	LEU
1	C	350	VAL
1	C	354	LYS
1	C	375	VAL
1	C	377	GLU
1	C	387	ARG
1	C	405	GLN
1	C	407	LEU
1	C	409	GLU
1	C	414	LYS
1	D	8	ILE
1	D	25	VAL
1	D	34	LYS
1	D	40	LEU
1	D	46	LYS
1	D	48	LEU
1	D	84	LEU
1	D	85	ASP
1	D	95	ILE
1	D	107	LEU
1	D	108	VAL
1	D	116	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	126	ARG
1	D	134	LEU
1	D	149	MET
1	D	156	LEU
1	D	162	ASN
1	D	163	GLN
1	D	165	LYS
1	D	175	VAL
1	D	181	ILE
1	D	189	SER
1	D	195	VAL
1	D	215	TYR
1	D	217	THR
1	D	237	ILE
1	D	243	GLU
1	D	249	ILE
1	D	253	GLU
1	D	278	LEU
1	D	307	LEU
1	D	308	LEU
1	D	309	ARG
1	D	311	THR
1	D	317	ARG
1	D	323	GLU
1	D	327	LEU
1	D	329	THR
1	D	332	LEU
1	D	350	VAL
1	D	354	LYS
1	D	375	VAL
1	D	377	GLU
1	D	387	ARG
1	D	407	LEU
1	D	409	GLU
1	D	414	LYS
1	F	8	ILE
1	F	25	VAL
1	F	34	LYS
1	F	40	LEU
1	F	46	LYS
1	F	48	LEU
1	F	57	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	84	LEU
1	F	85	ASP
1	F	95	ILE
1	F	107	LEU
1	F	108	VAL
1	F	116	VAL
1	F	126	ARG
1	F	134	LEU
1	F	149	MET
1	F	156	LEU
1	F	162	ASN
1	F	163	GLN
1	F	165	LYS
1	F	175	VAL
1	F	181	ILE
1	F	189	SER
1	F	195	VAL
1	F	215	TYR
1	F	217	THR
1	F	237	ILE
1	F	243	GLU
1	F	249	ILE
1	F	253	GLU
1	F	278	LEU
1	F	307	LEU
1	F	308	LEU
1	F	309	ARG
1	F	311	THR
1	F	317	ARG
1	F	323	GLU
1	F	327	LEU
1	F	329	THR
1	F	332	LEU
1	F	350	VAL
1	F	354	LYS
1	F	375	VAL
1	F	377	GLU
1	F	387	ARG
1	F	405	GLN
1	F	407	LEU
1	F	409	GLU
1	F	414	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	H	8	ILE
1	H	25	VAL
1	H	34	LYS
1	H	40	LEU
1	H	46	LYS
1	H	48	LEU
1	H	84	LEU
1	H	85	ASP
1	H	95	ILE
1	H	107	LEU
1	H	108	VAL
1	H	116	VAL
1	H	126	ARG
1	H	134	LEU
1	H	149	MET
1	H	156	LEU
1	H	162	ASN
1	H	163	GLN
1	H	165	LYS
1	H	175	VAL
1	H	181	ILE
1	H	189	SER
1	H	195	VAL
1	H	215	TYR
1	H	217	THR
1	H	237	ILE
1	H	243	GLU
1	H	249	ILE
1	H	253	GLU
1	H	278	LEU
1	H	307	LEU
1	H	308	LEU
1	H	309	ARG
1	H	311	THR
1	H	317	ARG
1	H	323	GLU
1	H	327	LEU
1	H	329	THR
1	H	332	LEU
1	H	350	VAL
1	H	354	LYS
1	H	375	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	H	377	GLU
1	H	387	ARG
1	H	407	LEU
1	H	409	GLU
1	H	414	LYS
1	I	8	ILE
1	I	25	VAL
1	I	34	LYS
1	I	40	LEU
1	I	46	LYS
1	I	48	LEU
1	I	84	LEU
1	I	85	ASP
1	I	95	ILE
1	I	107	LEU
1	I	108	VAL
1	I	116	VAL
1	I	126	ARG
1	I	134	LEU
1	I	149	MET
1	I	156	LEU
1	I	162	ASN
1	I	163	GLN
1	I	165	LYS
1	I	175	VAL
1	I	181	ILE
1	I	189	SER
1	I	195	VAL
1	I	215	TYR
1	I	217	THR
1	I	237	ILE
1	I	243	GLU
1	I	249	ILE
1	I	253	GLU
1	I	278	LEU
1	I	307	LEU
1	I	308	LEU
1	I	309	ARG
1	I	311	THR
1	I	317	ARG
1	I	323	GLU
1	I	327	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	I	329	THR
1	I	332	LEU
1	I	350	VAL
1	I	354	LYS
1	I	375	VAL
1	I	377	GLU
1	I	387	ARG
1	I	407	LEU
1	I	409	GLU
1	I	414	LYS
1	J	8	ILE
1	J	25	VAL
1	J	34	LYS
1	J	40	LEU
1	J	46	LYS
1	J	48	LEU
1	J	84	LEU
1	J	85	ASP
1	J	95	ILE
1	J	107	LEU
1	J	108	VAL
1	J	116	VAL
1	J	126	ARG
1	J	134	LEU
1	J	149	MET
1	J	156	LEU
1	J	162	ASN
1	J	163	GLN
1	J	165	LYS
1	J	175	VAL
1	J	181	ILE
1	J	189	SER
1	J	195	VAL
1	J	215	TYR
1	J	217	THR
1	J	237	ILE
1	J	243	GLU
1	J	249	ILE
1	J	253	GLU
1	J	278	LEU
1	J	307	LEU
1	J	308	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	J	309	ARG
1	J	311	THR
1	J	317	ARG
1	J	323	GLU
1	J	327	LEU
1	J	329	THR
1	J	332	LEU
1	J	350	VAL
1	J	354	LYS
1	J	375	VAL
1	J	377	GLU
1	J	387	ARG
1	J	405	GLN
1	J	407	LEU
1	J	409	GLU
1	J	414	LYS
1	K	8	ILE
1	K	25	VAL
1	K	34	LYS
1	K	40	LEU
1	K	46	LYS
1	K	48	LEU
1	K	84	LEU
1	K	85	ASP
1	K	95	ILE
1	K	107	LEU
1	K	108	VAL
1	K	116	VAL
1	K	126	ARG
1	K	134	LEU
1	K	149	MET
1	K	156	LEU
1	K	162	ASN
1	K	163	GLN
1	K	165	LYS
1	K	175	VAL
1	K	181	ILE
1	K	189	SER
1	K	195	VAL
1	K	215	TYR
1	K	217	THR
1	K	237	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	K	243	GLU
1	K	249	ILE
1	K	253	GLU
1	K	278	LEU
1	K	307	LEU
1	K	308	LEU
1	K	309	ARG
1	K	311	THR
1	K	317	ARG
1	K	323	GLU
1	K	327	LEU
1	K	329	THR
1	K	332	LEU
1	K	350	VAL
1	K	354	LYS
1	K	375	VAL
1	K	377	GLU
1	K	387	ARG
1	K	407	LEU
1	K	409	GLU
1	K	414	LYS
1	L	8	ILE
1	L	25	VAL
1	L	34	LYS
1	L	40	LEU
1	L	46	LYS
1	L	48	LEU
1	L	57	GLN
1	L	84	LEU
1	L	85	ASP
1	L	95	ILE
1	L	107	LEU
1	L	108	VAL
1	L	116	VAL
1	L	126	ARG
1	L	134	LEU
1	L	149	MET
1	L	156	LEU
1	L	162	ASN
1	L	163	GLN
1	L	165	LYS
1	L	175	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	L	181	ILE
1	L	189	SER
1	L	195	VAL
1	L	215	TYR
1	L	217	THR
1	L	237	ILE
1	L	243	GLU
1	L	249	ILE
1	L	253	GLU
1	L	278	LEU
1	L	307	LEU
1	L	308	LEU
1	L	309	ARG
1	L	311	THR
1	L	317	ARG
1	L	323	GLU
1	L	327	LEU
1	L	329	THR
1	L	332	LEU
1	L	350	VAL
1	L	354	LYS
1	L	375	VAL
1	L	377	GLU
1	L	387	ARG
1	L	405	GLN
1	L	407	LEU
1	L	409	GLU
1	L	414	LYS
1	M	8	ILE
1	M	25	VAL
1	M	34	LYS
1	M	40	LEU
1	M	46	LYS
1	M	48	LEU
1	M	84	LEU
1	M	85	ASP
1	M	95	ILE
1	M	107	LEU
1	M	108	VAL
1	M	116	VAL
1	M	126	ARG
1	M	134	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	M	149	MET
1	M	156	LEU
1	M	162	ASN
1	M	163	GLN
1	M	165	LYS
1	M	175	VAL
1	M	181	ILE
1	M	189	SER
1	M	195	VAL
1	M	215	TYR
1	M	217	THR
1	M	237	ILE
1	M	243	GLU
1	M	249	ILE
1	M	253	GLU
1	M	278	LEU
1	M	307	LEU
1	M	308	LEU
1	M	309	ARG
1	M	311	THR
1	M	317	ARG
1	M	323	GLU
1	M	327	LEU
1	M	329	THR
1	M	332	LEU
1	M	350	VAL
1	M	354	LYS
1	M	375	VAL
1	M	377	GLU
1	M	387	ARG
1	M	407	LEU
1	M	409	GLU
1	M	414	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (94) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	ASN
1	A	148	GLN
1	A	163	GLN
1	A	168	ASN
1	A	187	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	251	ASN
1	A	266	GLN
1	A	318	GLN
1	A	346	GLN
1	A	347	GLN
1	A	385	GLN
1	C	70	ASN
1	C	148	GLN
1	C	163	GLN
1	C	168	ASN
1	C	187	ASN
1	C	251	ASN
1	C	266	GLN
1	C	346	GLN
1	C	385	GLN
1	D	70	ASN
1	D	148	GLN
1	D	163	GLN
1	D	168	ASN
1	D	187	ASN
1	D	251	ASN
1	D	266	GLN
1	D	346	GLN
1	D	385	GLN
1	F	70	ASN
1	F	148	GLN
1	F	163	GLN
1	F	168	ASN
1	F	187	ASN
1	F	251	ASN
1	F	266	GLN
1	F	346	GLN
1	F	385	GLN
1	H	70	ASN
1	H	148	GLN
1	H	163	GLN
1	H	168	ASN
1	H	187	ASN
1	H	251	ASN
1	H	266	GLN
1	H	318	GLN
1	H	346	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	H	347	GLN
1	H	385	GLN
1	I	70	ASN
1	I	148	GLN
1	I	163	GLN
1	I	168	ASN
1	I	187	ASN
1	I	251	ASN
1	I	266	GLN
1	I	346	GLN
1	I	385	GLN
1	J	70	ASN
1	J	148	GLN
1	J	163	GLN
1	J	168	ASN
1	J	187	ASN
1	J	266	GLN
1	J	346	GLN
1	J	347	GLN
1	J	385	GLN
1	K	70	ASN
1	K	148	GLN
1	K	163	GLN
1	K	168	ASN
1	K	187	ASN
1	K	251	ASN
1	K	266	GLN
1	K	346	GLN
1	K	385	GLN
1	L	70	ASN
1	L	148	GLN
1	L	163	GLN
1	L	168	ASN
1	L	187	ASN
1	L	251	ASN
1	L	266	GLN
1	L	346	GLN
1	L	385	GLN
1	M	70	ASN
1	M	148	GLN
1	M	163	GLN
1	M	168	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	M	187	ASN
1	M	251	ASN
1	M	266	GLN
1	M	346	GLN
1	M	385	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	R	44/45 (97%)	34 (77%)	1 (2%)
2	S	44/45 (97%)	34 (77%)	1 (2%)
All	All	88/90 (97%)	68 (77%)	2 (2%)

All (68) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	R	19	U
2	R	21	U
2	R	23	U
2	R	24	U
2	R	25	U
2	R	26	U
2	R	27	U
2	R	28	U
2	R	30	U
2	R	32	U
2	R	33	U
2	R	34	U
2	R	35	U
2	R	36	U
2	R	37	U
2	R	39	U
2	R	41	U
2	R	42	U
2	R	43	U
2	R	44	U
2	R	45	U
2	R	46	U
2	R	48	U
2	R	50	U
2	R	51	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	R	52	U
2	R	53	U
2	R	54	U
2	R	55	U
2	R	57	U
2	R	59	U
2	R	60	U
2	R	61	U
2	R	62	U
2	S	19	U
2	S	21	U
2	S	23	U
2	S	24	U
2	S	25	U
2	S	26	U
2	S	27	U
2	S	28	U
2	S	30	U
2	S	32	U
2	S	33	U
2	S	34	U
2	S	35	U
2	S	36	U
2	S	37	U
2	S	39	U
2	S	41	U
2	S	42	U
2	S	43	U
2	S	44	U
2	S	45	U
2	S	46	U
2	S	48	U
2	S	50	U
2	S	51	U
2	S	52	U
2	S	53	U
2	S	54	U
2	S	55	U
2	S	57	U
2	S	59	U
2	S	60	U
2	S	61	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	S	62	U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	R	24	U
2	S	24	U

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.

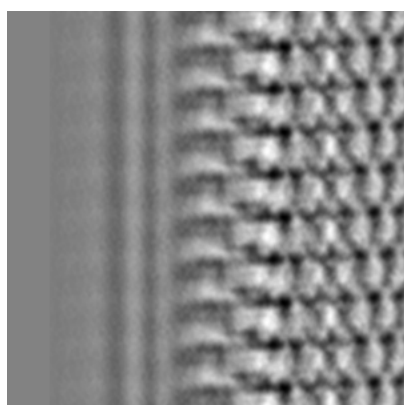
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1663. These allow visual inspection of the internal detail of the map and identification of artifacts.

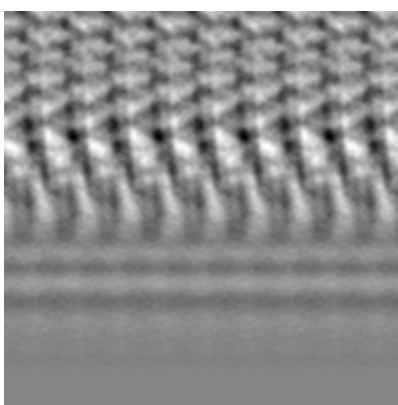
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

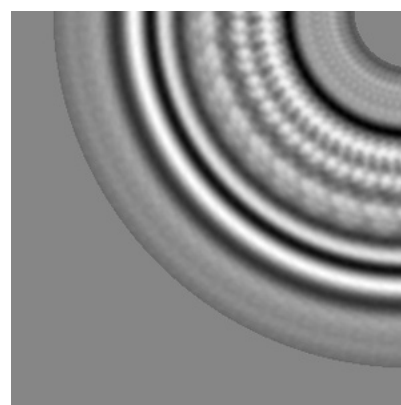
6.1.1 Primary map



X



Y

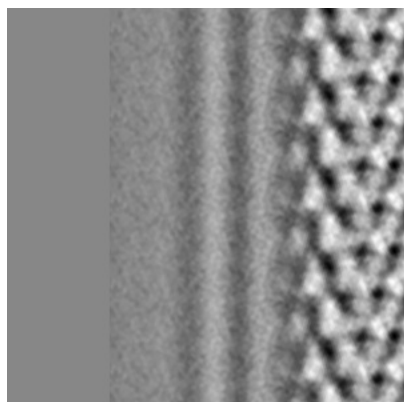


Z

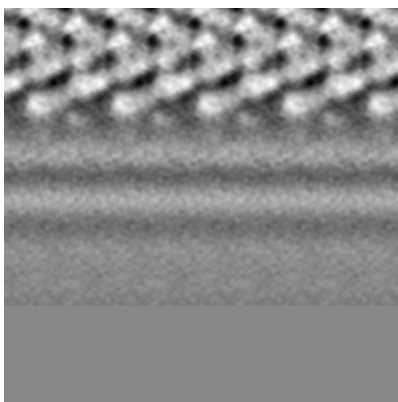
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

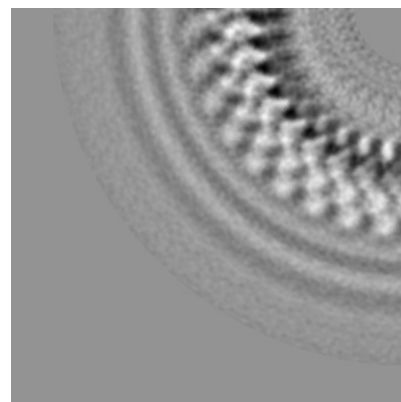
6.2.1 Primary map



X Index: 160



Y Index: 160

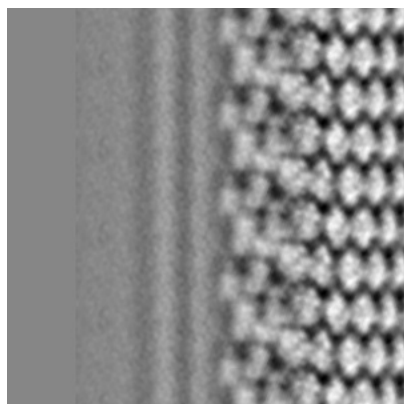


Z Index: 160

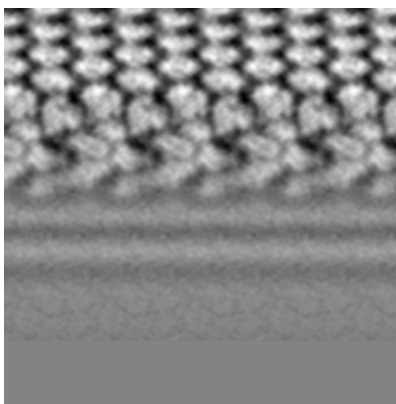
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

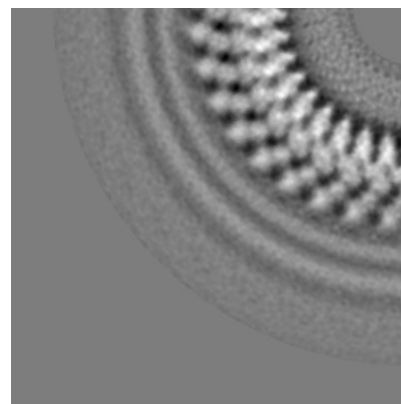
6.3.1 Primary map



X Index: 212



Y Index: 213

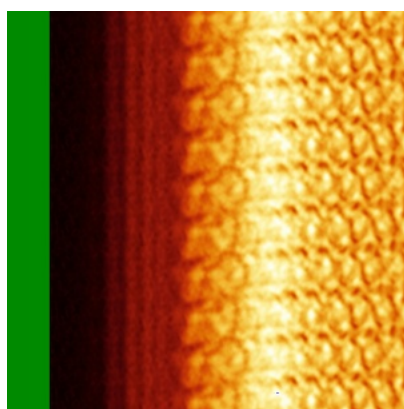


Z Index: 317

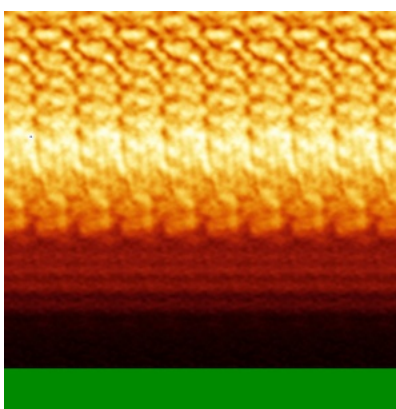
The images above show the largest variance slices of the map in three orthogonal directions.

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

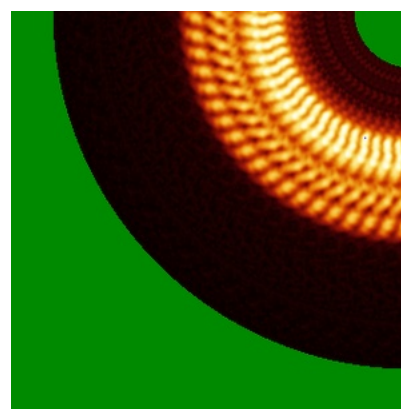
6.4.1 Primary map



X



Y

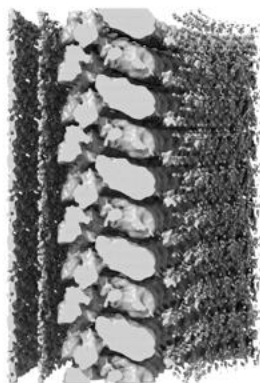


Z

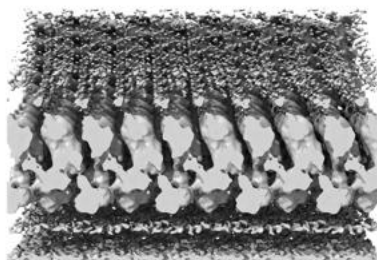
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

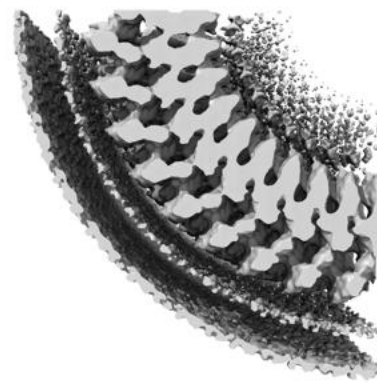
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

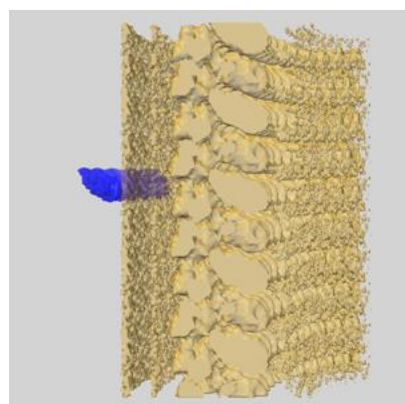
6.6 Mask visualisation [i](#)

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

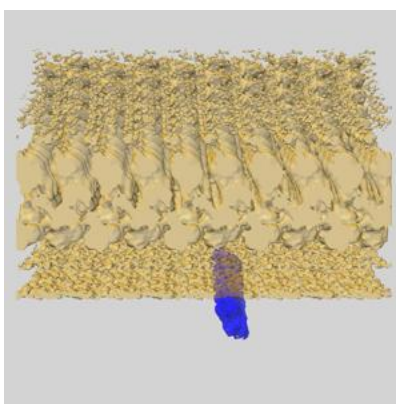
A mask typically either:

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

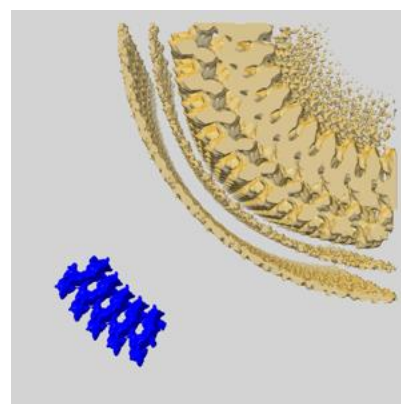
6.6.1 emd_1663_msk_1.map [i](#)



X

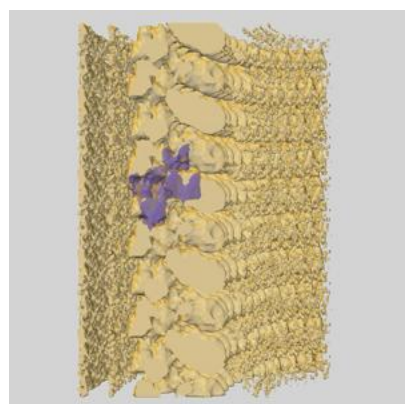


Y

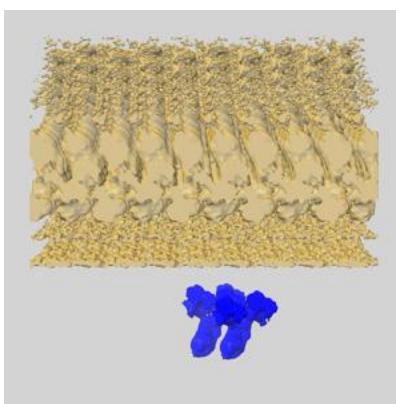


Z

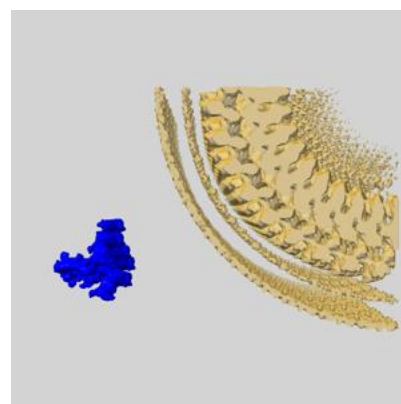
6.6.2 emd_1663_msk_2.map [i](#)



X



Y

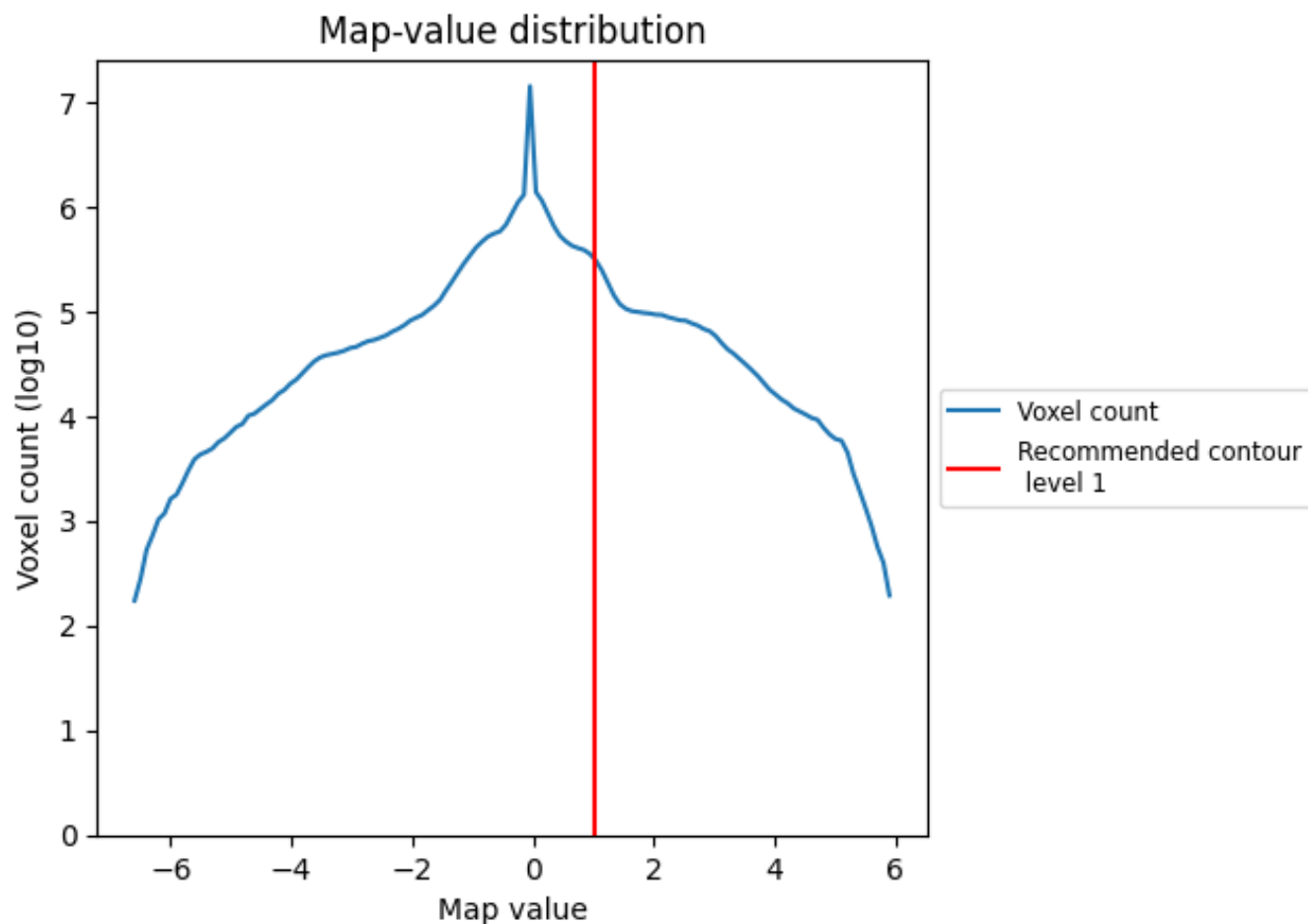


Z

7 Map analysis [i](#)

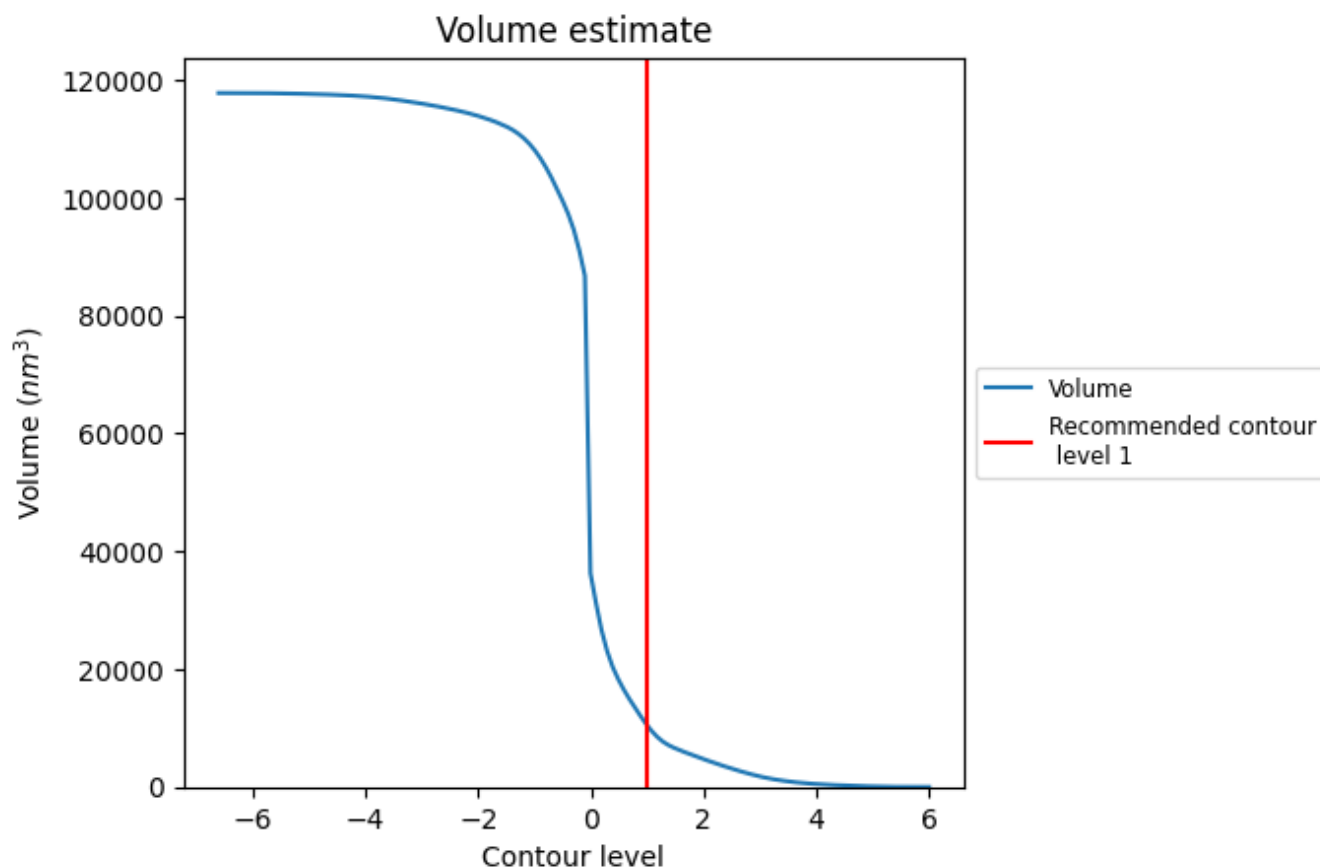
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

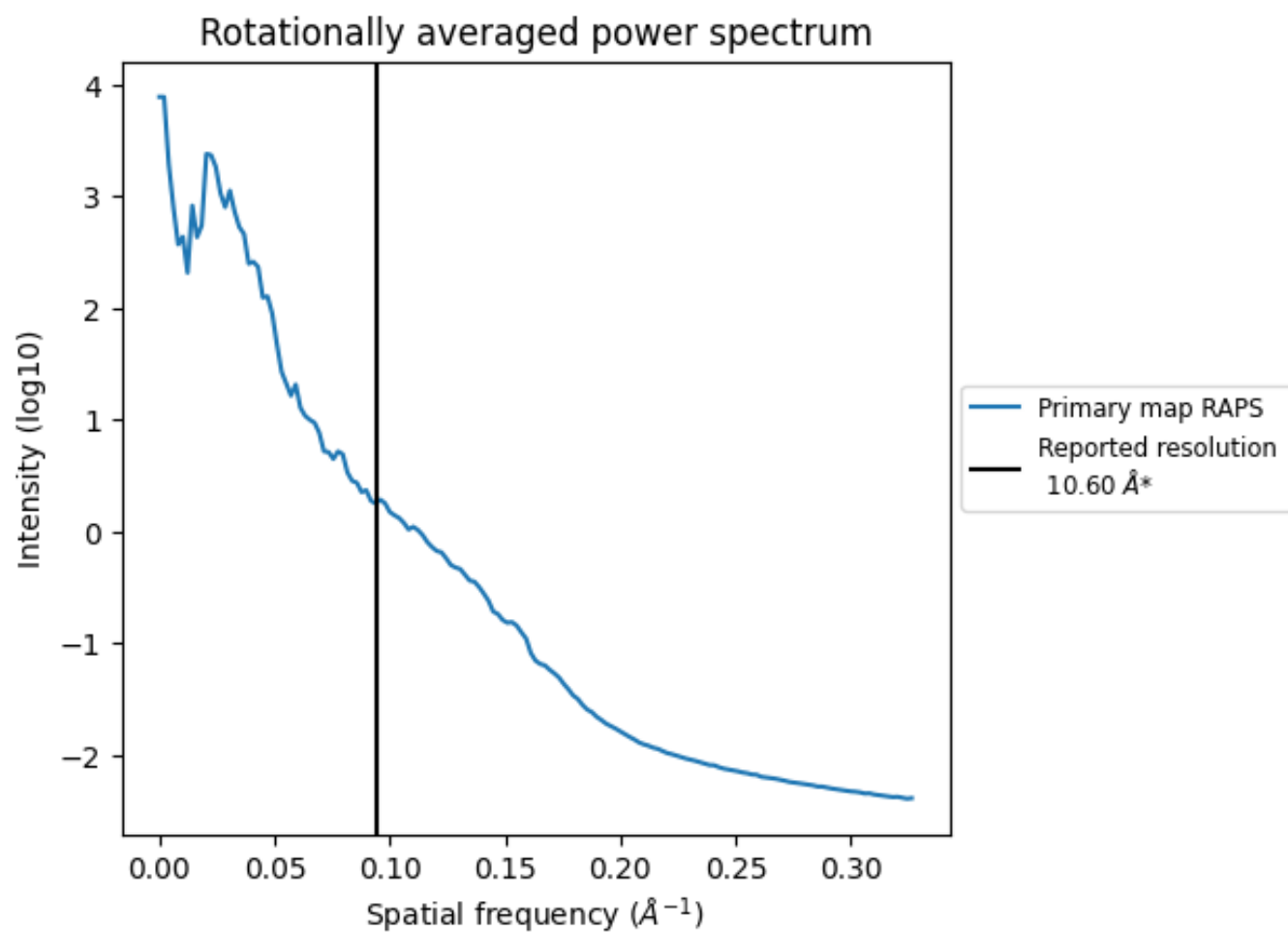
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 10476 nm³; this corresponds to an approximate mass of 9463 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 0.094 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

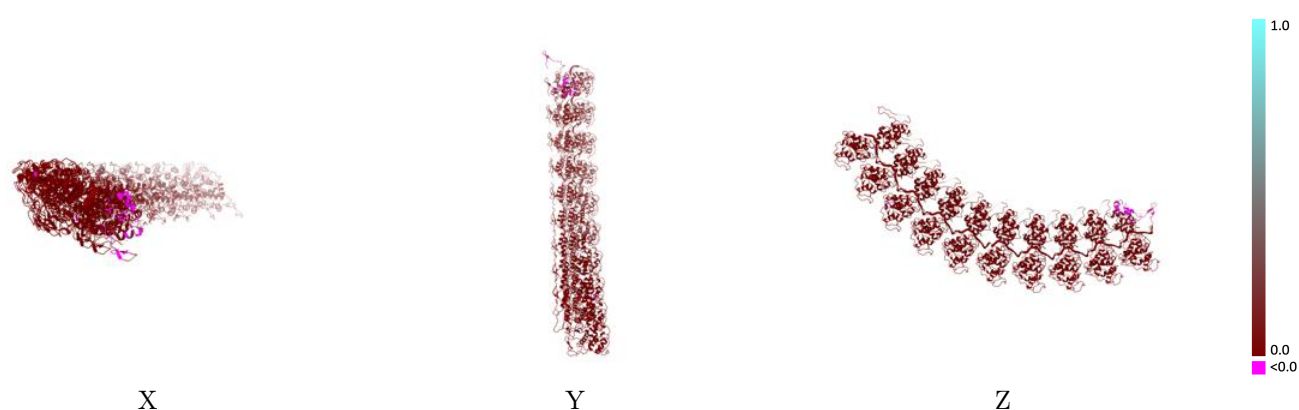
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1663 and PDB model 2WYY. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)

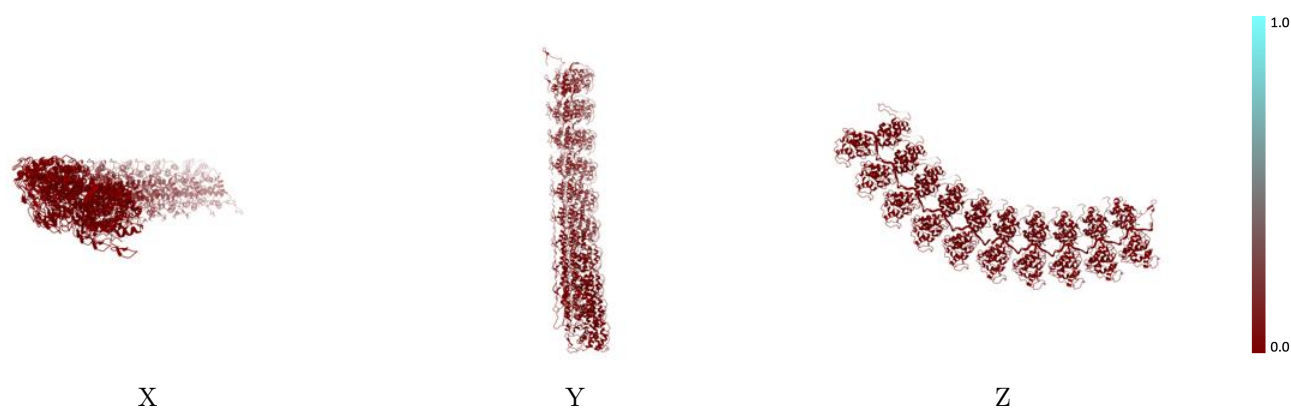
This section was not generated.

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



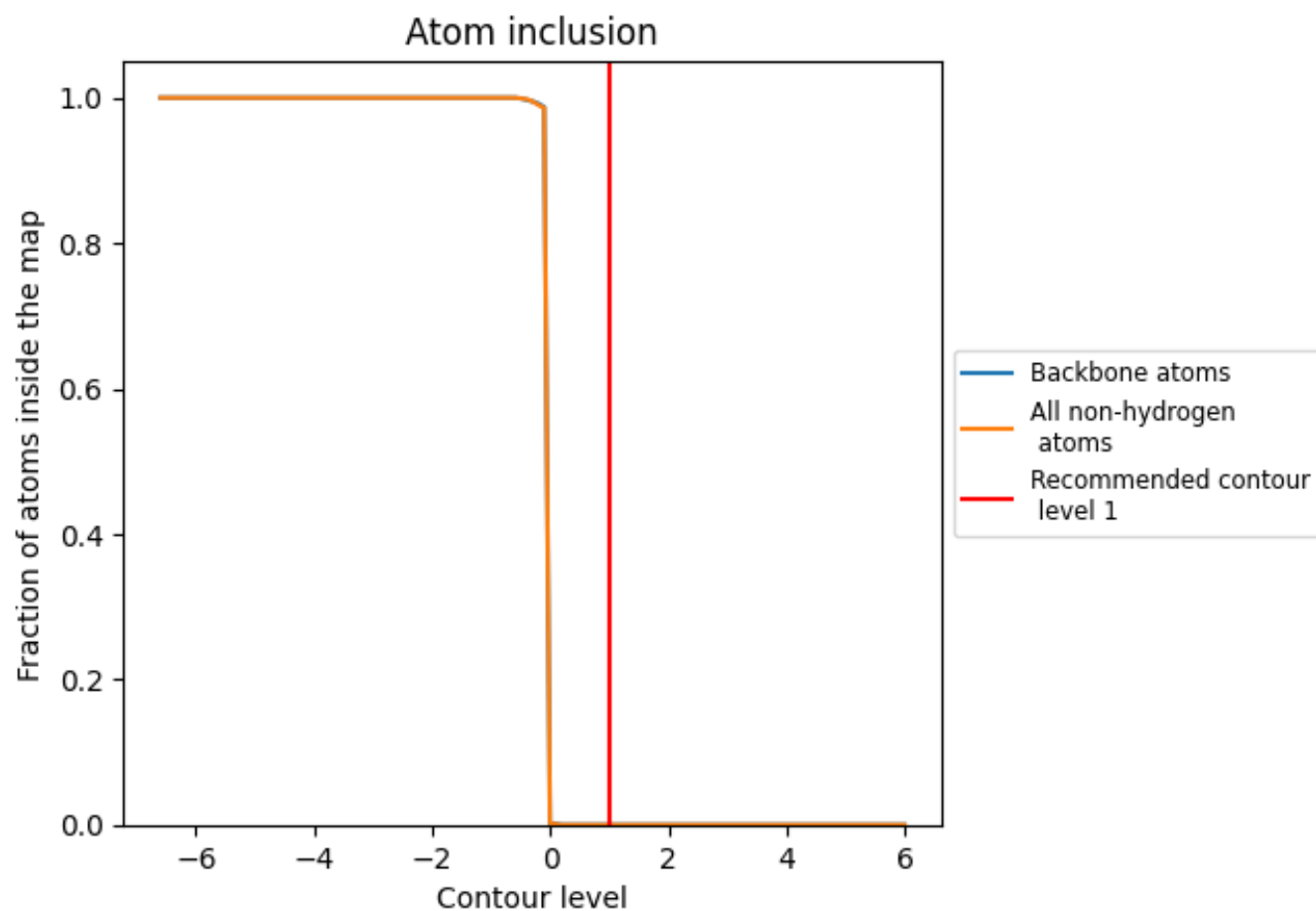
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 0% of all backbone atoms, 0% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.0000	0.0000
A	0.0000	0.0000
C	0.0000	-0.0000
D	0.0000	0.0000
F	0.0000	0.0000
H	0.0000	0.0000
I	0.0000	0.0010
J	0.0000	0.0030
K	0.0000	0.0000
L	0.0000	-0.0000
M	0.0000	0.0000
R	0.0000	0.0000
S	0.0000	0.0010

1.0

0.0

<0.0