



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 07:34 AM UTC

PDB ID : 9H2H / pdb_00009h2h
EMDB ID : EMD-51803
Title : AcMNPV apical cap - composite map of the C2 plug
Authors : Effantin, G.; Kandiah, E.; Pelosse, M.
Deposited on : 2024-10-11
Resolution : 6.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

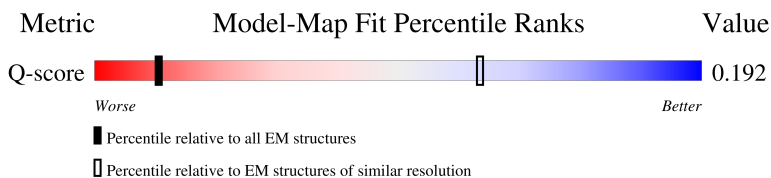
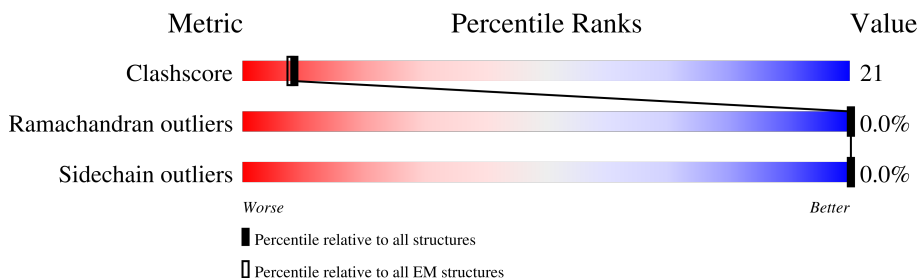
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 6.10 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.



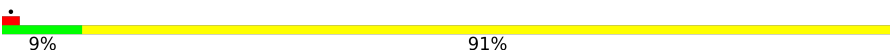
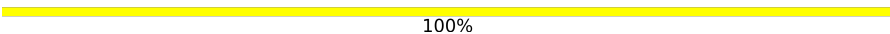
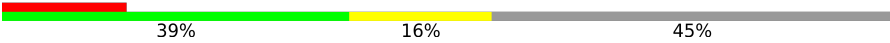
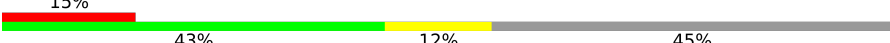
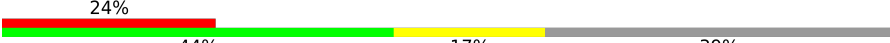
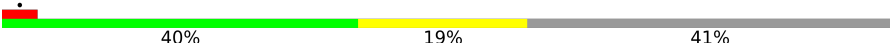
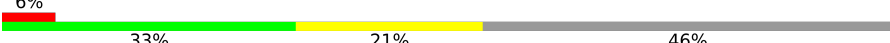
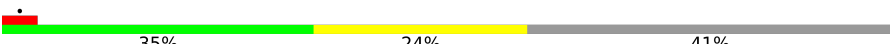
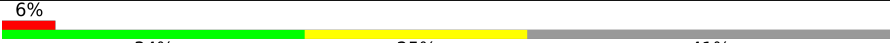
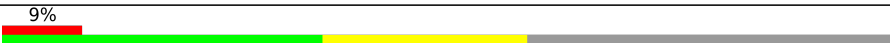
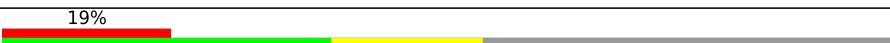
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	531 (5.60 - 6.60)

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	365	 6% 56% 35% 9%
1	B	365	 5% 54% 39% 8%
1	C	365	 1% 52% 37% 11%
1	D	365	 1% 50% 39% 11%

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Mol	Chain	Length	Quality of chain
2	E	58	
3	F	58	
4	G	290	
4	H	290	
4	K	290	
4	L	290	
4	O	290	
4	P	290	
4	S	290	
4	T	290	
5	I	361	
5	J	361	
5	M	361	
5	N	361	
5	Q	361	
5	R	361	
5	U	361	
5	V	361	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 39098 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 Protein AC54.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	332	Total	C	N	O	S	0	0
			2717	1723	479	497	18		
1	B	337	Total	C	N	O	S	0	0
			2757	1752	484	502	19		
1	C	324	Total	C	N	O	S	0	0
			2660	1691	468	483	18		
1	D	325	Total	C	N	O	S	0	0
			2666	1700	469	478	19		

- Molecule 2 is a DNA chain called DNA (58-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	58	Total	C	N	O	P	0	0
			1198	574	233	333	58		

- Molecule 3 is a DNA chain called DNA (58-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	58	Total	C	N	O	P	0	0
			1177	573	186	361	57		

- Molecule 4 is a protein called Occlusion-derived virus envelope protein E27.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	240	Total	C	N	O	S	0	0
			1941	1247	312	373	9		
4	H	160	Total	C	N	O	S	0	0
			1301	844	215	234	8		
4	K	228	Total	C	N	O	S	0	0
			1850	1191	296	354	9		
4	L	130	Total	C	N	O	S	0	0
			1061	692	172	190	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	O	238	Total	C	N	O	S	0	0
			1926	1238	309	370	9		
4	P	160	Total	C	N	O	S	0	0
			1302	847	212	235	8		
4	S	222	Total	C	N	O	S	0	0
			1805	1164	284	349	8		
4	T	178	Total	C	N	O	S	0	0
			1440	938	234	260	8		

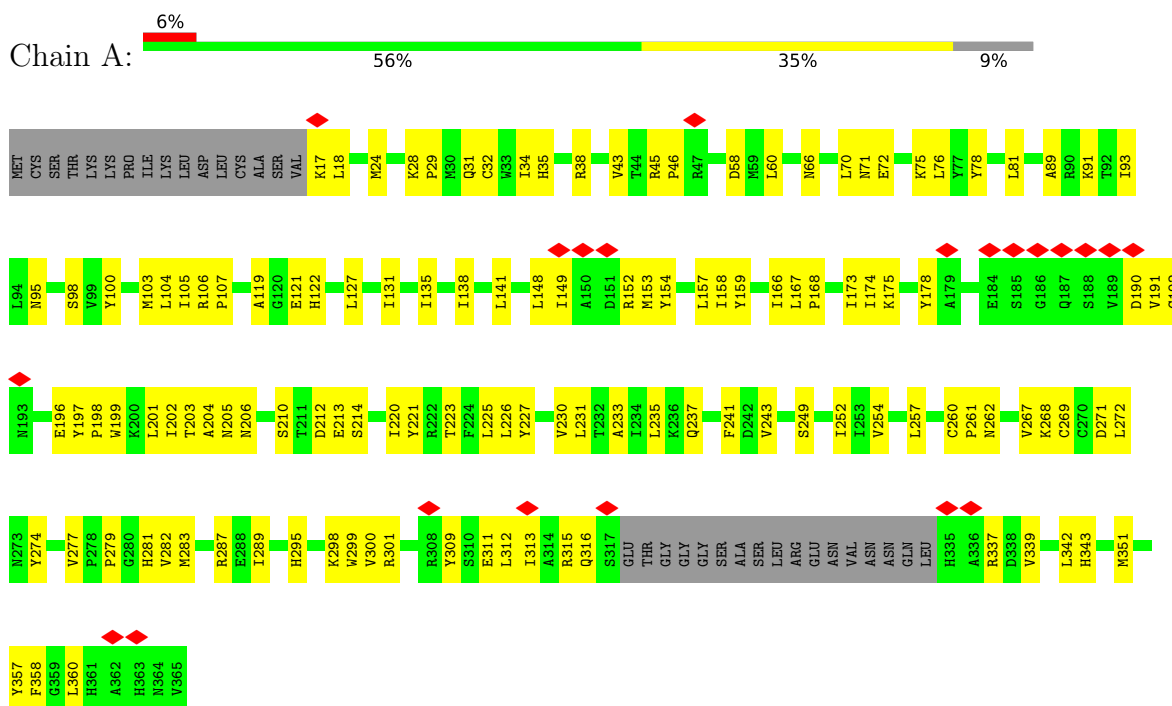
- Molecule 5 is a protein called Protein C42.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	213	Total	C	N	O	S	0	0
			1760	1117	296	331	16		
5	J	194	Total	C	N	O	S	0	0
			1622	1033	275	301	13		
5	M	213	Total	C	N	O	S	0	0
			1760	1117	296	331	16		
5	N	181	Total	C	N	O	S	0	0
			1517	966	257	282	12		
5	Q	213	Total	C	N	O	S	0	0
			1760	1117	296	331	16		
5	R	178	Total	C	N	O	S	0	0
			1488	943	253	279	13		
5	U	213	Total	C	N	O	S	0	0
			1760	1117	296	331	16		
5	V	196	Total	C	N	O	S	0	0
			1630	1036	276	306	12		

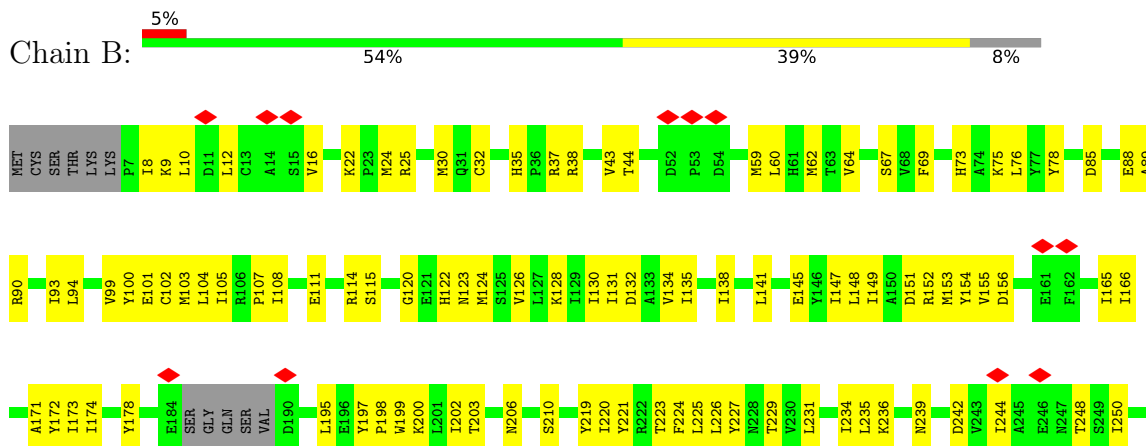
3 Residue-property plots

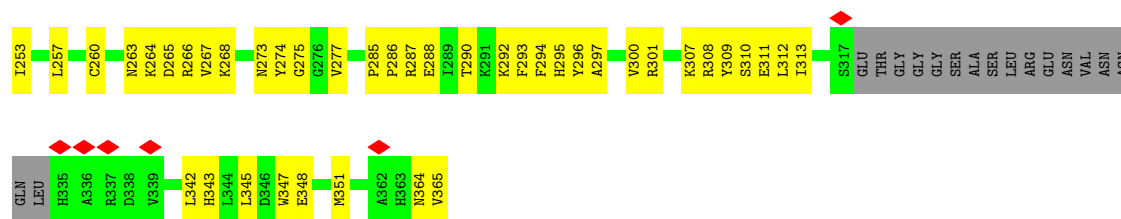
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Protein AC54



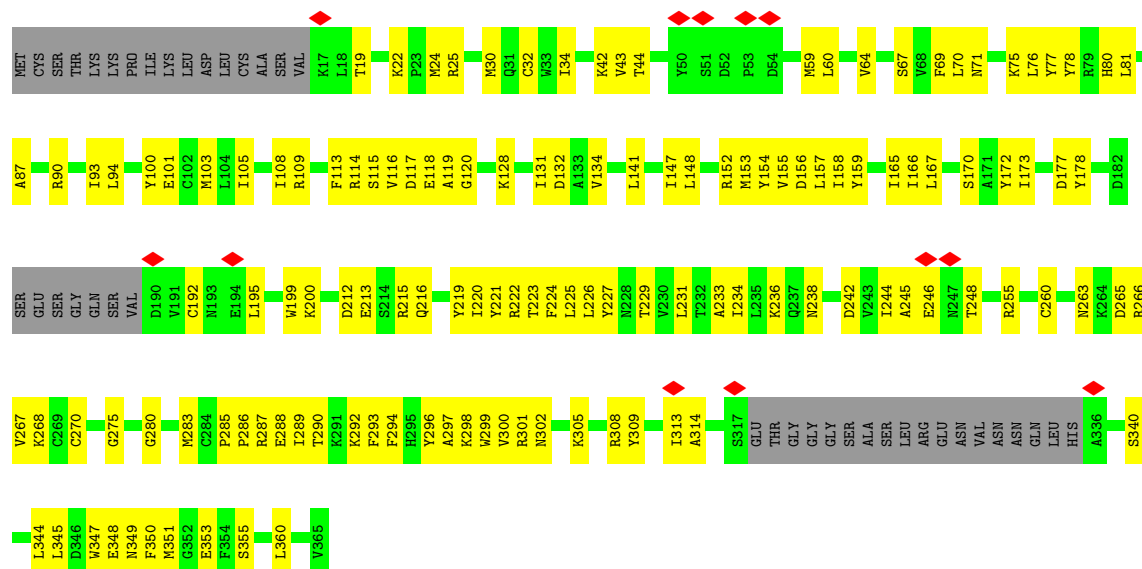
• Molecule 1: Protein AC54





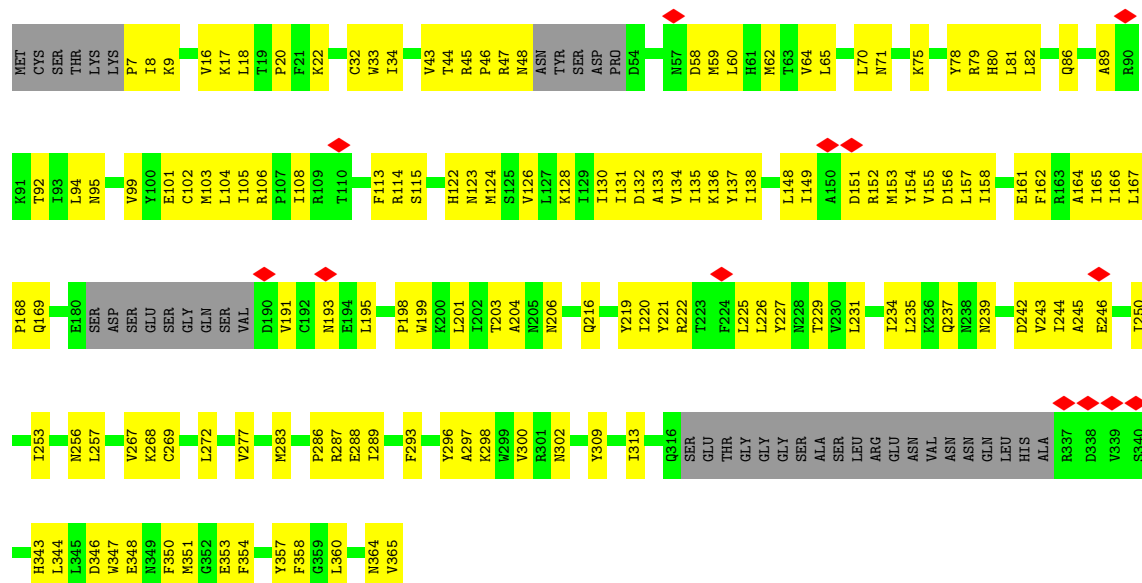
• Molecule 1: Protein AC54

Chain C: 52% 37% 11%



• Molecule 1: Protein AC54

Chain D: 50% 39% 11%

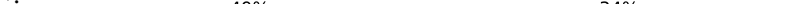


• Molecule 2: DNA (58-MER)

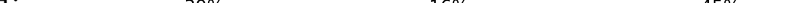
T1	A2	T3	T4	C5	C6	A7	A8	A9	C10	G11	T12	T13	A14	A15	A16	A17	C18	C19	T20	T21	T22	G25	A26	G27	A28	A29	G30	T31	A32	A33	A34	A35	C36	A37	A38	A39	A40	A41	A42	A43	A44	A45	T46	T47	T48	A49	A50	T51	T52	A53	A54	A55	T56	G57	A58
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- Chain F: 100%

C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15	C16	C17	C18	C19	C20	C21	C22	C23	C24	C25	C26	C27	C28	C29	C30	C31	C32	C33	C34	C35	C36	C37	C38	C39	C40	C41	C42	C43	C44	C45	C46	C47	C48	C49	C50	C51	C52	C53	C54	C55	C56	C57	C58	C59	C60	C61	C62	C63	C64	C65	C66	C67	C68	C69	C70	C71	C72	C73	C74	C75	C76	C77	C78	C79	C80	C81	C82	C83	C84	C85	C86	C87	C88	C89	C90	C91	C92	C93	C94	C95	C96	C97	C98	C99	C100
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- Chain G: 

[illegible]

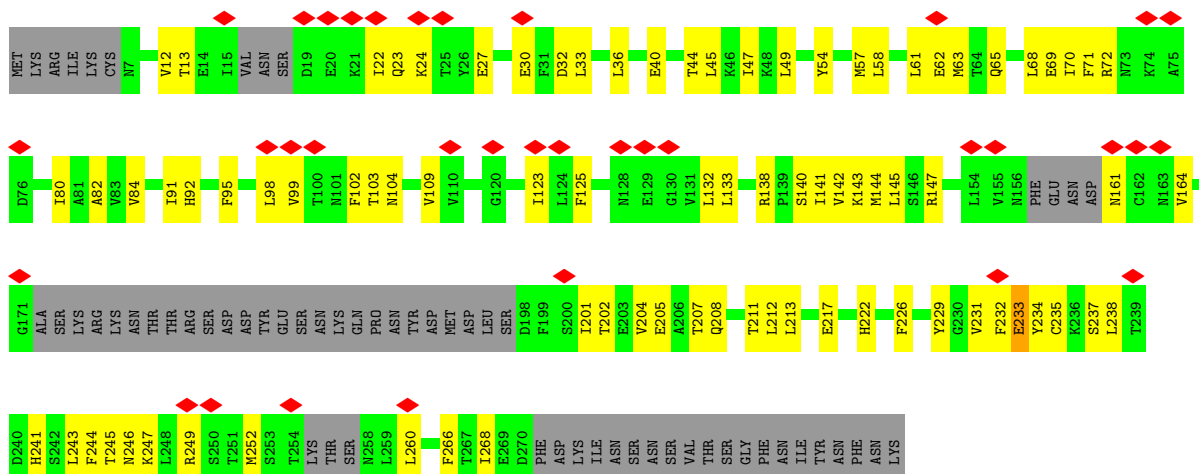
- Chain H: 

[illegible]

PHE
ASN
ILE
TYR
ASN
PHE
ASN
LYS

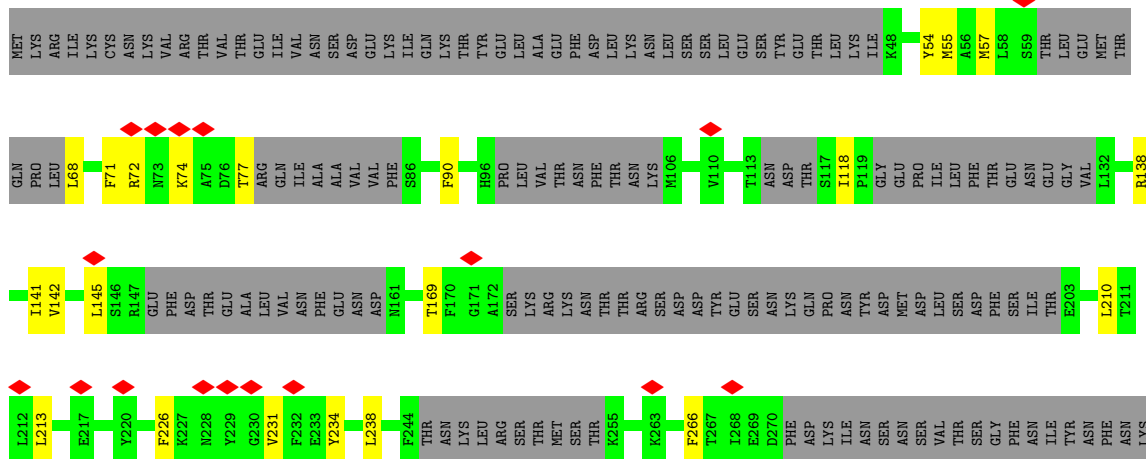
• Molecule 4: Occlusion-derived virus envelope protein E27

Chain K: 12% 50% 29% 21%



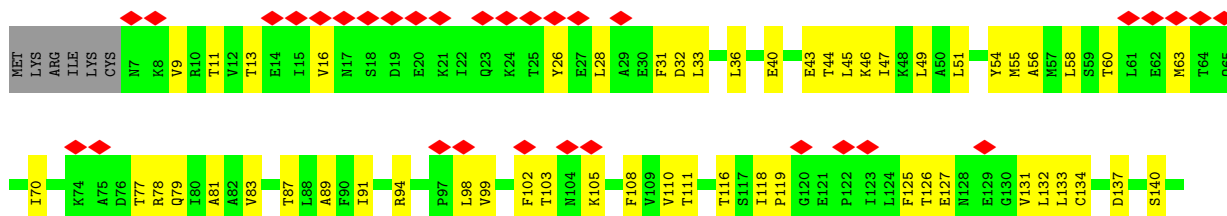
• Molecule 4: Occlusion-derived virus envelope protein E27

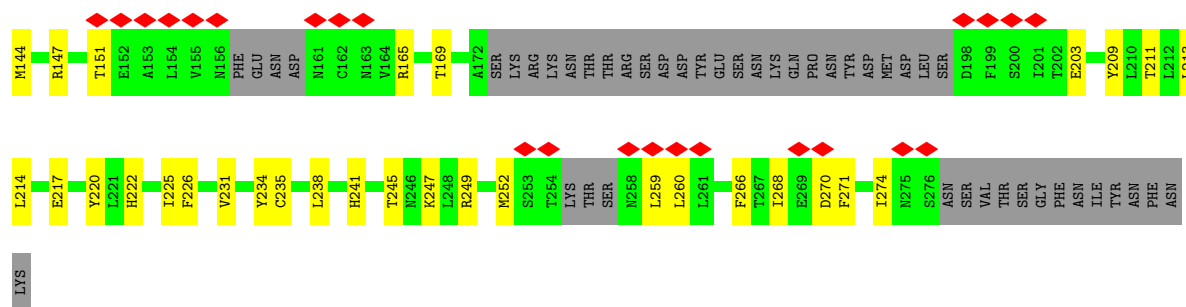
Chain L: 6% 37% 8% 55%



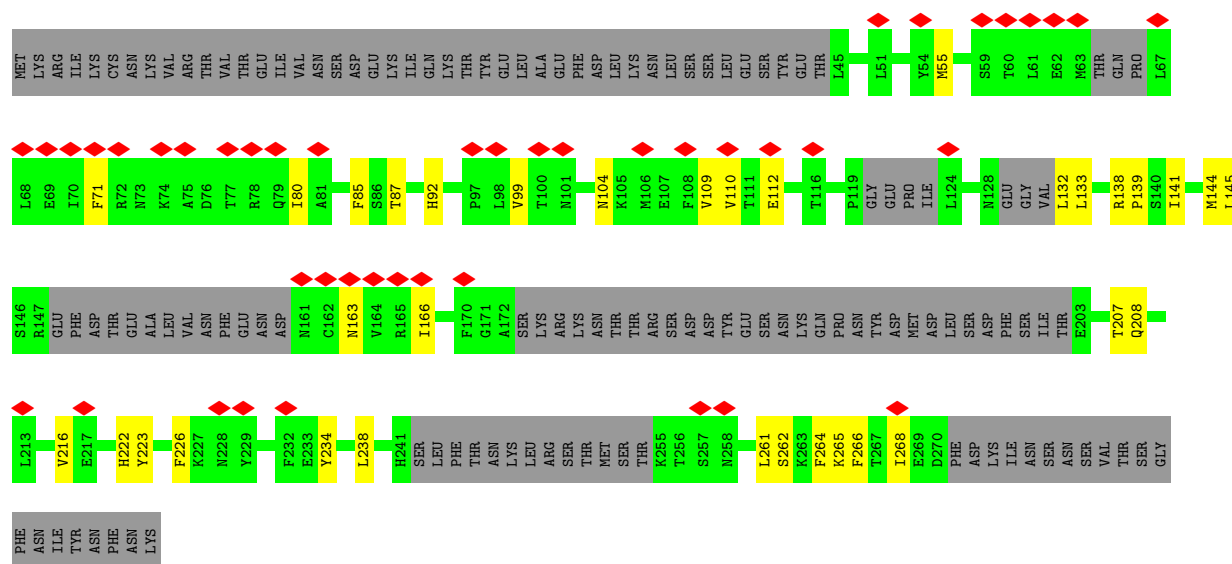
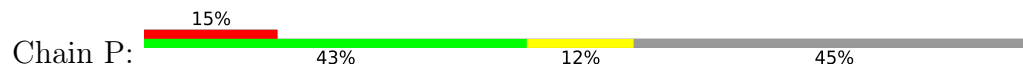
• Molecule 4: Occlusion-derived virus envelope protein E27

Chain O: 19% 53% 29% 18%

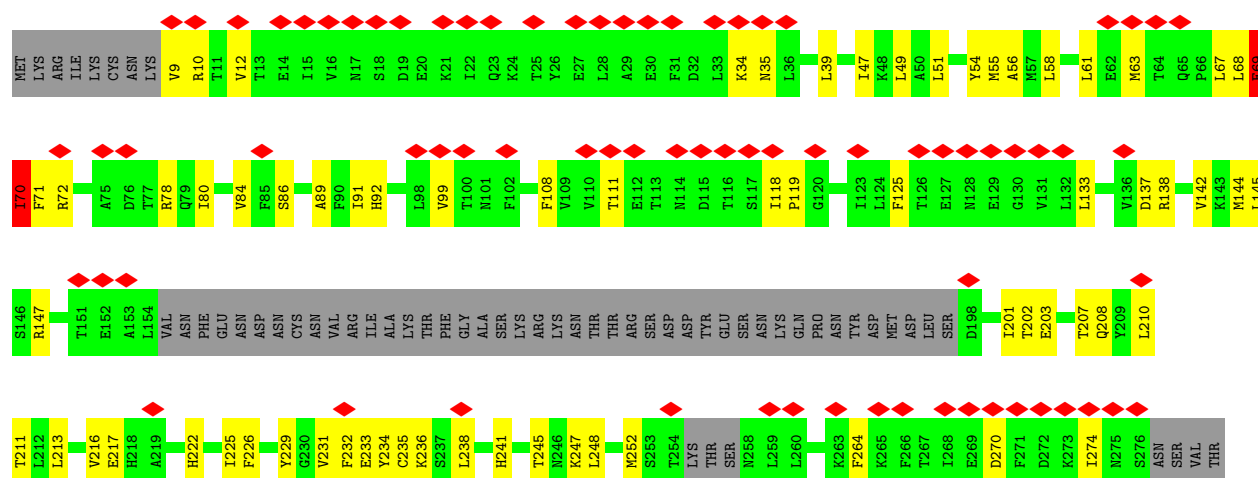


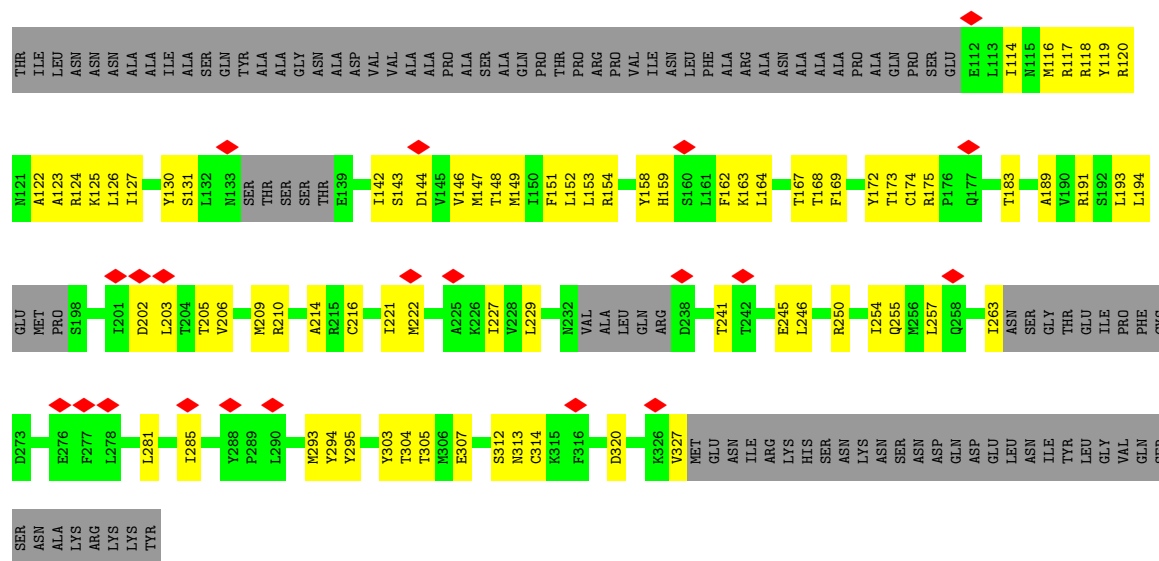


• Molecule 4: Occlusion-derived virus envelope protein E27



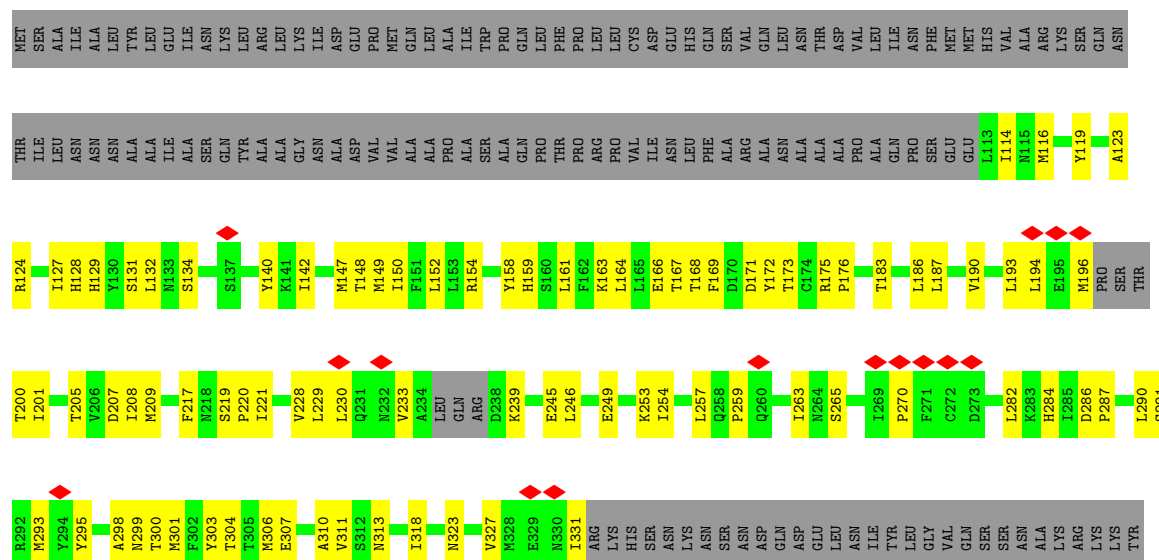
• Molecule 4: Occlusion-derived virus envelope protein E27





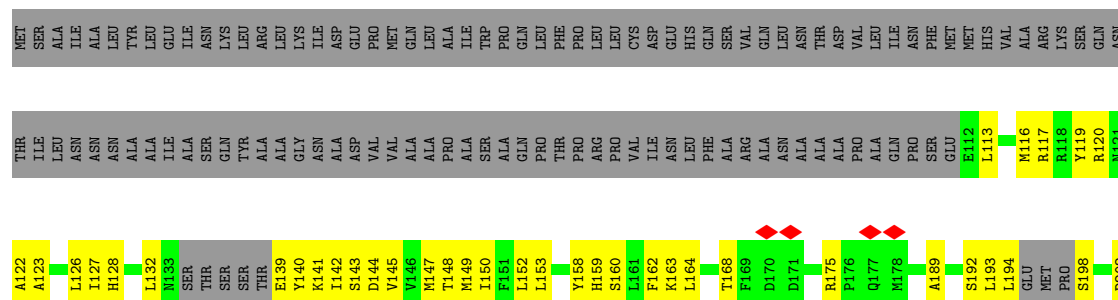
• Molecule 5: Protein C42

Chain M: 35% 24% 41%

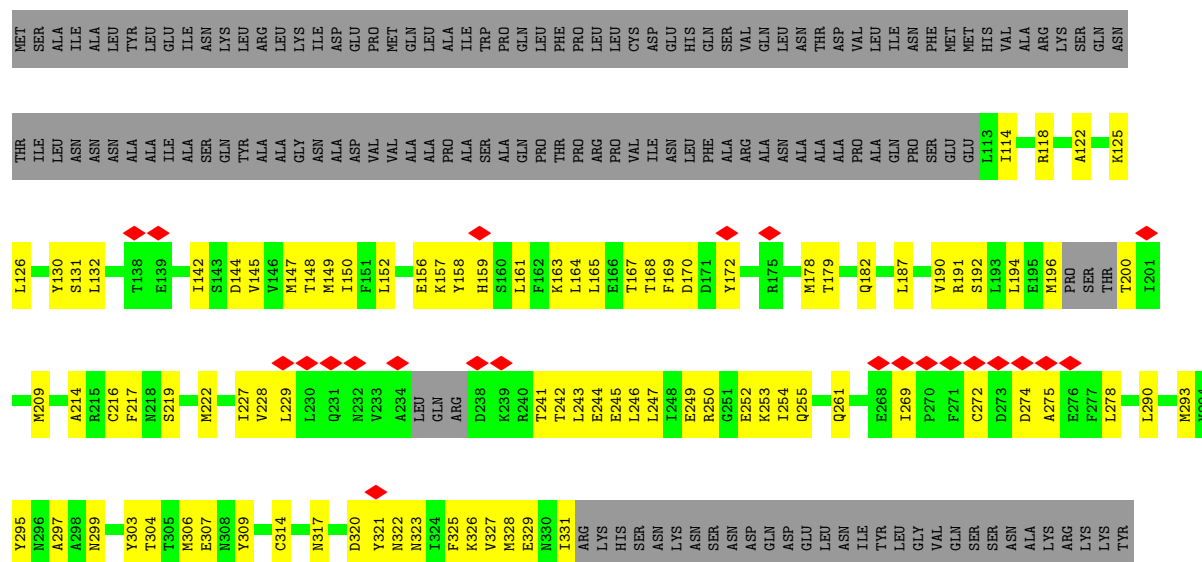
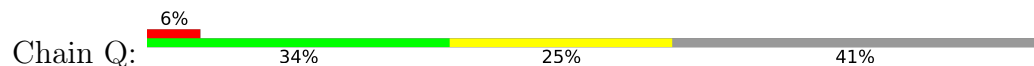


• Molecule 5: Protein C42

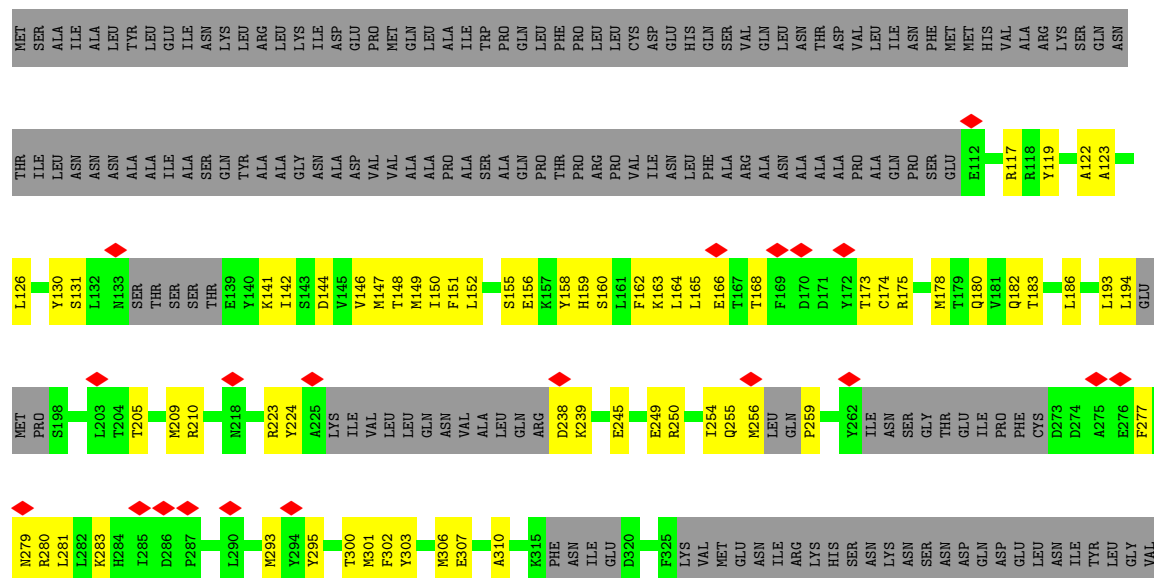
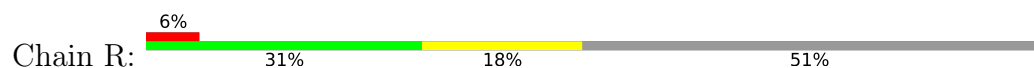
Chain N: 6% 33% 17% 50%



- Molecule 5: Protein C42



- Molecule 5: Protein C42



GLN
SER
SER
SER
ALA
LYS
LYS
ARG
LYS
TYR

● Molecule 5: Protein C42



MET
SER
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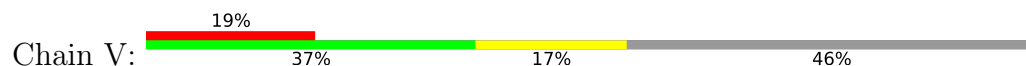
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E195
M196
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THR
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M209
R210
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S219
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M222
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Y224
A225
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I227
V228
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L230
A234
LEU
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L243
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E245
L246
E249
R250
G251
E252
K253
Q254
Q255
P259
Q260
Q261
Y262
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I269
P270
F271
C272
D273
E277
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A297
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● Molecule 5: Protein C42



MET
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Y119
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I127
H128
H129

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S136
S137
T138
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L164
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E166
T167
T168
F169
D170
P176
GLN
MET
THR
Q180
L187
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A189
V190
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M232
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L246
L247
I248
E249
R250
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N279
R280
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H284
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P287
Y288
P289
L290
S291
T300
M301
F302
M306
E307
V311
C314
K315
F316
N317
I318
E319
D320
Y321
I324
F325
K326
V327
MET
GLU
ILE
ARG
LYS
HIS
SER
ASN
LYS
ASN
ASN
SER
SER
ASN
ASP
GLN
ASP
LEU
GLU
ASN
ILE
TYR
LEU
GLY
VAL

GLN
SER
SER
SER
ALA
LYS
ARG
LYS
TYR

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12477	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.027	Depositor
Minimum map value	-0.007	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0065	Depositor
Map size (Å)	405.0, 405.0, 405.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.15	0/2783	0.37	0/3772
1	B	0.16	0/2823	0.37	0/3825
1	C	0.16	0/2724	0.41	0/3691
1	D	0.17	0/2728	0.42	0/3693
2	E	0.19	0/1350	0.34	0/2081
3	F	0.19	0/1313	0.40	0/2025
4	G	0.14	0/1973	0.34	0/2664
4	H	0.13	0/1321	0.32	0/1774
4	K	0.16	0/1880	0.42	2/2538 (0.1%)
4	L	0.11	0/1076	0.25	0/1439
4	O	0.15	0/1958	0.37	0/2645
4	P	0.13	0/1322	0.31	0/1778
4	S	0.17	0/1837	0.40	2/2484 (0.1%)
4	T	0.12	0/1464	0.29	0/1972
5	I	0.14	0/1790	0.35	0/2415
5	J	0.16	0/1648	0.36	0/2219
5	M	0.16	0/1790	0.38	0/2415
5	N	0.14	0/1539	0.37	0/2065
5	Q	0.17	0/1790	0.40	0/2415
5	R	0.14	0/1511	0.36	0/2030
5	U	0.16	0/1790	0.35	0/2415
5	V	0.12	0/1656	0.30	0/2231
All	All	0.15	0/40066	0.37	4/54586 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	K	233	GLU	CA-C-N	-5.48	112.51	120.29
4	K	233	GLU	C-N-CA	-5.48	112.51	120.29
4	S	69	GLU	N-CA-C	-5.43	106.49	113.23
4	S	70	ILE	N-CA-C	-5.34	104.20	111.89

There are no chirality outliers.

There are no planarity outliers.

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	2717	0	2673	112	0
1	B	2757	0	2724	139	0
1	C	2660	0	2624	124	0
1	D	2666	0	2655	135	0
2	E	1198	0	654	113	0
3	F	1177	0	670	156	0
4	G	1941	0	1954	114	0
4	H	1301	0	1330	46	0
4	K	1850	0	1862	84	0
4	L	1061	0	1072	20	0
4	O	1926	0	1936	86	0
4	P	1302	0	1328	27	0
4	S	1805	0	1811	72	0
4	T	1440	0	1476	46	0
5	I	1760	0	1756	74	0
5	J	1622	0	1623	89	0
5	M	1760	0	1756	84	0
5	N	1517	0	1507	65	0
5	Q	1760	0	1756	89	0
5	R	1488	0	1469	74	0
5	U	1760	0	1756	92	0
5	V	1630	0	1628	65	0
All	All	39098	0	38020	1633	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 21.

All (1633) 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)
4:K:47:ILE:HD12	4:K:260:LEU:HD12	1.46	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:220:ILE:HD11	1:C:313:ILE:HG21	1.43	0.96
5:V:152:LEU:HD12	5:V:161:LEU:HD11	1.57	0.85
4:G:248:LEU:HD12	4:G:252:MET:HB2	1.59	0.85
4:O:54:TYR:OH	4:O:87:THR:HG22	1.78	0.83
3:F:21:DT:H2''	3:F:22:DT:H71	1.60	0.82
1:A:269:CYS:HA	1:A:272:LEU:HD23	1.62	0.80
1:B:348:GLU:HA	1:B:351:MET:HE2	1.62	0.80
3:F:5:DT:H2'	3:F:6:DT:C6	2.17	0.79
1:C:305:LYS:HD2	3:F:15:DT:H3'	1.63	0.79
3:F:4:DT:H2'	3:F:5:DT:C6	2.17	0.79
4:S:245:THR:OG1	5:U:327:VAL:HG22	1.82	0.79
5:R:160:SER:HB2	5:R:186:LEU:HD11	1.66	0.78
3:F:18:DT:H2''	3:F:19:DT:OP2	1.81	0.78
4:T:145:LEU:HD12	4:T:208:GLN:HG3	1.64	0.78
1:D:34:ILE:HG21	1:D:158:ILE:HD12	1.65	0.77
3:F:10:DT:H1'	3:F:11:DA:O5'	1.84	0.77
5:U:168:THR:HG22	5:U:210:ARG:HG3	1.67	0.77
4:S:226:PHE:CE1	4:S:231:VAL:HG22	2.20	0.77
1:B:126:VAL:O	1:B:130:ILE:HD12	1.85	0.76
3:F:30:DT:H2''	3:F:31:DT:H72	1.67	0.76
5:M:171:ASP:O	5:M:173:THR:HG23	1.86	0.76
1:A:32:CYS:HA	1:A:43:VAL:HG12	1.68	0.76
5:Q:144:ASP:O	5:Q:148:THR:HG23	1.85	0.76
1:C:156:ASP:HB3	1:C:167:LEU:HD12	1.66	0.76
4:S:144:MET:SD	5:U:300:THR:HG22	2.26	0.76
3:F:21:DT:C2'	3:F:22:DT:H71	2.15	0.76
5:M:228:VAL:HG22	5:N:223:ARG:O	1.86	0.76
3:F:33:DT:H2'	3:F:34:DC:C6	2.21	0.75
5:U:149:MET:HE1	5:V:150:ILE:HD11	1.68	0.75
3:F:20:DT:H1'	3:F:21:DT:O5'	1.86	0.75
2:E:50:DA:H1'	2:E:51:DT:O5'	1.86	0.75
4:H:70:ILE:HG21	4:H:79:GLN:OE1	1.86	0.75
4:G:57:MET:HE1	4:G:86:SER:HB2	1.69	0.75
4:K:132:LEU:HD21	4:K:226:PHE:CE2	2.21	0.74
2:E:6:DC:H2''	2:E:7:DA:OP2	1.85	0.74
1:D:43:VAL:HG23	1:D:59:MET:HE1	1.70	0.74
3:F:33:DT:H2''	3:F:34:DC:C5'	2.18	0.74
1:A:72:GLU:OE2	1:B:93:ILE:HG23	1.88	0.74
1:C:32:CYS:HA	1:C:43:VAL:HG12	1.68	0.73
3:F:19:DT:H2''	3:F:20:DT:OP2	1.85	0.73
1:C:308:ARG:CD	3:F:15:DT:H5''	2.17	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:17:DT:H2''	3:F:18:DT:OP2	1.85	0.73
4:K:266:PHE:CE1	5:N:229:LEU:HD22	2.23	0.73
1:D:148:LEU:HB3	1:D:300:VAL:HG12	1.70	0.73
2:E:6:DC:H1'	2:E:7:DA:O5'	1.89	0.73
5:Q:164:LEU:O	5:Q:168:THR:HG23	1.87	0.72
3:F:49:DG:H2'	3:F:49:DG:OP2	1.89	0.72
4:H:87:THR:HG21	4:H:216:VAL:HG11	1.72	0.72
4:K:245:THR:OG1	5:M:327:VAL:HG22	1.89	0.72
1:B:147:ILE:HD11	1:B:171:ALA:HB1	1.70	0.72
5:J:126:LEU:HD22	5:J:148:THR:HG21	1.70	0.72
3:F:1:DC:H1'	3:F:2:DC:O4'	1.90	0.72
5:R:130:TYR:C	5:R:209:MET:HE1	2.15	0.71
3:F:37:DA:H1'	3:F:38:DA:H5'	1.72	0.71
1:B:141:LEU:HD11	1:B:145:GLU:O	1.91	0.71
3:F:45:DT:H1'	3:F:46:DA:H5'	1.72	0.71
5:N:290:LEU:HD11	5:N:294:TYR:CZ	2.25	0.71
1:C:157:LEU:HB3	1:C:166:ILE:HD12	1.73	0.71
3:F:46:DA:H1'	3:F:47:DA:O5'	1.91	0.70
3:F:57:DT:H2''	3:F:58:DA:OP2	1.89	0.70
5:M:124:ARG:HE	5:M:193:LEU:HD12	1.55	0.70
2:E:43:DA:H2''	2:E:44:DA:OP2	1.90	0.70
2:E:52:DT:H1'	2:E:53:DA:O5'	1.92	0.70
3:F:42:DT:H2''	3:F:43:DT:OP2	1.90	0.70
1:B:128:LYS:HA	1:B:131:ILE:HG12	1.72	0.70
3:F:4:DT:H2'	3:F:5:DT:H6	1.55	0.70
5:Q:172:TYR:CD2	5:Q:214:ALA:HB1	2.27	0.70
2:E:30:DG:H2''	2:E:31:DT:OP2	1.91	0.70
2:E:52:DT:H2''	2:E:53:DA:OP2	1.92	0.70
1:B:231:LEU:O	1:B:235:LEU:HD23	1.92	0.70
1:C:220:ILE:CD1	1:C:313:ILE:HG21	2.18	0.70
3:F:17:DT:H1'	3:F:18:DT:O5'	1.92	0.69
3:F:41:DG:H1'	3:F:42:DT:O5'	1.92	0.69
5:V:164:LEU:O	5:V:168:THR:HG23	1.91	0.69
5:R:144:ASP:O	5:R:148:THR:HG23	1.92	0.69
5:M:163:LYS:O	5:M:167:THR:HG23	1.91	0.69
4:K:231:VAL:HA	4:K:234:TYR:CE1	2.28	0.69
4:O:54:TYR:CE2	4:O:58:LEU:HD11	2.28	0.69
5:R:152:LEU:CD2	5:R:165:LEU:HD12	2.23	0.69
5:I:323:ASN:O	5:I:327:VAL:HG23	1.92	0.69
3:F:5:DT:H2'	3:F:6:DT:H6	1.57	0.68
4:O:11:THR:HG22	4:P:268:ILE:HG23	1.73	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:45:LEU:O	4:O:49:LEU:HD23	1.93	0.68
4:K:138:ARG:O	4:K:142:VAL:HG23	1.93	0.68
5:Q:149:MET:HE1	5:R:150:ILE:HD11	1.76	0.68
1:A:119:ALA:HB1	1:A:159:TYR:OH	1.93	0.68
2:E:27:DG:H2''	2:E:28:DA:C8	2.28	0.68
5:U:183:THR:HG23	5:U:203:LEU:HD11	1.75	0.68
4:G:67:LEU:HD12	4:G:212:LEU:HD11	1.75	0.68
5:I:127:ILE:HD13	5:I:193:LEU:HD22	1.76	0.68
3:F:35:DC:H1'	3:F:36:DT:O5'	1.94	0.67
5:Q:126:LEU:HD11	5:Q:130:TYR:CE2	2.29	0.67
4:T:45:LEU:HD23	4:T:48:LYS:HE2	1.74	0.67
1:D:113:PHE:HB3	1:D:158:ILE:HG12	1.76	0.67
2:E:10:DC:H1'	2:E:11:DG:O5'	1.94	0.67
3:F:44:DT:H2''	3:F:45:DT:OP2	1.95	0.67
4:K:145:LEU:HD22	4:K:208:GLN:CG	2.25	0.67
4:O:83:VAL:O	4:O:87:THR:HG23	1.95	0.67
3:F:14:DT:H2''	3:F:15:DT:H71	1.77	0.67
3:F:29:DC:H1'	3:F:30:DT:O5'	1.95	0.67
5:M:323:ASN:O	5:M:327:VAL:HG23	1.94	0.67
3:F:29:DC:C2'	3:F:30:DT:H71	2.25	0.67
3:F:37:DA:H1'	3:F:38:DA:C5'	2.24	0.67
5:M:142:ILE:HD12	5:N:216:CYS:O	1.94	0.67
4:S:35:ASN:O	4:S:39:LEU:HD23	1.95	0.67
4:S:241:HIS:O	5:U:327:VAL:HG21	1.95	0.67
5:U:290:LEU:HA	5:U:293:MET:HE2	1.75	0.67
4:S:61:LEU:HB2	4:S:63:MET:HE1	1.76	0.67
1:A:311:GLU:HB2	1:A:315:ARG:HE	1.60	0.66
2:E:47:DT:H1'	2:E:48:DT:O5'	1.94	0.66
3:F:6:DT:H2''	3:F:7:DA:C8	2.29	0.66
5:Q:168:THR:HB	5:Q:214:ALA:HB2	1.75	0.66
5:U:146:VAL:HG13	5:V:149:MET:HE3	1.74	0.66
4:G:245:THR:OG1	5:I:327:VAL:HG22	1.95	0.66
5:U:149:MET:HE3	5:V:146:VAL:HG13	1.76	0.66
4:T:87:THR:HB	4:T:216:VAL:HG11	1.78	0.66
1:A:221:TYR:O	1:A:225:LEU:HD23	1.95	0.66
2:E:51:DT:H2''	2:E:52:DT:OP2	1.94	0.66
5:U:144:ASP:O	5:U:148:THR:HG23	1.95	0.66
1:C:154:TYR:HB2	1:C:229:THR:HG22	1.76	0.66
1:D:33:TRP:CE3	1:D:43:VAL:HG11	2.30	0.66
4:G:138:ARG:O	4:G:142:VAL:HG23	1.96	0.66
5:I:144:ASP:O	5:I:148:THR:HG23	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:47:ILE:HD12	4:K:260:LEU:CD1	2.23	0.66
3:F:25:DT:H2''	3:F:26:DT:H71	1.77	0.66
3:F:51:DT:H2''	3:F:52:DT:OP2	1.94	0.66
2:E:4:DT:H2'	2:E:5:DC:C6	2.31	0.66
5:N:158:TYR:CE2	5:N:193:LEU:HD21	2.30	0.65
4:T:234:TYR:CE2	4:T:238:LEU:HD11	2.30	0.65
1:A:254:VAL:HG22	1:A:287:ARG:HH11	1.60	0.65
1:C:231:LEU:HD13	1:C:234:ILE:HD11	1.76	0.65
2:E:20:DT:H2''	2:E:21:DT:OP2	1.95	0.65
5:M:116:MET:HA	5:M:116:MET:HE3	1.78	0.65
5:N:126:LEU:HD11	5:N:144:ASP:HB3	1.78	0.65
3:F:47:DA:H1'	3:F:48:DC:O5'	1.95	0.65
4:K:71:PHE:HB3	4:K:142:VAL:HG22	1.77	0.65
1:C:219:TYR:O	1:C:223:THR:HG23	1.95	0.65
4:G:49:LEU:HD22	5:I:282:LEU:HD13	1.79	0.65
2:E:17:DA:H2''	2:E:18:DC:OP2	1.96	0.65
3:F:33:DT:H2''	3:F:34:DC:H5'	1.77	0.65
3:F:29:DC:H2''	3:F:30:DT:OP2	1.97	0.65
4:G:241:HIS:O	5:I:327:VAL:HG21	1.96	0.65
4:O:125:PHE:HB3	4:O:132:LEU:HD22	1.78	0.65
1:A:316:GLN:OE1	1:A:337:ARG:HA	1.97	0.65
3:F:21:DT:H2''	3:F:22:DT:OP2	1.95	0.65
4:O:266:PHE:CD2	5:Q:328:MET:HE2	2.32	0.65
1:B:248:THR:CG2	1:B:253:ILE:HD11	2.27	0.64
1:D:124:MET:HE3	5:N:139:GLU:HB2	1.79	0.64
3:F:25:DT:H2''	3:F:26:DT:OP2	1.98	0.64
4:H:106:MET:HE1	4:H:134:CYS:HB2	1.79	0.64
4:H:226:PHE:CE2	4:H:231:VAL:HG22	2.32	0.64
1:B:60:LEU:HA	1:B:103:MET:O	1.98	0.64
2:E:15:DA:H1'	2:E:16:DA:H5'	1.80	0.64
4:K:54:TYR:CE2	4:K:58:LEU:HD21	2.33	0.64
4:S:61:LEU:HD11	4:S:86:SER:CB	2.28	0.64
2:E:6:DC:H2'	2:E:6:DC:OP2	1.97	0.64
3:F:45:DT:H1'	3:F:46:DA:C5'	2.27	0.64
1:B:219:TYR:CE1	1:B:365:VAL:HG13	2.32	0.64
4:S:78:ARG:HA	5:U:261:GLN:NE2	2.13	0.64
3:F:30:DT:H2''	3:F:31:DT:C7	2.27	0.64
5:Q:169:PHE:CE2	5:R:147:MET:HE3	2.33	0.64
4:T:67:LEU:HD13	4:T:209:TYR:CZ	2.31	0.64
2:E:20:DT:H1'	2:E:21:DT:O5'	1.97	0.64
4:O:47:ILE:O	4:O:51:LEU:HD23	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:GLU:HB3	1:A:311:GLU:OE1	1.97	0.64
5:I:182:GLN:O	5:I:186:LEU:HD23	1.98	0.63
5:Q:149:MET:HE3	5:R:146:VAL:HG13	1.79	0.63
3:F:8:DA:H1'	3:F:9:DT:C5'	2.28	0.63
5:M:307:GLU:O	5:M:311:VAL:HG22	1.97	0.63
1:B:345:LEU:HD23	1:B:348:GLU:OE1	1.98	0.63
4:G:71:PHE:HE2	4:G:212:LEU:HD21	1.64	0.63
4:G:91:ILE:HD12	4:G:216:VAL:HG12	1.80	0.63
2:E:16:DA:H2''	2:E:17:DA:OP2	1.97	0.63
5:U:164:LEU:O	5:U:168:THR:HG23	1.98	0.63
3:F:34:DC:H2''	3:F:35:DC:C6	2.34	0.63
4:K:54:TYR:O	4:K:58:LEU:HD23	1.99	0.63
5:I:216:CYS:O	5:J:142:ILE:HD11	1.98	0.63
5:N:175:ARG:HD3	5:N:203:LEU:HD21	1.80	0.63
1:A:157:LEU:HB3	1:A:166:ILE:HD12	1.80	0.63
1:B:257:LEU:HD11	1:B:268:LYS:O	1.99	0.63
4:G:232:PHE:CD2	4:K:33:LEU:HD21	2.34	0.63
1:A:135:ILE:HG22	1:A:226:LEU:HD13	1.80	0.63
4:S:147:ARG:HD2	5:U:300:THR:HG23	1.81	0.63
1:C:24:MET:HB3	1:D:203:THR:HG21	1.80	0.62
1:C:227:TYR:O	1:C:231:LEU:HD23	1.99	0.62
5:U:161:LEU:HD11	5:U:189:ALA:HB3	1.80	0.62
2:E:33:DA:H2''	2:E:34:DA:OP2	2.00	0.62
4:G:109:VAL:HG23	5:I:257:LEU:HD22	1.81	0.62
5:N:128:HIS:NE2	5:N:132:LEU:HD11	2.14	0.62
2:E:39:DA:H1'	2:E:40:DA:O5'	1.99	0.62
3:F:25:DT:H1'	3:F:26:DT:O5'	2.00	0.62
4:P:234:TYR:CZ	4:P:238:LEU:HD11	2.34	0.62
5:I:168:THR:HG22	5:I:210:ARG:HG3	1.82	0.62
4:G:67:LEU:HD11	4:G:208:GLN:HB3	1.81	0.62
5:M:183:THR:O	5:M:187:LEU:HD23	1.99	0.62
1:C:227:TYR:CZ	1:C:231:LEU:HD21	2.35	0.62
2:E:56:DT:H1'	2:E:57:DG:O5'	1.99	0.62
2:E:5:DC:H2''	2:E:6:DC:OP2	1.99	0.62
4:G:111:THR:HG22	5:I:254:ILE:CD1	2.30	0.62
1:C:113:PHE:HB3	1:C:158:ILE:HG22	1.81	0.62
2:E:7:DA:H1'	2:E:8:DA:O5'	2.00	0.62
4:T:91:ILE:HD13	4:T:217:GLU:HA	1.82	0.62
5:Q:191:ARG:HH12	5:Q:194:LEU:HD22	1.65	0.62
1:A:24:MET:CE	1:B:203:THR:HG21	2.29	0.61
1:A:227:TYR:CZ	1:A:231:LEU:HD11	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:8:DA:H1'	3:F:9:DT:O5'	1.99	0.61
4:K:231:VAL:HA	4:K:234:TYR:CD1	2.34	0.61
5:U:158:TYR:CD1	5:U:189:ALA:HB1	2.35	0.61
1:C:267:VAL:HG12	1:C:287:ARG:HG2	1.82	0.61
2:E:44:DA:H2''	2:E:45:DA:OP2	2.01	0.61
5:I:142:ILE:HD12	5:J:216:CYS:O	2.00	0.61
4:K:144:MET:CE	5:M:304:THR:HG21	2.30	0.61
3:F:51:DT:C6	3:F:52:DT:H72	2.35	0.61
5:Q:228:VAL:HG22	5:R:223:ARG:O	2.00	0.61
5:U:158:TYR:HD1	5:U:189:ALA:HB1	1.64	0.61
1:A:148:LEU:HB2	1:A:300:VAL:HG12	1.82	0.61
1:B:105:ILE:HG22	1:B:107:PRO:HD3	1.81	0.61
1:C:308:ARG:HD3	3:F:15:DT:H5''	1.81	0.61
2:E:42:DA:H2''	2:E:43:DA:OP2	2.01	0.61
1:B:147:ILE:HD12	1:B:172:TYR:O	2.01	0.61
2:E:35:DA:H1'	2:E:36:DC:C5'	2.31	0.61
1:B:147:ILE:HD13	1:B:173:ILE:HD13	1.83	0.61
1:D:32:CYS:HA	1:D:43:VAL:HG12	1.83	0.61
4:G:45:LEU:O	4:G:49:LEU:HD23	2.01	0.61
1:A:153:MET:HE3	1:A:241:PHE:O	2.01	0.60
5:I:122:ALA:C	5:I:148:THR:HG22	2.26	0.60
4:K:144:MET:HE2	5:M:304:THR:HG21	1.83	0.60
1:A:149:ILE:HG22	1:A:221:TYR:OH	2.01	0.60
1:C:255:ARG:HH22	3:F:6:DT:H3'	1.65	0.60
4:G:226:PHE:CE2	4:G:231:VAL:HG22	2.35	0.60
4:O:226:PHE:CE2	4:O:231:VAL:HG22	2.36	0.60
5:U:146:VAL:HG11	5:V:169:PHE:CZ	2.37	0.60
1:B:138:ILE:HD13	1:B:226:LEU:HD21	1.81	0.60
1:B:342:LEU:HD11	5:J:191:ARG:HB2	1.83	0.60
4:H:92:HIS:NE2	4:H:99:VAL:HG12	2.16	0.60
5:N:149:MET:HE3	5:N:149:MET:O	2.01	0.60
4:O:47:ILE:HG22	4:O:260:LEU:CD1	2.31	0.60
1:C:114:ARG:NH1	1:C:119:ALA:HA	2.17	0.60
1:C:244:ILE:O	1:C:244:ILE:HG22	2.01	0.60
4:O:9:VAL:HG21	4:O:28:LEU:HD21	1.82	0.60
3:F:13:DA:C2'	3:F:14:DT:H71	2.31	0.60
4:H:79:GLN:NE2	4:H:83:VAL:HG21	2.16	0.60
4:T:256:THR:HG23	4:T:259:LEU:HD12	1.84	0.60
4:G:171:GLY:HA2	4:S:231:VAL:HG21	1.82	0.60
5:Q:272:CYS:O	5:Q:278:LEU:HD11	2.02	0.60
5:U:290:LEU:HG	5:U:294:TYR:HE2	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:119:TYR:HB3	5:R:151:PHE:HB2	1.84	0.60
1:C:308:ARG:NE	3:F:15:DT:H5''	2.17	0.60
1:D:155:VAL:HG12	1:D:229:THR:HG21	1.83	0.60
5:I:146:VAL:HG22	5:J:149:MET:SD	2.42	0.60
5:V:148:THR:O	5:V:152:LEU:HD23	2.01	0.60
1:B:267:VAL:HG22	1:B:287:ARG:HG2	1.83	0.59
3:F:9:DT:H2''	3:F:10:DT:H71	1.85	0.59
3:F:51:DT:OP2	3:F:51:DT:H6	1.85	0.59
1:C:153:MET:HE1	1:C:294:PHE:CD2	2.38	0.59
4:L:118:ILE:HD12	5:N:247:LEU:HD13	1.84	0.59
1:B:108:ILE:HG12	1:B:111:GLU:HB2	1.83	0.59
3:F:13:DA:H1'	3:F:14:DT:O5'	2.02	0.59
4:S:274:ILE:HD11	5:U:227:ILE:HG22	1.84	0.59
3:F:14:DT:H1'	3:F:15:DT:O5'	2.01	0.59
4:H:226:PHE:CZ	4:H:231:VAL:HG22	2.37	0.59
5:I:181:VAL:O	5:I:184:ASP:OD1	2.21	0.59
1:B:32:CYS:HA	1:B:43:VAL:HG12	1.85	0.59
4:K:125:PHE:HB3	4:K:132:LEU:HD22	1.85	0.59
2:E:34:DA:H1'	2:E:35:DA:H5'	1.84	0.59
5:J:263:ILE:O	5:J:263:ILE:HG22	2.02	0.59
3:F:36:DT:H1'	3:F:37:DA:O5'	2.03	0.59
4:H:87:THR:CG2	4:H:216:VAL:HG11	2.32	0.59
1:A:34:ILE:HG13	1:A:43:VAL:HG11	1.85	0.59
2:E:41:DA:H1'	2:E:42:DA:O5'	2.01	0.59
1:C:155:VAL:CG2	1:C:166:ILE:HD11	2.33	0.59
3:F:52:DT:H2''	3:F:53:DG:OP2	2.02	0.59
5:U:222:MET:HE1	5:U:226:LYS:HE3	1.85	0.59
1:A:153:MET:HE3	1:A:241:PHE:C	2.27	0.58
4:G:111:THR:HG22	5:I:254:ILE:HD11	1.85	0.58
4:O:58:LEU:C	4:O:63:MET:HE1	2.28	0.58
5:Q:246:LEU:HD12	5:Q:249:GLU:OE2	2.03	0.58
1:A:121:GLU:HB3	1:A:127:LEU:HD21	1.84	0.58
4:K:207:THR:OG1	5:M:293:MET:HG3	2.03	0.58
4:L:72:ARG:HH12	4:L:142:VAL:HG13	1.67	0.58
3:F:50:DT:H2''	3:F:51:DT:OP2	2.02	0.58
4:H:234:TYR:CE2	4:H:238:LEU:HD11	2.39	0.58
2:E:21:DT:H2''	2:E:22:DT:OP2	2.03	0.58
4:G:226:PHE:CZ	4:G:231:VAL:HG22	2.39	0.58
4:G:235:CYS:HA	4:G:238:LEU:HD12	1.84	0.58
4:G:166:ILE:HD11	5:U:244:GLU:HB2	1.83	0.58
1:C:221:TYR:CE2	1:C:225:LEU:HD11	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:M:246:LEU:HD12	5:M:249:GLU:OE2	2.03	0.58
5:Q:323:ASN:O	5:Q:327:VAL:HG23	2.04	0.58
4:S:61:LEU:HD21	4:S:86:SER:OG	2.03	0.58
1:D:221:TYR:HA	1:D:293:PHE:CE1	2.39	0.58
3:F:16:DT:H1'	3:F:17:DT:O5'	2.04	0.58
1:C:212:ASP:O	1:C:216:GLN:OE1	2.21	0.58
1:D:220:ILE:HG23	1:D:347:TRP:NE1	2.19	0.58
5:U:122:ALA:C	5:U:148:THR:HG22	2.29	0.58
4:S:226:PHE:HE1	4:S:231:VAL:HG22	1.65	0.58
1:A:283:MET:HE2	1:A:283:MET:HA	1.86	0.57
1:C:223:THR:HG21	1:C:347:TRP:HZ2	1.69	0.57
4:G:266:PHE:HD1	5:I:328:MET:HE2	1.68	0.57
5:N:122:ALA:O	5:N:126:LEU:HD13	2.04	0.57
5:U:152:LEU:HG	5:U:165:LEU:HD11	1.84	0.57
1:B:286:PRO:O	1:B:290:THR:HG23	2.04	0.57
3:F:29:DC:H2'	3:F:30:DT:H71	1.86	0.57
1:B:148:LEU:HD13	1:B:300:VAL:HG12	1.86	0.57
4:L:57:MET:HE1	4:L:90:PHE:CB	2.33	0.57
1:B:307:LYS:CE	2:E:18:DC:H5''	2.34	0.57
3:F:35:DC:H2''	3:F:36:DT:H71	1.84	0.57
5:Q:149:MET:HE3	5:R:146:VAL:CG1	2.35	0.57
1:D:138:ILE:HD12	1:D:222:ARG:HB3	1.86	0.57
2:E:25:DG:H1'	2:E:26:DA:C5'	2.34	0.57
3:F:20:DT:OP2	3:F:20:DT:H2'	2.05	0.57
3:F:28:DA:H2''	3:F:29:DC:OP2	2.05	0.57
4:G:92:HIS:HB3	4:G:102:PHE:HZ	1.70	0.57
4:G:171:GLY:N	4:S:231:VAL:HG11	2.19	0.57
1:B:155:VAL:HG21	1:B:166:ILE:HD11	1.85	0.57
1:B:307:LYS:HE3	2:E:18:DC:H5''	1.85	0.57
4:K:36:LEU:O	4:K:40:GLU:OE1	2.21	0.57
4:T:235:CYS:O	4:T:239:THR:HG23	2.05	0.57
4:H:144:MET:SD	5:J:304:THR:OG1	2.61	0.57
4:S:68:LEU:HA	4:S:145:LEU:HD23	1.87	0.57
5:V:127:ILE:HD11	5:V:152:LEU:HD21	1.87	0.57
1:D:75:LYS:HZ3	1:D:79:ARG:HB2	1.68	0.57
1:D:225:LEU:O	1:D:229:THR:HG23	2.05	0.57
4:K:161:ASN:HB3	4:K:164:VAL:HG12	1.87	0.57
1:B:308:ARG:NH2	2:E:18:DC:H2'	2.20	0.57
4:O:56:ALA:O	4:O:60:THR:HG23	2.04	0.57
5:Q:152:LEU:HD23	5:Q:165:LEU:HD13	1.87	0.57
1:A:34:ILE:HG22	1:A:35:HIS:CE1	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:22:ILE:HG21	5:J:295:TYR:CE1	2.40	0.57
5:R:178:MET:HE2	5:R:183:THR:HA	1.87	0.57
2:E:50:DA:H1'	2:E:51:DT:C5'	2.35	0.56
3:F:13:DA:H2''	3:F:14:DT:H71	1.87	0.56
3:F:56:DA:H2''	3:F:57:DT:OP2	2.04	0.56
5:R:245:GLU:O	5:R:249:GLU:OE1	2.23	0.56
1:A:254:VAL:HG22	1:A:287:ARG:NH1	2.20	0.56
1:B:250:ILE:HA	1:B:253:ILE:HD12	1.87	0.56
4:K:63:MET:SD	4:K:63:MET:O	2.63	0.56
1:A:282:VAL:HG21	1:A:357:TYR:CE1	2.40	0.56
2:E:35:DA:H1'	2:E:36:DC:H5'	1.88	0.56
3:F:9:DT:C2'	3:F:10:DT:H71	2.36	0.56
3:F:35:DC:C2'	3:F:36:DT:H71	2.35	0.56
5:I:146:VAL:HG11	5:J:169:PHE:HZ	1.69	0.56
5:U:160:SER:O	5:U:164:LEU:HD23	2.05	0.56
5:I:146:VAL:HG11	5:J:169:PHE:CZ	2.40	0.56
4:O:36:LEU:O	4:O:40:GLU:OE1	2.23	0.56
1:A:105:ILE:HG22	1:A:107:PRO:HD3	1.88	0.56
1:B:101:GLU:HG3	1:B:103:MET:HE3	1.88	0.56
3:F:19:DT:H1'	3:F:20:DT:O5'	2.06	0.56
3:F:30:DT:OP2	3:F:30:DT:H2'	2.06	0.56
5:J:241:THR:HG23	5:J:313:ASN:HD22	1.70	0.56
5:N:153:LEU:HA	5:N:162:PHE:CZ	2.40	0.56
5:R:178:MET:HE1	5:R:186:LEU:HG	1.86	0.56
1:D:44:THR:HG23	1:D:44:THR:O	2.05	0.56
2:E:25:DG:H1'	2:E:26:DA:O5'	2.06	0.56
2:E:13:DT:H2''	2:E:14:DA:H8	1.70	0.56
2:E:54:DA:H2''	2:E:55:DA:C8	2.39	0.56
4:K:145:LEU:HD22	4:K:208:GLN:HG3	1.87	0.56
5:U:153:LEU:HD23	5:V:153:LEU:HD23	1.88	0.56
1:A:135:ILE:HG22	1:A:226:LEU:CD1	2.35	0.56
5:N:159:HIS:HD2	5:N:162:PHE:CE2	2.24	0.56
4:T:54:TYR:CE1	4:T:87:THR:HG23	2.40	0.56
1:B:174:ILE:HG23	1:B:174:ILE:O	2.06	0.56
2:E:15:DA:H1'	2:E:16:DA:C5'	2.36	0.56
4:G:234:TYR:CE2	4:G:238:LEU:HD11	2.40	0.56
4:L:71:PHE:CE1	4:L:141:ILE:HG21	2.41	0.56
5:M:228:VAL:C	5:M:229:LEU:HD22	2.31	0.56
5:I:126:LEU:HD11	5:I:130:TYR:CZ	2.41	0.56
5:M:254:ILE:HD13	5:M:257:LEU:HD12	1.88	0.56
5:N:175:ARG:CD	5:N:203:LEU:HD21	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:131:SER:N	5:R:209:MET:HE1	2.21	0.56
1:A:91:LYS:HZ3	1:B:199:TRP:CD1	2.24	0.55
2:E:6:DC:H1'	2:E:7:DA:C5'	2.36	0.55
5:I:175:ARG:HD2	5:I:175:ARG:O	2.06	0.55
5:J:122:ALA:C	5:J:148:THR:HG22	2.31	0.55
3:F:19:DT:C6	3:F:20:DT:H72	2.41	0.55
4:K:204:VAL:O	4:K:208:GLN:OE1	2.25	0.55
1:D:8:ILE:HD12	1:D:18:LEU:O	2.05	0.55
4:P:85:PHE:HZ	4:P:104:ASN:HA	1.70	0.55
5:R:122:ALA:C	5:R:148:THR:HG22	2.31	0.55
1:C:34:ILE:HG22	1:C:115:SER:HB2	1.87	0.55
1:C:349:ASN:O	1:C:353:GLU:OE1	2.24	0.55
1:D:103:MET:HE3	1:D:168:PRO:HD3	1.87	0.55
2:E:55:DA:H2''	2:E:56:DT:OP2	2.07	0.55
5:N:113:LEU:HD23	5:N:113:LEU:H	1.72	0.55
4:T:103:THR:HG22	4:T:106:MET:SD	2.47	0.55
1:D:364:ASN:OD1	1:D:365:VAL:HG23	2.07	0.55
2:E:20:DT:OP1	2:E:20:DT:H3'	2.06	0.55
3:F:9:DT:H1'	3:F:10:DT:O5'	2.07	0.55
4:K:249:ARG:NH2	5:M:331:ILE:HG22	2.22	0.55
4:O:47:ILE:HG22	4:O:260:LEU:HD12	1.88	0.55
4:P:109:VAL:CG1	4:P:133:LEU:HD11	2.37	0.55
4:S:47:ILE:O	4:S:51:LEU:HD23	2.07	0.55
1:B:267:VAL:HG23	1:B:285:PRO:O	2.07	0.55
5:J:144:ASP:O	5:J:148:THR:HG23	2.07	0.55
5:U:298:ALA:HB1	5:V:227:ILE:HG21	1.88	0.55
1:A:119:ALA:HB3	1:A:233:ALA:O	2.07	0.55
1:C:225:LEU:O	1:C:229:THR:HG23	2.07	0.55
5:J:203:LEU:HA	5:J:206:VAL:HG22	1.89	0.55
4:O:44:THR:HG22	5:Q:290:LEU:CD1	2.36	0.55
2:E:35:DA:H1'	2:E:36:DC:O5'	2.07	0.55
3:F:53:DG:H2''	3:F:54:DG:OP2	2.07	0.55
3:F:54:DG:H2''	3:F:55:DA:OP2	2.05	0.55
2:E:16:DA:H1'	2:E:17:DA:O5'	2.07	0.55
5:Q:325:PHE:O	5:Q:329:GLU:OE1	2.25	0.55
1:B:60:LEU:HD13	1:B:104:LEU:HA	1.90	0.54
1:D:203:THR:HG22	1:D:204:ALA:H	1.71	0.54
4:G:141:ILE:HD11	4:G:212:LEU:HD23	1.89	0.54
4:K:44:THR:HG23	5:M:290:LEU:HD13	1.90	0.54
4:O:165:ARG:O	4:O:169:THR:HG23	2.07	0.54
1:C:299:TRP:CD2	1:C:309:TYR:HB2	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:71:PHE:CE2	4:G:212:LEU:HD21	2.43	0.54
4:L:68:LEU:HD12	4:L:71:PHE:HB2	1.89	0.54
4:T:114:ASN:HD22	5:V:311:VAL:HG11	1.72	0.54
4:T:214:LEU:HD23	4:T:217:GLU:OE2	2.08	0.54
1:A:72:GLU:OE1	1:B:24:MET:HG3	2.08	0.54
2:E:43:DA:H1'	2:E:44:DA:O5'	2.08	0.54
5:U:149:MET:HE1	5:V:150:ILE:CD1	2.37	0.54
3:F:23:DG:H2''	3:F:24:DT:OP2	2.08	0.54
4:K:91:ILE:HD13	4:K:217:GLU:HA	1.90	0.54
4:O:259:LEU:HD22	5:Q:331:ILE:HD11	1.88	0.54
4:S:47:ILE:HG21	5:U:294:TYR:OH	2.07	0.54
3:F:16:DT:C2'	3:F:17:DT:H72	2.37	0.54
3:F:33:DT:H2'	3:F:34:DC:H6	1.70	0.54
4:G:54:TYR:CZ	4:G:58:LEU:HD11	2.43	0.54
4:O:98:LEU:HG	4:O:99:VAL:HG23	1.88	0.54
4:O:235:CYS:HA	4:O:238:LEU:HD12	1.89	0.54
5:Q:142:ILE:HA	5:Q:145:VAL:HG22	1.88	0.54
3:F:32:DC:H2''	3:F:33:DT:OP2	2.07	0.54
4:O:125:PHE:CE1	4:O:134:CYS:HB3	2.43	0.54
4:S:80:ILE:O	4:S:84:VAL:HG23	2.08	0.54
5:V:158:TYR:CE1	5:V:189:ALA:HB1	2.42	0.54
1:A:46:PRO:HG3	1:A:60:LEU:HD11	1.90	0.54
1:C:25:ARG:O	1:D:203:THR:HG23	2.07	0.54
2:E:14:DA:H2''	2:E:15:DA:O5'	2.08	0.54
3:F:23:DG:C2'	3:F:24:DT:H71	2.37	0.54
4:G:88:LEU:HD12	4:G:102:PHE:HE2	1.71	0.54
4:O:32:ASP:O	4:O:36:LEU:HD23	2.08	0.54
4:O:70:ILE:HG23	4:O:79:GLN:OE1	2.07	0.54
1:A:122:HIS:CE1	1:A:277:VAL:HG13	2.43	0.54
2:E:42:DA:H1'	2:E:43:DA:O5'	2.08	0.54
3:F:8:DA:H1'	3:F:9:DT:H5'	1.90	0.54
5:J:164:LEU:O	5:J:168:THR:HG23	2.08	0.54
4:K:222:HIS:CE1	4:K:238:LEU:HD23	2.43	0.54
1:D:343:HIS:O	1:D:346:ASP:OD1	2.26	0.54
5:I:153:LEU:HD23	5:J:153:LEU:HD23	1.90	0.54
5:J:119:TYR:HB3	5:J:151:PHE:HB2	1.90	0.54
1:C:114:ARG:NH1	1:C:115:SER:O	2.41	0.53
3:F:18:DT:C6	3:F:19:DT:H72	2.43	0.53
4:L:55:MET:HB2	5:N:281:LEU:HD13	1.89	0.53
4:O:13:THR:HG23	4:P:266:PHE:HD2	1.71	0.53
1:B:155:VAL:HG12	1:B:229:THR:HG21	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:255:ARG:NH2	3:F:6:DT:H3'	2.22	0.53
1:D:94:LEU:HD23	1:D:94:LEU:H	1.73	0.53
1:D:135:ILE:HD12	1:D:138:ILE:HD11	1.90	0.53
3:F:23:DG:H2''	3:F:24:DT:H71	1.89	0.53
3:F:30:DT:C2'	3:F:31:DT:H72	2.36	0.53
3:F:48:DC:H2''	3:F:49:DG:OP2	2.07	0.53
4:G:54:TYR:CE2	4:G:58:LEU:HD11	2.43	0.53
4:K:237:SER:HB3	4:K:243:LEU:HD22	1.89	0.53
5:M:290:LEU:HA	5:M:293:MET:HE2	1.90	0.53
4:G:67:LEU:HD13	4:G:209:TYR:CE1	2.42	0.53
1:B:308:ARG:CZ	2:E:18:DC:H2'	2.39	0.53
4:L:68:LEU:HD13	4:L:145:LEU:HB2	1.90	0.53
4:O:11:THR:HG21	5:R:302:PHE:CE2	2.43	0.53
5:U:302:PHE:HE1	5:U:318:ILE:HD13	1.73	0.53
5:I:298:ALA:HB1	5:J:227:ILE:HG21	1.90	0.53
5:Q:187:LEU:HA	5:Q:190:VAL:HG22	1.91	0.53
1:D:203:THR:HG22	1:D:204:ALA:N	2.24	0.53
5:N:158:TYR:CE1	5:N:189:ALA:HB1	2.43	0.53
4:T:222:HIS:HB3	4:T:234:TYR:CE1	2.44	0.53
1:A:196:GLU:OE1	1:A:198:PRO:HD2	2.08	0.53
1:A:202:ILE:HD12	1:B:44:THR:HG21	1.91	0.53
1:B:250:ILE:HD13	1:B:294:PHE:CE2	2.44	0.53
1:D:157:LEU:HD21	1:D:164:ALA:HB1	1.90	0.53
2:E:48:DT:H1'	2:E:49:DA:C5'	2.38	0.53
5:U:142:ILE:O	5:U:146:VAL:HG23	2.09	0.53
5:V:158:TYR:CD1	5:V:189:ALA:HB1	2.44	0.53
1:C:345:LEU:HA	1:C:348:GLU:HG3	1.91	0.53
3:F:37:DA:H2''	3:F:38:DA:OP2	2.09	0.53
5:J:158:TYR:CE1	5:J:189:ALA:HB1	2.44	0.53
4:K:22:ILE:HG22	5:N:295:TYR:CZ	2.44	0.53
4:K:144:MET:O	5:M:300:THR:HG21	2.08	0.53
5:M:217:PHE:CE1	5:N:143:SER:HB2	2.44	0.53
4:S:91:ILE:HD12	4:S:216:VAL:HG12	1.91	0.53
2:E:25:DG:H1'	2:E:26:DA:H5'	1.91	0.53
4:G:174:LYS:HE3	5:U:252:GLU:HA	1.90	0.53
5:J:168:THR:HB	5:J:214:ALA:HB2	1.90	0.53
1:A:72:GLU:OE2	1:B:93:ILE:HA	2.09	0.53
4:G:108:PHE:CZ	5:I:263:ILE:HD12	2.44	0.53
4:G:234:TYR:CZ	4:G:238:LEU:HD11	2.44	0.53
4:H:62:GLU:O	4:H:62:GLU:CD	2.52	0.53
5:N:123:ALA:O	5:N:127:ILE:HG12	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:81:LEU:HD21	1:C:141:LEU:HD23	1.91	0.52
1:D:78:TYR:OH	1:D:101:GLU:HG2	2.09	0.52
2:E:16:DA:H1'	2:E:17:DA:C5'	2.39	0.52
5:N:160:SER:O	5:N:164:LEU:HD13	2.09	0.52
4:O:214:LEU:HD21	5:Q:297:ALA:HB1	1.90	0.52
5:Q:132:LEU:HD12	5:Q:303:TYR:CG	2.44	0.52
1:D:124:MET:HB2	1:D:358:PHE:HE1	1.75	0.52
1:D:243:VAL:HG12	1:D:245:ALA:H	1.73	0.52
2:E:13:DT:H2''	2:E:14:DA:C8	2.44	0.52
4:G:63:MET:O	4:G:63:MET:SD	2.67	0.52
4:L:74:LYS:O	4:L:77:THR:HG23	2.09	0.52
1:D:148:LEU:HD13	1:D:300:VAL:HA	1.91	0.52
5:Q:152:LEU:HD11	5:Q:161:LEU:HB2	1.90	0.52
1:B:102:CYS:O	1:B:103:MET:HE2	2.09	0.52
1:B:277:VAL:HG11	5:N:198:SER:OG	2.09	0.52
1:C:155:VAL:HG21	1:C:166:ILE:HD11	1.91	0.52
1:D:267:VAL:HG22	1:D:287:ARG:HG2	1.91	0.52
2:E:51:DT:H1'	2:E:52:DT:H5'	1.91	0.52
4:O:268:ILE:HB	4:O:271:PHE:CE1	2.44	0.52
4:K:147:ARG:HD2	5:M:300:THR:HG23	1.90	0.52
4:O:9:VAL:CG2	4:O:28:LEU:HD21	2.39	0.52
5:R:163:LYS:HA	5:R:166:GLU:HG2	1.89	0.52
5:J:254:ILE:HD13	5:J:257:LEU:HD11	1.91	0.52
4:K:47:ILE:HG23	4:K:260:LEU:CD1	2.39	0.52
4:K:232:PHE:HE2	4:O:33:LEU:HD13	1.75	0.52
4:O:213:LEU:O	4:O:217:GLU:HG2	2.09	0.52
4:P:87:THR:CG2	4:P:216:VAL:HG11	2.40	0.52
4:T:80:ILE:CG2	4:T:136:VAL:HG11	2.40	0.52
3:F:4:DT:H2'	3:F:5:DT:O4'	2.09	0.52
4:H:51:LEU:HD22	5:J:285:ILE:HD13	1.91	0.52
5:J:173:THR:C	5:U:174:CYS:HB2	2.35	0.52
5:M:116:MET:HE1	5:M:154:ARG:HG2	1.92	0.52
5:N:119:TYR:CD2	5:N:147:MET:SD	3.02	0.52
5:N:203:LEU:C	5:N:203:LEU:HD23	2.35	0.52
5:Q:275:ALA:HA	5:Q:278:LEU:HD12	1.91	0.52
5:R:164:LEU:O	5:R:168:THR:HG23	2.10	0.52
1:D:8:ILE:HD11	1:D:20:PRO:HB3	1.91	0.52
2:E:31:DT:H2''	2:E:32:DA:OP2	2.09	0.52
4:G:81:ALA:HB2	5:I:261:GLN:HG3	1.91	0.52
5:J:146:VAL:HG13	5:J:149:MET:HE2	1.92	0.52
4:K:49:LEU:HD23	5:M:282:LEU:HD22	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:235:CYS:HA	4:K:238:LEU:HD12	1.90	0.52
1:C:30:MET:HE2	1:C:64:VAL:HG23	1.92	0.52
1:C:263:ASN:OD1	1:C:265:ASP:OD1	2.27	0.52
1:D:105:ILE:HG12	1:D:165:ILE:HD13	1.92	0.52
2:E:31:DT:H1'	2:E:32:DA:H5'	1.92	0.52
4:H:54:TYR:HH	4:H:87:THR:HG1	1.58	0.52
1:D:227:TYR:O	1:D:231:LEU:HG	2.10	0.52
2:E:4:DT:H2''	2:E:5:DC:O4'	2.10	0.52
2:E:32:DA:H2''	2:E:33:DA:C8	2.45	0.52
4:O:56:ALA:HB1	5:Q:272:CYS:HB3	1.92	0.52
5:Q:243:LEU:HD12	5:Q:246:LEU:HD23	1.91	0.52
4:S:67:LEU:HD11	4:S:208:GLN:HB3	1.91	0.52
4:S:235:CYS:HA	4:S:238:LEU:HD12	1.91	0.52
1:A:35:HIS:CD2	1:A:38:ARG:NH2	2.77	0.51
1:B:236:LYS:HD3	1:B:275:GLY:HA2	1.92	0.51
1:C:71:ASN:O	1:D:94:LEU:HD21	2.10	0.51
4:O:118:ILE:CD1	5:Q:247:LEU:HD23	2.40	0.51
5:Q:250:ARG:O	5:Q:254:ILE:HG12	2.10	0.51
2:E:16:DA:H1'	2:E:17:DA:H5'	1.92	0.51
4:O:77:THR:HG22	4:O:110:VAL:HG21	1.91	0.51
4:O:119:PRO:HD2	5:Q:246:LEU:HD21	1.92	0.51
5:Q:152:LEU:HD12	5:Q:158:TYR:HB3	1.91	0.51
1:D:114:ARG:HD2	1:D:115:SER:O	2.10	0.51
4:G:262:SER:HA	5:I:328:MET:SD	2.50	0.51
5:I:158:TYR:CD2	5:I:193:LEU:HD12	2.45	0.51
1:D:82:LEU:O	1:D:82:LEU:HD12	2.11	0.51
2:E:49:DA:H2''	2:E:50:DA:OP2	2.10	0.51
4:H:265:LYS:HE3	5:J:327:VAL:HB	1.91	0.51
4:K:252:MET:HE1	5:M:331:ILE:HB	1.93	0.51
3:F:40:DG:H1'	3:F:41:DG:O5'	2.10	0.51
4:K:241:HIS:O	5:M:327:VAL:HG21	2.10	0.51
5:M:164:LEU:O	5:M:168:THR:HG23	2.10	0.51
1:D:130:ILE:CD1	1:D:164:ALA:HB2	2.41	0.51
1:D:293:PHE:HD1	1:D:313:ILE:HD11	1.75	0.51
1:D:297:ALA:O	1:D:300:VAL:HG13	2.10	0.51
3:F:29:DC:H2''	3:F:30:DT:H71	1.92	0.51
5:R:277:PHE:CE1	5:R:281:LEU:HD11	2.46	0.51
4:S:68:LEU:HD12	4:S:69:GLU:N	2.26	0.51
4:T:93:ASN:OD1	4:T:100:THR:HA	2.10	0.51
1:A:260:CYS:SG	1:A:281:HIS:CE1	3.04	0.51
4:P:138:ARG:O	4:P:141:ILE:HG22	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Q:216:CYS:O	5:R:142:ILE:HD11	2.10	0.51
4:S:144:MET:CE	4:S:211:THR:HG23	2.41	0.51
1:B:221:TYR:CD1	1:B:293:PHE:CE1	2.99	0.51
1:B:231:LEU:C	1:B:235:LEU:HD23	2.35	0.51
1:D:59:MET:O	1:D:104:LEU:HD12	2.10	0.51
2:E:38:DA:H2''	2:E:39:DA:C8	2.45	0.51
4:G:67:LEU:HD22	4:G:209:TYR:CZ	2.46	0.51
5:I:159:HIS:HB3	5:I:163:LYS:HZ3	1.75	0.51
4:O:270:ASP:O	4:O:274:ILE:HG12	2.11	0.51
4:O:274:ILE:HD11	5:Q:227:ILE:HB	1.92	0.51
2:E:8:DA:H2''	2:E:9:DA:OP2	2.11	0.51
4:H:247:LYS:HD2	5:J:327:VAL:HG22	1.92	0.51
4:P:133:LEU:HD13	5:R:259:PRO:HG3	1.92	0.51
1:D:153:MET:HE1	1:D:297:ALA:HB3	1.92	0.51
3:F:43:DT:H2''	3:F:44:DT:OP2	2.09	0.51
5:J:241:THR:HB	5:J:245:GLU:OE2	2.11	0.51
1:B:124:MET:HE2	5:N:194:LEU:HB2	1.92	0.50
3:F:41:DG:H2''	3:F:42:DT:H71	1.93	0.50
4:K:133:LEU:HD13	5:M:259:PRO:HB3	1.93	0.50
1:B:197:TYR:HB2	1:B:198:PRO:HD3	1.93	0.50
3:F:25:DT:C2'	3:F:26:DT:H71	2.41	0.50
3:F:56:DA:H2''	3:F:57:DT:H71	1.93	0.50
4:G:201:ILE:O	5:I:284:HIS:NE2	2.43	0.50
4:S:91:ILE:HD13	4:S:217:GLU:HA	1.93	0.50
1:B:297:ALA:O	1:B:300:VAL:HG13	2.12	0.50
1:C:267:VAL:HG13	1:C:285:PRO:O	2.11	0.50
5:J:122:ALA:O	5:J:126:LEU:HD13	2.11	0.50
5:J:175:ARG:O	5:J:175:ARG:HG2	2.11	0.50
1:A:198:PRO:O	1:A:201:LEU:HB3	2.12	0.50
1:D:220:ILE:HG23	1:D:347:TRP:HE1	1.76	0.50
5:N:247:LEU:HB3	4:P:166:ILE:HD11	1.94	0.50
4:O:241:HIS:O	5:Q:327:VAL:HG21	2.11	0.50
4:S:69:GLU:HA	4:S:72:ARG:HB3	1.92	0.50
4:T:261:LEU:HD11	5:V:325:PHE:CD1	2.45	0.50
4:T:268:ILE:HD13	5:V:302:PHE:CE1	2.46	0.50
1:B:288:GLU:OE1	1:B:343:HIS:CD2	2.65	0.50
1:C:220:ILE:HG22	1:C:347:TRP:CZ2	2.47	0.50
4:G:67:LEU:HD13	4:G:209:TYR:CD1	2.46	0.50
4:O:140:SER:O	4:O:144:MET:HG3	2.11	0.50
5:V:147:MET:HE2	5:V:147:MET:HA	1.94	0.50
1:D:149:ILE:O	1:D:300:VAL:HG11	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:153:MET:HE2	1:D:244:ILE:HG22	1.93	0.50
3:F:44:DT:H1'	3:F:45:DT:O5'	2.11	0.50
5:I:164:LEU:O	5:I:168:THR:HG23	2.12	0.50
4:K:57:MET:SD	4:K:58:LEU:HD22	2.51	0.50
1:B:267:VAL:HG22	1:B:287:ARG:CG	2.42	0.50
1:C:103:MET:HG3	1:C:105:ILE:HD11	1.94	0.50
1:C:212:ASP:HA	1:C:215:ARG:HD2	1.93	0.50
1:D:191:VAL:HG23	1:D:193:ASN:OD1	2.11	0.50
2:E:14:DA:H2''	2:E:15:DA:C5'	2.42	0.50
4:H:212:LEU:O	4:H:216:VAL:HG23	2.12	0.50
4:K:268:ILE:HD13	5:M:318:ILE:HD11	1.92	0.50
1:A:257:LEU:HD23	1:A:267:VAL:CG2	2.42	0.50
1:A:267:VAL:HG13	1:A:269:CYS:SG	2.52	0.50
1:D:86:GLN:HE21	1:D:165:ILE:HA	1.76	0.50
3:F:43:DT:H1'	3:F:44:DT:O5'	2.12	0.50
4:H:51:LEU:HD23	4:H:51:LEU:C	2.37	0.50
5:R:164:LEU:HD21	5:R:210:ARG:HG3	1.94	0.50
5:V:278:LEU:HD23	5:V:278:LEU:C	2.37	0.50
1:A:197:TYR:HB3	1:A:198:PRO:HD3	1.93	0.50
1:C:70:LEU:HD13	1:C:76:LEU:N	2.27	0.50
1:C:116:VAL:HA	1:C:159:TYR:HE1	1.76	0.50
1:D:60:LEU:HD12	1:D:103:MET:O	2.12	0.50
3:F:52:DT:H1'	3:F:53:DG:C8	2.47	0.50
4:G:202:THR:HG23	4:G:204:VAL:H	1.76	0.50
4:G:266:PHE:CD1	5:I:328:MET:HE2	2.47	0.50
5:N:158:TYR:HE1	5:N:189:ALA:HB1	1.76	0.50
4:S:144:MET:SD	5:U:304:THR:OG1	2.68	0.50
1:A:342:LEU:HD12	1:A:343:HIS:N	2.27	0.49
1:D:7:PRO:N	1:D:17:LYS:HZ3	2.10	0.49
2:E:48:DT:H1'	2:E:49:DA:O5'	2.12	0.49
5:M:129:HIS:HB2	5:M:140:TYR:OH	2.11	0.49
5:U:172:TYR:CG	5:U:214:ALA:HB1	2.46	0.49
1:A:223:THR:HB	1:A:351:MET:SD	2.52	0.49
1:A:274:TYR:CD2	1:A:279:PRO:HD2	2.48	0.49
1:A:295:HIS:HB3	1:A:312:LEU:HD11	1.93	0.49
1:D:193:ASN:OD1	1:D:193:ASN:O	2.31	0.49
4:G:109:VAL:HG13	4:G:135:SER:HA	1.93	0.49
4:O:151:THR:HG22	4:O:151:THR:O	2.11	0.49
1:C:78:TYR:OH	1:C:101:GLU:HG2	2.11	0.49
1:C:227:TYR:CE1	1:C:231:LEU:HD21	2.48	0.49
5:M:208:ILE:HG12	5:M:230:LEU:HD21	1.92	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:245:THR:OG1	5:Q:327:VAL:HG13	2.13	0.49
4:T:240:ASP:HA	5:V:320:ASP:OD1	2.12	0.49
1:D:89:ALA:HB3	1:D:104:LEU:HB3	1.94	0.49
1:D:253:ILE:O	1:D:256:ASN:OD1	2.31	0.49
2:E:45:DA:H1'	2:E:46:DT:O5'	2.12	0.49
3:F:11:DA:H1'	3:F:12:DA:O5'	2.12	0.49
3:F:25:DT:H1'	3:F:26:DT:C5'	2.42	0.49
4:G:222:HIS:ND1	4:G:238:LEU:HD23	2.27	0.49
5:J:146:VAL:HA	5:J:149:MET:HE2	1.94	0.49
5:J:152:LEU:HG	5:J:162:PHE:CD1	2.47	0.49
4:O:44:THR:HG22	5:Q:290:LEU:HD13	1.94	0.49
4:T:55:MET:HG3	5:V:281:LEU:HD13	1.94	0.49
5:V:302:PHE:CE1	5:V:306:MET:HE3	2.48	0.49
1:B:138:ILE:CD1	1:B:226:LEU:HD21	2.40	0.49
1:D:47:ARG:HD2	4:G:272:ASP:O	2.13	0.49
5:J:123:ALA:N	5:J:148:THR:HG22	2.27	0.49
5:Q:156:GLU:O	5:Q:159:HIS:CD2	2.66	0.49
4:S:234:TYR:CE2	4:S:238:LEU:HD11	2.47	0.49
1:B:103:MET:HB3	1:B:105:ILE:HD11	1.94	0.49
1:D:358:PHE:HB2	1:D:360:LEU:HD23	1.95	0.49
2:E:30:DG:H3'	2:E:30:DG:OP1	2.12	0.49
3:F:30:DT:H2'	3:F:30:DT:P	2.52	0.49
5:I:149:MET:SD	5:J:149:MET:HE3	2.52	0.49
4:K:61:LEU:HD21	5:M:270:PRO:HG3	1.95	0.49
4:K:95:PHE:CZ	4:K:217:GLU:OE2	2.65	0.49
4:S:9:VAL:HG13	4:T:270:ASP:HA	1.93	0.49
4:T:222:HIS:HB3	4:T:234:TYR:HE1	1.78	0.49
5:V:168:THR:HG21	5:V:210:ARG:CG	2.42	0.49
1:A:227:TYR:CE2	1:A:231:LEU:HD11	2.47	0.49
1:B:223:THR:HG21	1:B:351:MET:HG2	1.95	0.49
1:C:236:LYS:HZ2	1:C:275:GLY:HA2	1.77	0.49
1:B:290:THR:O	1:B:294:PHE:CD2	2.65	0.49
2:E:48:DT:H1'	2:E:49:DA:H5'	1.94	0.49
3:F:9:DT:H1'	3:F:10:DT:C5'	2.43	0.49
4:K:211:THR:HG23	5:M:301:MET:HE3	1.94	0.49
4:L:138:ARG:NH1	4:L:142:VAL:HG21	2.27	0.49
5:M:128:HIS:HB3	5:M:134:SER:HB2	1.94	0.49
4:O:13:THR:HG21	5:R:295:TYR:HA	1.94	0.49
5:R:303:TYR:O	5:R:307:GLU:HG3	2.12	0.49
4:T:226:PHE:HB2	4:T:234:TYR:CD1	2.46	0.49
2:E:17:DA:H1'	2:E:18:DC:H5'	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:226:PHE:HB2	4:H:234:TYR:CD1	2.47	0.49
5:N:164:LEU:O	5:N:168:THR:HG23	2.13	0.49
5:J:159:HIS:CD2	5:J:162:PHE:CE2	3.00	0.49
4:S:49:LEU:HD23	5:U:282:LEU:HD22	1.95	0.49
1:C:347:TRP:CZ2	1:C:351:MET:HG3	2.48	0.48
2:E:5:DC:H2''	2:E:6:DC:C6	2.48	0.48
3:F:43:DT:H1'	3:F:44:DT:C5'	2.43	0.48
4:G:121:GLU:HB2	4:G:124:LEU:HD21	1.95	0.48
5:R:280:ARG:HA	5:R:283:LYS:HE2	1.95	0.48
1:B:347:TRP:CD1	1:B:351:MET:HE1	2.48	0.48
1:C:340:SER:O	1:C:344:LEU:HG	2.13	0.48
1:D:59:MET:HE3	1:D:60:LEU:O	2.12	0.48
2:E:6:DC:H2'	2:E:6:DC:P	2.53	0.48
3:F:45:DT:H1'	3:F:46:DA:O5'	2.13	0.48
5:U:169:PHE:CE2	5:V:147:MET:HE3	2.48	0.48
1:A:213:GLU:OE2	1:A:315:ARG:HA	2.12	0.48
1:D:92:THR:HG22	1:D:101:GLU:OE1	2.14	0.48
1:D:94:LEU:HD23	1:D:94:LEU:N	2.27	0.48
4:G:68:LEU:HD13	4:G:145:LEU:HB3	1.96	0.48
5:M:158:TYR:CE2	5:M:193:LEU:HD13	2.48	0.48
1:C:298:LYS:HG3	1:C:301:ARG:NH1	2.29	0.48
2:E:19:DC:H1'	2:E:20:DT:O5'	2.12	0.48
4:K:102:PHE:CG	4:K:103:THR:N	2.81	0.48
4:K:229:TYR:HB3	4:K:233:GLU:HG3	1.94	0.48
5:Q:157:LYS:NZ	5:Q:192:SER:OG	2.46	0.48
5:Q:219:SER:HB2	5:Q:222:MET:HE1	1.96	0.48
4:S:210:LEU:HD22	5:U:297:ALA:HB3	1.96	0.48
1:B:149:ILE:HD11	1:B:151:ASP:HB3	1.96	0.48
1:D:235:LEU:HD12	1:D:239:ASN:HB2	1.95	0.48
5:N:243:LEU:HD13	5:N:314:CYS:SG	2.54	0.48
5:R:152:LEU:HD23	5:R:165:LEU:HD12	1.93	0.48
4:S:67:LEU:HA	4:S:70:ILE:HB	1.93	0.48
1:A:158:ILE:HG23	1:A:167:LEU:HD11	1.94	0.48
1:C:195:LEU:HB2	1:C:200:LYS:HB3	1.96	0.48
4:O:119:PRO:CD	5:Q:246:LEU:HD21	2.44	0.48
5:R:178:MET:HE2	5:R:182:GLN:C	2.39	0.48
1:B:135:ILE:HD12	1:B:138:ILE:HD11	1.95	0.48
1:D:32:CYS:HA	1:D:43:VAL:CG1	2.44	0.48
3:F:26:DT:C2'	3:F:27:DT:H71	2.44	0.48
4:O:252:MET:HE2	5:Q:331:ILE:HB	1.95	0.48
4:P:71:PHE:HD1	4:P:80:ILE:HD12	1.76	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:U:298:ALA:HA	5:U:301:MET:HE2	1.94	0.48
1:A:81:LEU:HD11	1:A:141:LEU:HD21	1.95	0.48
2:E:1:DT:H73	2:E:1:DT:OP1	2.14	0.48
4:K:226:PHE:CD2	4:K:234:TYR:CD1	3.01	0.48
4:P:144:MET:SD	5:R:301:MET:HE1	2.53	0.48
1:C:22:LYS:HD2	1:D:206:ASN:ND2	2.28	0.48
1:D:250:ILE:HA	1:D:253:ILE:HD12	1.96	0.48
4:G:94:ARG:HE	4:G:260:LEU:HD22	1.78	0.48
4:G:151:THR:HG22	5:I:293:MET:HE1	1.96	0.48
4:H:231:VAL:O	4:H:234:TYR:HB3	2.14	0.48
5:I:153:LEU:HD23	5:J:153:LEU:CD2	2.43	0.48
5:M:171:ASP:OD1	5:R:174:CYS:HA	2.13	0.48
5:Q:196:MET:HE1	5:Q:200:THR:OG1	2.14	0.48
5:U:249:GLU:HA	5:U:252:GLU:HG2	1.96	0.48
5:U:290:LEU:HG	5:U:294:TYR:CE2	2.48	0.48
1:B:155:VAL:CG2	1:B:166:ILE:HD11	2.42	0.48
1:B:239:ASN:O	1:B:242:ASP:OD1	2.32	0.48
1:C:25:ARG:HG3	1:D:206:ASN:OD1	2.14	0.48
1:D:65:LEU:O	1:D:99:VAL:HG22	2.14	0.48
1:D:350:PHE:O	1:D:353:GLU:HG2	2.14	0.48
3:F:37:DA:H1'	3:F:38:DA:O5'	2.14	0.48
5:I:277:PHE:CE1	5:I:281:LEU:HD11	2.49	0.48
4:P:92:HIS:NE2	4:P:99:VAL:HG12	2.29	0.48
4:S:229:TYR:HB3	4:S:233:GLU:HG3	1.96	0.48
1:C:155:VAL:HG12	1:C:229:THR:HG21	1.96	0.47
1:D:105:ILE:HG22	1:D:106:ARG:N	2.29	0.47
4:H:210:LEU:HD21	5:J:294:TYR:HA	1.95	0.47
4:K:65:GLN:HG3	4:K:69:GLU:OE1	2.14	0.47
5:Q:290:LEU:O	5:Q:293:MET:HB2	2.13	0.47
4:G:24:LYS:HZ2	5:J:295:TYR:HE1	1.59	0.47
4:H:241:HIS:HD1	5:J:320:ASP:CG	2.22	0.47
5:J:255:GLN:HG3	4:L:169:THR:HG22	1.96	0.47
4:O:16:VAL:HG22	4:P:265:LYS:NZ	2.29	0.47
5:R:255:GLN:C	5:R:256:MET:HE2	2.39	0.47
5:U:281:LEU:O	5:U:285:ILE:HG12	2.14	0.47
5:V:168:THR:HB	5:V:214:ALA:HB2	1.96	0.47
4:G:92:HIS:HB3	4:G:102:PHE:CZ	2.49	0.47
4:S:264:PHE:HE2	5:U:294:TYR:CE2	2.33	0.47
1:D:161:GLU:N	1:D:161:GLU:OE1	2.46	0.47
2:E:17:DA:H1'	2:E:18:DC:C5'	2.44	0.47
4:G:55:MET:SD	4:G:209:TYR:CZ	3.07	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:125:LYS:HG3	5:J:126:LEU:HD12	1.96	0.47
5:J:143:SER:O	5:J:147:MET:HG2	2.15	0.47
5:U:119:TYR:HB3	5:U:151:PHE:HB2	1.96	0.47
5:U:131:SER:N	5:U:209:MET:HE1	2.29	0.47
1:D:234:ILE:O	1:D:234:ILE:HG13	2.14	0.47
5:I:146:VAL:HG13	5:J:149:MET:SD	2.54	0.47
5:J:246:LEU:HD21	5:J:312:SER:HB2	1.95	0.47
4:O:274:ILE:CD1	5:Q:227:ILE:HB	2.44	0.47
4:P:132:LEU:HD13	4:P:223:TYR:CE1	2.49	0.47
5:Q:118:ARG:HG2	5:Q:147:MET:CE	2.43	0.47
5:R:147:MET:HE2	5:R:147:MET:HA	1.97	0.47
4:S:108:PHE:CE1	5:U:263:ILE:HD12	2.50	0.47
5:U:135:THR:HG22	5:U:303:TYR:CD2	2.50	0.47
1:A:28:LYS:N	1:A:29:PRO:CD	2.77	0.47
1:B:22:LYS:HD3	1:B:24:MET:O	2.15	0.47
1:C:93:ILE:HD12	1:C:100:TYR:O	2.15	0.47
1:C:178:TYR:CD1	1:C:215:ARG:NH2	2.83	0.47
4:G:88:LEU:HD12	4:G:102:PHE:CE2	2.50	0.47
4:H:221:LEU:O	4:H:225:ILE:HG12	2.15	0.47
5:I:119:TYR:HA	5:I:147:MET:HG3	1.96	0.47
5:M:161:LEU:HD21	5:M:190:VAL:HG12	1.96	0.47
1:A:89:ALA:HB3	1:A:104:LEU:HB3	1.95	0.47
1:B:124:MET:N	1:B:124:MET:SD	2.88	0.47
1:C:131:ILE:HD12	1:C:360:LEU:HD11	1.97	0.47
1:C:345:LEU:O	1:C:348:GLU:HG3	2.15	0.47
1:D:126:VAL:O	1:D:130:ILE:HG12	2.14	0.47
1:D:131:ILE:HA	1:D:134:VAL:HG22	1.96	0.47
2:E:14:DA:H2''	2:E:15:DA:H5'	1.96	0.47
2:E:47:DT:H1'	2:E:48:DT:C5'	2.45	0.47
2:E:51:DT:H1'	2:E:52:DT:C5'	2.45	0.47
3:F:30:DT:H1'	3:F:31:DT:C6	2.49	0.47
4:G:81:ALA:HB1	4:G:108:PHE:CD1	2.49	0.47
5:I:113:LEU:N	5:J:163:LYS:HZ1	2.13	0.47
5:J:172:TYR:CD2	5:U:174:CYS:HB3	2.50	0.47
5:M:217:PHE:O	5:N:143:SER:HB3	2.15	0.47
5:Q:229:LEU:HD11	5:Q:306:MET:HB2	1.95	0.47
4:S:138:ARG:O	4:S:142:VAL:HG23	2.15	0.47
1:A:71:ASN:O	1:B:94:LEU:HD23	2.15	0.47
1:A:227:TYR:OH	1:A:283:MET:O	2.33	0.47
1:D:128:LYS:O	1:D:131:ILE:HG22	2.15	0.47
2:E:33:DA:OP2	2:E:33:DA:H8	1.98	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:30:DT:H2''	3:F:31:DT:OP2	2.15	0.47
4:G:111:THR:OG1	4:G:137:ASP:HA	2.15	0.47
4:K:45:LEU:O	4:K:49:LEU:HG	2.15	0.47
4:L:118:ILE:HG23	5:N:247:LEU:HD11	1.97	0.47
4:S:49:LEU:CD2	5:U:282:LEU:HD22	2.45	0.47
4:T:72:ARG:HH21	4:T:142:VAL:HG11	1.80	0.47
5:V:164:LEU:HD21	5:V:210:ARG:HD2	1.96	0.47
1:A:260:CYS:SG	1:A:261:PRO:HD2	2.55	0.47
4:G:125:PHE:HD2	4:G:132:LEU:HD22	1.79	0.47
5:J:116:MET:HE3	5:J:151:PHE:CE1	2.50	0.47
5:Q:228:VAL:HG23	5:R:224:TYR:CD2	2.50	0.47
4:S:111:THR:HG1	4:S:137:ASP:HA	1.80	0.47
4:T:256:THR:O	4:T:256:THR:HG22	2.14	0.47
5:U:244:GLU:HG2	5:U:245:GLU:N	2.30	0.47
1:D:79:ARG:HA	1:D:82:LEU:HD23	1.97	0.47
3:F:12:DA:H1'	3:F:13:DA:C8	2.49	0.47
3:F:23:DG:H1'	3:F:24:DT:O5'	2.15	0.47
4:G:72:ARG:HD3	4:G:142:VAL:HG13	1.97	0.47
4:G:249:ARG:HA	5:I:331:ILE:HG22	1.97	0.47
5:J:173:THR:O	5:U:174:CYS:HB2	2.15	0.47
1:D:237:GLN:HE21	1:D:272:LEU:HD12	1.81	0.46
3:F:54:DG:H1'	3:F:55:DA:H5'	1.97	0.46
3:F:56:DA:C2'	3:F:57:DT:H71	2.45	0.46
4:G:61:LEU:HD11	4:G:86:SER:CB	2.44	0.46
4:K:71:PHE:CE2	4:K:141:ILE:HG22	2.50	0.46
5:N:142:ILE:HA	5:N:145:VAL:HG12	1.97	0.46
5:N:209:MET:HE2	5:N:213:PHE:CZ	2.49	0.46
4:O:222:HIS:ND1	4:O:238:LEU:HD23	2.30	0.46
1:A:138:ILE:HD11	1:A:226:LEU:HD11	1.97	0.46
1:C:155:VAL:HG22	1:C:166:ILE:HD11	1.96	0.46
1:C:221:TYR:CD1	1:C:296:TYR:HD2	2.34	0.46
1:D:60:LEU:HA	1:D:103:MET:O	2.15	0.46
1:D:289:ILE:HB	1:D:343:HIS:CD2	2.50	0.46
2:E:14:DA:H2''	2:E:15:DA:C8	2.51	0.46
3:F:36:DT:OP1	3:F:36:DT:H3'	2.16	0.46
4:G:56:ALA:HB1	5:I:272:CYS:HB3	1.97	0.46
4:G:274:ILE:HD11	5:I:227:ILE:HB	1.96	0.46
5:I:140:TYR:O	5:J:221:ILE:HG12	2.15	0.46
5:M:175:ARG:O	5:M:176:PRO:C	2.58	0.46
4:O:268:ILE:HB	4:O:271:PHE:CZ	2.50	0.46
1:A:249:SER:O	1:A:252:ILE:HG22	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:108:ILE:HG22	1:C:109:ARG:N	2.31	0.46
1:C:224:PHE:CZ	1:C:347:TRP:HD1	2.33	0.46
1:D:32:CYS:SG	1:D:34:ILE:HB	2.55	0.46
1:D:60:LEU:HD11	1:D:102:CYS:HB3	1.96	0.46
1:D:123:ASN:CG	1:D:126:VAL:HG23	2.41	0.46
1:D:154:TYR:HB2	1:D:229:THR:HG22	1.97	0.46
2:E:51:DT:H3'	2:E:51:DT:OP1	2.16	0.46
4:H:264:PHE:C	4:H:265:LYS:HD2	2.40	0.46
5:J:114:ILE:HD11	5:J:154:ARG:HE	1.78	0.46
5:J:123:ALA:O	5:J:127:ILE:HG12	2.16	0.46
5:M:299:ASN:ND2	5:N:227:ILE:H	2.12	0.46
4:P:163:ASN:O	4:P:166:ILE:HG22	2.16	0.46
5:Q:249:GLU:HA	5:Q:252:GLU:HG2	1.98	0.46
5:R:123:ALA:N	5:R:148:THR:HG22	2.30	0.46
1:A:72:GLU:OE1	1:B:94:LEU:O	2.32	0.46
1:A:262:ASN:HB2	1:A:281:HIS:CE1	2.50	0.46
1:B:85:ASP:CG	1:B:90:ARG:HE	2.23	0.46
1:B:236:LYS:HE3	1:B:273:ASN:OD1	2.15	0.46
2:E:28:DA:H2''	2:E:29:DA:N7	2.31	0.46
3:F:34:DC:H2''	3:F:35:DC:C5	2.50	0.46
4:G:111:THR:HG22	5:I:254:ILE:HD12	1.98	0.46
4:L:234:TYR:CZ	4:L:238:LEU:HD11	2.50	0.46
5:M:164:LEU:HD11	5:M:186:LEU:HD22	1.97	0.46
5:R:301:MET:N	5:R:301:MET:HE2	2.30	0.46
4:S:144:MET:HE2	4:S:211:THR:HG23	1.95	0.46
4:T:68:LEU:HB2	4:T:208:GLN:NE2	2.30	0.46
5:U:302:PHE:CE2	5:U:306:MET:CE	2.99	0.46
1:A:24:MET:N	1:B:206:ASN:HB2	2.31	0.46
1:A:131:ILE:HG22	1:A:230:VAL:HG12	1.96	0.46
1:D:231:LEU:O	1:D:235:LEU:HG	2.15	0.46
2:E:31:DT:H1'	2:E:32:DA:C5'	2.45	0.46
5:J:303:TYR:O	5:J:307:GLU:HG3	2.16	0.46
5:M:194:LEU:HD13	5:M:201:ILE:HD11	1.96	0.46
5:R:159:HIS:O	5:R:162:PHE:HB3	2.16	0.46
5:R:205:THR:O	5:R:209:MET:HG2	2.15	0.46
4:S:248:LEU:HD12	4:S:252:MET:HB2	1.97	0.46
1:A:148:LEU:HD12	1:A:148:LEU:O	2.15	0.46
1:B:122:HIS:O	1:B:122:HIS:CG	2.69	0.46
4:G:141:ILE:HD11	4:G:212:LEU:CD2	2.45	0.46
4:H:47:ILE:HG21	5:J:294:TYR:OH	2.16	0.46
4:H:210:LEU:HD23	5:J:293:MET:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:68:LEU:HD11	4:K:145:LEU:HB3	1.97	0.46
5:R:168:THR:HG22	5:R:210:ARG:CZ	2.45	0.46
1:D:123:ASN:ND2	1:D:126:VAL:HG23	2.30	0.46
2:E:55:DA:C2	2:E:56:DT:C2	3.04	0.46
5:I:242:THR:HG22	5:I:315:LYS:HZ3	1.81	0.46
5:N:243:LEU:O	5:N:247:LEU:HD23	2.16	0.46
1:B:220:ILE:HB	1:B:313:ILE:HG21	1.98	0.46
1:B:307:LYS:NZ	2:E:18:DC:H3'	2.30	0.46
3:F:9:DT:OP1	3:F:9:DT:H3'	2.16	0.46
4:K:92:HIS:NE2	4:K:99:VAL:HG11	2.30	0.46
5:N:159:HIS:HB3	5:N:163:LYS:NZ	2.31	0.46
5:Q:327:VAL:O	5:Q:331:ILE:HG12	2.16	0.46
5:R:300:THR:C	5:R:301:MET:HE2	2.40	0.46
5:R:301:MET:HE2	5:R:301:MET:HA	1.98	0.46
1:A:153:MET:HE2	1:A:243:VAL:O	2.16	0.46
1:C:152:ARG:HD3	1:C:242:ASP:OD2	2.16	0.46
5:J:202:ASP:OD1	5:J:205:THR:HG23	2.16	0.46
5:M:220:PRO:HA	5:N:141:LYS:HA	1.97	0.46
5:N:158:TYR:CE1	5:N:193:LEU:HD11	2.51	0.46
5:R:178:MET:HE1	5:R:186:LEU:CG	2.46	0.46
4:T:54:TYR:CZ	4:T:58:LEU:HD11	2.51	0.46
5:U:307:GLU:O	5:U:311:VAL:HG12	2.15	0.46
1:A:24:MET:HE2	1:B:203:THR:OG1	2.15	0.46
1:A:131:ILE:CG2	1:A:230:VAL:HG12	2.46	0.46
1:D:124:MET:HB2	1:D:358:PHE:CE1	2.51	0.46
2:E:54:DA:H2''	2:E:55:DA:H8	1.81	0.46
4:G:10:ARG:HA	4:G:24:LYS:O	2.16	0.46
4:G:61:LEU:O	4:G:62:GLU:HG3	2.15	0.46
4:L:141:ILE:O	4:L:145:LEU:HD23	2.16	0.46
5:M:114:ILE:HD13	5:M:150:ILE:HG22	1.98	0.46
4:P:222:HIS:HB3	4:P:234:TYR:HE1	1.81	0.46
4:S:222:HIS:CE1	4:S:238:LEU:HD23	2.51	0.46
1:C:114:ARG:C	1:C:158:ILE:HG23	2.41	0.45
1:C:227:TYR:OH	1:C:285:PRO:HD3	2.16	0.45
1:C:266:ARG:HA	1:C:286:PRO:HA	1.98	0.45
3:F:9:DT:H1'	3:F:10:DT:H5'	1.99	0.45
3:F:14:DT:C2'	3:F:15:DT:H71	2.44	0.45
5:V:166:GLU:OE2	5:V:167:THR:HG23	2.16	0.45
1:C:355:SER:HB3	1:C:360:LEU:HB2	1.98	0.45
3:F:14:DT:OP1	3:F:14:DT:H3'	2.16	0.45
4:G:13:THR:HG21	5:J:295:TYR:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:120:GLY:HA2	5:I:305:THR:HG23	1.99	0.45
5:N:116:MET:HA	5:N:119:TYR:CD1	2.51	0.45
1:B:141:LEU:HD11	1:B:145:GLU:C	2.42	0.45
1:C:76:LEU:CD2	1:C:78:TYR:HE1	2.29	0.45
1:D:101:GLU:HG3	1:D:103:MET:SD	2.56	0.45
2:E:45:DA:C8	2:E:46:DT:H72	2.51	0.45
5:R:193:LEU:C	5:R:194:LEU:HD22	2.41	0.45
1:A:269:CYS:HB2	1:A:283:MET:O	2.16	0.45
1:B:62:MET:SD	1:B:100:TYR:HB3	2.57	0.45
1:B:234:ILE:HG13	1:B:274:TYR:HD1	1.82	0.45
1:C:128:LYS:HA	1:C:131:ILE:HG12	1.98	0.45
1:C:134:VAL:HG11	1:C:226:LEU:CD1	2.47	0.45
1:C:153:MET:N	1:C:242:ASP:OD1	2.49	0.45
1:C:224:PHE:HZ	1:C:289:ILE:HD12	1.81	0.45
4:H:116:THR:HA	5:J:254:ILE:HD11	1.98	0.45
5:I:119:TYR:HB3	5:I:151:PHE:HB2	1.97	0.45
5:I:148:THR:O	5:I:152:LEU:HD23	2.17	0.45
5:I:149:MET:HE3	5:J:146:VAL:HG13	1.99	0.45
5:J:175:ARG:NH2	5:U:170:ASP:HB3	2.32	0.45
5:M:207:ASP:OD2	5:M:233:VAL:HG12	2.17	0.45
5:M:295:TYR:CD1	5:M:299:ASN:OD1	2.69	0.45
4:P:55:MET:HB3	5:R:281:LEU:HD13	1.98	0.45
1:A:205:ASN:HA	1:B:24:MET:SD	2.56	0.45
1:A:212:ASP:OD1	1:A:213:GLU:N	2.48	0.45
1:B:124:MET:SD	5:N:192:SER:HA	2.57	0.45
1:D:8:ILE:O	1:D:9:LYS:HE2	2.17	0.45
1:D:80:HIS:O	1:D:81:LEU:HD23	2.16	0.45
3:F:57:DT:H1'	3:F:58:DA:C8	2.51	0.45
4:G:205:GLU:O	4:G:209:TYR:CD2	2.70	0.45
4:H:117:SER:HG	4:H:137:ASP:CG	2.25	0.45
4:H:225:ILE:HG23	4:H:233:GLU:OE1	2.17	0.45
4:K:80:ILE:O	4:K:84:VAL:HG23	2.16	0.45
4:O:56:ALA:HB1	5:Q:272:CYS:CB	2.46	0.45
5:Q:114:ILE:CG2	5:R:166:GLU:OE1	2.65	0.45
5:R:164:LEU:C	5:R:164:LEU:HD23	2.41	0.45
1:A:70:LEU:HD13	1:A:76:LEU:N	2.32	0.45
1:B:178:TYR:N	1:B:210:SER:HB3	2.32	0.45
4:G:136:VAL:O	4:G:136:VAL:HG23	2.16	0.45
5:V:168:THR:HG21	5:V:210:ARG:HG2	1.97	0.45
5:V:306:MET:HE1	5:V:316:PHE:CG	2.52	0.45
1:A:235:LEU:HD23	1:A:274:TYR:CD1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:267:VAL:HG12	1:D:268:LYS:N	2.31	0.45
2:E:38:DA:H1'	2:E:39:DA:O5'	2.16	0.45
3:F:48:DC:H1'	3:F:49:DG:C8	2.51	0.45
4:H:138:ARG:HB3	4:H:139:PRO:HD3	1.98	0.45
5:M:291:SER:O	5:N:229:LEU:HD11	2.16	0.45
5:N:301:MET:HG3	5:N:321:TYR:OH	2.16	0.45
5:R:300:THR:HG22	5:R:301:MET:CE	2.46	0.45
1:A:227:TYR:O	1:A:230:VAL:HG22	2.16	0.45
4:K:72:ARG:HH22	4:K:142:VAL:HG21	1.82	0.45
5:M:207:ASP:OD2	5:M:233:VAL:HA	2.17	0.45
4:O:43:GLU:HA	4:O:46:LYS:HG2	1.99	0.45
4:O:77:THR:CG2	4:O:110:VAL:HG21	2.47	0.45
4:O:105:LYS:HG3	4:O:131:VAL:HG11	1.98	0.45
1:B:30:MET:HE2	1:B:64:VAL:HG23	1.98	0.45
1:B:101:GLU:OE2	1:B:103:MET:CE	2.65	0.45
1:C:246:GLU:OE2	1:D:16:VAL:HG22	2.17	0.45
1:C:299:TRP:CH2	1:C:302:ASN:O	2.70	0.45
4:G:252:MET:HE2	4:G:259:LEU:HG	1.98	0.45
4:H:141:ILE:O	4:H:145:LEU:HD23	2.16	0.45
4:K:70:ILE:O	4:K:80:ILE:HD11	2.16	0.45
4:K:123:ILE:HD11	4:K:141:ILE:HD11	1.99	0.45
5:M:131:SER:N	5:M:209:MET:HE1	2.31	0.45
4:O:81:ALA:HB1	4:O:108:PHE:CD2	2.52	0.45
4:P:132:LEU:HD13	4:P:223:TYR:HE1	1.81	0.45
1:B:59:MET:C	1:B:60:LEU:HD22	2.42	0.45
1:B:93:ILE:HG22	1:B:100:TYR:HD2	1.81	0.45
1:D:48:ASN:C	4:G:275:ASN:HB3	2.42	0.45
1:D:122:HIS:HE1	1:D:277:VAL:HG22	1.82	0.45
1:D:132:ASP:HA	1:D:135:ILE:HG22	1.99	0.45
3:F:18:DT:H6	3:F:18:DT:H2'	1.61	0.45
5:I:216:CYS:HB2	5:J:222:MET:HE2	1.98	0.45
4:K:12:VAL:HG22	4:K:23:GLN:HG3	1.99	0.45
4:K:24:LYS:HB2	5:N:295:TYR:OH	2.17	0.45
5:M:219:SER:O	5:N:142:ILE:HG12	2.17	0.45
4:O:31:PHE:O	5:R:310:ALA:HB1	2.17	0.45
4:P:138:ARG:HB3	4:P:139:PRO:HD3	1.98	0.45
5:Q:156:GLU:HA	5:Q:159:HIS:NE2	2.32	0.45
5:U:243:LEU:HD12	5:U:244:GLU:N	2.32	0.45
1:B:260:CYS:HB2	1:B:267:VAL:O	2.17	0.44
4:H:54:TYR:CE2	4:H:58:LEU:HD11	2.52	0.44
4:H:166:ILE:HD13	5:V:248:ILE:HG13	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:171:ASP:O	5:I:172:TYR:CG	2.69	0.44
4:K:47:ILE:HG23	4:K:260:LEU:HD11	1.98	0.44
5:M:194:LEU:HD13	5:M:201:ILE:CD1	2.47	0.44
4:O:87:THR:O	4:O:91:ILE:HG12	2.17	0.44
5:Q:178:MET:HB2	5:Q:182:GLN:OE1	2.17	0.44
5:R:250:ARG:O	5:R:254:ILE:HG13	2.17	0.44
4:T:222:HIS:CE1	4:T:238:LEU:HD23	2.52	0.44
5:U:146:VAL:HG11	5:V:169:PHE:HZ	1.78	0.44
1:A:235:LEU:HD22	1:A:237:GLN:HG3	1.98	0.44
1:A:267:VAL:HG23	1:A:287:ARG:HH22	1.82	0.44
4:G:43:GLU:O	4:G:47:ILE:HG12	2.17	0.44
4:G:144:MET:HE1	5:I:301:MET:HG2	2.00	0.44
4:G:148:GLU:O	5:I:133:ASN:O	2.36	0.44
4:H:55:MET:CG	5:J:281:LEU:HD13	2.48	0.44
4:K:27:GLU:HB3	4:K:30:GLU:OE1	2.17	0.44
4:S:133:LEU:CD1	5:U:259:PRO:HB3	2.47	0.44
5:V:202:ASP:O	5:V:206:VAL:HG23	2.17	0.44
1:C:154:TYR:HD1	1:C:242:ASP:OD1	2.00	0.44
1:C:213:GLU:CG	1:C:314:ALA:HB3	2.47	0.44
1:D:130:ILE:HD13	1:D:164:ALA:HB2	1.99	0.44
1:D:151:ASP:OD1	1:D:152:ARG:N	2.50	0.44
1:D:257:LEU:HD11	1:D:268:LYS:O	2.17	0.44
4:K:202:THR:OG1	4:K:205:GLU:HG3	2.18	0.44
5:M:132:LEU:HD11	5:M:303:TYR:CD1	2.52	0.44
5:Q:295:TYR:CE1	5:Q:299:ASN:OD1	2.70	0.44
5:R:155:SER:OG	5:R:158:TYR:HB2	2.18	0.44
1:B:131:ILE:O	1:B:135:ILE:HG22	2.17	0.44
1:C:59:MET:C	1:C:60:LEU:HD22	2.42	0.44
1:C:75:LYS:NZ	1:C:80:HIS:HB2	2.33	0.44
1:C:117:ASP:O	1:C:118:GLU:HB2	2.16	0.44
1:C:177:ASP:HB2	1:C:192:CYS:SG	2.58	0.44
1:C:245:ALA:HB3	1:C:248:THR:OG1	2.18	0.44
1:D:216:GLN:HA	1:D:219:TYR:HD2	1.82	0.44
3:F:24:DT:H1'	3:F:25:DT:O5'	2.17	0.44
4:G:107:GLU:OE2	4:G:131:VAL:HG11	2.17	0.44
4:L:226:PHE:CE2	4:L:231:VAL:HG22	2.52	0.44
5:N:158:TYR:CZ	5:N:193:LEU:HD21	2.53	0.44
4:O:44:THR:HG22	5:Q:290:LEU:HD11	1.99	0.44
5:R:193:LEU:O	5:R:194:LEU:HD22	2.18	0.44
5:R:303:TYR:HA	5:R:306:MET:HE3	1.99	0.44
5:V:163:LYS:HA	5:V:166:GLU:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:V:187:LEU:O	5:V:201:ILE:HD11	2.18	0.44
5:V:277:PHE:CE1	5:V:281:LEU:HD11	2.52	0.44
1:A:46:PRO:HG2	1:A:58:ASP:HB2	1.99	0.44
1:B:22:LYS:HD2	1:B:22:LYS:O	2.18	0.44
1:B:195:LEU:HB2	1:B:200:LYS:HG2	2.00	0.44
1:B:197:TYR:HB2	1:B:198:PRO:CD	2.47	0.44
1:B:286:PRO:HB3	1:B:343:HIS:CE1	2.52	0.44
2:E:18:DC:H2''	2:E:19:DC:C5	2.53	0.44
2:E:44:DA:O5'	2:E:44:DA:H2'	2.18	0.44
3:F:44:DT:H1'	3:F:45:DT:C5'	2.47	0.44
5:J:152:LEU:O	5:J:162:PHE:CE1	2.69	0.44
5:J:193:LEU:C	5:J:194:LEU:HD22	2.42	0.44
4:K:201:ILE:HB	5:M:284:HIS:CD2	2.52	0.44
5:Q:122:ALA:HB2	5:Q:147:MET:HE2	2.00	0.44
5:Q:163:LYS:HA	5:Q:163:LYS:HE2	1.99	0.44
5:V:152:LEU:CD1	5:V:161:LEU:HD11	2.36	0.44
1:B:67:SER:HA	1:B:99:VAL:HG21	2.00	0.44
1:B:76:LEU:CD2	1:B:78:TYR:HE2	2.31	0.44
1:C:77:TYR:HB3	1:C:173:ILE:HD11	2.00	0.44
2:E:56:DT:O2	2:E:57:DG:O4'	2.36	0.44
5:I:179:THR:HG23	5:I:182:GLN:H	1.82	0.44
5:M:114:ILE:HG21	5:M:150:ILE:HG21	1.98	0.44
5:N:159:HIS:O	5:N:162:PHE:HB2	2.17	0.44
4:O:16:VAL:HG22	4:P:265:LYS:CE	2.47	0.44
4:S:58:LEU:O	4:S:63:MET:HE1	2.18	0.44
4:S:118:ILE:HD12	4:S:119:PRO:HD2	2.00	0.44
5:U:145:VAL:O	5:U:149:MET:HG3	2.18	0.44
1:C:286:PRO:O	1:C:290:THR:HG23	2.18	0.44
1:D:64:VAL:C	1:D:65:LEU:HD12	2.42	0.44
3:F:33:DT:H2''	3:F:34:DC:O4'	2.18	0.44
4:G:247:LYS:C	4:G:248:LEU:HD22	2.43	0.44
4:K:211:THR:CG2	5:M:301:MET:HE3	2.47	0.44
5:N:128:HIS:CD2	5:N:132:LEU:HD11	2.52	0.44
5:R:126:LEU:HD11	5:R:130:TYR:CZ	2.53	0.44
4:S:144:MET:HE1	5:U:301:MET:N	2.32	0.44
5:U:280:ARG:HE	5:U:281:LEU:HD22	1.82	0.44
5:V:166:GLU:HA	5:V:169:PHE:CD1	2.53	0.44
2:E:14:DA:C2'	2:E:15:DA:C8	3.00	0.44
3:F:36:DT:H1'	3:F:37:DA:C8	2.53	0.44
4:G:232:PHE:CE2	4:K:164:VAL:HA	2.53	0.44
5:I:286:ASP:N	5:I:287:PRO:HD2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:159:HIS:HA	5:J:162:PHE:CG	2.53	0.44
5:M:166:GLU:O	5:M:169:PHE:HB2	2.18	0.44
4:O:245:THR:OG1	5:Q:327:VAL:HG22	2.17	0.44
5:R:279:ASN:HB3	5:R:283:LYS:NZ	2.33	0.44
4:T:55:MET:HE1	5:V:285:ILE:HG21	2.00	0.44
5:V:321:TYR:HA	5:V:324:ILE:HD12	2.00	0.44
1:C:119:ALA:HB3	1:C:233:ALA:O	2.17	0.44
3:F:21:DT:H1'	3:F:22:DT:H5'	2.00	0.44
4:G:212:LEU:O	4:G:216:VAL:HG23	2.17	0.44
5:J:246:LEU:HG	5:J:250:ARG:HE	1.83	0.44
4:L:138:ARG:HH12	4:L:142:VAL:HG21	1.83	0.44
5:N:158:TYR:CD1	5:N:193:LEU:HD11	2.53	0.44
4:O:249:ARG:NE	4:O:249:ARG:HA	2.32	0.44
5:Q:165:LEU:HD23	5:Q:169:PHE:HE1	1.83	0.44
5:Q:167:THR:O	5:Q:170:ASP:OD1	2.36	0.44
5:Q:241:THR:HG22	5:Q:242:THR:O	2.18	0.44
5:R:302:PHE:CD2	5:R:306:MET:HE2	2.53	0.44
1:A:339:VAL:O	1:A:342:LEU:HG	2.18	0.43
1:A:342:LEU:HD12	1:A:342:LEU:C	2.43	0.43
1:B:120:GLY:HA2	1:B:234:ILE:C	2.42	0.43
1:C:221:TYR:CD1	1:C:293:PHE:CE1	3.05	0.43
1:D:221:TYR:HA	1:D:293:PHE:HE1	1.80	0.43
3:F:32:DC:P	3:F:32:DC:H2'	2.58	0.43
4:G:144:MET:HE1	5:I:301:MET:CG	2.48	0.43
4:G:174:LYS:HE3	5:U:252:GLU:OE1	2.18	0.43
5:J:152:LEU:O	5:J:162:PHE:HE1	2.01	0.43
4:S:89:ALA:HB1	5:U:269:ILE:CD1	2.48	0.43
1:B:266:ARG:HA	1:B:286:PRO:HA	2.00	0.43
1:D:153:MET:HB2	1:D:242:ASP:HA	2.00	0.43
2:E:32:DA:H2''	2:E:33:DA:H8	1.83	0.43
3:F:44:DT:H3'	3:F:44:DT:OP1	2.18	0.43
4:G:89:ALA:HA	4:G:102:PHE:CZ	2.52	0.43
5:J:120:ARG:HG2	5:J:151:PHE:CE1	2.53	0.43
5:M:286:ASP:N	5:M:287:PRO:HD2	2.33	0.43
5:R:152:LEU:HD11	5:R:158:TYR:O	2.18	0.43
4:S:270:ASP:O	4:S:274:ILE:HG12	2.19	0.43
5:V:243:LEU:HD22	5:V:314:CYS:SG	2.58	0.43
1:D:46:PRO:HG3	1:D:60:LEU:HB3	1.99	0.43
1:D:46:PRO:HD3	1:D:60:LEU:N	2.33	0.43
1:D:80:HIS:O	1:D:80:HIS:ND1	2.45	0.43
2:E:33:DA:H2''	2:E:34:DA:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:46:DT:H1'	2:E:47:DT:O5'	2.18	0.43
3:F:50:DT:H2''	3:F:51:DT:C6	2.54	0.43
4:G:67:LEU:HD12	4:G:212:LEU:CD1	2.48	0.43
4:L:54:TYR:CD1	4:L:213:LEU:HD21	2.52	0.43
5:M:149:MET:HE2	5:N:150:ILE:HG13	2.00	0.43
5:M:298:ALA:HB1	5:N:227:ILE:HG21	2.00	0.43
5:R:238:ASP:CG	5:R:239:LYS:H	2.26	0.43
1:A:17:LYS:C	1:A:18:LEU:HD22	2.43	0.43
1:B:154:TYR:CE2	1:B:156:ASP:OD1	2.71	0.43
2:E:55:DA:C8	2:E:56:DT:H72	2.53	0.43
3:F:50:DT:P	3:F:50:DT:H2'	2.58	0.43
4:G:233:GLU:OE2	4:K:30:GLU:HG3	2.18	0.43
5:J:131:SER:HA	5:J:209:MET:CE	2.48	0.43
4:K:243:LEU:O	4:K:246:ASN:OD1	2.36	0.43
4:L:210:LEU:HD11	5:N:297:ALA:HB2	2.00	0.43
5:M:196:MET:HE1	5:M:200:THR:HG23	1.99	0.43
4:O:211:THR:O	4:O:214:LEU:HG	2.19	0.43
5:R:164:LEU:HD21	5:R:210:ARG:CD	2.49	0.43
1:A:28:LYS:HG3	1:A:29:PRO:HD3	2.01	0.43
1:A:89:ALA:HB3	1:A:104:LEU:CB	2.49	0.43
1:C:227:TYR:OH	1:C:283:MET:O	2.37	0.43
1:D:45:ARG:HE	4:G:276:SER:HB2	1.83	0.43
1:D:154:TYR:HA	1:D:225:LEU:HG	2.01	0.43
1:D:195:LEU:HD12	1:D:199:TRP:HB3	2.00	0.43
4:H:222:HIS:HB3	4:H:234:TYR:CE1	2.54	0.43
4:H:248:LEU:HA	4:H:256:THR:HB	2.00	0.43
4:H:262:SER:HA	5:J:327:VAL:HG21	2.00	0.43
4:K:49:LEU:CD2	5:M:282:LEU:HD22	2.49	0.43
4:K:132:LEU:HD21	4:K:226:PHE:CZ	2.53	0.43
5:M:142:ILE:HD11	5:M:221:ILE:HG13	2.00	0.43
5:N:202:ASP:OD1	5:N:205:THR:HG23	2.18	0.43
4:P:264:PHE:C	4:P:265:LYS:HD3	2.44	0.43
5:U:302:PHE:HD1	5:U:321:TYR:CE2	2.37	0.43
5:V:161:LEU:C	5:V:161:LEU:HD12	2.44	0.43
5:V:301:MET:HE2	5:V:301:MET:N	2.33	0.43
1:A:191:VAL:HG22	1:A:192:CYS:N	2.34	0.43
1:C:147:ILE:HD12	1:C:173:ILE:HD13	2.01	0.43
1:C:152:ARG:HA	1:C:152:ARG:HE	1.81	0.43
1:C:297:ALA:O	1:C:300:VAL:HG12	2.18	0.43
2:E:28:DA:P	2:E:28:DA:H2'	2.57	0.43
3:F:16:DT:H2''	3:F:17:DT:C7	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:48:DC:C2'	3:F:49:DG:OP2	2.67	0.43
4:H:81:ALA:HB3	5:J:263:ILE:HD12	2.01	0.43
4:K:12:VAL:HG22	4:K:23:GLN:CG	2.48	0.43
4:L:54:TYR:CE1	4:L:213:LEU:HD21	2.53	0.43
4:O:126:THR:O	4:O:133:LEU:HG	2.19	0.43
5:R:277:PHE:HE1	5:R:281:LEU:HD11	1.83	0.43
4:S:207:THR:OG1	5:U:293:MET:HG3	2.18	0.43
4:T:87:THR:HG22	4:T:91:ILE:HD11	1.99	0.43
1:A:66:ASN:HD22	1:B:8:ILE:HG21	1.84	0.43
1:A:214:SER:HB3	1:A:311:GLU:OE2	2.19	0.43
1:A:358:PHE:HB2	1:A:360:LEU:HD23	2.01	0.43
1:B:151:ASP:O	1:B:152:ARG:HG3	2.18	0.43
1:C:94:LEU:HG	1:C:94:LEU:O	2.18	0.43
1:D:286:PRO:HB2	1:D:289:ILE:HG22	1.98	0.43
2:E:2:DA:H2'	2:E:3:DT:H71	2.00	0.43
2:E:6:DC:H1'	2:E:7:DA:H5'	2.00	0.43
4:G:94:ARG:HE	4:G:260:LEU:CD2	2.32	0.43
4:G:140:SER:O	4:G:143:LYS:HG2	2.19	0.43
5:J:126:LEU:O	5:J:130:TYR:HD1	2.01	0.43
4:K:104:ASN:O	5:M:265:SER:N	2.52	0.43
5:N:298:ALA:HA	5:N:301:MET:HE2	2.00	0.43
4:O:108:PHE:CD2	4:O:134:CYS:SG	3.12	0.43
4:S:225:ILE:HD12	4:S:247:LYS:HG3	2.00	0.43
4:T:114:ASN:ND2	5:V:311:VAL:HG11	2.34	0.43
1:A:203:THR:HG22	1:A:204:ALA:N	2.34	0.43
1:A:220:ILE:HD12	1:A:313:ILE:HG21	2.00	0.43
1:D:298:LYS:HE3	1:D:309:TYR:OH	2.19	0.43
4:H:55:MET:HG2	5:J:281:LEU:HD22	2.01	0.43
5:J:124:ARG:HG3	5:J:193:LEU:HD12	2.00	0.43
4:P:145:LEU:CD1	4:P:208:GLN:HB3	2.48	0.43
4:S:108:PHE:HE1	5:U:263:ILE:HD12	1.83	0.43
1:A:72:GLU:OE2	1:B:93:ILE:CG2	2.62	0.43
1:A:173:ILE:HG22	1:A:174:ILE:N	2.34	0.43
1:A:262:ASN:HB2	1:A:281:HIS:ND1	2.33	0.43
5:J:117:ARG:CG	5:J:118:ARG:N	2.82	0.43
4:K:205:GLU:HA	4:K:208:GLN:OE1	2.19	0.43
4:K:252:MET:C	4:K:252:MET:SD	3.02	0.43
5:M:295:TYR:CE1	5:M:299:ASN:OD1	2.72	0.43
4:O:119:PRO:CG	5:Q:246:LEU:HD21	2.49	0.43
4:O:270:ASP:O	4:O:271:PHE:C	2.62	0.43
4:S:111:THR:OG1	4:S:137:ASP:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:T:147:ARG:CB	5:V:300:THR:HG23	2.48	0.43
5:U:142:ILE:HA	5:U:145:VAL:HG22	2.00	0.43
1:A:206:ASN:HA	1:B:25:ARG:NH1	2.34	0.43
1:C:154:TYR:CD1	1:C:242:ASP:OD1	2.72	0.43
1:D:296:TYR:CE2	1:D:309:TYR:O	2.72	0.43
2:E:53:DA:H2''	2:E:54:DA:OP2	2.18	0.43
3:F:30:DT:H2''	3:F:31:DT:C5	2.54	0.43
3:F:50:DT:H2''	3:F:51:DT:H71	2.01	0.43
5:J:146:VAL:O	5:J:149:MET:HG2	2.19	0.43
4:O:54:TYR:HH	4:O:87:THR:HG22	1.82	0.43
4:O:147:ARG:CZ	5:Q:132:LEU:O	2.67	0.43
4:O:225:ILE:HD12	4:O:247:LYS:HG3	2.00	0.43
5:R:175:ARG:NH2	5:R:178:MET:SD	2.92	0.43
4:T:214:LEU:HA	4:T:217:GLU:HG2	2.00	0.43
1:B:73:HIS:CB	1:B:75:LYS:HE2	2.49	0.42
1:B:123:ASN:ND2	1:B:126:VAL:HG23	2.33	0.42
1:D:239:ASN:ND2	1:D:242:ASP:OD1	2.51	0.42
1:D:351:MET:HE3	1:D:365:VAL:HG21	2.00	0.42
2:E:20:DT:C2	3:F:40:DG:N2	2.87	0.42
2:E:31:DT:H6	2:E:31:DT:H2'	1.71	0.42
4:K:147:ARG:CD	5:M:300:THR:HG23	2.49	0.42
5:M:173:THR:OG1	5:R:173:THR:N	2.52	0.42
4:O:78:ARG:HA	5:Q:261:GLN:HG2	2.01	0.42
4:O:91:ILE:HG21	4:O:220:TYR:CG	2.54	0.42
5:R:178:MET:CE	5:R:186:LEU:HD23	2.49	0.42
5:V:123:ALA:HA	5:V:148:THR:HG23	2.00	0.42
1:A:24:MET:HE2	1:B:203:THR:HG21	2.01	0.42
1:C:43:VAL:HG22	1:C:44:THR:N	2.34	0.42
1:C:199:TRP:NE1	1:D:102:CYS:HB2	2.34	0.42
3:F:57:DT:H1'	3:F:58:DA:O5'	2.19	0.42
4:G:133:LEU:N	4:G:133:LEU:HD12	2.34	0.42
4:G:155:VAL:CG1	5:J:229:LEU:HD12	2.49	0.42
4:H:119:PRO:O	5:J:305:THR:HG23	2.19	0.42
4:K:109:VAL:N	4:K:133:LEU:HD11	2.34	0.42
5:N:123:ALA:HA	5:N:148:THR:OG1	2.19	0.42
4:O:26:TYR:CD2	5:R:306:MET:HE1	2.54	0.42
4:O:89:ALA:O	5:Q:269:ILE:HD11	2.19	0.42
5:Q:126:LEU:CD2	5:Q:148:THR:HG21	2.49	0.42
5:Q:172:TYR:CG	5:Q:214:ALA:HB1	2.54	0.42
5:R:164:LEU:HD21	5:R:210:ARG:CG	2.49	0.42
4:S:144:MET:HE2	5:U:301:MET:SD	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:U:318:ILE:HD12	5:U:321:TYR:HB3	2.00	0.42
5:V:119:TYR:HB3	5:V:151:PHE:HB2	2.00	0.42
5:V:163:LYS:HA	5:V:166:GLU:CG	2.49	0.42
1:A:295:HIS:HB2	1:A:312:LEU:HD21	2.01	0.42
1:C:260:CYS:HB2	1:C:267:VAL:O	2.19	0.42
1:D:269:CYS:HA	1:D:272:LEU:HD23	2.01	0.42
3:F:58:DA:O5'	3:F:58:DA:H8	2.02	0.42
5:N:298:ALA:O	5:N:301:MET:HG2	2.19	0.42
5:Q:249:GLU:O	5:Q:253:LYS:HG2	2.19	0.42
5:R:301:MET:HE2	5:R:301:MET:CA	2.49	0.42
4:S:54:TYR:CE1	4:S:213:LEU:HD21	2.54	0.42
1:A:301:ARG:HH11	1:B:16:VAL:HG13	1.85	0.42
1:B:290:THR:O	1:B:294:PHE:HD2	2.02	0.42
1:C:288:GLU:O	1:C:292:LYS:HG2	2.20	0.42
4:G:62:GLU:OE1	4:G:62:GLU:O	2.37	0.42
4:G:202:THR:HG22	4:G:205:GLU:CD	2.44	0.42
5:I:161:LEU:HD12	5:I:186:LEU:HD13	2.01	0.42
5:M:229:LEU:HB3	5:M:306:MET:HE2	2.01	0.42
4:O:270:ASP:C	4:O:274:ILE:HG12	2.44	0.42
5:Q:217:PHE:C	5:R:141:LYS:HZ2	2.27	0.42
5:Q:272:CYS:SG	5:Q:274:ASP:OD1	2.74	0.42
4:S:233:GLU:HA	4:S:236:LYS:HG2	2.01	0.42
1:B:105:ILE:HG12	1:B:165:ILE:HD13	2.00	0.42
1:C:94:LEU:HD23	1:C:94:LEU:H	1.83	0.42
1:D:344:LEU:O	1:D:348:GLU:HG2	2.19	0.42
1:D:354:PHE:O	1:D:357:TYR:HB3	2.20	0.42
2:E:1:DT:H2''	2:E:2:DA:O5'	2.20	0.42
4:H:74:LYS:NZ	4:H:138:ARG:NH2	2.67	0.42
5:M:123:ALA:HA	5:M:148:THR:HG23	2.01	0.42
5:M:239:LYS:C	5:M:313:ASN:ND2	2.78	0.42
4:S:92:HIS:HE2	4:S:99:VAL:HG21	1.84	0.42
4:S:201:ILE:HG22	4:S:202:THR:N	2.35	0.42
4:T:67:LEU:HD11	4:T:212:LEU:CD2	2.49	0.42
5:V:161:LEU:HD12	5:V:162:PHE:N	2.33	0.42
5:V:213:PHE:HB3	5:V:217:PHE:CZ	2.54	0.42
1:A:58:ASP:OD1	1:A:106:ARG:HB2	2.19	0.42
1:B:69:PHE:O	1:B:76:LEU:HD12	2.20	0.42
1:B:153:MET:HG3	1:B:242:ASP:O	2.19	0.42
1:C:69:PHE:CE1	1:C:170:SER:C	2.98	0.42
1:C:238:ASN:OD1	1:C:238:ASN:O	2.37	0.42
1:D:45:ARG:HG3	1:D:58:ASP:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:108:ILE:HD11	1:D:162:PHE:CE2	2.53	0.42
3:F:34:DC:H2''	3:F:35:DC:H6	1.81	0.42
4:G:167:ALA:CB	4:S:232:PHE:HD1	2.31	0.42
5:I:250:ARG:O	5:I:254:ILE:HG12	2.20	0.42
5:N:117:ARG:HA	5:N:120:ARG:HG2	2.00	0.42
5:R:156:GLU:HA	5:R:159:HIS:CG	2.54	0.42
4:S:125:PHE:HA	4:S:133:LEU:O	2.20	0.42
1:A:71:ASN:ND2	1:A:75:LYS:HE3	2.35	0.42
1:A:257:LEU:HD23	1:A:267:VAL:HG22	2.01	0.42
1:B:88:GLU:HB3	1:B:104:LEU:HG	2.02	0.42
1:C:19:THR:OG1	1:D:302:ASN:HA	2.20	0.42
1:C:30:MET:CE	1:C:64:VAL:HG23	2.50	0.42
1:C:147:ILE:HD12	1:C:173:ILE:CD1	2.50	0.42
2:E:27:DG:H2''	2:E:28:DA:H8	1.78	0.42
2:E:34:DA:C8	2:E:34:DA:O5'	2.73	0.42
4:K:140:SER:O	4:K:144:MET:HG2	2.20	0.42
5:Q:131:SER:CA	5:Q:209:MET:HE1	2.50	0.42
5:Q:304:THR:HA	5:Q:307:GLU:HG2	2.01	0.42
5:V:129:HIS:CE1	5:V:137:SER:CB	3.02	0.42
5:V:190:VAL:HB	5:V:201:ILE:CD1	2.49	0.42
1:A:45:ARG:H	1:A:45:ARG:HD3	1.85	0.42
1:A:93:ILE:HG23	1:A:100:TYR:HB2	2.01	0.42
1:C:213:GLU:HG2	1:C:314:ALA:HB3	2.01	0.42
1:D:62:MET:HA	1:D:101:GLU:O	2.19	0.42
1:D:104:LEU:C	1:D:105:ILE:HD12	2.45	0.42
2:E:1:DT:H1'	2:E:2:DA:O4'	2.20	0.42
3:F:43:DT:H1'	3:F:44:DT:H5'	2.02	0.42
4:H:144:MET:CE	4:H:147:ARG:HE	2.32	0.42
4:H:210:LEU:HD21	5:J:294:TYR:HD1	1.84	0.42
5:M:171:ASP:C	5:M:172:TYR:CD2	2.98	0.42
4:S:51:LEU:O	4:S:55:MET:SD	2.78	0.42
4:T:213:LEU:HD23	4:T:260:LEU:HD11	2.02	0.42
5:V:306:MET:HE1	5:V:316:PHE:CD1	2.55	0.42
5:V:317:ASN:CG	5:V:320:ASP:HB3	2.44	0.42
1:A:149:ILE:HG21	1:A:152:ARG:O	2.20	0.42
1:C:147:ILE:C	1:C:148:LEU:HD12	2.44	0.42
2:E:27:DG:N2	3:F:33:DT:O2	2.53	0.42
2:E:34:DA:H2''	2:E:35:DA:O5'	2.20	0.42
3:F:11:DA:O5'	3:F:11:DA:C8	2.72	0.42
4:G:43:GLU:O	4:G:46:LYS:HG2	2.20	0.42
5:I:249:GLU:OE2	5:I:253:LYS:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:297:ALA:O	5:I:300:THR:HG22	2.20	0.42
5:M:127:ILE:HD11	5:M:194:LEU:HA	2.01	0.42
5:M:233:VAL:CG2	5:M:310:ALA:HB1	2.49	0.42
4:O:137:ASP:OD2	4:O:140:SER:HB3	2.20	0.42
4:P:226:PHE:HB2	4:P:234:TYR:CD1	2.55	0.42
5:Q:245:GLU:O	5:Q:249:GLU:HG3	2.19	0.42
4:T:138:ARG:NH1	4:T:142:VAL:HG21	2.35	0.42
5:U:246:LEU:HD11	5:U:250:ARG:NH1	2.35	0.42
5:U:302:PHE:CD1	5:V:227:ILE:HD11	2.55	0.42
1:A:78:TYR:CZ	1:A:168:PRO:HA	2.54	0.42
1:B:8:ILE:C	1:B:9:LYS:HD3	2.45	0.42
1:B:195:LEU:HB3	1:B:199:TRP:HB2	2.02	0.42
1:C:30:MET:HA	1:C:42:LYS:HG3	2.02	0.42
1:C:219:TYR:O	1:C:222:ARG:HG2	2.20	0.42
1:D:283:MET:HE1	1:D:354:PHE:CE2	2.54	0.42
4:G:118:ILE:CD1	5:I:247:LEU:HD23	2.50	0.42
4:G:138:ARG:NH1	4:G:142:VAL:HG21	2.35	0.42
5:J:130:TYR:HB3	5:J:209:MET:SD	2.60	0.42
4:K:61:LEU:C	4:K:62:GLU:HG3	2.45	0.42
4:K:98:LEU:HG	4:K:99:VAL:HG23	2.02	0.42
5:N:123:ALA:HA	5:N:148:THR:HG23	2.02	0.42
4:O:151:THR:O	4:O:151:THR:CG2	2.68	0.42
4:S:145:LEU:HD11	4:S:208:GLN:CB	2.50	0.42
4:S:226:PHE:HB2	4:S:234:TYR:CD1	2.55	0.42
1:A:152:ARG:HD3	1:A:154:TYR:CE1	2.55	0.41
1:A:271:ASP:OD1	1:A:272:LEU:HD22	2.20	0.41
1:B:153:MET:SD	1:B:294:PHE:CE1	3.13	0.41
1:C:69:PHE:CE1	1:C:172:TYR:CD1	3.08	0.41
1:D:288:GLU:HG2	1:D:343:HIS:NE2	2.35	0.41
1:D:293:PHE:CD1	1:D:313:ILE:HD11	2.55	0.41
2:E:17:DA:H1'	2:E:18:DC:C6	2.55	0.41
3:F:53:DG:H2''	3:F:54:DG:C8	2.55	0.41
4:G:201:ILE:C	5:I:284:HIS:HE2	2.27	0.41
4:G:263:LYS:HE3	5:I:290:LEU:HD11	2.02	0.41
4:K:32:ASP:O	4:K:36:LEU:HD23	2.20	0.41
5:N:246:LEU:HD22	5:N:312:SER:HB2	2.02	0.41
4:P:207:THR:OG1	5:R:293:MET:HE3	2.20	0.41
1:C:94:LEU:HD11	1:D:70:LEU:HD23	2.01	0.41
3:F:53:DG:H2''	3:F:54:DG:H8	1.85	0.41
4:H:166:ILE:HD13	5:V:248:ILE:CG1	2.50	0.41
5:N:153:LEU:HD23	5:N:153:LEU:C	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Q:317:ASN:ND2	5:Q:320:ASP:HB2	2.35	0.41
5:Q:322:ASN:O	5:Q:326:LYS:HG2	2.20	0.41
5:U:297:ALA:O	5:U:301:MET:SD	2.78	0.41
1:A:190:ASP:OD1	1:A:190:ASP:O	2.38	0.41
1:B:292:LYS:HG2	1:B:312:LEU:HD23	2.01	0.41
1:C:67:SER:HA	1:C:70:LEU:HD23	2.01	0.41
1:D:65:LEU:HB2	1:D:99:VAL:HG23	2.01	0.41
1:D:137:TYR:CD1	1:D:137:TYR:C	2.97	0.41
3:F:25:DT:H1'	3:F:26:DT:H5'	2.03	0.41
3:F:53:DG:H1'	3:F:54:DG:O5'	2.19	0.41
5:I:126:LEU:CD2	5:I:148:THR:HG21	2.51	0.41
5:J:130:TYR:O	5:J:209:MET:HE1	2.20	0.41
5:J:205:THR:O	5:J:209:MET:HG2	2.19	0.41
5:M:245:GLU:O	5:M:249:GLU:HG3	2.20	0.41
5:M:249:GLU:HB2	5:M:253:LYS:NZ	2.35	0.41
5:M:311:VAL:C	5:M:313:ASN:N	2.78	0.41
5:Q:179:THR:HG23	5:Q:182:GLN:H	1.85	0.41
5:Q:196:MET:HE1	5:Q:200:THR:HA	2.02	0.41
4:S:56:ALA:CB	5:U:278:LEU:HD23	2.50	0.41
4:S:233:GLU:CD	4:S:236:LYS:HZ3	2.28	0.41
4:S:248:LEU:HD12	4:S:252:MET:CB	2.51	0.41
4:T:111:THR:HG22	5:V:257:LEU:CD1	2.50	0.41
5:U:132:LEU:HD11	5:U:303:TYR:CD1	2.55	0.41
1:B:10:LEU:HD12	1:B:12:LEU:HD13	2.01	0.41
1:B:131:ILE:HA	1:B:134:VAL:HG12	2.01	0.41
1:B:257:LEU:O	1:B:268:LYS:HB3	2.20	0.41
1:B:296:TYR:CD1	1:B:309:TYR:O	2.73	0.41
1:C:220:ILE:HD11	1:C:313:ILE:CG2	2.32	0.41
1:D:138:ILE:HD11	1:D:226:LEU:HD11	2.01	0.41
1:D:156:ASP:H	1:D:169:GLN:NE2	2.18	0.41
1:D:246:GLU:OE1	1:D:246:GLU:N	2.52	0.41
3:F:30:DT:H2'	3:F:30:DT:H6	1.70	0.41
4:K:232:PHE:CE2	4:O:33:LEU:HD13	2.54	0.41
5:N:116:MET:SD	5:R:180:GLN:CD	3.04	0.41
4:P:110:VAL:HG12	4:P:112:GLU:OE2	2.20	0.41
5:Q:132:LEU:HD12	5:Q:303:TYR:CD2	2.55	0.41
4:S:34:LYS:HE3	5:V:307:GLU:OE2	2.19	0.41
5:U:219:SER:O	5:V:142:ILE:HD12	2.20	0.41
1:A:257:LEU:CD2	1:A:267:VAL:HG22	2.51	0.41
1:A:289:ILE:HD11	1:A:343:HIS:O	2.20	0.41
1:D:46:PRO:HG3	1:D:60:LEU:CB	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:133:ALA:O	1:D:136:LYS:HG3	2.20	0.41
3:F:44:DT:H6	3:F:44:DT:H2'	1.70	0.41
4:G:88:LEU:CD1	4:G:102:PHE:HE2	2.33	0.41
4:G:92:HIS:O	4:G:96:HIS:N	2.53	0.41
4:G:104:ASN:O	5:I:265:SER:N	2.54	0.41
4:G:201:ILE:HB	5:I:284:HIS:NE2	2.35	0.41
4:K:82:ALA:HA	5:M:263:ILE:HD11	2.02	0.41
5:M:152:LEU:O	5:M:159:HIS:HD2	2.02	0.41
5:M:233:VAL:HG22	5:M:310:ALA:HB1	2.02	0.41
5:Q:150:ILE:HD11	5:R:149:MET:HE1	2.02	0.41
5:Q:228:VAL:HG23	5:R:224:TYR:CE2	2.56	0.41
5:Q:244:GLU:HG2	5:Q:245:GLU:N	2.36	0.41
1:B:89:ALA:HB3	1:B:104:LEU:HB3	2.01	0.41
1:B:244:ILE:O	1:B:301:ARG:NH2	2.54	0.41
1:B:295:HIS:HB2	1:B:312:LEU:HD21	2.02	0.41
1:C:71:ASN:ND2	1:C:75:LYS:HE3	2.36	0.41
1:C:166:ILE:HD12	1:C:166:ILE:HA	1.96	0.41
3:F:14:DT:H1'	3:F:15:DT:C5'	2.50	0.41
3:F:26:DT:H2''	3:F:27:DT:H71	2.02	0.41
4:G:137:ASP:OD2	4:G:140:SER:HB2	2.21	0.41
5:I:146:VAL:HG12	5:I:150:ILE:HD12	2.02	0.41
4:O:151:THR:HG23	4:O:203:GLU:HG2	2.02	0.41
4:O:234:TYR:CE2	4:O:238:LEU:HD11	2.55	0.41
4:S:203:GLU:HG3	5:U:293:MET:SD	2.61	0.41
4:T:48:LYS:HG3	5:V:282:LEU:HD11	2.02	0.41
4:T:231:VAL:O	4:T:234:TYR:HB3	2.21	0.41
5:U:151:PHE:CE2	5:U:193:LEU:HD13	2.56	0.41
5:U:171:ASP:O	5:U:172:TYR:CD2	2.74	0.41
1:B:10:LEU:HD23	1:B:10:LEU:H	1.86	0.41
1:B:225:LEU:O	1:B:229:THR:HG23	2.20	0.41
1:C:32:CYS:HA	1:C:43:VAL:H	1.86	0.41
1:D:71:ASN:ND2	1:D:75:LYS:HB3	2.34	0.41
2:E:15:DA:H1'	2:E:16:DA:O5'	2.20	0.41
3:F:17:DT:C1'	3:F:18:DT:O5'	2.67	0.41
4:H:235:CYS:HA	4:H:238:LEU:HD12	2.02	0.41
5:I:277:PHE:HE1	5:I:281:LEU:HD11	1.85	0.41
4:O:102:PHE:CG	4:O:103:THR:N	2.89	0.41
4:O:151:THR:HG23	4:O:203:GLU:CG	2.50	0.41
4:P:109:VAL:HB	4:P:133:LEU:HD11	2.03	0.41
5:R:117:ARG:HA	5:R:117:ARG:NE	2.36	0.41
4:S:108:PHE:HB2	5:U:261:GLN:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:S:144:MET:HE1	5:U:300:THR:HB	2.01	0.41
4:T:123:ILE:HG21	4:T:219:ALA:HB1	2.02	0.41
1:A:31:GLN:NE2	1:A:43:VAL:O	2.54	0.41
1:A:298:LYS:O	1:A:301:ARG:HG2	2.21	0.41
1:B:286:PRO:HD2	1:B:347:TRP:CE3	2.56	0.41
1:C:131:ILE:HA	1:C:134:VAL:HG12	2.02	0.41
1:C:349:ASN:O	1:C:350:PHE:C	2.64	0.41
3:F:3:DA:C2'	3:F:4:DT:H71	2.51	0.41
3:F:11:DA:H1'	3:F:12:DA:C5'	2.51	0.41
3:F:15:DT:H2''	3:F:16:DT:C6	2.56	0.41
4:G:56:ALA:HB1	5:I:272:CYS:CB	2.51	0.41
4:G:58:LEU:O	4:G:61:LEU:HB2	2.21	0.41
4:G:145:LEU:HD22	4:G:208:GLN:HG2	2.02	0.41
4:G:244:PHE:CB	5:I:327:VAL:HG11	2.51	0.41
5:J:124:ARG:CG	5:J:193:LEU:HD12	2.51	0.41
5:J:241:THR:O	5:J:314:CYS:HA	2.21	0.41
4:O:268:ILE:HD11	5:Q:321:TYR:HD2	1.85	0.41
4:T:210:LEU:O	4:T:214:LEU:HG	2.20	0.41
1:A:24:MET:HA	1:B:206:ASN:N	2.36	0.41
1:A:196:GLU:O	1:A:199:TRP:N	2.54	0.41
1:A:220:ILE:CD1	1:A:313:ILE:HG21	2.51	0.41
1:B:78:TYR:OH	1:B:101:GLU:HG2	2.21	0.41
1:B:220:ILE:HG23	1:B:347:TRP:CD1	2.55	0.41
1:B:227:TYR:O	1:B:231:LEU:HG	2.20	0.41
1:B:267:VAL:HG12	1:B:268:LYS:N	2.36	0.41
2:E:53:DA:C6	2:E:54:DA:C6	3.09	0.41
4:G:37:SER:O	4:G:40:GLU:HG2	2.21	0.41
5:J:117:ARG:HG3	5:J:118:ARG:N	2.35	0.41
4:K:13:THR:HG23	4:L:266:PHE:HD1	1.86	0.41
4:K:143:LYS:HG2	5:M:307:GLU:OE2	2.20	0.41
4:K:243:LEU:CD2	4:K:247:LYS:HG3	2.50	0.41
4:L:68:LEU:HD11	4:L:72:ARG:NH1	2.35	0.41
5:M:119:TYR:CG	5:M:147:MET:SD	3.14	0.41
5:M:171:ASP:O	5:M:172:TYR:CG	2.73	0.41
5:N:152:LEU:O	5:N:162:PHE:HE1	2.04	0.41
5:N:250:ARG:O	5:N:254:ILE:HG12	2.21	0.41
4:O:55:MET:HE1	4:O:209:TYR:CD1	2.56	0.41
4:O:91:ILE:HG23	4:O:94:ARG:NH2	2.36	0.41
4:O:132:LEU:HD21	4:O:226:PHE:CE1	2.56	0.41
4:T:67:LEU:HD13	4:T:209:TYR:CE1	2.56	0.41
4:T:138:ARG:O	4:T:141:ILE:HG22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:U:140:TYR:HB3	5:V:221:ILE:HD11	2.02	0.41
5:U:286:ASP:N	5:U:287:PRO:HD2	2.36	0.41
5:V:243:LEU:O	5:V:247:LEU:HD13	2.21	0.41
5:V:244:GLU:HG2	5:V:245:GLU:N	2.36	0.41
1:A:60:LEU:HA	1:A:103:MET:O	2.21	0.41
1:A:178:TYR:HB3	1:A:210:SER:O	2.21	0.41
1:B:9:LYS:HA	1:B:16:VAL:O	2.20	0.41
1:B:37:ARG:HD2	1:B:37:ARG:N	2.36	0.41
1:B:132:ASP:HA	1:B:135:ILE:HG22	2.03	0.41
1:B:154:TYR:HB2	1:B:229:THR:HG22	2.03	0.41
1:B:347:TRP:O	1:B:351:MET:SD	2.79	0.41
1:D:155:VAL:CG2	1:D:166:ILE:HD11	2.51	0.41
1:D:156:ASP:HB3	1:D:167:LEU:HD12	2.03	0.41
2:E:17:DA:H1'	2:E:18:DC:O5'	2.21	0.41
2:E:34:DA:P	2:E:34:DA:H2'	2.60	0.41
4:G:24:LYS:HD2	5:J:295:TYR:OH	2.20	0.41
4:G:147:ARG:HD2	5:I:300:THR:OG1	2.21	0.41
4:G:203:GLU:HG2	5:I:293:MET:CE	2.51	0.41
4:H:248:LEU:O	4:H:248:LEU:HD23	2.21	0.41
5:J:126:LEU:HD22	5:J:148:THR:CG2	2.45	0.41
5:J:164:LEU:HD23	5:J:210:ARG:HE	1.85	0.41
5:J:167:THR:O	5:J:173:THR:HG21	2.21	0.41
4:P:261:LEU:HD12	4:P:262:SER:N	2.36	0.41
5:U:226:LYS:HE2	5:U:226:LYS:HA	2.03	0.41
1:A:95:ASN:HB3	1:A:98:SER:OG	2.21	0.40
1:B:221:TYR:CD1	1:B:296:TYR:HD2	2.39	0.40
1:C:87:ALA:HB2	1:C:165:ILE:HD11	2.03	0.40
1:C:120:GLY:HA2	1:C:234:ILE:O	2.21	0.40
1:C:244:ILE:O	1:C:244:ILE:CG2	2.68	0.40
1:C:270:CYS:HA	1:C:280:GLY:HA2	2.03	0.40
1:D:22:LYS:HB2	1:D:95:ASN:OD1	2.20	0.40
3:F:39:DA:H2''	3:F:40:DG:O5'	2.21	0.40
5:J:174:CYS:SG	5:U:176:PRO:HA	2.61	0.40
5:M:295:TYR:O	5:M:299:ASN:OD1	2.39	0.40
4:O:126:THR:O	4:O:126:THR:HG23	2.21	0.40
4:O:127:GLU:HA	4:O:132:LEU:HA	2.04	0.40
5:Q:122:ALA:HA	5:Q:125:LYS:HG2	2.04	0.40
4:S:51:LEU:HB3	4:S:55:MET:HE1	2.03	0.40
4:T:116:THR:HG21	5:V:257:LEU:HD11	2.03	0.40
5:U:251:GLY:HA2	5:U:254:ILE:HG22	2.03	0.40
5:U:254:ILE:HG23	5:U:255:GLN:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:35:HIS:HA	1:B:38:ARG:NH2	2.35	0.40
1:B:148:LEU:HD13	1:B:300:VAL:HA	2.03	0.40
1:B:198:PRO:O	1:B:202:ILE:HD12	2.21	0.40
1:B:260:CYS:HB3	1:B:263:ASN:O	2.21	0.40
1:B:310:SER:OG	1:B:311:GLU:OE1	2.39	0.40
1:C:90:ARG:HB3	1:C:101:GLU:OE2	2.21	0.40
1:C:157:LEU:HA	1:C:167:LEU:HG	2.02	0.40
1:C:224:PHE:HD2	1:C:293:PHE:HB2	1.87	0.40
1:D:198:PRO:O	1:D:201:LEU:HG	2.21	0.40
1:D:235:LEU:HD22	1:D:237:GLN:NE2	2.36	0.40
3:F:10:DT:C1'	3:F:11:DA:O5'	2.63	0.40
3:F:14:DT:H6	3:F:14:DT:H2'	1.65	0.40
3:F:28:DA:C4	3:F:29:DC:C4	3.09	0.40
3:F:51:DT:C2'	3:F:52:DT:H72	2.51	0.40
5:I:242:THR:CG2	5:I:315:LYS:HZ3	2.34	0.40
5:M:205:THR:HA	5:M:208:ILE:HD12	2.03	0.40
5:R:152:LEU:HG	5:R:162:PHE:HB2	2.03	0.40
4:S:10:ARG:HH11	4:S:12:VAL:HG23	1.87	0.40
4:S:71:PHE:O	4:S:138:ARG:HD2	2.20	0.40
5:U:124:ARG:O	5:U:128:HIS:CG	2.75	0.40
5:U:132:LEU:HD11	5:U:303:TYR:CE1	2.55	0.40
5:U:277:PHE:CZ	5:U:281:LEU:HD21	2.55	0.40
5:V:277:PHE:O	5:V:280:ARG:HG2	2.22	0.40
1:A:175:LYS:HG2	1:A:192:CYS:SG	2.62	0.40
1:B:250:ILE:HD12	1:B:253:ILE:HB	2.03	0.40
1:B:264:LYS:HD2	1:B:265:ASP:N	2.37	0.40
1:C:128:LYS:O	1:C:132:ASP:CG	2.64	0.40
1:C:268:LYS:HG3	1:C:268:LYS:O	2.21	0.40
1:D:153:MET:HE1	1:D:297:ALA:CB	2.51	0.40
1:D:198:PRO:HG2	1:D:199:TRP:CE3	2.56	0.40
2:E:45:DA:OP2	2:E:45:DA:H8	2.03	0.40
3:F:21:DT:H1'	3:F:22:DT:C5'	2.52	0.40
4:G:222:HIS:CE1	4:G:238:LEU:HD23	2.56	0.40
5:J:183:THR:HG23	5:J:203:LEU:HD21	2.03	0.40
4:K:244:PHE:HB2	5:M:327:VAL:HG11	2.03	0.40
5:N:140:TYR:C	5:N:141:LYS:HD3	2.47	0.40
5:N:306:MET:HA	5:N:306:MET:HE2	2.02	0.40
5:Q:295:TYR:CD1	5:Q:299:ASN:OD1	2.74	0.40
5:R:168:THR:HG21	5:R:210:ARG:HG3	2.03	0.40
4:S:144:MET:CE	5:U:301:MET:SD	3.09	0.40
1:B:135:ILE:HD11	1:B:364:ASN:OD1	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:69:PHE:CE2	1:C:170:SER:HB2	2.57	0.40
2:E:2:DA:C2'	2:E:3:DT:H71	2.52	0.40
2:E:53:DA:O5'	2:E:53:DA:C8	2.74	0.40
3:F:54:DG:P	3:F:54:DG:H2'	2.61	0.40
4:G:66:PRO:HD2	4:G:69:GLU:OE2	2.22	0.40
4:G:118:ILE:HG21	4:G:124:LEU:HD11	2.03	0.40
4:G:233:GLU:HA	4:G:236:LYS:HG2	2.03	0.40
4:H:138:ARG:HD2	4:H:138:ARG:C	2.47	0.40
5:I:115:ASN:O	5:I:119:TYR:HD1	2.03	0.40
5:I:124:ARG:O	5:I:128:HIS:CD2	2.75	0.40
4:K:141:ILE:O	4:K:144:MET:HB2	2.22	0.40
4:K:212:LEU:HD12	4:K:213:LEU:N	2.36	0.40
4:O:111:THR:HB	4:O:116:THR:HG23	2.02	0.40
5:Q:152:LEU:HD11	5:Q:161:LEU:CB	2.51	0.40
5:Q:227:ILE:CD1	5:R:223:ARG:HD3	2.52	0.40
4:T:80:ILE:HG22	4:T:136:VAL:HG11	2.02	0.40
4:T:221:LEU:HD21	4:T:259:LEU:HD12	2.04	0.40
5:U:128:HIS:CD2	5:U:194:LEU:HG	2.56	0.40
5:U:289:PRO:HB2	5:U:292:ARG:HG2	2.04	0.40
5:U:299:ASN:OD1	5:V:226:LYS:HG2	2.21	0.40
5:V:302:PHE:O	5:V:306:MET:HG2	2.21	0.40
1:A:260:CYS:HA	1:A:268:LYS:HG2	2.03	0.40
1:A:299:TRP:CG	1:A:309:TYR:HB2	2.57	0.40
1:B:114:ARG:NH1	1:B:115:SER:O	2.54	0.40
1:B:154:TYR:CE1	1:B:242:ASP:HB3	2.57	0.40
1:B:224:PHE:HB3	1:B:293:PHE:CE1	2.56	0.40
1:D:47:ARG:C	4:G:275:ASN:HB3	2.47	0.40
5:Q:114:ILE:HG23	5:R:166:GLU:OE1	2.22	0.40
5:Q:252:GLU:HA	5:Q:255:GLN:HG3	2.04	0.40
5:Q:309:TYR:HE1	5:Q:314:CYS:HG	1.67	0.40
4:S:55:MET:HA	4:S:58:LEU:HG	2.04	0.40
4:T:145:LEU:HD12	4:T:208:GLN:CG	2.44	0.40
5:U:153:LEU:HB2	5:U:162:PHE:CE1	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	328/365 (90%)	296 (90%)	32 (10%)	0	100	100
1	B	331/365 (91%)	305 (92%)	26 (8%)	0	100	100
1	C	318/365 (87%)	283 (89%)	35 (11%)	0	100	100
1	D	317/365 (87%)	286 (90%)	31 (10%)	0	100	100
4	G	232/290 (80%)	219 (94%)	13 (6%)	0	100	100
4	H	146/290 (50%)	141 (97%)	5 (3%)	0	100	100
4	K	218/290 (75%)	206 (94%)	12 (6%)	0	100	100
4	L	112/290 (39%)	111 (99%)	1 (1%)	0	100	100
4	O	230/290 (79%)	216 (94%)	14 (6%)	0	100	100
4	P	146/290 (50%)	140 (96%)	6 (4%)	0	100	100
4	S	216/290 (74%)	204 (94%)	12 (6%)	0	100	100
4	T	166/290 (57%)	161 (97%)	4 (2%)	1 (1%)	21	59
5	I	207/361 (57%)	196 (95%)	11 (5%)	0	100	100
5	J	184/361 (51%)	172 (94%)	12 (6%)	0	100	100
5	M	207/361 (57%)	194 (94%)	13 (6%)	0	100	100
5	N	165/361 (46%)	159 (96%)	6 (4%)	0	100	100
5	Q	207/361 (57%)	195 (94%)	12 (6%)	0	100	100
5	R	164/361 (45%)	156 (95%)	8 (5%)	0	100	100
5	U	207/361 (57%)	194 (94%)	13 (6%)	0	100	100
5	V	186/361 (52%)	174 (94%)	12 (6%)	0	100	100
All	All	4287/6668 (64%)	4008 (94%)	278 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	T	247	LYS

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	303/331 (92%)	303 (100%)	0	100	100
1	B	308/331 (93%)	308 (100%)	0	100	100
1	C	296/331 (89%)	296 (100%)	0	100	100
1	D	297/331 (90%)	297 (100%)	0	100	100
4	G	224/273 (82%)	224 (100%)	0	100	100
4	H	148/273 (54%)	148 (100%)	0	100	100
4	K	213/273 (78%)	213 (100%)	0	100	100
4	L	120/273 (44%)	120 (100%)	0	100	100
4	O	222/273 (81%)	222 (100%)	0	100	100
4	P	148/273 (54%)	148 (100%)	0	100	100
4	S	209/273 (77%)	207 (99%)	2 (1%)	68	78
4	T	164/273 (60%)	164 (100%)	0	100	100
5	I	201/326 (62%)	201 (100%)	0	100	100
5	J	184/326 (56%)	184 (100%)	0	100	100
5	M	201/326 (62%)	201 (100%)	0	100	100
5	N	171/326 (52%)	171 (100%)	0	100	100
5	Q	201/326 (62%)	201 (100%)	0	100	100
5	R	168/326 (52%)	168 (100%)	0	100	100
5	U	201/326 (62%)	201 (100%)	0	100	100
5	V	186/326 (57%)	186 (100%)	0	100	100
All	All	4165/6116 (68%)	4163 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	S	69	GLU
4	S	70	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	GLN
1	A	80	HIS
1	A	112	HIS
1	A	187	GLN
1	A	273	ASN
1	A	281	HIS
1	A	343	HIS
1	A	361	HIS
1	B	48	ASN
1	B	73	HIS
1	B	295	HIS
1	C	48	ASN
1	C	218	GLN
1	C	238	ASN
1	C	343	HIS
1	D	35	HIS
1	D	57	ASN
1	D	237	GLN
1	D	281	HIS
4	G	35	ASN
4	G	241	HIS
4	H	208	GLN
5	I	128	HIS
5	J	121	ASN
5	J	313	ASN
5	M	218	ASN
5	M	296	ASN
5	M	299	ASN
5	N	159	HIS
4	O	92	HIS
4	O	96	HIS
4	O	101	ASN
4	O	258	ASN
4	P	241	HIS
5	Q	159	HIS
5	R	129	HIS
5	R	284	HIS
4	T	93	ASN
4	T	114	ASN
5	U	261	GLN
5	U	322	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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.

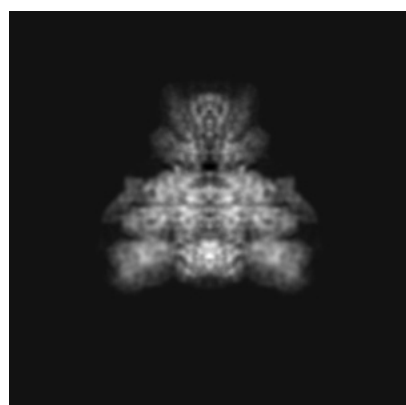
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51803. These allow visual inspection of the internal detail of the map and identification of artifacts.

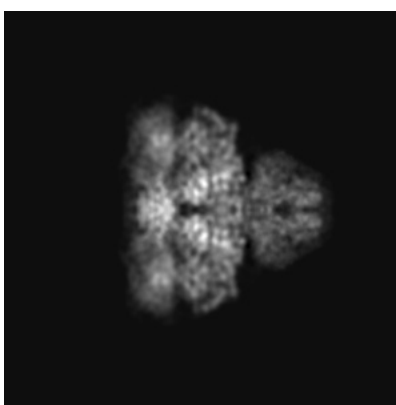
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

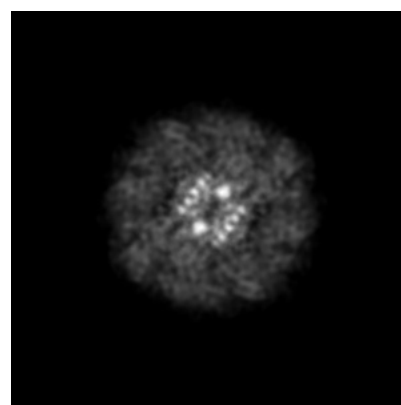
6.1.1 Primary map



X



Y

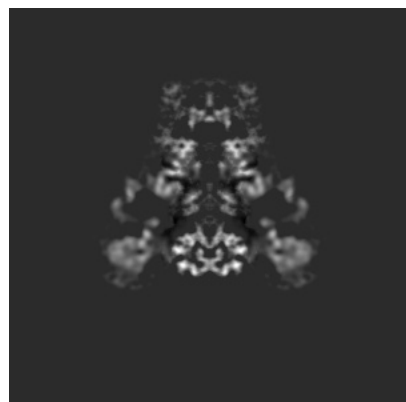


Z

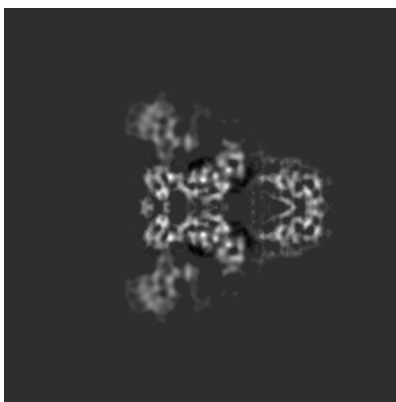
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

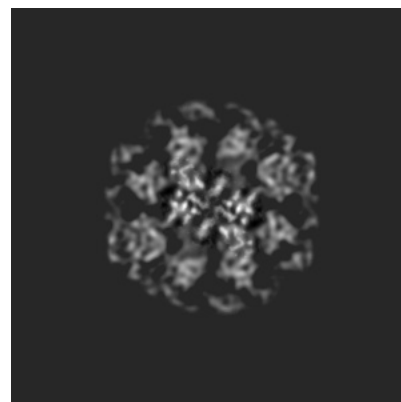
6.2.1 Primary map



X Index: 150



Y Index: 150

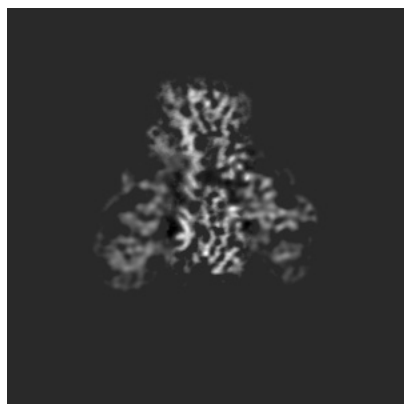


Z Index: 150

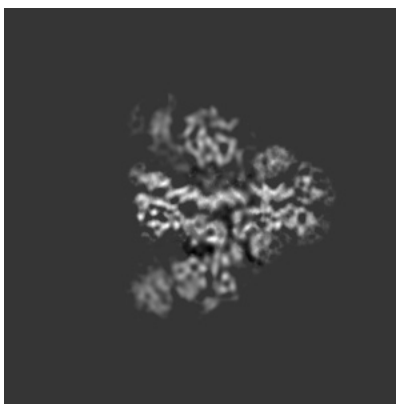
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

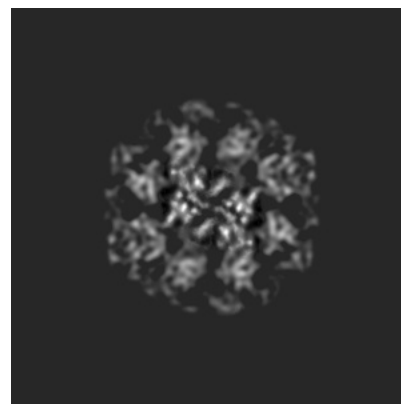
6.3.1 Primary map



X Index: 139



Y Index: 164

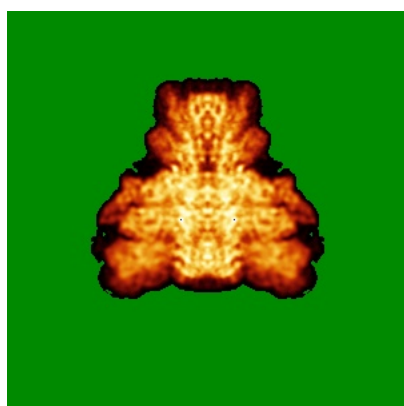


Z Index: 149

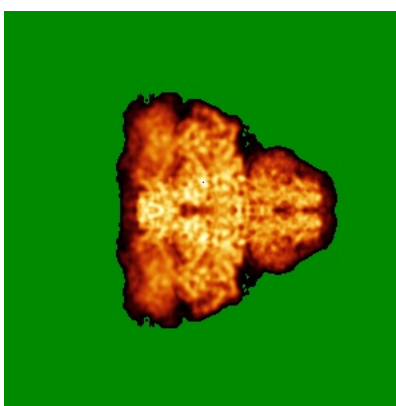
The images above show the largest variance slices of the map in three orthogonal directions.

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

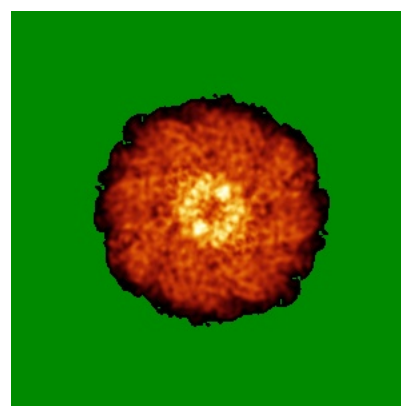
6.4.1 Primary map



X



Y

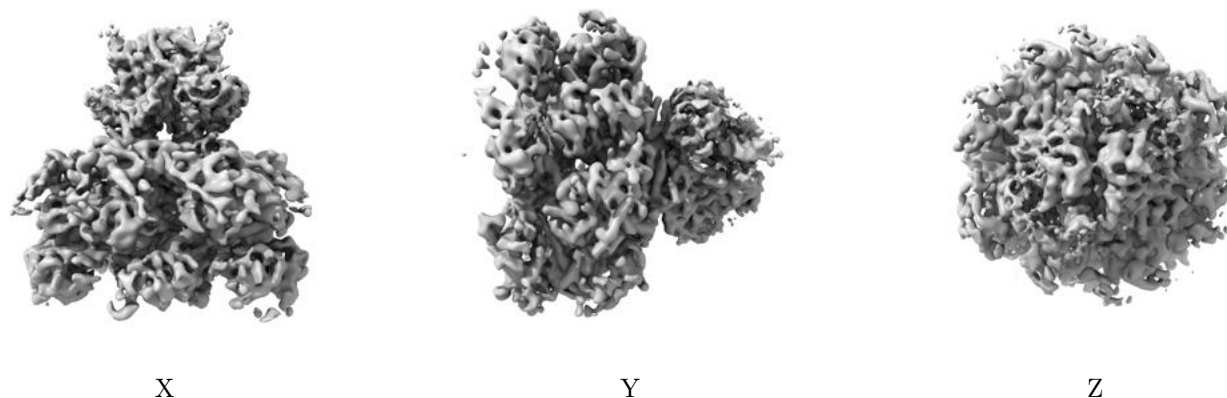


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0065. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

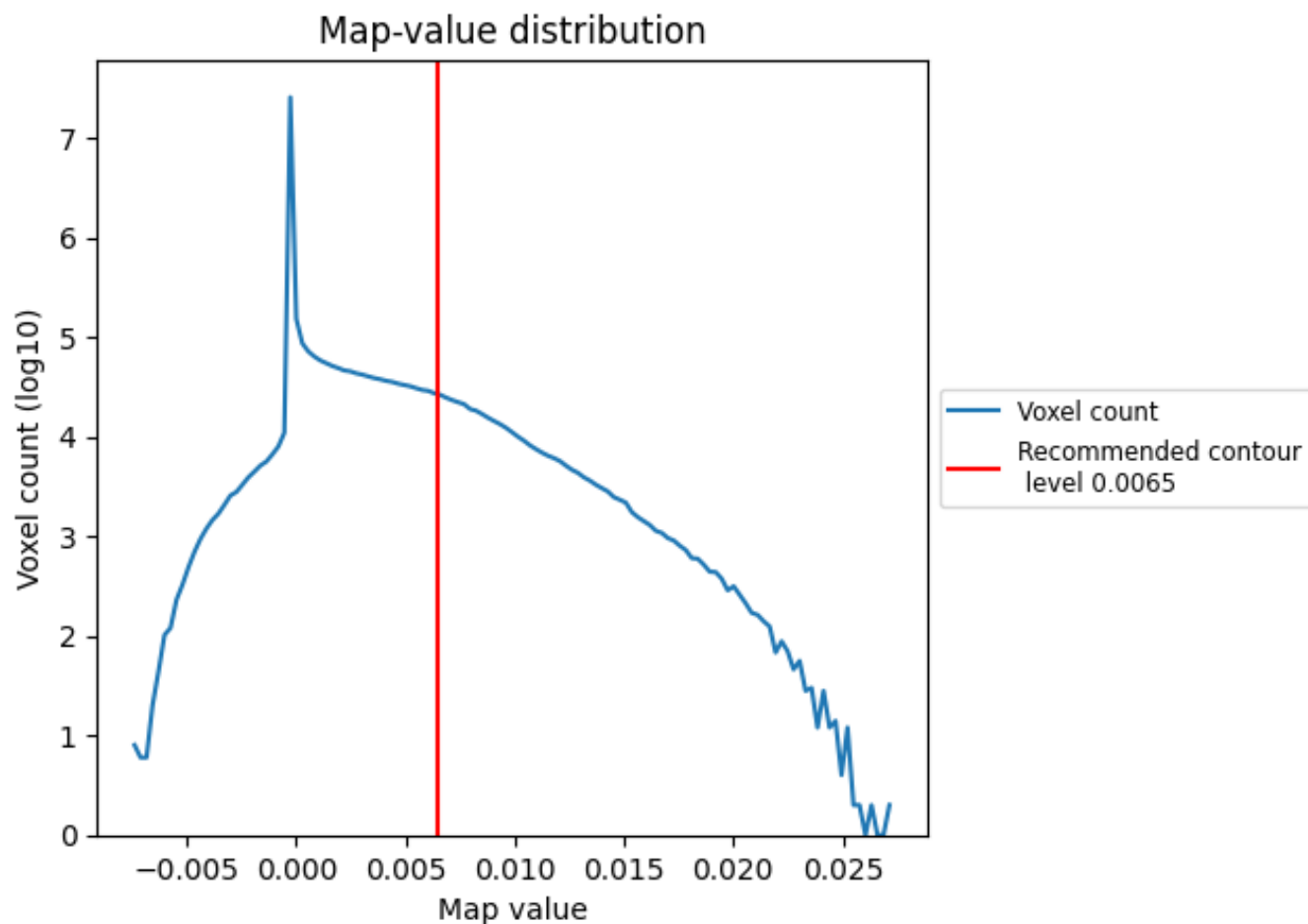
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

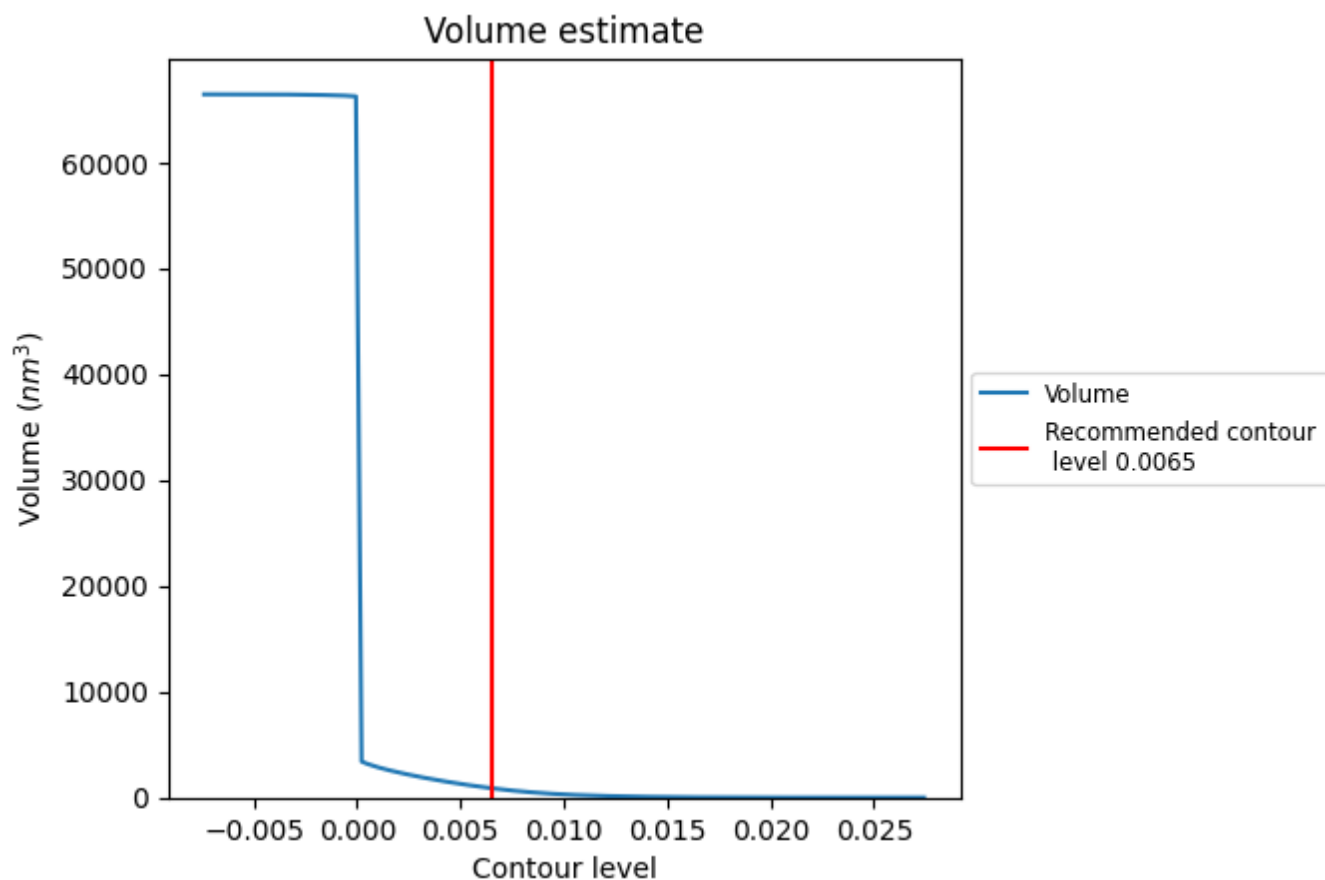
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

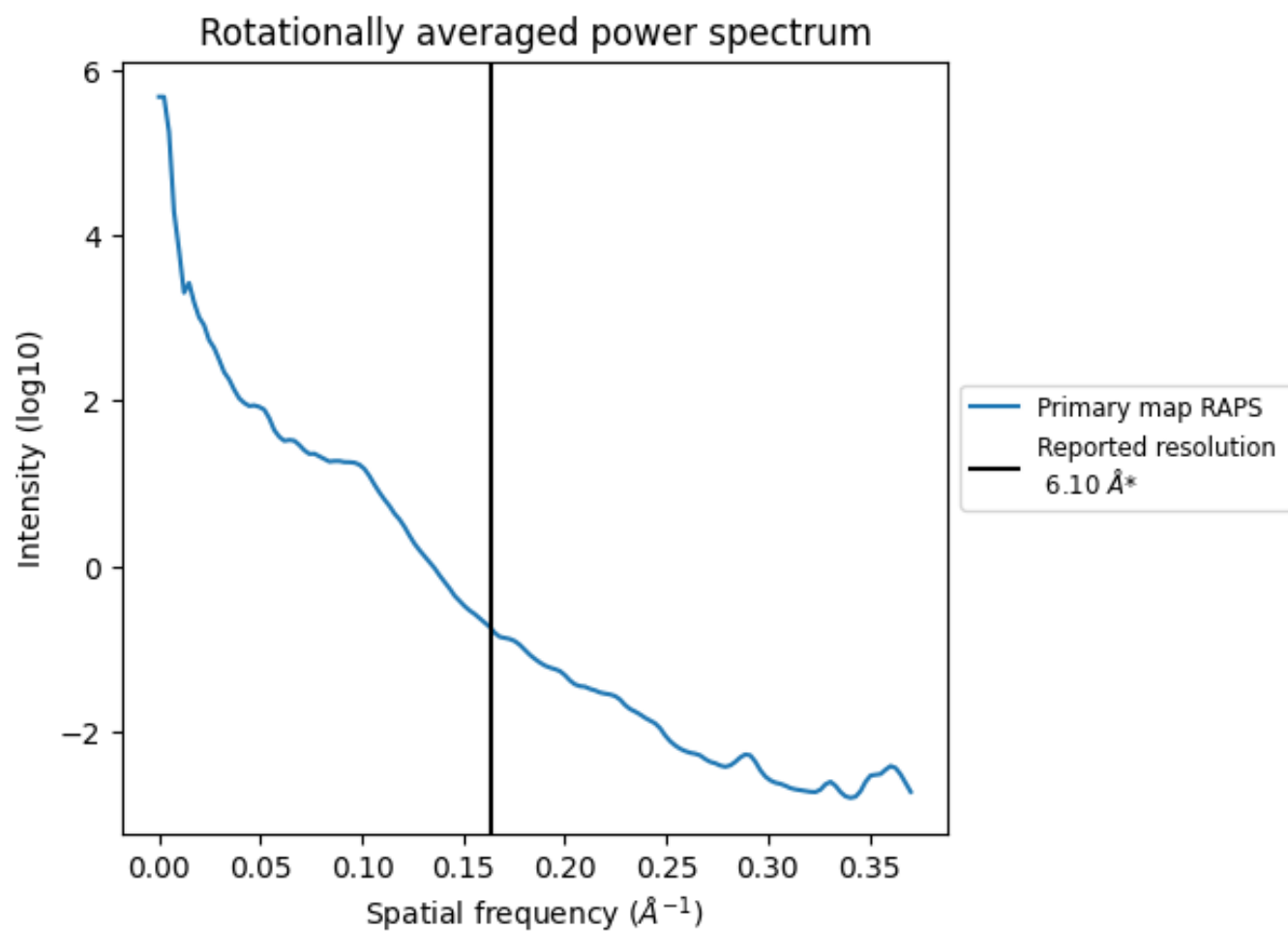
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 886 nm³; this corresponds to an approximate mass of 800 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 0.164 Å⁻¹

8 Fourier-Shell correlation ⓘ

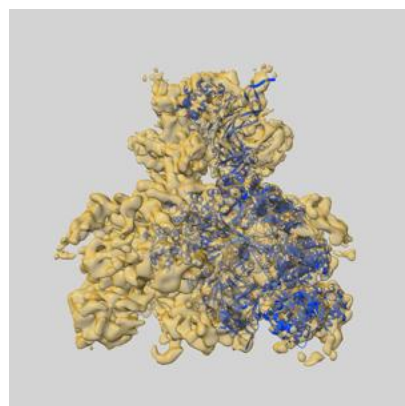
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

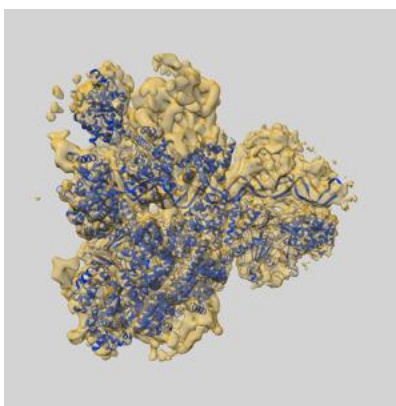
This section contains information regarding the fit between EMDB map EMD-51803 and PDB model 9H2H. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlays

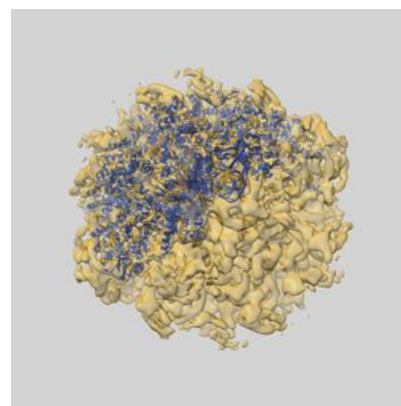
9.1.1 Map-model overlay [i](#)



X

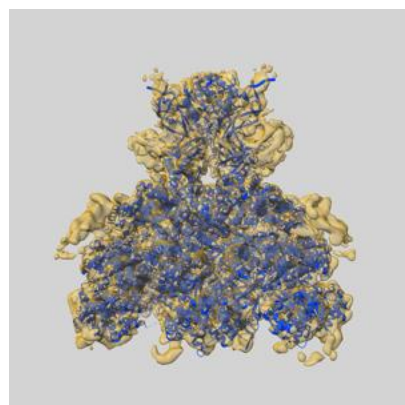


Y

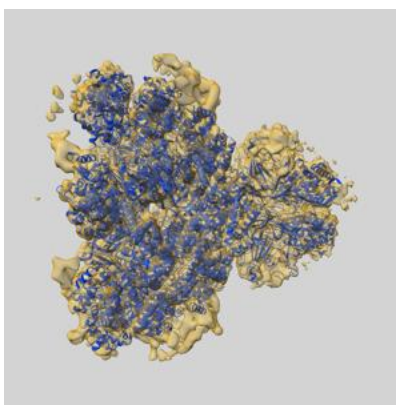


Z

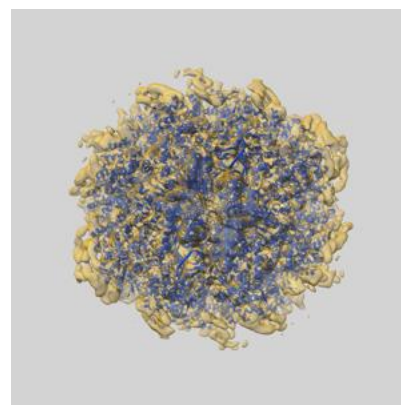
9.1.2 Map-model assembly overlay [i](#)



X



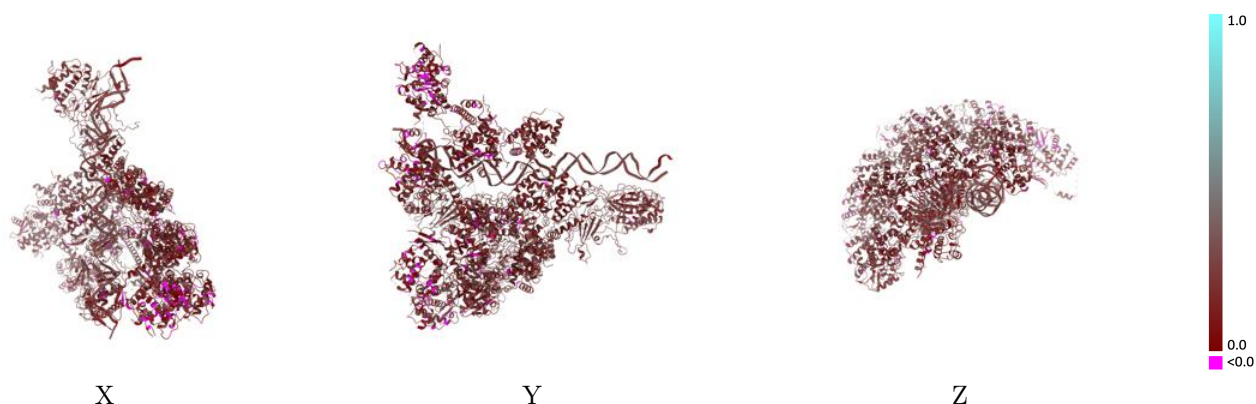
Y



Z

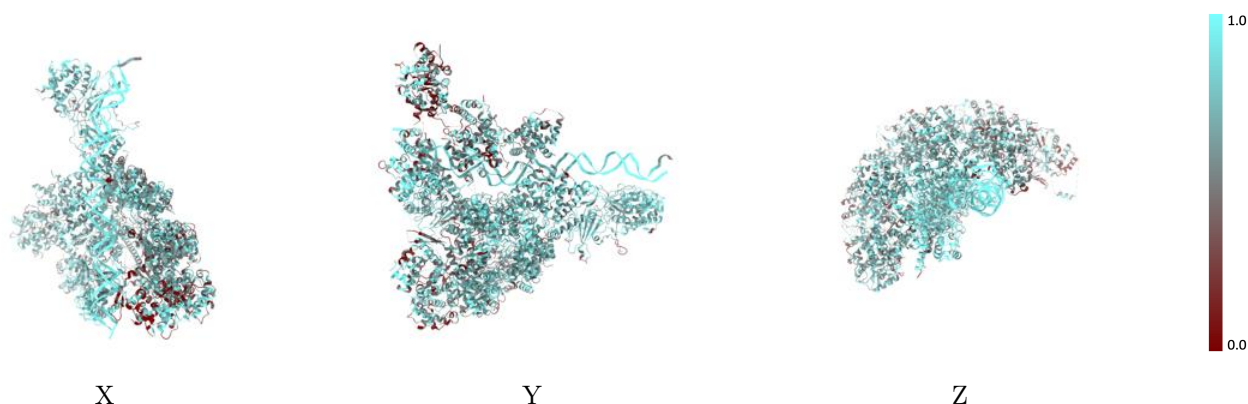
The images above show the 3D surface view of the map at the recommended contour level 0.0065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



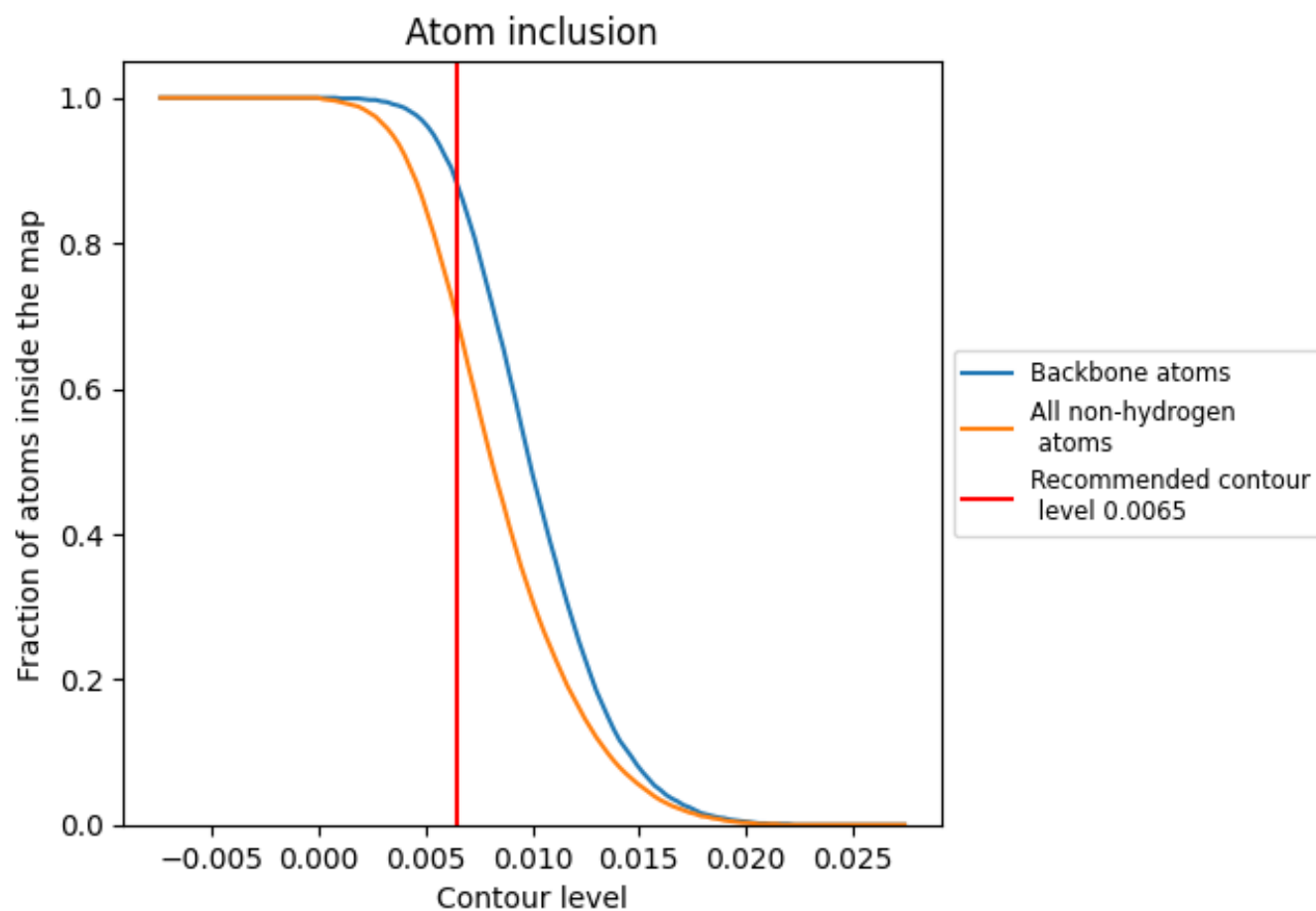
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0065).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 69% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6930	 0.1920
A	 0.7500	 0.2170
B	 0.7680	 0.2250
C	 0.7900	 0.2300
D	 0.7850	 0.2170
E	 0.9240	 0.2670
F	 0.9520	 0.2780
G	 0.6420	 0.1770
H	 0.6240	 0.1580
I	 0.7220	 0.1970
J	 0.7100	 0.1790
K	 0.6480	 0.1760
L	 0.7210	 0.1580
M	 0.7060	 0.1870
N	 0.7010	 0.1780
O	 0.5770	 0.1710
P	 0.6370	 0.1540
Q	 0.6640	 0.1880
R	 0.6730	 0.1840
S	 0.4990	 0.1580
T	 0.5360	 0.1260
U	 0.6310	 0.1760
V	 0.5370	 0.1650

