



Full wwPDB EM Validation Report ⓘ

Mar 12, 2026 – 06:56 AM UTC

PDB ID : 7C97 / pdb_00007c97
EMDB ID : EMD-30307
Title : Cryo-EM structure of an Escherichia coli RNAP-promoter open complex (RPo) with SspA
Authors : Lin, W.; Feng, Y.
Deposited on : 2020-06-05
Resolution : 3.68 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

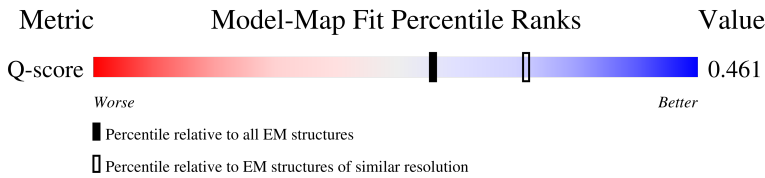
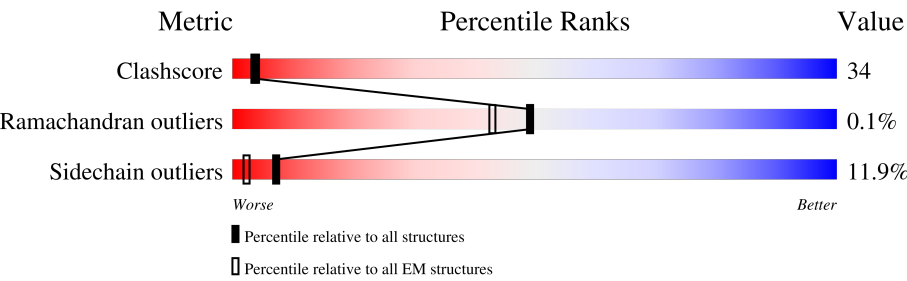
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.68 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	11376 (3.18 - 4.18)

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	H	63	 37% 35% 65%
2	I	212	 34% 37% 53% 7% .
2	J	212	 29% 33% 57% 5% 5%
3	A	329	 5% 34% 32% . 30%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	B	329	
3	K	329	
4	C	1342	
5	D	1407	
6	E	91	
7	F	613	
8	G	63	

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 35581 atoms, of which 532 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 DNA chain called DNA (63-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	63	Total	C	N	O	P	0	0
			1312	623	256	370	63		

- Molecule 2 is a protein called Stringent starvation protein A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	206	Total	C	N	O	S	0	0
			1663	1066	279	310	8		
2	J	201	Total	C	N	O	S	0	0
			1629	1046	272	303	8		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	K	67	Total	C	H	N	O	S	0	0
			1050	328	532	88	100	2		
3	A	230	Total	C	N	O	S		0	0
			1787	1112	317	352	6			
3	B	226	Total	C	N	O	S		0	0
			1755	1094	310	345	6			

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	1340	Total	C	N	O	S	0	0
			10569	6632	1841	2053	43		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	516	VAL	ASP	engineered mutation	UNP P0A8V2

- Molecule 5 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	1343	Total	C	N	O	S	0	0
			10368	6512	1846	1960	50		

- Molecule 6 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	79	Total	C	N	O	S	0	0
			627	382	118	126	1		

- Molecule 7 is a protein called RNA polymerase sigma factor RpoD.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	472	Total	C	N	O	S	0	0
			3845	2408	685	729	23		

- Molecule 8 is a DNA chain called DNA (63-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	48	Total	C	N	O	P	0	0
			973	469	161	295	48		

- Molecule 9 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
9	D	1	Total	Mg	0
			1	1	

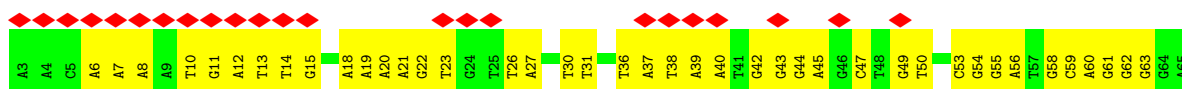
- Molecule 10 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
10	D	2	Total	Zn	0
			2	2	

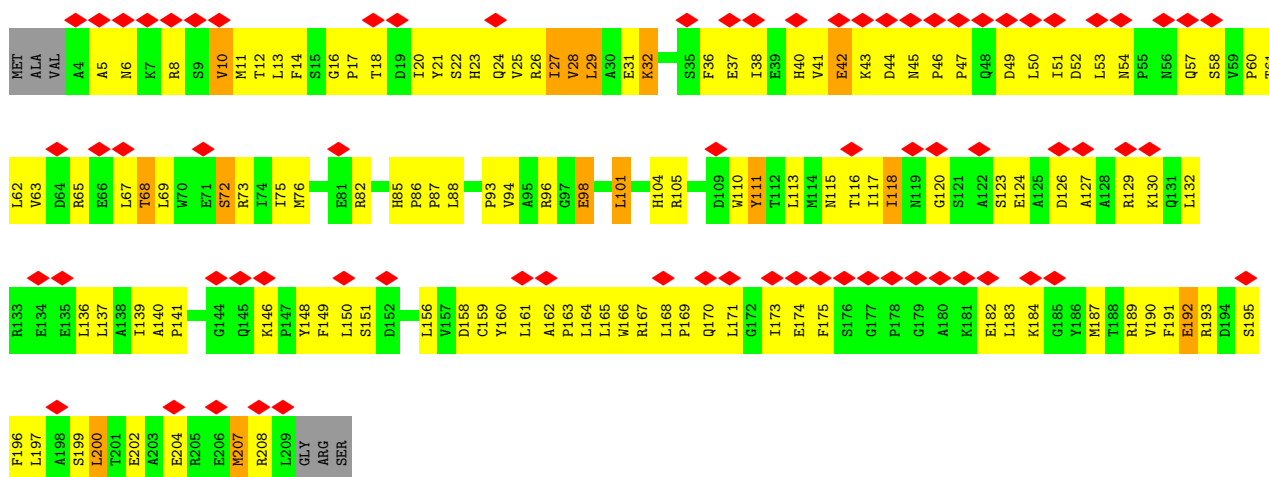
3 Residue-property plots

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.

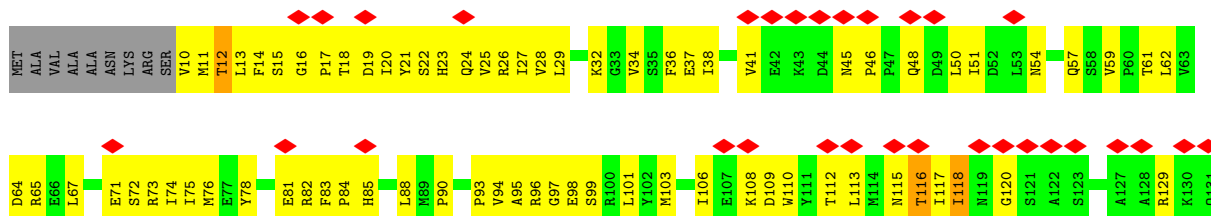
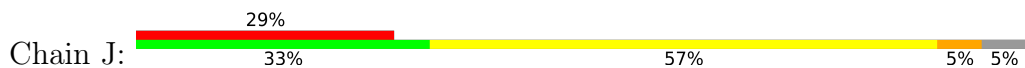
- Molecule 1: DNA (63-mer)

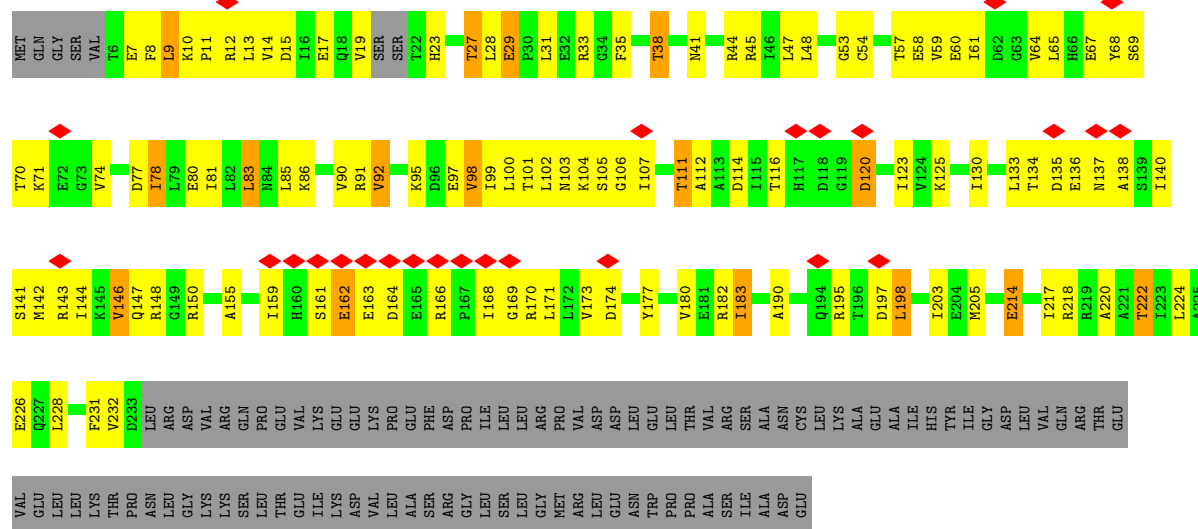


- Molecule 2: Stringent starvation protein A

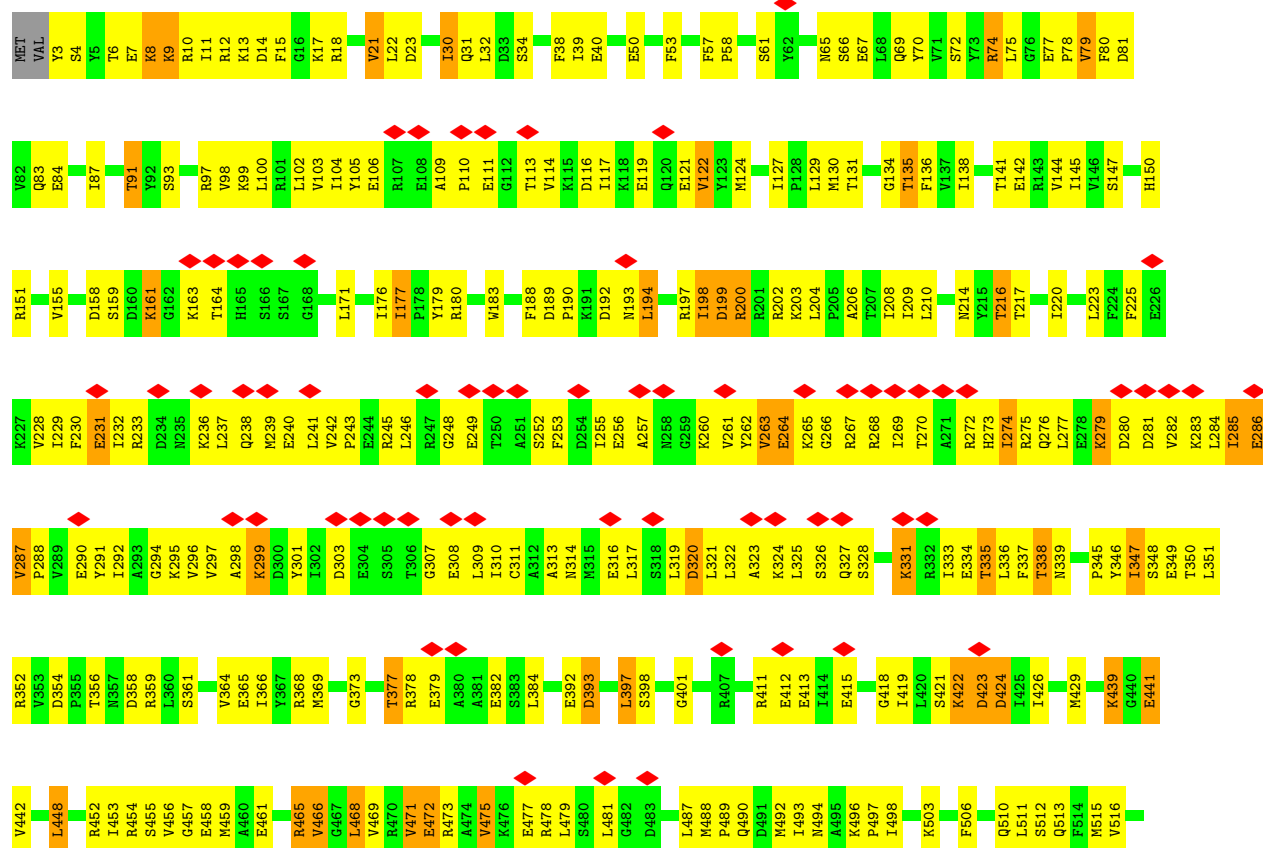


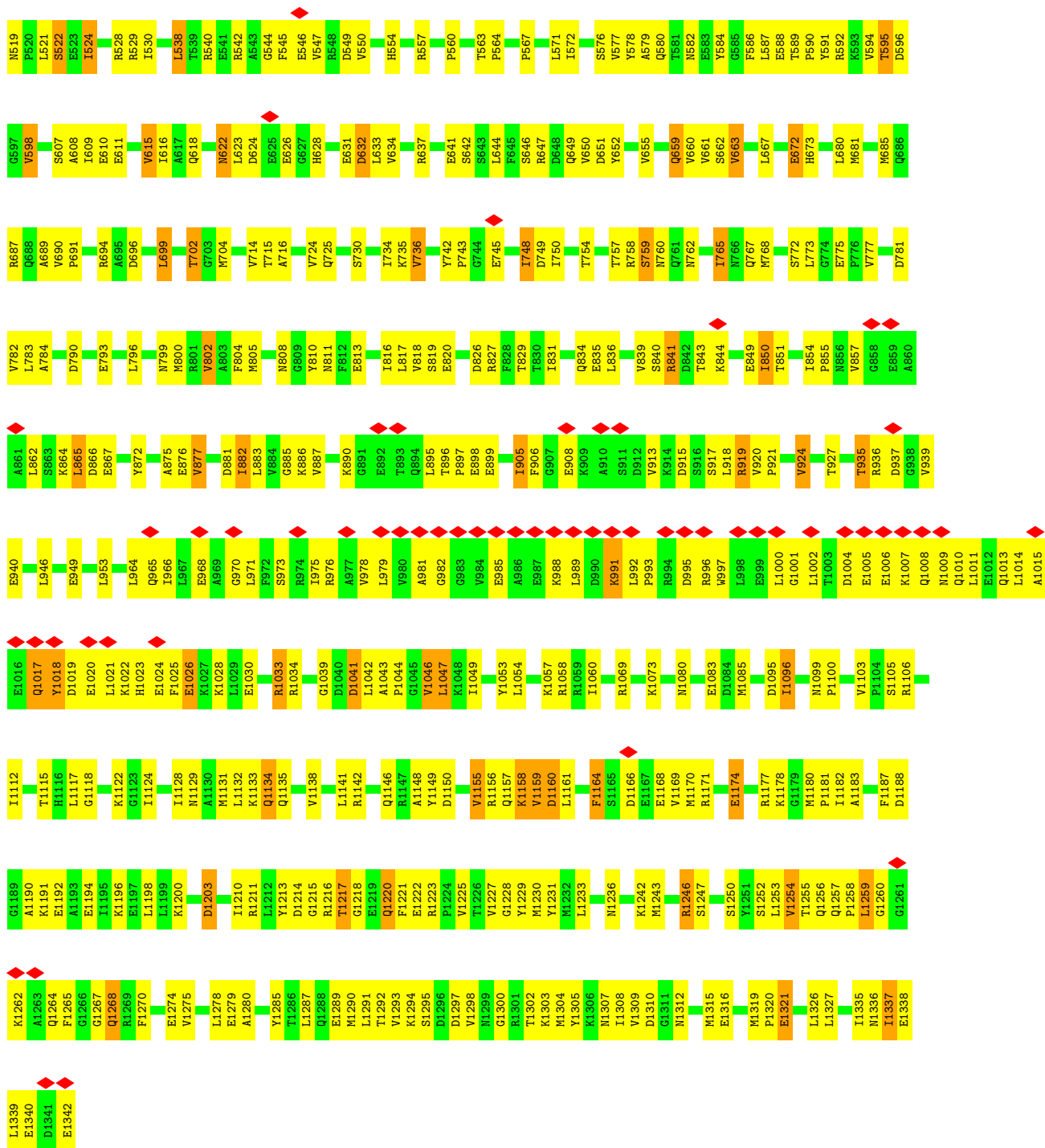
- Molecule 2: Stringent starvation protein A



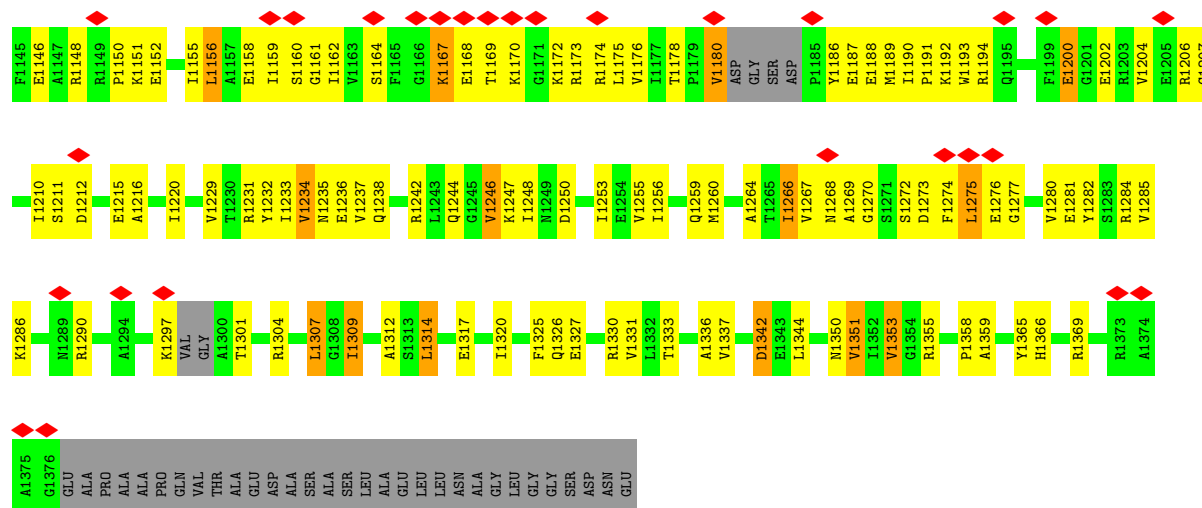


• Molecule 4: DNA-directed RNA polymerase subunit beta

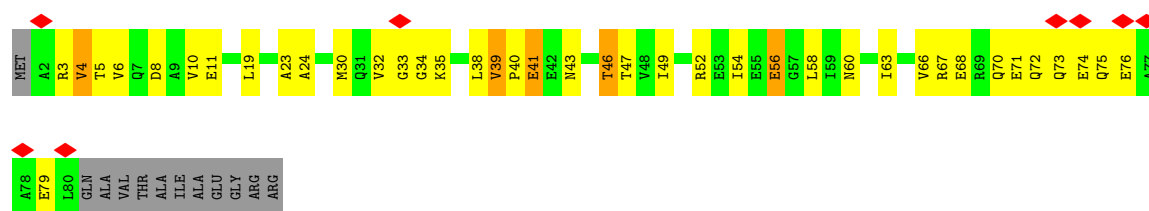
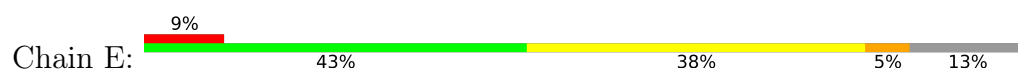




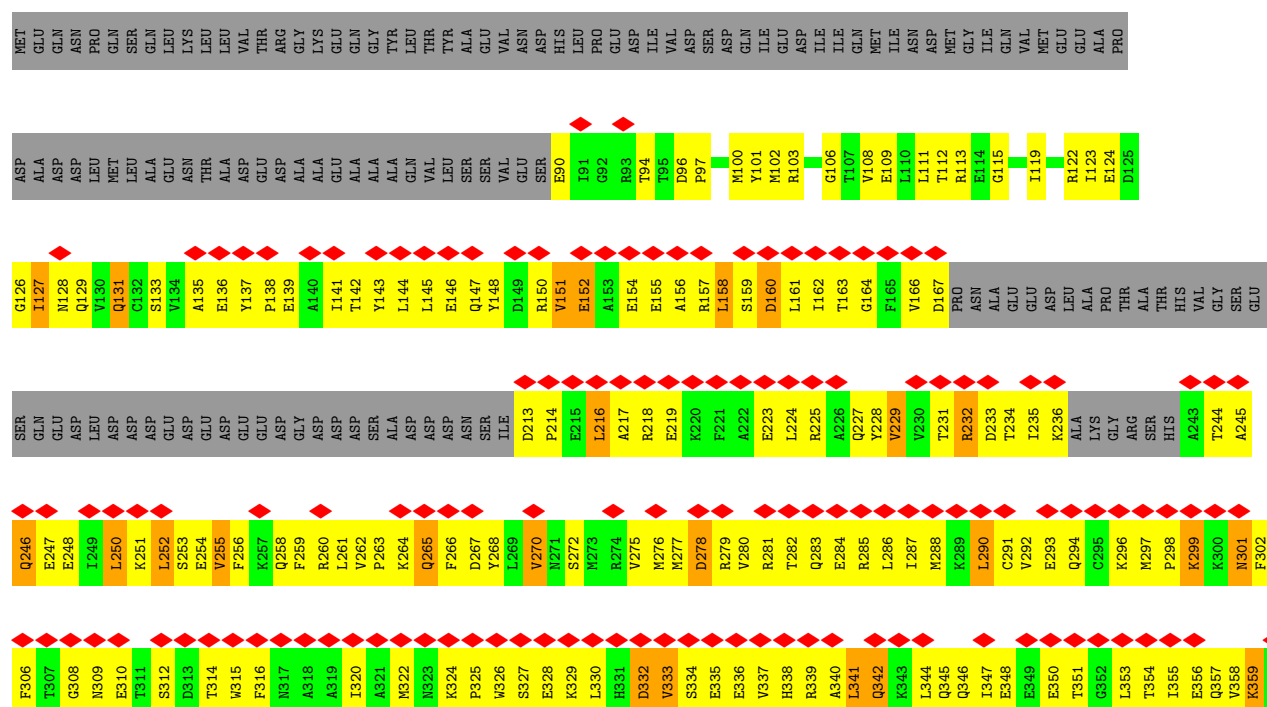


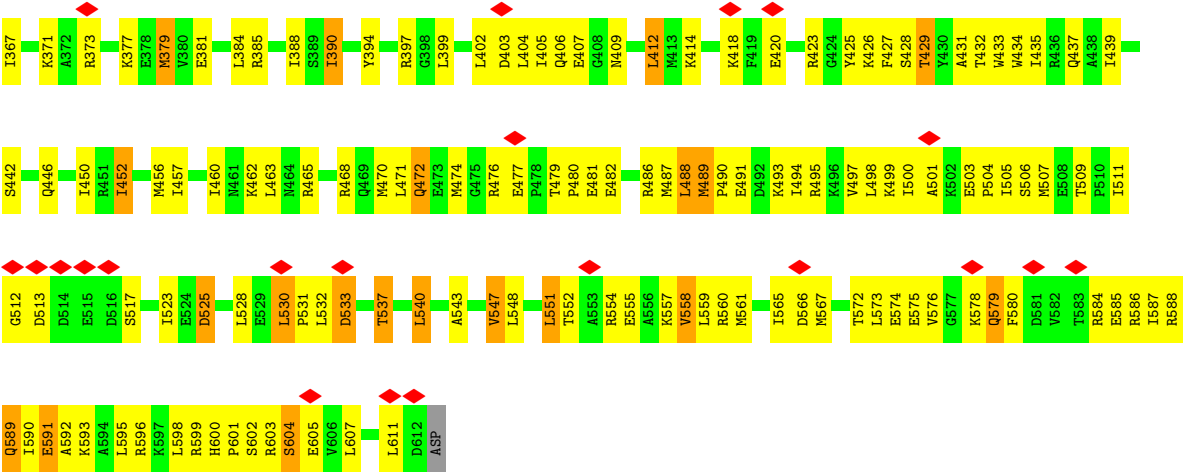


• Molecule 6: DNA-directed RNA polymerase subunit omega

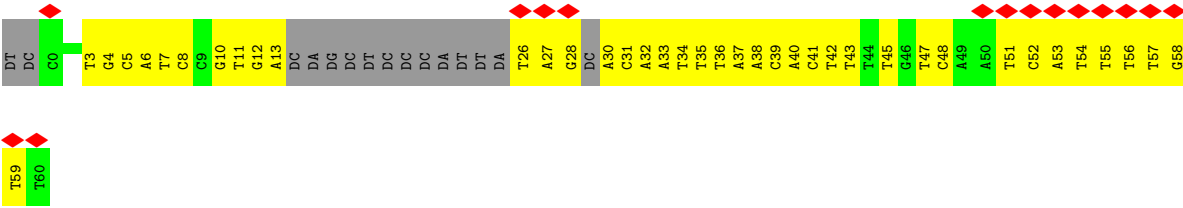
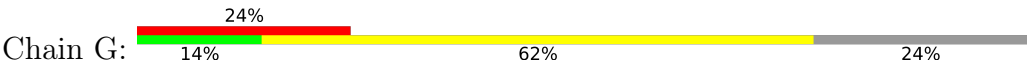


• Molecule 7: RNA polymerase sigma factor RpoD





● Molecule 8: DNA (63-mer)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	60145	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	59	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.170	Depositor
Minimum map value	-0.112	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.026	Depositor
Map size (Å)	261.4, 261.4, 261.4	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3069999, 1.3069999, 1.3069999	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	H	0.25	0/1478	0.39	0/2283
2	I	0.21	0/1704	0.48	0/2313
2	J	0.22	0/1670	0.49	0/2267
3	A	0.34	0/1809	0.52	0/2451
3	B	0.29	0/1776	0.48	0/2406
3	K	0.29	0/524	0.55	0/711
4	C	0.36	0/10738	0.52	2/14488 (0.0%)
5	D	0.35	0/10521	0.52	1/14208 (0.0%)
6	E	0.32	0/629	0.51	0/847
7	F	0.24	0/3896	0.48	0/5236
8	G	0.24	0/1084	0.39	0/1664
All	All	0.32	0/35829	0.50	3/48874 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	C	1159	VAL	N-CA-C	9.76	120.58	110.62
4	C	1160	ASP	N-CA-C	6.82	119.78	109.41
5	D	334	LYS	N-CA-C	-5.37	106.60	112.72

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	1312	0	709	82	0
2	I	1663	0	1646	146	0
2	J	1629	0	1613	158	0
3	A	1787	0	1810	106	0
3	B	1755	0	1778	117	0
3	K	518	532	531	13	0
4	C	10569	0	10587	666	0
5	D	10368	0	10517	724	0
6	E	627	0	634	35	0
7	F	3845	0	3913	405	0
8	G	973	0	550	47	0
9	D	1	0	0	0	0
10	D	2	0	0	0	0
All	All	35049	532	34288	2339	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 34.

All (2339) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:42:DG:O6	7:F:106:GLY:HA3	1.36	1.21
5:D:1089:LEU:HA	5:D:1096:PRO:HA	1.30	1.11
7:F:476:ARG:HG2	7:F:477:GLU:HG2	1.37	1.06
4:C:993:PRO:HG2	4:C:996:ARG:HB3	1.41	1.03
5:D:140:TYR:HB3	7:F:100:MET:HE1	1.40	1.03
2:I:12:THR:HB	2:I:63:VAL:HB	1.44	1.00
3:B:47:LEU:HD12	3:B:183:ILE:HD12	1.43	0.99
5:D:973:LEU:HB2	5:D:1003:LEU:HD12	1.45	0.99
4:C:560:PRO:HB2	5:D:776:THR:HG21	1.40	0.98
2:I:117:ILE:HG22	2:I:171:LEU:HD12	1.45	0.96
4:C:1146:GLN:OE1	4:C:1160:ASP:HB3	1.62	0.96
7:F:250:LEU:HD22	7:F:254:GLU:HG3	1.45	0.96
5:D:972:LYS:HG3	5:D:1002:VAL:HG23	1.48	0.96
4:C:228:VAL:HB	4:C:335:THR:HG23	1.48	0.95
1:H:39:DA:H2''	1:H:40:DA:H5''	1.46	0.95
5:D:1011:VAL:HG21	5:D:1017:VAL:HB	1.45	0.95
4:C:239:MET:HE3	4:C:241:LEU:HD13	1.48	0.95
4:C:398:SER:HB2	4:C:401:GLY:H	1.32	0.94

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:1079:LYS:HD3	5:D:1087:ASP:HB3	1.49	0.94
4:C:1160:ASP:OD2	4:C:1161:LEU:N	2.01	0.94
5:D:980:THR:HB	5:D:997:VAL:HB	1.49	0.94
7:F:561:MET:HE2	7:F:576:VAL:HG22	1.49	0.94
7:F:111:LEU:HD11	7:F:115:GLY:HA3	1.47	0.93
5:D:559:ALA:HB3	5:D:562:GLU:HG2	1.49	0.93
4:C:1017:GLN:HA	4:C:1020:GLU:HB2	1.52	0.91
5:D:746:LEU:HB3	5:D:758:PRO:HB3	1.52	0.91
1:H:42:DG:H1'	1:H:43:DG:C1'	2.01	0.90
7:F:141:ILE:HD13	7:F:224:LEU:HD21	1.50	0.90
7:F:585:GLU:HA	7:F:588:ARG:HH11	1.37	0.90
6:E:56:GLU:HB3	6:E:58:LEU:HD13	1.54	0.90
4:C:1260:GLY:HA3	4:C:1265:PHE:HA	1.52	0.89
2:J:175:PHE:HB3	2:J:180:ALA:HB2	1.53	0.89
5:D:925:GLU:HG3	5:D:926:PRO:HD3	1.53	0.89
4:C:1004:ASP:HA	4:C:1008:GLN:HG2	1.55	0.89
2:I:41:VAL:HG11	2:I:47:PRO:HD3	1.54	0.89
5:D:424:ASN:HB2	5:D:434:ILE:HG12	1.54	0.89
4:C:979:LEU:HD12	4:C:1007:LYS:HB2	1.55	0.88
1:H:38:DT:H2''	1:H:39:DA:H5'	1.55	0.88
7:F:160:ASP:HB3	7:F:264:LYS:HG3	1.55	0.88
5:D:704:GLU:HB2	5:D:718:SER:HB2	1.54	0.88
7:F:144:LEU:HD12	7:F:147:GLN:HB2	1.56	0.87
8:G:47:DT:H2''	8:G:48:DC:H5'	1.55	0.87
5:D:368:LEU:HD23	5:D:373:ALA:HB2	1.55	0.87
4:C:210:LEU:HD11	4:C:429:MET:HE1	1.55	0.86
4:C:198:ILE:HG22	4:C:199:ASP:H	1.38	0.86
5:D:1039:ASP:HB3	5:D:1074:LEU:HB3	1.58	0.86
1:H:37:DA:H61	7:F:420:GLU:HB3	1.41	0.86
3:B:105:SER:HB3	3:B:138:ALA:HB1	1.56	0.86
5:D:789:LYS:HE3	5:D:931:THR:HB	1.57	0.86
4:C:276:GLN:HA	4:C:279:LYS:HD3	1.57	0.85
4:C:876:GLU:HG2	4:C:927:THR:HG22	1.57	0.85
6:E:39:VAL:HG22	6:E:40:PRO:HD2	1.56	0.85
4:C:319:LEU:HD12	4:C:322:LEU:HD12	1.59	0.85
4:C:1149:TYR:CG	4:C:1159:VAL:HG11	2.11	0.84
5:D:1167:LYS:HE3	5:D:1170:LYS:HB2	1.58	0.84
4:C:1015:ALA:HA	4:C:1018:TYR:HB3	1.58	0.84
4:C:1117:LEU:HD11	4:C:1182:ILE:HG21	1.57	0.84
2:I:113:LEU:HD23	2:I:132:LEU:HB2	1.59	0.84
4:C:272:ARG:HA	4:C:275:ARG:HD2	1.59	0.84

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:1103:VAL:HG21	4:C:1112:ILE:HD11	1.60	0.84
1:H:42:DG:H1'	1:H:43:DG:H1'	1.57	0.83
5:D:747:MET:HG3	5:D:759:ILE:HD11	1.58	0.83
5:D:926:PRO:HG2	5:D:1248:ILE:HD11	1.59	0.83
2:I:82:ARG:HH12	2:J:94:VAL:HG13	1.44	0.83
3:A:104:LYS:HD3	3:A:110:VAL:HG22	1.61	0.83
4:C:238:GLN:HB3	4:C:284:LEU:HD11	1.58	0.83
5:D:194:LEU:HD12	5:D:224:LEU:HD22	1.61	0.82
5:D:1031:VAL:HG21	5:D:1088:VAL:HG21	1.60	0.82
6:E:4:VAL:HG23	6:E:5:THR:HG23	1.59	0.82
4:C:471:VAL:HB	4:C:498:ILE:HD11	1.61	0.82
2:I:85:HIS:HB3	7:F:557:LYS:HZ2	1.43	0.82
7:F:574:GLU:HG2	7:F:588:ARG:HH22	1.45	0.82
4:C:1327:LEU:HD22	4:C:1337:ILE:HG21	1.61	0.81
5:D:1031:VAL:HG13	5:D:1080:ILE:HG21	1.62	0.81
7:F:390:ILE:HD11	7:F:432:THR:HG23	1.59	0.81
4:C:106:GLU:HG2	4:C:109:ALA:HB3	1.61	0.81
3:A:111:THR:HG23	3:A:113:ALA:H	1.45	0.80
5:D:515:ARG:HH22	5:D:717:VAL:HB	1.47	0.80
7:F:320:ILE:HA	7:F:327:SER:HB2	1.61	0.80
5:D:958:ILE:HG22	5:D:960:LEU:HD21	1.64	0.79
4:C:1148:ALA:HB1	4:C:1180:MET:HE1	1.63	0.79
4:C:231:GLU:HG3	4:C:233:ARG:HG3	1.64	0.79
5:D:1155:ILE:HG13	5:D:1210:ILE:HB	1.65	0.79
5:D:322:ARG:HG2	5:D:323:PRO:HD2	1.63	0.79
4:C:1164:PHE:HB2	4:C:1168:GLU:HB2	1.65	0.79
4:C:985:GLU:HG2	4:C:988:LYS:HD3	1.65	0.78
4:C:1149:TYR:HB3	4:C:1159:VAL:HG11	1.65	0.78
7:F:224:LEU:HD22	7:F:259:PHE:HE2	1.48	0.78
3:B:166:ARG:HB3	3:B:170:ARG:HG3	1.64	0.78
5:D:1029:THR:HB	5:D:1119:ASP:H	1.47	0.78
2:I:204:GLU:HA	2:I:207:MET:HE2	1.65	0.78
6:E:76:GLU:HA	6:E:79:GLU:HB2	1.66	0.78
5:D:552:ILE:HD11	5:D:570:LYS:HG3	1.66	0.78
8:G:5:DC:H2''	8:G:6:DA:H5'	1.66	0.78
5:D:213:LYS:HA	5:D:216:LYS:HE3	1.64	0.77
7:F:286:LEU:HD21	7:F:290:LEU:HD23	1.66	0.77
5:D:983:LYS:HE3	5:D:991:THR:HB	1.63	0.77
5:D:1204:VAL:HG21	5:D:1210:ILE:HD11	1.66	0.77
2:I:23:HIS:HA	2:I:26:ARG:HG3	1.67	0.77
7:F:465:ARG:HH22	8:G:26:DT:H2'	1.48	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:46:PRO:HG2	2:I:51:ILE:HD11	1.66	0.77
5:D:1102:PRO:HG2	5:D:1124:ILE:HG12	1.68	0.76
5:D:706:VAL:HG12	5:D:715:LYS:HB3	1.67	0.76
4:C:57:PHE:HD1	4:C:70:TYR:HB2	1.51	0.76
4:C:979:LEU:HG	4:C:1002:LEU:HD22	1.68	0.76
4:C:423:ASP:OD1	4:C:423:ASP:N	2.17	0.76
2:I:14:PHE:HB3	2:I:50:LEU:HD22	1.68	0.76
4:C:199:ASP:O	4:C:200:ARG:HG2	1.85	0.76
7:F:530:LEU:HD23	7:F:531:PRO:HD2	1.67	0.76
2:I:168:LEU:HB3	2:I:169:PRO:HD3	1.67	0.76
4:C:690:VAL:HG23	4:C:1236:ASN:HB3	1.68	0.76
4:C:194:LEU:HB3	4:C:206:ALA:HB3	1.68	0.75
2:I:47:PRO:HD2	2:I:50:LEU:HD23	1.67	0.75
2:J:113:LEU:HD23	2:J:132:LEU:HD13	1.68	0.75
2:J:117:ILE:HG22	2:J:171:LEU:HD12	1.66	0.75
5:D:1011:VAL:HG12	5:D:1015:GLU:HB3	1.69	0.75
7:F:167:ASP:HB3	7:F:258:GLN:HE21	1.50	0.75
4:C:758:ARG:NH1	4:C:762:ASN:OD1	2.20	0.75
3:B:48:LEU:HD22	5:D:535:ARG:HG3	1.67	0.75
3:B:97:GLU:OE2	3:B:147:GLN:NE2	2.20	0.75
5:D:1049:GLN:HB2	5:D:1059:LEU:HD11	1.66	0.75
5:D:332:LYS:NZ	5:D:332:LYS:HB3	2.02	0.74
5:D:490:ILE:HD11	5:D:614:LEU:HD12	1.69	0.74
5:D:827:GLU:HB2	5:D:832:LYS:HG2	1.69	0.74
7:F:147:GLN:O	7:F:151:VAL:N	2.20	0.74
4:C:424:ASP:OD1	4:C:424:ASP:N	2.21	0.74
4:C:198:ILE:HG22	4:C:199:ASP:N	2.03	0.74
4:C:642:SER:HB3	5:D:770:LEU:HD21	1.69	0.74
5:D:156:ARG:NH2	5:D:191:SER:OG	2.21	0.74
5:D:986:ASP:OD1	5:D:986:ASP:N	2.20	0.74
4:C:609:ILE:HD12	4:C:610:GLU:HG3	1.69	0.73
5:D:1036:ARG:HB3	5:D:1079:LYS:HB3	1.70	0.73
2:J:17:PRO:HD3	2:J:41:VAL:HG22	1.69	0.73
5:D:537:TYR:OH	5:D:634:ARG:NH1	2.21	0.73
5:D:298:MET:HE1	7:F:406:GLN:HG3	1.70	0.73
2:J:133:ARG:HA	2:J:136:LEU:HG	1.68	0.73
7:F:490:PRO:HG2	7:F:493:LYS:HE2	1.70	0.73
7:F:530:LEU:HD22	7:F:532:LEU:H	1.52	0.73
3:A:214:GLU:OE2	3:A:218:ARG:NH2	2.21	0.73
4:C:270:THR:OG1	4:C:273:HIS:N	2.22	0.73
3:A:61:ILE:HB	3:A:64:VAL:HG12	1.70	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:205:MET:HE1	3:B:217:ILE:HG13	1.70	0.73
4:C:232:ILE:HG23	4:C:237:LEU:HD23	1.69	0.73
4:C:255:ILE:HG12	4:C:263:VAL:HB	1.71	0.73
4:C:736:VAL:HG23	4:C:748:ILE:HA	1.68	0.73
4:C:1033:ARG:O	4:C:1033:ARG:NE	2.21	0.73
5:D:310:GLY:HA2	5:D:314:ARG:HD2	1.69	0.73
2:I:6:ASN:OD1	2:I:65:ARG:N	2.21	0.73
2:J:51:ILE:HG22	2:J:57:GLN:HG2	1.69	0.73
4:C:11:ILE:HG21	4:C:1159:VAL:HG23	1.70	0.73
4:C:1191:LYS:N	4:C:1194:GLU:OE1	2.21	0.73
7:F:102:MET:HE1	7:F:388:ILE:HD13	1.71	0.73
3:B:61:ILE:HG22	3:B:64:VAL:H	1.54	0.72
4:C:314:ASN:HD21	4:C:352:ARG:HG3	1.53	0.72
4:C:1149:TYR:CB	4:C:1159:VAL:HG11	2.20	0.72
2:I:192:GLU:HA	2:I:197:LEU:HD21	1.71	0.72
4:C:1290:MET:SD	4:C:1294:LYS:NZ	2.61	0.72
5:D:81:ARG:NH1	5:D:81:ARG:O	2.22	0.72
4:C:161:LYS:HD3	4:C:161:LYS:H	1.54	0.72
4:C:528:ARG:NH2	4:C:576:SER:O	2.22	0.72
3:A:191:ARG:NH1	3:A:195:ARG:O	2.22	0.72
5:D:482:ALA:O	5:D:488:ASN:ND2	2.22	0.72
1:H:50:DT:OP2	4:C:542:ARG:NH1	2.22	0.72
4:C:3:TYR:N	4:C:7:GLU:OE1	2.22	0.72
4:C:378:ARG:NH1	4:C:382:GLU:OE2	2.21	0.72
5:D:1108:GLN:NE2	5:D:1120:THR:O	2.22	0.72
5:D:352:ARG:NH1	5:D:465:GLN:OE1	2.23	0.72
5:D:832:LYS:HE3	5:D:1242:ARG:HD3	1.72	0.72
2:J:41:VAL:HG12	2:J:46:PRO:HB3	1.72	0.72
3:A:27:THR:HG21	3:A:200:LYS:HE3	1.71	0.72
3:B:164:ASP:O	3:B:166:ARG:NH1	2.22	0.72
4:C:242:VAL:HG22	4:C:245:ARG:HE	1.55	0.72
5:D:1004:ALA:N	5:D:1017:VAL:O	2.21	0.72
8:G:7:DT:H1'	8:G:8:DC:H5'	1.71	0.72
5:D:70:CYS:SG	5:D:71:LEU:N	2.63	0.71
5:D:278:ARG:NH1	7:F:407:GLU:OE2	2.23	0.71
5:D:905:ARG:HH21	5:D:907:HIS:HB2	1.55	0.71
5:D:201:LEU:HD23	5:D:204:GLU:HB2	1.72	0.71
4:C:813:GLU:HB2	5:D:461:PHE:HD2	1.56	0.71
1:H:42:DG:C1'	1:H:43:DG:O4'	2.38	0.71
7:F:296:LYS:HG2	7:F:326:TRP:HB3	1.72	0.71
2:J:18:THR:O	2:J:167:ARG:NH2	2.24	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:100:LEU:HD12	4:C:122:VAL:HG11	1.73	0.71
5:D:475:GLU:HG3	6:E:24:ALA:HB1	1.72	0.71
4:C:1246:ARG:NH1	5:D:348:ASP:OD1	2.23	0.71
7:F:346:GLN:O	7:F:350:GLU:N	2.22	0.71
2:J:28:VAL:HG21	2:J:76:MET:HG2	1.73	0.71
4:C:1124:ILE:HG21	4:C:1180:MET:HE3	1.70	0.71
5:D:1172:LYS:HB3	5:D:1191:PRO:HA	1.73	0.71
5:D:573:THR:HG23	5:D:576:ARG:HD2	1.71	0.71
5:D:876:SER:OG	5:D:988:PHE:HB3	1.89	0.71
7:F:474:MET:SD	7:F:476:ARG:NH2	2.64	0.70
5:D:288:PRO:HB3	7:F:377:LYS:HE3	1.73	0.70
2:J:54:ASN:OD1	2:J:57:GLN:N	2.23	0.70
5:D:81:ARG:HB3	5:D:81:ARG:HH11	1.56	0.70
5:D:661:VAL:HG21	5:D:682:VAL:HG13	1.73	0.70
5:D:1024:THR:HG23	5:D:1124:ILE:H	1.55	0.70
5:D:1160:SER:OG	5:D:1206:ARG:N	2.25	0.70
1:H:42:DG:H2''	1:H:43:DG:O4'	1.92	0.70
3:A:155:ALA:HA	3:A:158:ARG:HD2	1.72	0.70
4:C:1002:LEU:HD23	4:C:1007:LYS:HD3	1.73	0.70
4:C:61:SER:OG	4:C:65:ASN:N	2.25	0.70
4:C:1149:TYR:HB3	4:C:1159:VAL:CG1	2.22	0.70
4:C:1293:VAL:HG11	4:C:1304:MET:HG2	1.74	0.70
2:J:147:PRO:HD2	2:J:152:ASP:HA	1.74	0.70
5:D:194:LEU:HD21	5:D:234:PRO:HG3	1.74	0.70
5:D:1105:ALA:HB1	5:D:1122:ALA:HB1	1.73	0.70
7:F:141:ILE:O	7:F:145:LEU:N	2.22	0.70
3:B:65:LEU:HD22	3:B:169:GLY:HA3	1.72	0.70
1:H:12:DA:H1'	1:H:13:DT:H5'	1.74	0.69
4:C:97:ARG:HG3	4:C:121:GLU:HB3	1.73	0.69
7:F:144:LEU:HD11	7:F:161:LEU:HD12	1.73	0.69
5:D:1144:LEU:HD21	5:D:1236:GLU:HB2	1.75	0.69
8:G:3:DT:H1'	8:G:4:DG:H5'	1.75	0.69
3:A:208:ASN:ND2	3:A:210:THR:OG1	2.25	0.69
4:C:103:VAL:HG12	4:C:116:ASP:HB3	1.75	0.69
4:C:229:ILE:HG23	4:C:240:GLU:HB2	1.74	0.69
4:C:622:ASN:N	4:C:622:ASN:OD1	2.24	0.69
4:C:1083:GLU:OE1	4:C:1083:GLU:N	2.25	0.69
5:D:193:ASP:OD1	5:D:193:ASP:N	2.25	0.69
5:D:518:VAL:HG12	5:D:707:ILE:HD12	1.75	0.69
5:D:1025:MET:HB3	5:D:1124:ILE:HB	1.75	0.69
5:D:641:ILE:O	5:D:764:ARG:NH2	2.26	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:425:ARG:NH1	5:D:458:ASN:O	2.25	0.69
7:F:144:LEU:HA	7:F:147:GLN:HG2	1.74	0.69
2:J:118:ILE:HD11	2:J:171:LEU:HD11	1.74	0.68
5:D:332:LYS:HB3	5:D:332:LYS:HZ2	1.58	0.68
5:D:1314:LEU:HB2	5:D:1326:GLN:HE22	1.58	0.68
7:F:336:GLU:HA	7:F:339:ARG:HG2	1.75	0.68
5:D:473:THR:OG1	5:D:474:LEU:N	2.26	0.68
5:D:510:LEU:O	5:D:514:THR:HG22	1.93	0.68
4:C:322:LEU:O	4:C:326:SER:N	2.25	0.68
4:C:452:ARG:NH2	4:C:584:TYR:O	2.25	0.68
7:F:460:ILE:HD13	7:F:501:ALA:HB2	1.76	0.68
7:F:574:GLU:O	7:F:578:LYS:NZ	2.27	0.68
3:A:190:ALA:HB2	3:A:200:LYS:HG3	1.76	0.68
5:D:73:GLY:O	5:D:76:LYS:NZ	2.26	0.68
5:D:972:LYS:HZ2	5:D:974:VAL:HG23	1.59	0.68
5:D:1037:PHE:HB3	5:D:1041:ILE:HD13	1.76	0.68
5:D:1267:VAL:N	5:D:1301:THR:O	2.24	0.68
4:C:236:LYS:HE2	4:C:236:LYS:HA	1.75	0.68
5:D:275:ARG:NH2	7:F:403:ASP:OD1	2.27	0.68
5:D:816:THR:HG22	5:D:818:GLU:H	1.58	0.68
7:F:147:GLN:OE1	7:F:150:ARG:NH2	2.26	0.68
4:C:255:ILE:HG21	4:C:263:VAL:HG23	1.76	0.67
4:C:820:GLU:HB2	4:C:1080:ASN:O	1.93	0.67
5:D:966:VAL:O	5:D:974:VAL:N	2.22	0.67
4:C:264:GLU:HB2	4:C:267:ARG:HD3	1.76	0.67
5:D:130:MET:HE1	5:D:157:GLN:HB3	1.75	0.67
2:J:82:ARG:NH2	5:D:91:GLU:OE1	2.28	0.67
2:J:132:LEU:HG	2:J:136:LEU:HD21	1.76	0.67
4:C:1297:ASP:OD2	4:C:1300:GLY:N	2.24	0.67
5:D:640:GLY:N	5:D:643:ASP:OD2	2.20	0.67
5:D:741:ALA:O	5:D:762:ASN:ND2	2.27	0.67
7:F:277:MET:O	7:F:281:ARG:N	2.24	0.67
5:D:205:LEU:HB2	5:D:217:LEU:HD12	1.75	0.67
3:B:101:THR:HG22	3:B:143:ARG:HD2	1.77	0.67
4:C:265:LYS:O	4:C:267:ARG:NH1	2.27	0.67
5:D:19:ALA:HA	5:D:1342:ASP:O	1.93	0.67
5:D:558:ASP:OD1	5:D:558:ASP:N	2.25	0.67
4:C:1254:VAL:O	5:D:99:ARG:NH2	2.27	0.67
4:C:1339:LEU:HB3	5:D:17:PHE:HD2	1.60	0.67
5:D:17:PHE:HZ	5:D:1353:VAL:HG11	1.60	0.67
5:D:210:SER:HB3	5:D:213:LYS:HB2	1.75	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:1017:GLN:O	4:C:1021:LEU:N	2.27	0.66
5:D:652:GLU:N	5:D:652:GLU:OE1	2.28	0.66
3:B:58:GLU:OE2	3:B:170:ARG:NH2	2.28	0.66
5:D:760:THR:O	5:D:760:THR:OG1	2.13	0.66
5:D:1002:VAL:N	5:D:1019:ASN:O	2.28	0.66
2:I:63:VAL:HG22	2:I:68:THR:HA	1.75	0.66
4:C:615:VAL:HG12	4:C:650:VAL:HA	1.77	0.66
5:D:1167:LYS:HG3	5:D:1174:ARG:HE	1.60	0.66
3:A:110:VAL:HG23	3:A:133:LEU:HD23	1.78	0.66
4:C:30:ILE:HG22	4:C:31:GLN:HG2	1.78	0.66
7:F:214:PRO:O	7:F:218:ARG:NE	2.24	0.66
2:I:82:ARG:HH21	7:F:578:LYS:HB3	1.60	0.66
2:I:184:LYS:HA	2:I:187:MET:HE3	1.78	0.66
4:C:321:LEU:HA	4:C:324:LYS:HB2	1.77	0.66
5:D:423:LEU:HD23	5:D:466:MET:HE1	1.77	0.66
5:D:925:GLU:HG3	5:D:926:PRO:CD	2.25	0.66
3:B:155:ALA:N	3:B:174:ASP:OD1	2.25	0.66
1:H:63:DG:H5"	5:D:1170:LYS:HG2	1.77	0.66
2:I:126:ASP:O	2:I:130:LYS:N	2.26	0.66
3:A:191:ARG:NH2	3:A:196:THR:O	2.27	0.66
4:C:439:LYS:O	4:C:439:LYS:NZ	2.24	0.66
4:C:1009:ASN:O	4:C:1013:GLN:HB2	1.95	0.66
7:F:124:GLU:O	7:F:128:ASN:ND2	2.29	0.66
3:A:192:VAL:HG12	3:A:195:ARG:HB2	1.78	0.65
4:C:242:VAL:HG23	4:C:245:ARG:HB2	1.78	0.65
4:C:379:GLU:N	4:C:379:GLU:OE1	2.29	0.65
5:D:709:ARG:NH1	5:D:714:GLU:OE1	2.30	0.65
4:C:702:THR:O	4:C:702:THR:OG1	2.13	0.65
5:D:799:ARG:NH1	5:D:1146:GLU:OE2	2.29	0.65
2:J:169:PRO:HD3	2:J:208:ARG:NH2	2.12	0.65
3:B:41:ASN:OD1	3:B:44:ARG:NH2	2.30	0.65
5:D:704:GLU:HB2	5:D:718:SER:CB	2.26	0.65
5:D:959:LYS:HE3	5:D:985:ILE:HG13	1.78	0.65
5:D:1144:LEU:HD23	5:D:1237:VAL:HG23	1.77	0.65
5:D:968:ASN:ND2	5:D:970:SER:OG	2.27	0.65
4:C:189:ASP:HB2	4:C:190:PRO:HD2	1.79	0.65
4:C:633:LEU:HD12	4:C:644:LEU:HD12	1.78	0.65
4:C:1161:LEU:HD12	4:C:1161:LEU:O	1.96	0.65
5:D:1105:ALA:HA	5:D:1123:ARG:O	1.97	0.65
4:C:1267:GLY:HA3	5:D:347:VAL:O	1.97	0.65
5:D:1158:GLU:OE1	5:D:1158:GLU:N	2.30	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:404:LEU:HD22	7:F:439:ILE:HG23	1.79	0.65
1:H:44:DG:H1'	1:H:45:DA:H5'	1.79	0.65
4:C:632:ASP:OD1	4:C:632:ASP:N	2.29	0.65
4:C:839:VAL:HG12	4:C:1049:ILE:HG23	1.78	0.65
5:D:980:THR:CB	5:D:997:VAL:HB	2.26	0.65
6:E:3:ARG:HH21	6:E:52:ARG:HG3	1.60	0.65
1:H:14:DT:H5''	7:F:584:ARG:HD2	1.79	0.65
4:C:320:ASP:O	4:C:324:LYS:N	2.25	0.65
5:D:749:LYS:NZ	5:D:753:SER:OG	2.30	0.65
3:K:263:THR:O	3:K:267:ALA:N	2.29	0.64
3:B:61:ILE:HG21	3:B:64:VAL:HB	1.79	0.64
5:D:709:ARG:HH21	5:D:712:GLN:HB2	1.63	0.64
2:J:165:LEU:O	2:J:208:ARG:NH2	2.30	0.64
4:C:699:LEU:HB2	4:C:799:ASN:HD22	1.61	0.64
4:C:1021:LEU:O	4:C:1025:PHE:HB3	1.98	0.64
6:E:23:ALA:HB2	6:E:54:ILE:HD11	1.78	0.64
4:C:975:ILE:HG22	4:C:1010:GLN:HG2	1.80	0.64
4:C:716:ALA:HB3	4:C:784:ALA:HB3	1.78	0.64
5:D:703:THR:HG21	5:D:715:LYS:HD3	1.78	0.64
5:D:959:LYS:HG3	5:D:985:ILE:HG13	1.79	0.64
2:I:146:LYS:HG3	2:I:150:LEU:HA	1.79	0.64
3:B:83:LEU:HD11	5:D:527:LEU:O	1.98	0.64
3:B:104:LYS:NZ	3:B:105:SER:O	2.31	0.64
4:C:299:LYS:HE2	4:C:334:GLU:OE1	1.97	0.64
5:D:314:ARG:HH22	5:D:323:PRO:HG3	1.62	0.64
5:D:507:VAL:HG21	5:D:598:LYS:HB2	1.78	0.64
3:B:135:ASP:OD1	3:B:136:GLU:N	2.30	0.64
5:D:1029:THR:HB	5:D:1118:GLY:H	1.62	0.64
2:I:96:ARG:NH2	2:J:81:GLU:OE2	2.30	0.64
4:C:545:PHE:CZ	5:D:781:LYS:HD3	2.32	0.64
4:C:836:LEU:HD21	4:C:921:PRO:HD3	1.80	0.64
5:D:850:LYS:HG3	5:D:855:ASP:HB3	1.78	0.64
7:F:341:LEU:HB3	7:F:344:LEU:HD21	1.80	0.64
2:I:18:THR:O	2:I:167:ARG:NH2	2.23	0.64
3:A:226:GLU:O	3:B:10:LYS:NZ	2.27	0.64
4:C:320:ASP:OD1	4:C:320:ASP:N	2.25	0.64
5:D:398:LYS:HD3	7:F:532:LEU:CD2	2.28	0.64
5:D:609:TYR:HE1	5:D:614:LEU:HD12	1.63	0.64
4:C:117:ILE:HD11	4:C:488:MET:HA	1.79	0.63
4:C:540:ARG:HH22	4:C:567:PRO:HG2	1.62	0.63
5:D:163:GLU:OE1	5:D:163:GLU:N	2.31	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:528:THR:O	5:D:528:THR:OG1	2.11	0.63
7:F:97:PRO:O	7:F:101:TYR:N	2.29	0.63
7:F:543:ALA:O	7:F:547:VAL:N	2.31	0.63
3:A:155:ALA:O	3:A:159:ILE:HG12	1.98	0.63
3:B:83:LEU:HD21	5:D:526:VAL:HG22	1.81	0.63
4:C:576:SER:OG	4:C:577:VAL:N	2.30	0.63
8:G:58:DG:H2'	8:G:59:DT:H71	1.79	0.63
3:B:100:LEU:HB2	3:B:144:ILE:CG1	2.29	0.63
4:C:335:THR:OG1	4:C:336:LEU:N	2.30	0.63
4:C:194:LEU:HB3	4:C:206:ALA:CB	2.28	0.63
4:C:557:ARG:NH2	4:C:611:GLU:OE1	2.25	0.63
5:D:978:ARG:HH12	5:D:999:TYR:HB2	1.63	0.63
7:F:283:GLN:HE22	7:F:340:ALA:HB1	1.63	0.63
2:I:6:ASN:HB3	2:I:65:ARG:HA	1.80	0.63
5:D:1152:GLU:OE1	5:D:1194:ARG:NH2	2.32	0.63
7:F:279:ARG:NH2	7:F:350:GLU:OE2	2.30	0.63
2:I:111:TYR:CE1	2:I:164:LEU:HD11	2.34	0.63
4:C:180:ARG:NH2	4:C:393:ASP:O	2.32	0.63
4:C:288:PRO:HG2	4:C:291:TYR:HB2	1.80	0.63
5:D:959:LYS:NZ	5:D:985:ILE:HG21	2.14	0.63
7:F:150:ARG:HD2	7:F:155:GLU:OE1	1.99	0.63
4:C:1004:ASP:OD1	4:C:1008:GLN:NE2	2.32	0.63
1:H:42:DG:H2''	1:H:43:DG:OP2	1.98	0.62
1:H:59:DC:H1'	1:H:60:DA:H5'	1.81	0.62
4:C:441:GLU:OE1	4:C:442:VAL:N	2.32	0.62
4:C:1142:ARG:HD3	4:C:1169:VAL:HG21	1.80	0.62
4:C:1338:GLU:O	4:C:1339:LEU:HD23	1.98	0.62
5:D:1280:VAL:HG11	5:D:1304:ARG:HH21	1.63	0.62
7:F:131:GLN:HB3	7:F:266:PHE:HZ	1.64	0.62
2:I:11:MET:SD	2:I:37:GLU:N	2.66	0.62
2:I:20:ILE:HD11	2:I:163:PRO:HB2	1.81	0.62
2:I:41:VAL:CG1	2:I:47:PRO:HD3	2.28	0.62
2:J:118:ILE:CD1	2:J:171:LEU:HD11	2.29	0.62
5:D:716:GLN:HG3	5:D:717:VAL:O	1.99	0.62
5:D:885:VAL:HG11	5:D:1255:VAL:HG12	1.81	0.62
6:E:75:GLN:O	6:E:79:GLU:N	2.32	0.62
7:F:163:THR:HG23	7:F:262:VAL:HG22	1.81	0.62
3:B:214:GLU:OE2	3:B:218:ARG:NH2	2.25	0.62
4:C:12:ARG:NH2	4:C:793:GLU:OE2	2.27	0.62
4:C:193:ASN:HB3	4:C:350:THR:HG22	1.81	0.62
5:D:694:SER:OG	5:D:738:ARG:NE	2.32	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:803:VAL:HG11	5:D:1309:ILE:HG22	1.80	0.62
7:F:228:TYR:CD2	7:F:229:VAL:HG13	2.34	0.62
5:D:611:ILE:HG22	5:D:612:LEU:HD12	1.80	0.62
5:D:255:LEU:HD23	5:D:261:ALA:HB2	1.82	0.62
5:D:1004:ALA:HB3	5:D:1017:VAL:HA	1.81	0.62
7:F:141:ILE:HG22	7:F:145:LEU:HB3	1.80	0.62
8:G:52:DC:H5'	8:G:52:DC:H6	1.62	0.62
2:J:154:PHE:CE1	2:J:158:ASP:HB2	2.34	0.62
3:A:222:THR:HG22	3:B:232:VAL:HA	1.82	0.62
4:C:866:ASP:HB3	4:C:872:TYR:CE1	2.34	0.62
8:G:11:DT:H2''	8:G:12:DG:H5''	1.82	0.62
1:H:42:DG:C2'	1:H:43:DG:O4'	2.47	0.62
4:C:494:ASN:OD1	7:F:468:ARG:NE	2.33	0.62
5:D:83:VAL:O	5:D:92:VAL:HG22	2.00	0.62
5:D:807:LEU:HD12	5:D:1259:GLN:OE1	2.00	0.62
7:F:347:ILE:HA	7:F:350:GLU:HB2	1.82	0.62
4:C:453:ILE:HD12	4:C:587:LEU:HD21	1.82	0.62
4:C:1134:GLN:O	4:C:1135:GLN:HG2	2.00	0.62
5:D:474:LEU:HD11	6:E:47:THR:HG22	1.82	0.62
5:D:801:VAL:CG2	5:D:917:VAL:HG13	2.28	0.62
5:D:860:ARG:O	5:D:862:THR:HG23	2.00	0.62
5:D:1027:VAL:O	5:D:1121:LEU:N	2.29	0.62
7:F:354:THR:HG22	7:F:357:GLN:HG3	1.82	0.62
7:F:479:THR:OG1	7:F:482:GLU:HG3	2.00	0.62
5:D:44:ILE:HD11	7:F:450:ILE:HD11	1.80	0.62
5:D:163:GLU:O	5:D:167:ASP:N	2.26	0.62
5:D:857:LEU:HD12	5:D:858:VAL:HG13	1.82	0.62
7:F:160:ASP:O	7:F:265:GLN:NE2	2.29	0.62
7:F:160:ASP:HA	7:F:262:VAL:HG11	1.80	0.62
7:F:305:LEU:O	7:F:314:THR:HG21	2.00	0.62
7:F:247:GLU:O	7:F:251:LYS:N	2.32	0.62
7:F:250:LEU:O	7:F:254:GLU:N	2.31	0.62
2:J:14:PHE:CD2	2:J:50:LEU:HD13	2.34	0.61
2:J:22:SER:O	2:J:26:ARG:HG3	2.00	0.61
3:K:264:VAL:O	3:K:268:ASN:N	2.32	0.61
3:B:222:THR:O	3:B:226:GLU:HG2	2.00	0.61
4:C:373:GLY:HA3	7:F:94:THR:HB	1.82	0.61
5:D:800:LEU:HD22	5:D:1256:ILE:HD13	1.82	0.61
2:I:169:PRO:HG2	2:I:208:ARG:HH12	1.64	0.61
3:B:86:LYS:HE2	3:B:174:ASP:HB2	1.83	0.61
4:C:667:LEU:HA	4:C:702:THR:HG21	1.81	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:453:ILE:HD11	4:C:587:LEU:HD11	1.82	0.61
7:F:565:ILE:O	7:F:567:MET:HG2	2.00	0.61
7:F:585:GLU:CG	7:F:588:ARG:HD2	2.31	0.61
2:J:11:MET:HE2	2:J:64:ASP:HB3	1.81	0.61
3:B:159:ILE:HD12	3:B:162:GLU:HB2	1.83	0.61
4:C:119:GLU:HB2	4:C:489:PRO:HD2	1.82	0.61
4:C:245:ARG:HG3	4:C:337:PHE:CZ	2.36	0.61
5:D:381:ILE:HD11	5:D:412:LEU:HB2	1.82	0.61
5:D:982:LEU:HD21	5:D:997:VAL:HG21	1.82	0.61
8:G:32:DA:H2''	8:G:33:DA:H5'	1.82	0.61
4:C:77:GLU:OE1	4:C:77:GLU:N	2.30	0.61
5:D:334:LYS:O	5:D:335:GLN:NE2	2.33	0.61
5:D:1175:LEU:HD12	5:D:1176:VAL:H	1.64	0.61
3:A:11:PRO:HA	3:A:30:PRO:HD2	1.83	0.61
3:A:57:THR:HG21	3:A:147:GLN:HE21	1.64	0.61
4:C:298:ALA:HB3	4:C:299:LYS:HZ1	1.65	0.61
5:D:1012:ALA:HB3	5:D:1015:GLU:HB2	1.83	0.61
5:D:1055:GLY:O	5:D:1108:GLN:HB2	2.01	0.61
2:I:183:LEU:HG	2:I:187:MET:HE2	1.83	0.61
5:D:210:SER:O	5:D:214:ARG:HG2	2.01	0.61
5:D:1111:ASP:OD1	5:D:1112:GLY:N	2.34	0.61
7:F:136:GLU:HG3	7:F:361:ILE:HG12	1.83	0.61
4:C:155:VAL:HG12	4:C:176:ILE:HG12	1.83	0.61
4:C:690:VAL:CG2	4:C:1236:ASN:HB3	2.31	0.61
5:D:62:PHE:CD1	5:D:247:PRO:HD3	2.36	0.61
7:F:150:ARG:O	7:F:154:GLU:N	2.33	0.61
7:F:329:LYS:O	7:F:329:LYS:HD3	2.01	0.61
3:B:170:ARG:HH11	3:B:170:ARG:HA	1.65	0.60
4:C:817:LEU:HD21	4:C:1080:ASN:HD21	1.66	0.60
5:D:948:SER:HA	5:D:1022:PRO:HG3	1.83	0.60
8:G:55:DT:H2'	8:G:56:DT:C2	2.35	0.60
2:J:162:ALA:HB3	2:J:163:PRO:HD3	1.83	0.60
3:A:74:VAL:HG23	3:A:76:GLU:H	1.67	0.60
4:C:268:ARG:NH2	4:C:270:THR:HA	2.16	0.60
4:C:336:LEU:O	4:C:338:THR:HG22	2.00	0.60
5:D:490:ILE:O	5:D:491:LEU:HD23	2.01	0.60
5:D:1062:LEU:HB2	5:D:1067:ARG:HE	1.64	0.60
2:I:174:GLU:OE1	2:I:175:PHE:N	2.32	0.60
2:J:166:TRP:NE1	2:J:204:GLU:O	2.28	0.60
4:C:321:LEU:HD23	4:C:324:LYS:HD2	1.81	0.60
4:C:546:GLU:HG2	4:C:547:VAL:HG13	1.82	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:806:ASP:OD1	5:D:806:ASP:N	2.30	0.60
7:F:277:MET:O	7:F:280:VAL:N	2.33	0.60
1:H:19:DA:H2''	1:H:20:DA:H5''	1.83	0.60
1:H:42:DG:O6	7:F:106:GLY:CA	2.31	0.60
2:J:168:LEU:HB2	2:J:169:PRO:HD3	1.82	0.60
5:D:516:ASP:OD1	5:D:516:ASP:N	2.34	0.60
4:C:538:LEU:HD21	4:C:547:VAL:HG21	1.83	0.60
5:D:1155:ILE:HG12	5:D:1211:SER:HB3	1.83	0.60
2:J:129:ARG:HA	2:J:173:ILE:HD11	1.83	0.60
4:C:757:THR:HG23	4:C:765:ILE:HG23	1.82	0.60
5:D:557:LYS:HA	5:D:562:GLU:O	2.01	0.60
5:D:1025:MET:N	5:D:1124:ILE:O	2.34	0.60
2:I:202:GLU:N	2:I:202:GLU:OE1	2.35	0.60
4:C:662:SER:OG	4:C:663:VAL:N	2.31	0.60
5:D:975:ILE:HG12	5:D:998:PRO:O	2.02	0.60
7:F:109:GLU:OE1	7:F:109:GLU:N	2.29	0.60
5:D:134:ASP:OD1	5:D:159:ILE:HG12	2.02	0.60
5:D:514:THR:HG21	5:D:596:LEU:HB3	1.84	0.60
5:D:847:ASP:OD1	5:D:860:ARG:HA	2.01	0.60
7:F:127:ILE:O	7:F:131:GLN:HG3	2.02	0.60
2:J:191:PHE:HA	2:J:196:PHE:HD2	1.66	0.60
3:B:54:CYS:SG	3:B:148:ARG:HG2	2.41	0.60
5:D:534:GLU:HA	5:D:578:ILE:HD11	1.84	0.60
5:D:978:ARG:HH22	5:D:999:TYR:HB2	1.67	0.60
7:F:320:ILE:HG12	7:F:327:SER:O	2.02	0.60
2:I:10:VAL:HG12	2:I:11:MET:H	1.67	0.60
4:C:415:GLU:OE1	4:C:415:GLU:N	2.30	0.60
4:C:979:LEU:HD11	4:C:1011:LEU:HD21	1.84	0.60
3:A:118:ASP:OD1	3:A:119:GLY:N	2.35	0.59
4:C:288:PRO:HG2	4:C:291:TYR:CB	2.32	0.59
4:C:775:GLU:OE1	4:C:775:GLU:N	2.35	0.59
5:D:443:GLU:OE2	5:D:444:GLY:N	2.33	0.59
5:D:960:LEU:HD22	5:D:981:GLU:O	2.02	0.59
7:F:138:PRO:HG2	7:F:353:LEU:HD11	1.84	0.59
8:G:47:DT:C2'	8:G:48:DC:H5'	2.28	0.59
2:I:124:GLU:HA	2:I:127:ALA:HB3	1.84	0.59
3:A:14:VAL:HG12	3:A:27:THR:O	2.00	0.59
4:C:1006:GLU:HA	4:C:1009:ASN:HB2	1.83	0.59
4:C:1164:PHE:HB2	4:C:1168:GLU:CB	2.32	0.59
5:D:450:HIS:NE2	5:D:625:MET:SD	2.76	0.59
5:D:1025:MET:HB3	5:D:1124:ILE:CG2	2.32	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:88:LEU:HD13	2:I:156:LEU:HD21	1.82	0.59
4:C:988:LYS:HA	4:C:991:LYS:HG2	1.84	0.59
7:F:456:MET:HE3	7:F:497:VAL:HG22	1.83	0.59
2:I:93:PRO:HD2	5:D:82:GLY:HA3	1.85	0.59
4:C:262:TYR:HE2	4:C:282:VAL:HG21	1.67	0.59
5:D:808:VAL:HG21	5:D:1359:ALA:HB2	1.83	0.59
5:D:1073:ASP:O	5:D:1074:LEU:HD23	2.03	0.59
7:F:298:PRO:HB2	7:F:301:ASN:HD21	1.67	0.59
2:I:27:ILE:HD11	2:I:163:PRO:HG3	1.83	0.59
3:B:135:ASP:O	3:B:137:ASN:ND2	2.35	0.59
4:C:98:VAL:O	4:C:121:GLU:HA	2.01	0.59
5:D:438:GLU:HG3	5:D:485:MET:HE1	1.85	0.59
5:D:955:LYS:HG2	5:D:1010:GLN:HB3	1.84	0.59
5:D:1088:VAL:O	5:D:1097:ALA:N	2.25	0.59
7:F:146:GLU:O	7:F:150:ARG:NE	2.35	0.59
7:F:572:THR:HG23	8:G:45:DT:OP2	2.02	0.59
1:H:19:DA:H2''	1:H:20:DA:C5'	2.32	0.59
2:J:103:MET:HE3	2:J:160:TYR:CE1	2.38	0.59
2:J:29:LEU:HG	2:J:34:VAL:HG11	1.84	0.59
4:C:857:VAL:HG11	4:C:862:LEU:HD21	1.85	0.59
7:F:144:LEU:HA	7:F:147:GLN:CG	2.32	0.59
2:I:104:HIS:CE1	2:J:71:GLU:HG3	2.38	0.59
3:A:26:VAL:HG21	3:A:217:ILE:HD12	1.85	0.59
4:C:940:GLU:OE1	4:C:940:GLU:N	2.36	0.59
2:I:104:HIS:NE2	2:J:71:GLU:HG3	2.18	0.59
2:J:103:MET:HE3	2:J:160:TYR:HE1	1.68	0.59
4:C:230:PHE:HB2	4:C:333:ILE:HB	1.85	0.59
4:C:232:ILE:O	4:C:331:LYS:HD3	2.02	0.59
4:C:243:PRO:HB3	4:C:277:LEU:HB2	1.83	0.59
4:C:324:LYS:O	4:C:328:SER:HB2	2.02	0.59
7:F:113:ARG:HB2	7:F:426:LYS:HE2	1.84	0.59
7:F:297:MET:HE2	7:F:330:LEU:HD11	1.83	0.59
2:J:28:VAL:O	2:J:32:LYS:HG2	2.03	0.59
2:J:23:HIS:O	2:J:27:ILE:HG12	2.03	0.58
3:A:100:LEU:HD21	3:A:121:VAL:HG11	1.85	0.58
3:B:98:VAL:HG13	3:B:146:VAL:HG13	1.85	0.58
7:F:142:THR:HA	7:F:145:LEU:CD2	2.34	0.58
7:F:166:VAL:HG12	7:F:260:ARG:NH2	2.17	0.58
1:H:55:DG:H2''	1:H:56:DA:H5''	1.85	0.58
2:J:15:SER:O	2:J:41:VAL:HG13	2.02	0.58
4:C:225:PHE:HE2	4:C:347:ILE:HG22	1.68	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:471:VAL:O	4:C:475:VAL:HG12	2.03	0.58
4:C:1020:GLU:O	4:C:1024:GLU:N	2.25	0.58
5:D:390:LEU:HD23	5:D:407:VAL:HG11	1.85	0.58
2:I:5:ALA:HB1	2:I:12:THR:HG21	1.85	0.58
5:D:152:THR:HG22	5:D:153:ASN:H	1.68	0.58
5:D:208:THR:CG2	5:D:213:LYS:HE3	2.34	0.58
5:D:232:ASN:OD1	5:D:232:ASN:N	2.33	0.58
5:D:1286:LYS:O	5:D:1290:ARG:N	2.27	0.58
3:A:27:THR:CG2	3:A:200:LYS:HE3	2.32	0.58
7:F:150:ARG:HB3	7:F:155:GLU:HB3	1.85	0.58
3:A:179:PRO:HA	3:A:208:ASN:OD1	2.02	0.58
4:C:1005:GLU:O	4:C:1008:GLN:HG3	2.03	0.58
5:D:120:LEU:HB2	5:D:121:PRO:HD3	1.86	0.58
5:D:697:MET:SD	5:D:741:ALA:HB3	2.43	0.58
5:D:825:VAL:CG1	5:D:832:LYS:HB2	2.33	0.58
5:D:975:ILE:HD11	5:D:977:SER:O	2.04	0.58
6:E:67:ARG:NH1	6:E:67:ARG:O	2.36	0.58
8:G:38:DA:H2'	8:G:39:DC:C6	2.38	0.58
2:J:154:PHE:HE1	2:J:158:ASP:HB2	1.67	0.58
2:J:194:ASP:HA	2:J:197:LEU:HB3	1.84	0.58
4:C:38:PHE:HD2	4:C:39:ILE:HG23	1.69	0.58
4:C:230:PHE:CE2	4:C:292:ILE:HD12	2.39	0.58
5:D:843:VAL:HG21	5:D:883:ARG:HD3	1.85	0.58
5:D:1021:ASP:CG	5:D:1024:THR:HB	2.29	0.58
2:I:182:GLU:N	2:I:182:GLU:OE1	2.36	0.58
2:J:20:ILE:O	2:J:24:GLN:HG3	2.02	0.58
5:D:127:LEU:HD22	5:D:227:PHE:HE1	1.69	0.58
5:D:1038:THR:HG21	5:D:1079:LYS:HB2	1.85	0.58
8:G:36:DT:H2''	8:G:37:DA:H5'	1.85	0.58
3:A:14:VAL:CG1	3:A:27:THR:HB	2.32	0.58
4:C:1008:GLN:HA	4:C:1011:LEU:CD1	2.34	0.58
5:D:1215:GLU:OE1	5:D:1215:GLU:N	2.37	0.58
2:J:129:ARG:NH2	2:J:171:LEU:O	2.37	0.58
4:C:242:VAL:CG2	4:C:245:ARG:HB2	2.34	0.58
4:C:473:ARG:HB2	4:C:473:ARG:NH1	2.19	0.58
4:C:979:LEU:CD1	4:C:1011:LEU:HD21	2.34	0.58
5:D:320:ASN:O	5:D:321:LYS:HD3	2.03	0.58
7:F:159:SER:O	7:F:262:VAL:HG21	2.03	0.58
1:H:18:DA:H1'	1:H:19:DA:H5'	1.85	0.58
3:B:161:SER:O	3:B:163:GLU:HG3	2.04	0.58
4:C:301:TYR:HB2	4:C:311:CYS:SG	2.44	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:578:TYR:HD2	4:C:659:GLN:HB2	1.68	0.58
5:D:317:THR:CG2	5:D:320:ASN:HB3	2.33	0.58
5:D:1029:THR:CG2	5:D:1117:SER:HA	2.34	0.58
8:G:41:DC:H2"	8:G:42:DT:N3	2.19	0.58
3:B:170:ARG:HA	3:B:170:ARG:NH1	2.18	0.57
2:I:25:VAL:O	2:I:29:LEU:HB2	2.04	0.57
3:B:57:THR:O	3:B:173:VAL:HG12	2.02	0.57
4:C:397:LEU:O	4:C:398:SER:OG	2.20	0.57
4:C:897:PRO:HG2	4:C:898:GLU:OE1	2.04	0.57
5:D:426:ALA:HB3	5:D:427:PRO:HD3	1.86	0.57
5:D:519:ASN:HA	5:D:523:GLU:OE1	2.04	0.57
5:D:718:SER:OG	5:D:719:PHE:N	2.35	0.57
7:F:558:VAL:HG23	7:F:580:PHE:HE2	1.69	0.57
2:I:94:VAL:HG13	2:J:67:LEU:HD22	1.86	0.57
2:J:90:PRO:HG2	2:J:96:ARG:HA	1.86	0.57
5:D:38:VAL:HG11	5:D:56:LEU:HD12	1.84	0.57
5:D:1005:LYS:HG3	5:D:1011:VAL:HG22	1.86	0.57
6:E:76:GLU:HA	6:E:79:GLU:HG3	1.86	0.57
7:F:214:PRO:HB2	7:F:218:ARG:HD3	1.86	0.57
2:J:32:LYS:NZ	2:J:83:PHE:O	2.23	0.57
4:C:58:PRO:HB3	4:C:69:GLN:HA	1.85	0.57
4:C:1022:LYS:O	4:C:1026:GLU:HB3	2.05	0.57
5:D:1027:VAL:HB	5:D:1121:LEU:HB2	1.87	0.57
5:D:1161:GLY:HA2	5:D:1180:VAL:HG22	1.86	0.57
7:F:463:LEU:HD12	7:F:487:MET:HE1	1.86	0.57
7:F:558:VAL:HG21	7:F:587:ILE:HD11	1.87	0.57
1:H:11:DG:N2	8:G:53:DA:N3	2.53	0.57
2:J:17:PRO:HD3	2:J:41:VAL:CG2	2.35	0.57
2:J:41:VAL:HG11	2:J:59:VAL:HG11	1.86	0.57
2:J:99:SER:O	2:J:103:MET:HG2	2.03	0.57
3:A:11:PRO:HB3	3:A:31:LEU:HD23	1.86	0.57
4:C:102:LEU:HB2	4:C:489:PRO:HG3	1.87	0.57
4:C:248:GLY:H	4:C:269:ILE:HD11	1.69	0.57
4:C:471:VAL:CB	4:C:498:ILE:HD11	2.33	0.57
5:D:388:ARG:HB2	5:D:390:LEU:HD13	1.86	0.57
5:D:697:MET:HE1	5:D:738:ARG:HA	1.86	0.57
5:D:1031:VAL:O	5:D:1080:ILE:HD13	2.04	0.57
4:C:164:THR:HG21	4:C:171:LEU:CD1	2.34	0.57
4:C:672:GLU:HB3	4:C:1187:PHE:CD1	2.40	0.57
5:D:218:THR:HA	5:D:221:ILE:CG2	2.35	0.57
3:A:100:LEU:HD13	3:A:115:ILE:HG21	1.84	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:208:ILE:HD11	4:C:365:GLU:HG2	1.86	0.57
4:C:826:ASP:OD1	4:C:829:THR:HB	2.05	0.57
4:C:979:LEU:CG	4:C:1002:LEU:HD22	2.33	0.57
5:D:134:ASP:O	5:D:138:VAL:HG23	2.04	0.57
5:D:1021:ASP:HB3	5:D:1024:THR:O	2.04	0.57
5:D:1095:MET:HG3	5:D:1096:PRO:O	2.04	0.57
7:F:136:GLU:CD	7:F:361:ILE:HA	2.30	0.57
7:F:145:LEU:HD22	7:F:228:TYR:OH	2.05	0.57
7:F:158:LEU:HD23	7:F:158:LEU:H	1.69	0.57
7:F:267:ASP:O	7:F:270:VAL:HG22	2.05	0.57
2:I:140:ALA:HB3	2:I:141:PRO:HD3	1.87	0.57
2:I:170:GLN:HG3	2:I:171:LEU:CD2	2.34	0.57
2:J:90:PRO:HD2	2:J:96:ARG:HG2	1.84	0.57
3:B:80:GLU:OE1	5:D:569:LEU:HD21	2.05	0.57
3:A:38:THR:OG1	3:B:45:ARG:HD3	2.05	0.57
4:C:993:PRO:CG	4:C:996:ARG:HB3	2.26	0.57
5:D:155:GLU:OE1	5:D:158:GLN:NE2	2.27	0.57
7:F:139:GLU:O	7:F:142:THR:OG1	2.22	0.57
7:F:224:LEU:HD11	7:F:252:LEU:CD1	2.34	0.57
7:F:335:GLU:O	7:F:339:ARG:N	2.37	0.57
2:I:62:LEU:HD12	2:I:63:VAL:H	1.70	0.57
3:B:28:LEU:HD12	3:B:29:GLU:H	1.70	0.57
4:C:117:ILE:HD11	4:C:489:PRO:HD3	1.87	0.57
4:C:263:VAL:HG12	4:C:264:GLU:H	1.70	0.57
5:D:836:ARG:NH1	5:D:837:ASP:OD1	2.37	0.57
5:D:930:LEU:HD22	5:D:1244:GLN:HB3	1.86	0.57
5:D:1042:ASP:OD2	5:D:1048:ARG:HD2	2.05	0.57
7:F:487:MET:O	7:F:488:LEU:HD22	2.05	0.57
2:I:21:TYR:HB3	2:I:60:PRO:CD	2.34	0.56
2:J:25:VAL:HG12	2:J:29:LEU:HD13	1.87	0.56
2:J:155:SER:OG	2:J:157:VAL:HG12	2.05	0.56
6:E:56:GLU:HB3	6:E:58:LEU:CD1	2.31	0.56
7:F:166:VAL:HG12	7:F:260:ARG:HH21	1.70	0.56
7:F:572:THR:O	7:F:576:VAL:HG23	2.05	0.56
3:A:181:GLU:OE2	3:A:208:ASN:HB3	2.05	0.56
3:B:102:LEU:O	3:B:141:SER:HA	2.05	0.56
4:C:38:PHE:CD2	4:C:39:ILE:HG23	2.40	0.56
5:D:847:ASP:OD1	5:D:847:ASP:N	2.38	0.56
5:D:1036:ARG:HD2	5:D:1079:LYS:HD2	1.86	0.56
2:J:112:THR:HG23	2:J:115:ASN:HD22	1.70	0.56
3:K:307:LEU:HD12	3:K:308:ALA:N	2.20	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:1001:GLY:HA2	4:C:1011:LEU:HD13	1.88	0.56
5:D:1005:LYS:NZ	5:D:1011:VAL:HA	2.19	0.56
5:D:1037:PHE:HB3	5:D:1041:ILE:CD1	2.36	0.56
5:D:1060:VAL:HA	5:D:1105:ALA:O	2.04	0.56
7:F:128:ASN:OD1	7:F:131:GLN:NE2	2.39	0.56
7:F:511:ILE:HD11	7:F:517:SER:OG	2.06	0.56
7:F:593:LYS:HA	7:F:596:ARG:NH1	2.20	0.56
1:H:38:DT:C2'	7:F:429:THR:HG21	2.36	0.56
3:K:302:GLU:OE1	3:K:302:GLU:N	2.38	0.56
4:C:98:VAL:HG21	4:C:124:MET:SD	2.45	0.56
5:D:795:TYR:CZ	5:D:799:ARG:HD3	2.41	0.56
5:D:902:ASP:OD1	5:D:903:LEU:N	2.39	0.56
5:D:956:GLY:C	5:D:1010:GLN:HG3	2.30	0.56
5:D:984:LEU:O	5:D:992:LYS:HB2	2.05	0.56
5:D:1109:LEU:HD21	5:D:1115:ILE:HG21	1.87	0.56
7:F:244:THR:OG1	7:F:247:GLU:HB2	2.05	0.56
7:F:278:ASP:O	7:F:282:THR:HG22	2.05	0.56
2:J:71:GLU:OE1	2:J:73:ARG:HB3	2.04	0.56
3:B:65:LEU:HD22	3:B:168:ILE:O	2.05	0.56
5:D:287:ALA:HB1	5:D:288:PRO:HD2	1.87	0.56
5:D:813:ASP:OD2	5:D:897:HIS:ND1	2.39	0.56
7:F:284:GLU:HA	7:F:287:ILE:CD1	2.36	0.56
1:H:37:DA:OP1	1:H:37:DA:H2'	2.04	0.56
2:J:148:TYR:HB3	2:J:158:ASP:OD2	2.06	0.56
4:C:865:LEU:HD23	4:C:865:LEU:H	1.71	0.56
1:H:40:DA:OP2	7:F:428:SER:HB2	2.06	0.56
3:A:155:ALA:HA	3:A:158:ARG:CD	2.34	0.56
4:C:1124:ILE:HG21	4:C:1180:MET:CE	2.36	0.56
5:D:707:ILE:HD11	5:D:716:GLN:HE22	1.71	0.56
5:D:751:ASP:OD1	5:D:751:ASP:N	2.37	0.56
5:D:870:ASP:HA	5:D:873:GLU:HB3	1.87	0.56
7:F:128:ASN:HA	7:F:131:GLN:NE2	2.20	0.56
7:F:333:VAL:O	7:F:337:VAL:HG22	2.06	0.56
7:F:572:THR:HB	7:F:575:GLU:HB3	1.87	0.56
1:H:18:DA:C1'	1:H:19:DA:H5'	2.35	0.56
1:H:61:DG:H1'	1:H:62:DG:C8	2.40	0.56
4:C:274:ILE:HA	4:C:277:LEU:CD1	2.36	0.56
4:C:324:LYS:HA	4:C:327:GLN:HE21	1.71	0.56
4:C:516:VAL:HG12	4:C:522:SER:OG	2.06	0.56
4:C:1131:MET:HE2	4:C:1141:LEU:HD12	1.88	0.56
5:D:235:GLU:OE1	5:D:235:GLU:N	2.28	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:798:ARG:HD2	5:D:798:ARG:O	2.05	0.56
5:D:1256:ILE:O	5:D:1260:MET:HB2	2.06	0.56
2:I:36:PHE:CE1	2:I:38:ILE:HG22	2.41	0.56
4:C:896:THR:HB	4:C:897:PRO:HD2	1.87	0.56
4:C:1339:LEU:HB3	5:D:17:PHE:CD2	2.40	0.56
5:D:870:ASP:O	5:D:874:GLU:HG3	2.06	0.56
5:D:929:GLN:O	5:D:930:LEU:HD23	2.05	0.56
6:E:76:GLU:HA	6:E:79:GLU:CB	2.33	0.56
7:F:246:GLN:O	7:F:250:LEU:HB2	2.05	0.56
3:A:41:ASN:ND2	4:C:1217:THR:O	2.39	0.56
3:A:61:ILE:HB	3:A:64:VAL:CG1	2.36	0.56
5:D:165:TYR:O	5:D:169:LEU:N	2.39	0.56
5:D:273:ILE:O	5:D:277:ASN:HB2	2.05	0.56
5:D:1272:SER:OG	5:D:1286:LYS:NZ	2.39	0.56
7:F:489:MET:HB2	7:F:494:ILE:HG13	1.88	0.56
2:I:24:GLN:OE1	2:I:160:TYR:HA	2.06	0.55
2:J:41:VAL:HB	2:J:46:PRO:N	2.20	0.55
3:A:14:VAL:HG22	3:A:15:ASP:H	1.70	0.55
3:B:107:ILE:HD13	3:B:135:ASP:HA	1.88	0.55
3:B:162:GLU:HG3	3:B:166:ARG:HH22	1.72	0.55
7:F:525:ASP:OD2	7:F:528:LEU:HD13	2.05	0.55
7:F:572:THR:HB	7:F:575:GLU:CB	2.35	0.55
4:C:1243:MET:HE3	5:D:445:LYS:HB3	1.88	0.55
4:C:1305:TYR:O	4:C:1309:VAL:HG13	2.06	0.55
6:E:32:VAL:O	6:E:34:GLY:N	2.38	0.55
7:F:336:GLU:HA	7:F:339:ARG:CG	2.36	0.55
8:G:40:DA:H2'	8:G:41:DC:C2	2.42	0.55
2:J:184:LYS:O	2:J:188:THR:HG22	2.06	0.55
2:J:201:THR:O	2:J:205:ARG:HG3	2.05	0.55
3:B:69:SER:OG	3:B:70:THR:N	2.39	0.55
3:B:105:SER:CB	3:B:138:ALA:HB1	2.32	0.55
4:C:81:ASP:HB2	4:C:84:GLU:OE1	2.05	0.55
4:C:268:ARG:NH2	4:C:269:ILE:O	2.39	0.55
4:C:297:VAL:HG13	4:C:313:ALA:HA	1.88	0.55
4:C:393:ASP:OD1	4:C:393:ASP:N	2.21	0.55
4:C:1020:GLU:O	4:C:1024:GLU:HG2	2.06	0.55
4:C:1034:ARG:NH1	4:C:1034:ARG:HB2	2.21	0.55
4:C:1340:GLU:HG2	5:D:19:ALA:O	2.06	0.55
5:D:707:ILE:HD11	5:D:716:GLN:NE2	2.21	0.55
5:D:1081:VAL:HG12	5:D:1086:ASN:O	2.07	0.55
6:E:71:GLU:O	6:E:75:GLN:N	2.36	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:36:DT:O4	7:F:437:GLN:HB2	2.07	0.55
4:C:982:GLY:HA3	4:C:1002:LEU:HG	1.89	0.55
5:D:709:ARG:HD2	5:D:714:GLU:OE1	2.06	0.55
5:D:1109:LEU:HD12	5:D:1121:LEU:HD22	1.87	0.55
7:F:108:VAL:HG21	7:F:381:GLU:O	2.06	0.55
7:F:136:GLU:O	7:F:138:PRO:HD3	2.07	0.55
2:J:145:GLN:O	2:J:146:LYS:HD2	2.06	0.55
3:A:222:THR:HG22	3:B:232:VAL:CB	2.37	0.55
3:B:47:LEU:HD12	3:B:183:ILE:CD1	2.28	0.55
3:B:100:LEU:HB2	3:B:144:ILE:HG12	1.89	0.55
4:C:634:VAL:O	4:C:644:LEU:HD13	2.07	0.55
4:C:772:SER:N	4:C:775:GLU:OE2	2.36	0.55
7:F:598:LEU:O	7:F:604:SER:OG	2.22	0.55
4:C:66:SER:O	4:C:479:LEU:HD21	2.07	0.55
4:C:192:ASP:HB3	4:C:346:TYR:CD1	2.42	0.55
4:C:589:THR:HG22	4:C:590:PRO:HD2	1.87	0.55
4:C:596:ASP:N	4:C:596:ASP:OD1	2.40	0.55
4:C:632:ASP:O	4:C:647:ARG:N	2.40	0.55
5:D:72:CYS:SG	5:D:73:GLY:N	2.79	0.55
5:D:110:PRO:C	5:D:111:THR:HG22	2.31	0.55
5:D:527:LEU:HD12	5:D:532:GLU:HG2	1.87	0.55
5:D:742:GLY:O	5:D:762:ASN:HB3	2.07	0.55
5:D:1020:TRP:O	5:D:1022:PRO:HD3	2.06	0.55
6:E:30:MET:HE2	6:E:46:THR:HG22	1.88	0.55
3:A:224:LEU:HD23	3:B:228:LEU:HD11	1.88	0.55
5:D:1040:MET:SD	5:D:1078:LEU:HG	2.47	0.55
5:D:1080:ILE:HD12	5:D:1097:ALA:HB1	1.88	0.55
7:F:219:GLU:O	7:F:223:GLU:N	2.40	0.55
4:C:67:GLU:HB3	4:C:103:VAL:CG2	2.37	0.55
4:C:102:LEU:CB	4:C:489:PRO:HG3	2.37	0.55
4:C:294:GLY:O	4:C:295:LYS:HD3	2.06	0.55
5:D:94:GLN:O	5:D:97:VAL:HG12	2.07	0.55
5:D:399:LYS:O	5:D:403:ARG:HG3	2.07	0.55
5:D:489:ASN:OD1	5:D:489:ASN:N	2.38	0.55
5:D:857:LEU:HD11	5:D:872:LEU:HD21	1.89	0.55
5:D:872:LEU:HD13	5:D:877:VAL:HG11	1.88	0.55
6:E:23:ALA:HB2	6:E:54:ILE:CD1	2.37	0.55
7:F:135:ALA:HB2	7:F:256:PHE:HD2	1.71	0.55
3:B:107:ILE:HG12	3:B:134:THR:O	2.07	0.55
4:C:646:SER:OG	4:C:649:GLN:HB2	2.07	0.55
5:D:1025:MET:O	5:D:1124:ILE:HD13	2.07	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:1282:TYR:O	5:D:1286:LYS:HG3	2.07	0.55
7:F:231:THR:HB	7:F:248:GLU:O	2.07	0.55
7:F:456:MET:CE	7:F:497:VAL:HG22	2.36	0.55
3:B:107:ILE:CD1	3:B:135:ASP:HA	2.37	0.55
5:D:120:LEU:HD11	8:G:10:DG:H4'	1.89	0.55
5:D:1001:ALA:HA	5:D:1020:TRP:HA	1.88	0.55
5:D:1314:LEU:HB2	5:D:1326:GLN:NE2	2.22	0.55
2:J:137:LEU:HA	2:J:140:ALA:HB2	1.88	0.54
4:C:413:GLU:OE1	4:C:413:GLU:N	2.38	0.54
5:D:26:SER:HB3	5:D:236:TRP:CE2	2.42	0.54
5:D:955:LYS:HG3	5:D:1011:VAL:O	2.08	0.54
5:D:986:ASP:OD2	5:D:990:ARG:HB2	2.07	0.54
6:E:3:ARG:NH1	6:E:3:ARG:HA	2.22	0.54
2:J:20:ILE:HG13	2:J:163:PRO:HB2	1.88	0.54
2:J:174:GLU:HG3	2:J:175:PHE:H	1.72	0.54
3:B:27:THR:OG1	3:B:28:LEU:N	2.41	0.54
4:C:1158:LYS:HZ2	4:C:1158:LYS:H	1.56	0.54
4:C:529:ARG:HD2	4:C:572:ILE:CG2	2.38	0.54
4:C:1015:ALA:CA	4:C:1018:TYR:HB3	2.33	0.54
5:D:44:ILE:HD11	7:F:450:ILE:CD1	2.37	0.54
5:D:1023:HIS:O	5:D:1125:PRO:HA	2.08	0.54
1:H:22:DG:H2''	1:H:23:DT:H72	1.89	0.54
3:A:197:ASP:O	3:A:198:LEU:HD23	2.08	0.54
4:C:598:VAL:HG12	4:C:628:HIS:NE2	2.23	0.54
4:C:685:MET:HE1	4:C:1073:LYS:HE2	1.90	0.54
4:C:1252:SER:HB3	4:C:1255:THR:O	2.07	0.54
4:C:1285:TYR:HB2	5:D:479:GLU:OE2	2.08	0.54
5:D:1025:MET:HB3	5:D:1124:ILE:CB	2.37	0.54
2:I:63:VAL:HG22	2:I:68:THR:CA	2.37	0.54
2:J:202:GLU:OE1	2:J:202:GLU:N	2.40	0.54
3:B:11:PRO:HB2	3:B:28:LEU:HD11	1.88	0.54
3:B:48:LEU:HD22	5:D:535:ARG:CG	2.37	0.54
4:C:298:ALA:CB	4:C:334:GLU:HB3	2.37	0.54
4:C:1030:GLU:HG3	4:C:1034:ARG:HH12	1.72	0.54
7:F:229:VAL:HB	7:F:232:ARG:NH2	2.23	0.54
7:F:231:THR:HA	7:F:248:GLU:HB3	1.88	0.54
2:I:13:LEU:HA	2:I:61:THR:O	2.06	0.54
2:I:23:HIS:HA	2:I:26:ARG:CG	2.37	0.54
3:B:65:LEU:CD2	3:B:169:GLY:HA3	2.37	0.54
3:B:197:ASP:O	3:B:198:LEU:HD22	2.07	0.54
4:C:490:GLN:NE2	7:F:472:GLN:HB3	2.22	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:1160:ASP:O	4:C:1161:LEU:HB3	2.07	0.54
4:C:1243:MET:HA	5:D:352:ARG:O	2.06	0.54
4:C:119:GLU:HB2	4:C:489:PRO:CG	2.38	0.54
4:C:130:MET:SD	4:C:134:GLY:HA2	2.47	0.54
4:C:276:GLN:HA	4:C:279:LYS:CD	2.33	0.54
4:C:854:ILE:HG23	4:C:855:PRO:HD2	1.88	0.54
5:D:1269:ALA:HB2	5:D:1274:PHE:HD1	1.72	0.54
6:E:30:MET:HE1	6:E:49:ILE:HB	1.89	0.54
2:J:54:ASN:ND2	2:J:61:THR:OG1	2.39	0.54
4:C:210:LEU:CD1	4:C:429:MET:HE1	2.34	0.54
4:C:714:VAL:O	4:C:767:GLN:NE2	2.40	0.54
4:C:802:VAL:CG2	4:C:1096:ILE:HB	2.38	0.54
4:C:988:LYS:O	4:C:991:LYS:HG3	2.07	0.54
7:F:148:TYR:OH	7:F:218:ARG:HA	2.07	0.54
7:F:229:VAL:O	7:F:232:ARG:HG3	2.08	0.54
2:I:72:SER:HA	2:I:75:ILE:HG13	1.89	0.54
4:C:398:SER:HB2	4:C:401:GLY:N	2.13	0.54
4:C:810:TYR:CE1	5:D:359:PRO:HD2	2.43	0.54
5:D:127:LEU:HD22	5:D:227:PHE:CE1	2.42	0.54
5:D:1039:ASP:OD1	5:D:1074:LEU:HD22	2.08	0.54
5:D:1155:ILE:HD11	5:D:1210:ILE:HG22	1.89	0.54
5:D:1167:LYS:CE	5:D:1170:LYS:HD3	2.38	0.54
4:C:577:VAL:HG23	4:C:661:VAL:O	2.08	0.54
4:C:618:GLN:NE2	5:D:770:LEU:HB2	2.23	0.54
4:C:819:SER:HB2	4:C:1085:MET:HG3	1.90	0.54
5:D:165:TYR:CZ	5:D:169:LEU:HD22	2.43	0.54
5:D:930:LEU:HD11	5:D:1246:VAL:CG2	2.37	0.54
7:F:292:VAL:HG21	7:F:299:LYS:HB2	1.89	0.54
4:C:158:ASP:OD1	4:C:159:SER:N	2.37	0.53
5:D:289:ASP:O	5:D:293:ARG:HB3	2.08	0.53
5:D:1186:TYR:OH	5:D:1188:GLU:OE1	2.21	0.53
2:I:8:ARG:HH12	2:I:10:VAL:HB	1.73	0.53
4:C:292:ILE:HG22	4:C:317:LEU:HD13	1.91	0.53
4:C:348:SER:O	4:C:351:LEU:HB2	2.09	0.53
4:C:622:ASN:O	4:C:623:LEU:HD23	2.09	0.53
7:F:596:ARG:O	7:F:600:HIS:ND1	2.40	0.53
3:K:307:LEU:HD13	3:K:313:SER:HA	1.89	0.53
5:D:255:LEU:HD12	5:D:256:ASP:OD1	2.08	0.53
2:I:21:TYR:HB3	2:I:60:PRO:HD3	1.89	0.53
4:C:549:ASP:OD1	4:C:550:VAL:N	2.37	0.53
4:C:1242:LYS:HD2	5:D:465:GLN:NE2	2.23	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:1295:SER:OG	5:D:346:ARG:O	2.22	0.53
5:D:227:PHE:CE2	5:D:1337:VAL:HG13	2.43	0.53
5:D:557:LYS:HB3	5:D:563:LEU:CD1	2.39	0.53
5:D:668:PHE:HB2	5:D:678:ARG:HG3	1.89	0.53
5:D:709:ARG:HD2	5:D:714:GLU:CD	2.33	0.53
5:D:744:ARG:HH12	5:D:747:MET:HE3	1.71	0.53
7:F:234:THR:CG2	7:F:245:ALA:HA	2.38	0.53
7:F:390:ILE:CD1	7:F:432:THR:HG23	2.34	0.53
2:I:14:PHE:CB	2:I:50:LEU:HD22	2.38	0.53
2:I:85:HIS:CE1	7:F:567:MET:HG3	2.43	0.53
2:J:157:VAL:HG13	2:J:158:ASP:OD1	2.08	0.53
3:K:282:VAL:O	3:K:316:MET:N	2.41	0.53
4:C:578:TYR:CD2	4:C:659:GLN:HB2	2.43	0.53
4:C:836:LEU:HD13	4:C:1054:LEU:HD13	1.90	0.53
5:D:233:LYS:HB3	5:D:235:GLU:OE1	2.08	0.53
5:D:1042:ASP:CG	5:D:1048:ARG:HD2	2.34	0.53
4:C:1132:LEU:HD23	4:C:1132:LEU:O	2.08	0.53
5:D:122:SER:OG	5:D:132:LEU:HD22	2.09	0.53
5:D:288:PRO:CB	7:F:377:LYS:HE3	2.38	0.53
5:D:1031:VAL:HG21	5:D:1088:VAL:HG11	1.89	0.53
4:C:18:ARG:HD3	4:C:1188:ASP:OD1	2.08	0.53
4:C:99:LYS:O	4:C:100:LEU:HD23	2.08	0.53
4:C:229:ILE:HD12	4:C:333:ILE:O	2.09	0.53
4:C:802:VAL:HG22	4:C:1096:ILE:HB	1.91	0.53
4:C:1095:ASP:O	4:C:1096:ILE:HG12	2.08	0.53
4:C:1158:LYS:HA	4:C:1158:LYS:NZ	2.23	0.53
4:C:1253:LEU:HD13	7:F:525:ASP:HB2	1.89	0.53
7:F:137:TYR:CE2	7:F:139:GLU:HB2	2.44	0.53
7:F:139:GLU:HA	7:F:142:THR:HG23	1.91	0.53
7:F:291:CYS:O	7:F:297:MET:HB3	2.09	0.53
2:J:139:ILE:HG21	2:J:149:PHE:HE2	1.74	0.53
2:J:165:LEU:O	2:J:168:LEU:HG	2.09	0.53
4:C:279:LYS:HG3	4:C:280:ASP:OD1	2.09	0.53
4:C:1308:ILE:HG21	5:D:379:PRO:HB2	1.91	0.53
5:D:144:TYR:CE1	5:D:180:MET:HE3	2.43	0.53
5:D:218:THR:HA	5:D:221:ILE:HG22	1.91	0.53
7:F:359:LYS:HA	7:F:359:LYS:HE3	1.91	0.53
8:G:31:DC:H2'	8:G:32:DA:O4'	2.09	0.53
2:J:29:LEU:HD23	2:J:36:PHE:CG	2.43	0.53
4:C:179:TYR:HB2	4:C:397:LEU:O	2.09	0.53
4:C:696:ASP:OD2	4:C:696:ASP:N	2.38	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:834:GLN:NE2	4:C:924:VAL:HG21	2.24	0.53
5:D:978:ARG:O	5:D:996:LYS:HD2	2.07	0.53
2:I:68:THR:C	2:I:69:LEU:HD12	2.34	0.53
5:D:213:LYS:O	5:D:217:LEU:HB2	2.09	0.53
7:F:281:ARG:O	7:F:285:ARG:HG2	2.09	0.53
2:J:113:LEU:HD21	2:J:132:LEU:HB2	1.91	0.52
2:J:185:GLY:O	2:J:189:ARG:HG3	2.09	0.52
4:C:179:TYR:HB2	4:C:398:SER:OG	2.09	0.52
4:C:595:THR:OG1	4:C:598:VAL:O	2.21	0.52
5:D:497:GLU:HG2	5:D:498:PRO:HD2	1.91	0.52
5:D:1167:LYS:H	5:D:1174:ARG:HH21	1.56	0.52
7:F:146:GLU:HB3	7:F:150:ARG:CZ	2.39	0.52
8:G:54:DT:C2	8:G:55:DT:H1'	2.43	0.52
2:J:10:VAL:HB	2:J:65:ARG:HG2	1.92	0.52
2:J:85:HIS:HB2	5:D:86:GLU:OE1	2.09	0.52
2:J:196:PHE:O	2:J:200:LEU:HG	2.10	0.52
3:A:49:SER:OG	4:C:1083:GLU:OE2	2.21	0.52
4:C:202:ARG:HE	4:C:369:MET:HG3	1.74	0.52
4:C:563:THR:HB	4:C:564:PRO:HD2	1.90	0.52
4:C:618:GLN:HE21	5:D:770:LEU:HB2	1.75	0.52
4:C:725:GLN:OE1	4:C:735:LYS:HB2	2.10	0.52
7:F:136:GLU:O	7:F:361:ILE:HD11	2.08	0.52
2:I:32:LYS:NZ	2:I:86:PRO:O	2.24	0.52
5:D:820:ILE:HD11	5:D:822:MET:SD	2.50	0.52
5:D:1024:THR:HG23	5:D:1124:ILE:N	2.24	0.52
7:F:137:TYR:HA	7:F:361:ILE:HD13	1.90	0.52
7:F:299:LYS:HA	7:F:302:PHE:HE2	1.74	0.52
2:J:140:ALA:CB	2:J:183:LEU:HD23	2.40	0.52
2:J:165:LEU:HD12	2:J:168:LEU:HD11	1.92	0.52
4:C:246:LEU:HA	4:C:249:GLU:CD	2.34	0.52
4:C:323:ALA:HA	4:C:326:SER:OG	2.09	0.52
4:C:817:LEU:HD21	4:C:1080:ASN:ND2	2.23	0.52
4:C:1327:LEU:HD22	4:C:1337:ILE:CG2	2.36	0.52
5:D:1232:TYR:O	5:D:1236:GLU:HG2	2.10	0.52
7:F:452:ILE:HD11	7:F:457:ILE:CD1	2.39	0.52
1:H:11:DG:H2''	1:H:12:DA:C5'	2.40	0.52
3:A:101:THR:O	3:A:115:ILE:HG23	2.09	0.52
3:B:111:THR:OG1	3:B:112:ALA:N	2.42	0.52
4:C:1158:LYS:NZ	4:C:1158:LYS:CA	2.73	0.52
5:D:616:PRO:HA	5:D:619:ILE:HG22	1.90	0.52
5:D:1024:THR:HG23	5:D:1123:ARG:HA	1.89	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:292:VAL:HA	7:F:297:MET:O	2.10	0.52
1:H:6:DA:OP2	1:H:7:DA:N6	2.42	0.52
3:A:7:GLU:HB3	3:B:150:ARG:NH2	2.25	0.52
3:A:185:TYR:HD2	3:A:201:LEU:HD11	1.74	0.52
4:C:199:ASP:O	4:C:200:ARG:CG	2.56	0.52
5:D:1087:ASP:O	5:D:1096:PRO:HB3	2.09	0.52
7:F:585:GLU:HA	7:F:588:ARG:NH1	2.17	0.52
2:I:8:ARG:NH1	2:I:10:VAL:HB	2.25	0.52
3:A:57:THR:HG21	3:A:147:GLN:NE2	2.24	0.52
4:C:468:LEU:O	4:C:471:VAL:HG12	2.10	0.52
4:C:494:ASN:O	4:C:498:ILE:HD13	2.09	0.52
4:C:1214:ASP:OD1	4:C:1215:GLY:N	2.43	0.52
5:D:905:ARG:NH1	5:D:910:ASN:OD1	2.42	0.52
5:D:982:LEU:HD21	5:D:997:VAL:CG2	2.39	0.52
7:F:290:LEU:HD22	7:F:294:GLN:OE1	2.10	0.52
2:I:162:ALA:HB3	2:I:163:PRO:HD3	1.91	0.52
5:D:208:THR:HG21	5:D:213:LYS:HE3	1.92	0.52
5:D:1029:THR:HG22	5:D:1117:SER:HA	1.91	0.52
5:D:1102:PRO:HG2	5:D:1124:ILE:CG1	2.37	0.52
5:D:1123:ARG:C	5:D:1124:ILE:HD12	2.34	0.52
1:H:8:DA:C2	8:G:56:DT:H1'	2.45	0.52
2:J:129:ARG:NH1	2:J:129:ARG:HB2	2.25	0.52
4:C:65:ASN:O	4:C:105:TYR:HB2	2.09	0.52
5:D:863:LEU:HD21	5:D:901:ARG:HG3	1.92	0.52
3:B:67:GLU:HA	3:B:78:ILE:HD12	1.91	0.52
5:D:425:ARG:HG2	5:D:426:ALA:H	1.75	0.52
5:D:839:VAL:HG23	5:D:882:VAL:HG11	1.91	0.52
5:D:958:ILE:CG2	5:D:960:LEU:HD21	2.38	0.52
5:D:1102:PRO:HG2	5:D:1124:ILE:CD1	2.40	0.52
7:F:138:PRO:CG	7:F:353:LEU:HD11	2.39	0.52
8:G:32:DA:H2''	8:G:33:DA:C5'	2.39	0.52
2:I:61:THR:HG23	2:I:68:THR:OG1	2.11	0.51
2:I:115:ASN:O	2:I:118:ILE:HG22	2.10	0.51
4:C:103:VAL:HG12	4:C:116:ASP:CB	2.40	0.51
5:D:288:PRO:O	5:D:292:VAL:HG12	2.10	0.51
5:D:948:SER:HA	5:D:1022:PRO:CG	2.40	0.51
7:F:229:VAL:HB	7:F:232:ARG:HH21	1.74	0.51
7:F:548:LEU:O	7:F:548:LEU:HD23	2.10	0.51
2:I:28:VAL:HG11	2:I:76:MET:HE3	1.91	0.51
2:I:85:HIS:CE1	7:F:561:MET:HA	2.45	0.51
3:A:79:LEU:O	3:A:83:LEU:HG	2.09	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:60:GLU:HA	3:B:170:ARG:HH12	1.75	0.51
4:C:243:PRO:HB3	4:C:277:LEU:CB	2.40	0.51
5:D:17:PHE:O	5:D:1369:ARG:NH2	2.44	0.51
5:D:673:VAL:HG22	5:D:674:THR:O	2.10	0.51
5:D:950:ILE:HD12	5:D:1018:ALA:O	2.11	0.51
5:D:972:LYS:NZ	5:D:1028:ILE:HD13	2.25	0.51
5:D:1104:LYS:HE2	5:D:1124:ILE:HG23	1.91	0.51
5:D:1229:VAL:O	5:D:1233:ILE:HG12	2.10	0.51
7:F:142:THR:HA	7:F:145:LEU:HG	1.93	0.51
7:F:278:ASP:OD1	7:F:278:ASP:N	2.26	0.51
7:F:347:ILE:HG12	7:F:350:GLU:OE1	2.10	0.51
3:B:101:THR:HG22	3:B:143:ARG:CD	2.38	0.51
4:C:189:ASP:OD2	4:C:193:ASN:HB2	2.10	0.51
4:C:303:ASP:O	4:C:307:GLY:N	2.42	0.51
4:C:1103:VAL:HG11	4:C:1112:ILE:CD1	2.40	0.51
4:C:1131:MET:CE	4:C:1141:LEU:HD12	2.40	0.51
4:C:1211:ARG:HD3	4:C:1220:GLN:HE22	1.75	0.51
5:D:1026:PRO:HA	5:D:1122:ALA:O	2.10	0.51
7:F:141:ILE:CD1	7:F:252:LEU:HD11	2.41	0.51
2:J:18:THR:HG23	2:J:207:MET:HE1	1.93	0.51
2:J:140:ALA:HB2	2:J:183:LEU:HD23	1.92	0.51
3:A:51:MET:HE1	3:A:216:ALA:HA	1.92	0.51
4:C:117:ILE:CD1	4:C:489:PRO:HD3	2.39	0.51
4:C:241:LEU:CD2	4:C:246:LEU:HD11	2.40	0.51
4:C:452:ARG:NH1	4:C:458:GLU:OE2	2.32	0.51
4:C:1336:ASN:HD22	5:D:33:TRP:HZ2	1.56	0.51
5:D:983:LYS:HG2	5:D:985:ILE:HD13	1.92	0.51
5:D:1000:GLY:HA3	5:D:1026:PRO:HD2	1.91	0.51
5:D:1038:THR:O	5:D:1038:THR:OG1	2.28	0.51
7:F:284:GLU:HA	7:F:287:ILE:HD12	1.92	0.51
7:F:288:MET:O	7:F:292:VAL:N	2.37	0.51
7:F:367:ILE:O	7:F:371:LYS:HB2	2.10	0.51
7:F:530:LEU:O	7:F:533:ASP:N	2.40	0.51
2:I:123:SER:O	2:I:127:ALA:N	2.29	0.51
3:A:12:ARG:HB3	3:A:12:ARG:NH1	2.25	0.51
3:A:40:GLY:HA3	3:A:185:TYR:CE2	2.45	0.51
3:B:71:LYS:HB3	3:B:74:VAL:HG21	1.92	0.51
4:C:1256:GLN:OE1	7:F:528:LEU:HD21	2.11	0.51
5:D:130:MET:HE1	5:D:157:GLN:CB	2.41	0.51
5:D:660:GLU:HG2	5:D:685:ILE:HD12	1.91	0.51
5:D:816:THR:OG1	5:D:889:ASP:HB2	2.11	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:825:VAL:HG13	5:D:832:LYS:HB2	1.91	0.51
5:D:1011:VAL:CG2	5:D:1017:VAL:HB	2.31	0.51
7:F:150:ARG:CB	7:F:155:GLU:HB3	2.40	0.51
7:F:327:SER:O	7:F:330:LEU:HB2	2.11	0.51
1:H:43:DG:H2'	1:H:44:DG:N7	2.26	0.51
4:C:12:ARG:HD3	4:C:1183:ALA:HB2	1.93	0.51
4:C:38:PHE:HE1	4:C:461:GLU:HB2	1.75	0.51
4:C:203:LYS:O	4:C:204:LEU:HD23	2.11	0.51
4:C:252:SER:C	4:C:265:LYS:HG3	2.35	0.51
4:C:260:LYS:HE2	4:C:261:VAL:O	2.10	0.51
4:C:680:LEU:O	4:C:680:LEU:HD23	2.10	0.51
4:C:867:GLU:OE1	4:C:867:GLU:N	2.44	0.51
4:C:1158:LYS:H	4:C:1158:LYS:NZ	2.09	0.51
5:D:833:GLU:HG2	5:D:838:ARG:HG3	1.92	0.51
5:D:973:LEU:HD12	5:D:973:LEU:H	1.74	0.51
5:D:1003:LEU:HA	5:D:1018:ALA:HA	1.93	0.51
5:D:1005:LYS:HB2	5:D:1017:VAL:HG23	1.93	0.51
5:D:1155:ILE:O	5:D:1156:LEU:HD22	2.10	0.51
4:C:742:TYR:HB3	4:C:743:PRO:HD2	1.93	0.51
5:D:264:ASP:OD2	7:F:506:SER:OG	2.24	0.51
5:D:511:TYR:CE2	5:D:515:ARG:HD2	2.46	0.51
5:D:744:ARG:NH1	5:D:747:MET:HE3	2.26	0.51
2:I:41:VAL:HB	2:I:46:PRO:HA	1.91	0.51
2:J:129:ARG:HG3	2:J:173:ILE:CD1	2.40	0.51
2:J:158:ASP:HB3	2:J:186:TYR:OH	2.11	0.51
3:A:228:LEU:HD11	3:B:224:LEU:HD23	1.92	0.51
3:B:83:LEU:CD1	5:D:528:THR:HB	2.41	0.51
4:C:303:ASP:N	4:C:310:ILE:HG12	2.26	0.51
4:C:1008:GLN:HA	4:C:1011:LEU:HD12	1.93	0.51
5:D:1151:LYS:O	5:D:1152:GLU:HG2	2.11	0.51
2:J:140:ALA:HB3	2:J:141:PRO:HD3	1.92	0.51
4:C:397:LEU:HB2	4:C:418:GLY:O	2.11	0.51
5:D:1167:LYS:HE3	5:D:1170:LYS:CB	2.35	0.51
7:F:286:LEU:HD23	7:F:290:LEU:HB2	1.93	0.51
7:F:341:LEU:O	7:F:345:GLN:HG3	2.11	0.51
7:F:552:THR:OG1	7:F:555:GLU:HB2	2.11	0.51
7:F:558:VAL:HG21	7:F:587:ILE:CD1	2.40	0.51
3:A:82:LEU:HD11	3:A:171:LEU:HD23	1.92	0.51
3:A:194:GLN:O	3:A:195:ARG:HG2	2.11	0.51
4:C:188:PHE:HE1	4:C:194:LEU:HD12	1.76	0.51
4:C:615:VAL:CG1	4:C:650:VAL:HA	2.41	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:745:GLU:OE1	4:C:971:LEU:HD11	2.11	0.51
4:C:886:LYS:N	4:C:917:SER:OG	2.30	0.51
4:C:1304:MET:O	4:C:1308:ILE:HG12	2.10	0.51
4:C:1339:LEU:HD13	5:D:17:PHE:CE2	2.46	0.51
5:D:749:LYS:HB2	5:D:750:PRO:CD	2.41	0.51
2:I:63:VAL:HG22	2:I:68:THR:HB	1.93	0.50
2:I:101:LEU:HD23	2:J:74:ILE:HD12	1.93	0.50
3:B:47:LEU:HB3	3:B:180:VAL:HG11	1.92	0.50
4:C:256:GLU:OE1	4:C:286:GLU:HB2	2.11	0.50
4:C:1217:THR:OG1	4:C:1218:GLY:N	2.44	0.50
4:C:1268:GLN:NE2	5:D:352:ARG:HE	2.09	0.50
5:D:1350:ASN:OD1	5:D:1355:ARG:HG3	2.11	0.50
7:F:338:HIS:HA	7:F:341:LEU:HD11	1.92	0.50
1:H:37:DA:C2	7:F:423:ARG:HB2	2.45	0.50
3:B:35:PHE:HA	3:B:38:THR:CG2	2.41	0.50
4:C:1309:VAL:HG23	4:C:1310:ASP:OD1	2.11	0.50
5:D:827:GLU:HB2	5:D:832:LYS:CG	2.41	0.50
7:F:276:MET:O	7:F:280:VAL:HG22	2.11	0.50
4:C:411:ARG:HG2	4:C:412:GLU:H	1.76	0.50
4:C:516:VAL:O	4:C:522:SER:OG	2.29	0.50
4:C:1034:ARG:HB2	4:C:1034:ARG:HH11	1.75	0.50
5:D:398:LYS:HD3	7:F:532:LEU:HD23	1.92	0.50
5:D:841:GLY:HA2	5:D:901:ARG:HD3	1.94	0.50
5:D:1068:THR:HG22	5:D:1069:ALA:H	1.76	0.50
7:F:530:LEU:HD23	7:F:531:PRO:CD	2.38	0.50
1:H:63:DG:C3'	5:D:1170:LYS:HD2	2.41	0.50
2:J:82:ARG:O	2:J:84:PRO:HD3	2.10	0.50
2:J:109:ASP:O	2:J:113:LEU:HB2	2.11	0.50
3:B:57:THR:C	3:B:173:VAL:HG12	2.37	0.50
3:B:85:LEU:HD21	3:B:130:ILE:HD13	1.93	0.50
4:C:164:THR:HG21	4:C:171:LEU:HD12	1.93	0.50
4:C:745:GLU:OE2	4:C:1014:LEU:HA	2.11	0.50
5:D:114:ILE:HB	5:D:304:ASP:OD1	2.11	0.50
5:D:1087:ASP:OD2	5:D:1096:PRO:HG2	2.11	0.50
5:D:1168:GLU:HG2	5:D:1169:THR:H	1.76	0.50
2:I:21:TYR:O	2:I:25:VAL:HG23	2.12	0.50
2:J:202:GLU:HB2	2:J:205:ARG:HH21	1.76	0.50
3:A:29:GLU:HB3	3:A:30:PRO:HD3	1.92	0.50
4:C:303:ASP:OD2	4:C:310:ILE:HD11	2.12	0.50
4:C:1326:LEU:HD21	5:D:337:ARG:NH2	2.26	0.50
5:D:978:ARG:NH1	5:D:999:TYR:HB2	2.26	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:1109:LEU:HD11	5:D:1115:ILE:HD13	1.93	0.50
5:D:1314:LEU:HD21	5:D:1331:VAL:CG2	2.41	0.50
1:H:11:DG:H4'	3:K:264:VAL:HG21	1.92	0.50
2:I:24:GLN:NE2	2:I:111:TYR:OH	2.45	0.50
2:I:73:ARG:NH1	2:I:73:ARG:HB3	2.26	0.50
2:J:117:ILE:CG2	2:J:171:LEU:HD12	2.39	0.50
2:J:134:GLU:OE1	2:J:137:LEU:HD11	2.12	0.50
4:C:255:ILE:HG21	4:C:263:VAL:H	1.76	0.50
4:C:349:GLU:OE1	4:C:352:ARG:NH1	2.45	0.50
4:C:672:GLU:OE2	4:C:1187:PHE:HA	2.11	0.50
5:D:665:GLN:HE21	5:D:669:GLN:HE21	1.58	0.50
5:D:810:THR:HG21	5:D:892:PHE:O	2.10	0.50
5:D:1040:MET:HE3	5:D:1061:VAL:CG2	2.42	0.50
5:D:1065:ALA:HB2	5:D:1193:TRP:O	2.12	0.50
5:D:1164:SER:O	5:D:1175:LEU:HD12	2.12	0.50
5:D:1276:GLU:HG2	5:D:1277:GLY:H	1.74	0.50
4:C:192:ASP:HB3	4:C:346:TYR:HD1	1.76	0.50
5:D:351:GLY:O	5:D:467:ALA:HA	2.11	0.50
5:D:1005:LYS:HZ2	5:D:1011:VAL:HA	1.77	0.50
5:D:1063:ASP:OD1	5:D:1063:ASP:N	2.44	0.50
5:D:1215:GLU:CG	5:D:1220:ILE:HD11	2.42	0.50
5:D:1264:ALA:HB2	5:D:1280:VAL:HG22	1.94	0.50
6:E:3:ARG:NH2	6:E:52:ARG:HG3	2.26	0.50
7:F:277:MET:HA	7:F:280:VAL:HG22	1.94	0.50
7:F:310:GLU:HB2	7:F:355:ILE:HG21	1.92	0.50
1:H:42:DG:H4'	1:H:43:DG:O5'	2.11	0.50
2:I:16:GLY:N	2:I:22:SER:OG	2.27	0.50
2:I:113:LEU:O	2:I:117:ILE:HG13	2.12	0.50
4:C:53:PHE:HD1	4:C:468:LEU:HD11	1.76	0.50
5:D:320:ASN:OD1	5:D:321:LYS:N	2.41	0.50
5:D:1150:PRO:CD	5:D:1216:ALA:HB2	2.42	0.50
5:D:1215:GLU:HG3	5:D:1220:ILE:HD11	1.92	0.50
1:H:27:DA:H2'	1:H:27:DA:OP2	2.12	0.50
1:H:40:DA:H62	7:F:429:THR:HA	1.77	0.50
2:I:72:SER:HA	2:I:75:ILE:CG1	2.42	0.50
2:I:166:TRP:CE2	2:I:200:LEU:HD11	2.47	0.50
3:A:50:SER:HB3	3:B:8:PHE:HZ	1.76	0.50
3:A:61:ILE:HG22	3:A:62:ASP:H	1.76	0.50
4:C:303:ASP:HB2	4:C:310:ILE:HD11	1.94	0.50
4:C:1002:LEU:HD23	4:C:1007:LYS:CD	2.41	0.50
5:D:107:LEU:HD13	5:D:111:THR:CG2	2.42	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:619:ILE:O	5:D:619:ILE:HG12	2.12	0.50
2:J:103:MET:HB2	2:J:160:TYR:CE1	2.46	0.49
3:B:60:GLU:O	3:B:142:MET:HA	2.12	0.49
4:C:358:ASP:OD1	4:C:361:SER:HB3	2.12	0.49
4:C:571:LEU:O	4:C:572:ILE:HD13	2.12	0.49
4:C:1095:ASP:C	4:C:1096:ILE:HG12	2.36	0.49
4:C:1157:GLN:HG3	4:C:1159:VAL:HB	1.94	0.49
4:C:1213:TYR:CD2	4:C:1220:GLN:HB2	2.47	0.49
6:E:6:VAL:O	6:E:10:VAL:HG23	2.12	0.49
7:F:167:ASP:HB3	7:F:258:GLN:NE2	2.24	0.49
7:F:591:GLU:HG3	7:F:595:LEU:HD23	1.92	0.49
1:H:37:DA:C2	7:F:425:TYR:HB2	2.46	0.49
2:J:116:THR:HA	2:J:120:GLY:N	2.27	0.49
3:K:280:ASP:N	3:K:280:ASP:OD1	2.45	0.49
4:C:1002:LEU:HD23	4:C:1007:LYS:HB2	1.93	0.49
4:C:1250:SER:OG	4:C:1259:LEU:O	2.29	0.49
5:D:116:PHE:O	5:D:124:ILE:HG13	2.11	0.49
5:D:217:LEU:O	5:D:221:ILE:HG22	2.12	0.49
5:D:664:ILE:CD1	5:D:681:LYS:HG2	2.42	0.49
7:F:233:ASP:OD1	7:F:236:LYS:HD3	2.11	0.49
7:F:286:LEU:HD21	7:F:290:LEU:CD2	2.41	0.49
7:F:499:LYS:O	7:F:500:ILE:HD13	2.11	0.49
3:B:99:ILE:HD11	3:B:143:ARG:HB3	1.94	0.49
4:C:303:ASP:HB2	4:C:308:GLU:O	2.11	0.49
4:C:715:THR:CG2	4:C:782:VAL:HG13	2.42	0.49
4:C:936:ARG:O	4:C:939:VAL:HG12	2.12	0.49
7:F:251:LYS:O	7:F:255:VAL:HG13	2.12	0.49
7:F:470:MET:O	7:F:474:MET:HB3	2.12	0.49
7:F:489:MET:HG3	7:F:494:ILE:HD11	1.94	0.49
2:I:111:TYR:HE1	2:I:164:LEU:HD11	1.77	0.49
2:J:175:PHE:CZ	2:J:183:LEU:HG	2.47	0.49
4:C:292:ILE:HG22	4:C:317:LEU:CD1	2.42	0.49
4:C:524:ILE:O	4:C:524:ILE:HD13	2.13	0.49
4:C:1155:VAL:HG12	4:C:1156:ARG:H	1.77	0.49
5:D:747:MET:CG	5:D:759:ILE:HD11	2.38	0.49
5:D:1023:HIS:NE2	5:D:1127:GLU:HG2	2.27	0.49
5:D:1024:THR:CG2	5:D:1123:ARG:HA	2.43	0.49
5:D:1033:GLY:HA2	5:D:1114:GLN:HE22	1.75	0.49
6:E:67:ARG:NH1	6:E:71:GLU:OE2	2.31	0.49
6:E:76:GLU:HA	6:E:79:GLU:CG	2.42	0.49
1:H:42:DG:H8	7:F:385:ARG:HG3	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:87:PRO:HD3	7:F:567:MET:SD	2.52	0.49
2:J:19:ASP:OD2	2:J:21:TYR:HB2	2.13	0.49
4:C:297:VAL:CG1	4:C:313:ALA:HA	2.42	0.49
5:D:198:CYS:O	5:D:202:ARG:HG2	2.12	0.49
7:F:137:TYR:HA	7:F:361:ILE:CD1	2.42	0.49
7:F:325:PRO:O	7:F:329:LYS:HB2	2.11	0.49
1:H:53:DC:H2''	1:H:54:DG:O5'	2.13	0.49
3:K:255:ARG:HB2	3:K:278:ILE:HD12	1.93	0.49
5:D:552:ILE:HD12	5:D:589:TYR:CD1	2.46	0.49
7:F:160:ASP:O	7:F:262:VAL:HB	2.12	0.49
8:G:36:DT:H2''	8:G:37:DA:C5'	2.43	0.49
2:I:42:GLU:OE1	2:I:43:LYS:HD2	2.12	0.49
3:B:164:ASP:O	3:B:166:ARG:HG3	2.12	0.49
4:C:953:LEU:HD11	4:C:1033:ARG:HG3	1.93	0.49
4:C:1041:ASP:N	4:C:1041:ASP:OD1	2.42	0.49
7:F:151:VAL:HG23	7:F:156:ALA:HB3	1.94	0.49
4:C:8:LYS:HD3	4:C:1168:GLU:OE2	2.12	0.49
4:C:91:THR:HG21	4:C:503:LYS:NZ	2.27	0.49
4:C:131:THR:HG23	4:C:135:THR:O	2.12	0.49
4:C:150:HIS:CD2	4:C:454:ARG:HG3	2.48	0.49
4:C:230:PHE:HE2	4:C:292:ILE:HD12	1.77	0.49
4:C:1287:LEU:O	4:C:1287:LEU:HD23	2.13	0.49
5:D:394:ILE:HG12	7:F:532:LEU:HD11	1.94	0.49
7:F:261:LEU:HG	7:F:262:VAL:H	1.78	0.49
7:F:586:ARG:HG3	7:F:590:ILE:HD11	1.95	0.49
2:J:64:ASP:OD1	2:J:64:ASP:N	2.44	0.49
3:A:8:PHE:CE1	3:A:32:GLU:HG2	2.47	0.49
4:C:239:MET:HB3	4:C:287:VAL:HG11	1.94	0.49
4:C:255:ILE:HB	4:C:263:VAL:O	2.13	0.49
4:C:296:VAL:CG1	4:C:336:LEU:HD12	2.42	0.49
5:D:972:LYS:NZ	5:D:974:VAL:HA	2.27	0.49
5:D:1040:MET:HE3	5:D:1061:VAL:HG21	1.94	0.49
7:F:561:MET:SD	7:F:576:VAL:HG13	2.53	0.49
2:I:46:PRO:CB	2:I:50:LEU:HD23	2.42	0.49
4:C:119:GLU:HB2	4:C:489:PRO:CD	2.42	0.49
4:C:257:ALA:HB3	4:C:262:TYR:CE2	2.48	0.49
4:C:981:ALA:O	4:C:1002:LEU:HD21	2.13	0.49
4:C:1053:TYR:C	4:C:1054:LEU:HD12	2.38	0.49
4:C:1158:LYS:NZ	4:C:1158:LYS:N	2.60	0.49
5:D:405:GLU:O	5:D:408:VAL:HG22	2.12	0.49
5:D:499:ILE:O	5:D:500:ILE:HD13	2.13	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:615:LYS:HB2	5:D:616:PRO:HD3	1.95	0.49
5:D:966:VAL:HG12	5:D:967:VAL:O	2.13	0.49
5:D:1270:GLY:HA3	5:D:1297:LYS:O	2.13	0.49
2:J:139:ILE:O	2:J:142:VAL:HG13	2.13	0.48
4:C:210:LEU:HB3	4:C:220:ILE:CD1	2.43	0.48
4:C:264:GLU:HB2	4:C:267:ARG:CZ	2.43	0.48
4:C:607:SER:OG	4:C:608:ALA:N	2.46	0.48
4:C:1192:GLU:O	4:C:1196:LYS:HG2	2.13	0.48
5:D:1082:ASP:OD2	5:D:1086:ASN:HB3	2.13	0.48
5:D:1143:ASP:OD1	5:D:1148:ARG:HD2	2.12	0.48
5:D:1314:LEU:HD23	5:D:1326:GLN:CD	2.38	0.48
7:F:262:VAL:HG13	7:F:263:PRO:HD2	1.94	0.48
7:F:267:ASP:OD1	7:F:268:TYR:N	2.46	0.48
7:F:465:ARG:NH2	8:G:26:DT:H2'	2.25	0.48
1:H:22:DG:H2''	1:H:23:DT:C5	2.47	0.48
1:H:40:DA:C6	7:F:429:THR:HG22	2.47	0.48
1:H:62:DG:C8	1:H:62:DG:H5'	2.48	0.48
2:I:17:PRO:HG3	2:I:40:HIS:HB3	1.94	0.48
4:C:453:ILE:CD1	4:C:587:LEU:HD11	2.43	0.48
4:C:631:GLU:OE1	4:C:631:GLU:N	2.45	0.48
4:C:1115:THR:CG2	4:C:1228:GLY:HA3	2.43	0.48
5:D:416:ILE:CG2	5:D:439:PRO:HG2	2.43	0.48
5:D:514:THR:HG21	5:D:596:LEU:CB	2.42	0.48
5:D:820:ILE:O	5:D:881:LYS:HA	2.13	0.48
5:D:960:LEU:HD22	5:D:982:LEU:HA	1.95	0.48
7:F:344:LEU:HA	7:F:347:ILE:HG13	1.94	0.48
3:A:16:ILE:CD1	3:A:214:GLU:HB2	2.44	0.48
5:D:120:LEU:HD12	5:D:1330:ARG:NH2	2.28	0.48
5:D:905:ARG:HH21	5:D:907:HIS:CB	2.24	0.48
7:F:585:GLU:CB	7:F:588:ARG:HD2	2.43	0.48
1:H:58:DG:H2''	1:H:59:DC:H5''	1.94	0.48
2:I:82:ARG:HD3	2:J:93:PRO:HB2	1.96	0.48
4:C:413:GLU:HB2	4:C:415:GLU:OE1	2.13	0.48
4:C:689:ALA:CB	4:C:1233:LEU:HD12	2.43	0.48
5:D:475:GLU:O	5:D:479:GLU:HG3	2.13	0.48
5:D:710:ASP:OD1	5:D:710:ASP:N	2.44	0.48
5:D:980:THR:O	5:D:997:VAL:N	2.46	0.48
5:D:1038:THR:HG23	5:D:1077:ALA:O	2.13	0.48
5:D:1194:ARG:HD3	5:D:1211:SER:OG	2.12	0.48
7:F:347:ILE:HA	7:F:350:GLU:OE1	2.13	0.48
2:I:193:ARG:O	2:I:197:LEU:N	2.28	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:103:MET:HB2	2:J:160:TYR:HE1	1.77	0.48
4:C:147:SER:HB2	4:C:530:ILE:HD13	1.96	0.48
4:C:796:LEU:N	4:C:1231:TYR:OH	2.47	0.48
4:C:1247:SER:HB2	5:D:375:GLU:O	2.12	0.48
5:D:801:VAL:HG21	5:D:917:VAL:HG13	1.95	0.48
5:D:985:ILE:HG23	5:D:990:ARG:O	2.12	0.48
7:F:305:LEU:HB2	7:F:314:THR:HB	1.95	0.48
7:F:322:MET:HG3	7:F:324:LYS:HD3	1.94	0.48
8:G:51:DT:H2''	8:G:52:DC:C6	2.48	0.48
4:C:204:LEU:HG	4:C:369:MET:HE2	1.94	0.48
4:C:1043:ALA:HB1	4:C:1044:PRO:HD2	1.94	0.48
4:C:1340:GLU:HB2	5:D:18:ASP:O	2.13	0.48
5:D:298:MET:SD	7:F:402:LEU:HG	2.53	0.48
7:F:354:THR:HG23	7:F:356:GLU:N	2.28	0.48
1:H:10:DT:H2''	1:H:11:DG:C8	2.48	0.48
1:H:61:DG:H4'	1:H:62:DG:C5'	2.43	0.48
2:J:41:VAL:HB	2:J:45:ASN:C	2.38	0.48
5:D:502:PRO:HG2	5:D:601:ILE:HG21	1.95	0.48
5:D:530:PRO:HB2	5:D:581:MET:HE2	1.95	0.48
5:D:681:LYS:O	5:D:685:ILE:HG22	2.14	0.48
5:D:1119:ASP:OD1	5:D:1120:THR:N	2.47	0.48
7:F:148:TYR:HH	7:F:218:ARG:HA	1.79	0.48
7:F:462:LYS:HE2	7:F:462:LYS:HB3	1.59	0.48
2:I:17:PRO:HG3	2:I:40:HIS:C	2.39	0.48
2:J:201:THR:N	2:J:204:GLU:OE2	2.43	0.48
3:A:222:THR:HG22	3:B:232:VAL:CA	2.43	0.48
5:D:975:ILE:HD12	5:D:976:THR:H	1.78	0.48
7:F:145:LEU:HD12	7:F:146:GLU:N	2.29	0.48
7:F:533:ASP:O	7:F:537:THR:HG23	2.14	0.48
8:G:42:DT:H2''	8:G:43:DT:C6	2.49	0.48
3:B:19:VAL:O	3:B:23:HIS:HB3	2.14	0.48
4:C:377:THR:HG22	4:C:378:ARG:H	1.78	0.48
4:C:899:GLU:HG2	7:F:540:LEU:CD1	2.44	0.48
5:D:1046:ILE:CG2	5:D:1059:LEU:HD23	2.44	0.48
5:D:1314:LEU:HD21	5:D:1331:VAL:HG22	1.95	0.48
7:F:266:PHE:O	7:F:270:VAL:HG13	2.14	0.48
8:G:26:DT:H2''	8:G:27:DA:OP2	2.14	0.48
3:A:155:ALA:O	3:A:158:ARG:HG2	2.14	0.48
4:C:216:THR:O	4:C:220:ILE:HG12	2.14	0.48
4:C:589:THR:CG2	4:C:590:PRO:HD2	2.43	0.48
4:C:953:LEU:O	4:C:953:LEU:HD12	2.14	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:1024:GLU:O	4:C:1028:LYS:HG3	2.12	0.48
5:D:959:LYS:CG	5:D:985:ILE:HG13	2.43	0.48
5:D:980:THR:O	5:D:996:LYS:HD3	2.14	0.48
5:D:1031:VAL:CG2	5:D:1088:VAL:HG11	2.43	0.48
7:F:102:MET:CE	7:F:388:ILE:HD13	2.42	0.48
7:F:283:GLN:O	7:F:287:ILE:HG13	2.14	0.48
7:F:427:PHE:CE2	7:F:431:ALA:HB2	2.49	0.48
1:H:19:DA:H4'	1:H:20:DA:OP1	2.14	0.47
2:I:67:LEU:HD12	2:I:68:THR:H	1.79	0.47
2:J:202:GLU:HA	2:J:205:ARG:NE	2.29	0.47
3:A:47:LEU:HB2	3:A:183:ILE:HD12	1.96	0.47
3:B:91:ARG:O	3:B:91:ARG:HG2	2.14	0.47
4:C:83:GLN:O	4:C:87:ILE:HG13	2.14	0.47
4:C:323:ALA:O	4:C:327:GLN:HG3	2.14	0.47
4:C:734:ILE:CD1	4:C:777:VAL:HG21	2.44	0.47
4:C:985:GLU:HG2	4:C:988:LYS:CD	2.39	0.47
4:C:1105:SER:HA	5:D:736:GLN:OE1	2.13	0.47
5:D:395:LYS:O	5:D:399:LYS:NZ	2.41	0.47
5:D:532:GLU:HG3	5:D:532:GLU:O	2.13	0.47
5:D:1234:VAL:O	5:D:1238:GLN:HB2	2.13	0.47
8:G:58:DG:H2'	8:G:59:DT:C7	2.43	0.47
2:I:159:CYS:O	2:I:163:PRO:HD2	2.14	0.47
3:A:77:ASP:OD1	3:A:77:ASP:N	2.46	0.47
4:C:117:ILE:HD12	4:C:488:MET:HE2	1.96	0.47
4:C:241:LEU:N	4:C:283:LYS:O	2.41	0.47
4:C:985:GLU:O	4:C:989:LEU:HD13	2.14	0.47
5:D:634:ARG:H	5:D:634:ARG:HG2	1.52	0.47
5:D:1029:THR:CB	5:D:1118:GLY:H	2.26	0.47
7:F:248:GLU:HA	7:F:251:LYS:HB2	1.97	0.47
7:F:315:TRP:CH2	7:F:337:VAL:HB	2.48	0.47
7:F:575:GLU:HA	7:F:578:LYS:NZ	2.29	0.47
4:C:163:LYS:HZ3	4:C:164:THR:HA	1.79	0.47
4:C:782:VAL:O	4:C:783:LEU:HD23	2.14	0.47
4:C:836:LEU:CD1	4:C:1054:LEU:HD13	2.44	0.47
5:D:491:LEU:HB2	5:D:904:ALA:O	2.14	0.47
5:D:947:GLU:HG2	5:D:1020:TRP:CZ2	2.49	0.47
7:F:119:ILE:CG2	7:F:379:MET:HE2	2.45	0.47
7:F:560:ARG:HG3	7:F:565:ILE:CG2	2.45	0.47
7:F:600:HIS:HB3	7:F:601:PRO:HD2	1.97	0.47
8:G:57:DT:H2''	8:G:58:DG:O4'	2.14	0.47
1:H:58:DG:H2''	1:H:59:DC:O4'	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:67:GLU:HA	3:B:78:ILE:CD1	2.44	0.47
4:C:298:ALA:HB3	4:C:334:GLU:HB3	1.95	0.47
4:C:849:GLU:O	4:C:886:LYS:HG3	2.14	0.47
4:C:1138:VAL:HG11	4:C:1166:ASP:HA	1.96	0.47
5:D:317:THR:HG21	5:D:320:ASN:HB3	1.94	0.47
7:F:231:THR:HG21	7:F:252:LEU:HB2	1.95	0.47
7:F:481:GLU:OE1	7:F:491:GLU:HG3	2.13	0.47
2:J:50:LEU:O	2:J:54:ASN:HB3	2.14	0.47
2:J:90:PRO:HG2	2:J:96:ARG:CA	2.44	0.47
2:J:169:PRO:HD3	2:J:208:ARG:HH21	1.77	0.47
4:C:238:GLN:CB	4:C:284:LEU:HD11	2.37	0.47
4:C:970:GLY:HA2	4:C:973:SER:OG	2.14	0.47
4:C:1295:SER:OG	5:D:347:VAL:HA	2.14	0.47
4:C:1307:ASN:HB3	4:C:1312:ASN:O	2.14	0.47
4:C:1338:GLU:C	4:C:1339:LEU:HD23	2.38	0.47
5:D:245:LEU:HD12	5:D:245:LEU:HA	1.73	0.47
5:D:682:VAL:HA	5:D:685:ILE:CG2	2.45	0.47
7:F:306:PHE:CZ	7:F:341:LEU:HD22	2.50	0.47
7:F:588:ARG:O	7:F:592:ALA:HB2	2.14	0.47
3:B:28:LEU:HD12	3:B:29:GLU:N	2.30	0.47
3:B:104:LYS:HE3	3:B:114:ASP:OD2	2.14	0.47
4:C:519:ASN:HB3	4:C:521:LEU:H	1.79	0.47
4:C:1158:LYS:HA	4:C:1158:LYS:CE	2.44	0.47
5:D:1030:GLU:OE1	5:D:1099:TYR:OH	2.32	0.47
5:D:1150:PRO:HD3	5:D:1216:ALA:HB2	1.95	0.47
7:F:290:LEU:HD12	7:F:337:VAL:CG1	2.45	0.47
2:I:132:LEU:O	2:I:136:LEU:HG	2.15	0.47
2:I:148:TYR:HB3	2:I:158:ASP:OD2	2.14	0.47
2:J:90:PRO:HB2	2:J:96:ARG:HG3	1.96	0.47
3:A:133:LEU:HD12	3:A:138:ALA:CB	2.45	0.47
3:A:133:LEU:HD12	3:A:138:ALA:HB1	1.97	0.47
4:C:13:LYS:HD2	4:C:14:ASP:H	1.79	0.47
4:C:378:ARG:HB3	4:C:379:GLU:OE1	2.15	0.47
4:C:594:VAL:HG23	4:C:652:TYR:HA	1.96	0.47
4:C:816:ILE:HG22	4:C:817:LEU:O	2.14	0.47
4:C:1270:PHE:CE2	4:C:1290:MET:HG2	2.50	0.47
5:D:211:GLU:O	5:D:215:LYS:HB2	2.13	0.47
5:D:364:HIS:HB3	5:D:487:THR:CG2	2.44	0.47
5:D:661:VAL:CG2	5:D:682:VAL:HG13	2.44	0.47
5:D:872:LEU:HD22	5:D:877:VAL:CG1	2.44	0.47
5:D:967:VAL:HA	5:D:973:LEU:HA	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:70:GLN:O	6:E:74:GLU:N	2.28	0.47
7:F:129:GLN:O	7:F:133:SER:OG	2.24	0.47
7:F:164:GLY:O	7:F:260:ARG:HD2	2.14	0.47
7:F:332:ASP:OD1	7:F:332:ASP:N	2.48	0.47
7:F:560:ARG:HG3	7:F:565:ILE:HB	1.96	0.47
7:F:572:THR:O	7:F:575:GLU:HB3	2.14	0.47
2:J:197:LEU:O	2:J:200:LEU:HD12	2.14	0.47
4:C:12:ARG:HG3	4:C:1181:PRO:O	2.15	0.47
5:D:58:CYS:SG	5:D:59:ALA:N	2.88	0.47
5:D:959:LYS:CE	5:D:985:ILE:HG21	2.45	0.47
7:F:250:LEU:HD22	7:F:254:GLU:CG	2.31	0.47
7:F:373:ARG:HH12	7:F:377:LYS:HD2	1.78	0.47
1:H:38:DT:H2'	7:F:429:THR:HG21	1.97	0.47
1:H:63:DG:C4'	5:D:1170:LYS:HD2	2.45	0.47
2:I:195:SER:O	2:I:199:SER:OG	2.33	0.47
2:J:14:PHE:CE2	2:J:50:LEU:HD13	2.50	0.47
4:C:53:PHE:CD1	4:C:468:LEU:HD11	2.49	0.47
4:C:177:ILE:HG22	4:C:183:TRP:CE2	2.50	0.47
4:C:354:ASP:OD1	4:C:356:THR:HG22	2.15	0.47
4:C:716:ALA:CB	4:C:784:ALA:HB3	2.43	0.47
4:C:964:LEU:HB3	4:C:968:GLU:OE2	2.15	0.47
5:D:452:LEU:HD13	5:D:500:ILE:HG22	1.96	0.47
5:D:1280:VAL:HG21	5:D:1304:ARG:HE	1.80	0.47
7:F:161:LEU:H	7:F:161:LEU:HD23	1.80	0.47
1:H:13:DT:OP2	7:F:586:ARG:HD3	2.15	0.47
1:H:42:DG:C8	7:F:385:ARG:HG3	2.50	0.47
2:I:72:SER:HA	2:I:75:ILE:CD1	2.45	0.47
2:I:192:GLU:HA	2:I:197:LEU:CD2	2.42	0.47
2:J:113:LEU:CD2	2:J:132:LEU:HB2	2.44	0.47
3:B:103:ASN:HA	3:B:141:SER:HA	1.97	0.47
3:B:120:ASP:OD1	3:B:120:ASP:N	2.48	0.47
4:C:448:LEU:HD12	4:C:554:HIS:ND1	2.30	0.47
4:C:471:VAL:CG2	4:C:498:ILE:HD11	2.45	0.47
4:C:976:ARG:HB2	4:C:976:ARG:NH1	2.30	0.47
4:C:1259:LEU:HD12	4:C:1260:GLY:N	2.31	0.47
5:D:1002:VAL:O	5:D:1019:ASN:N	2.39	0.47
7:F:96:ASP:OD1	7:F:96:ASP:N	2.47	0.47
7:F:297:MET:HG2	7:F:298:PRO:O	2.15	0.47
7:F:586:ARG:O	7:F:590:ILE:HG13	2.15	0.47
2:I:22:SER:O	2:I:26:ARG:HG3	2.14	0.46
2:I:72:SER:HA	2:I:75:ILE:HD12	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:134:THR:OG1	4:C:773:LEU:HD11	2.14	0.46
4:C:104:ILE:O	4:C:114:VAL:HB	2.15	0.46
4:C:887:VAL:HG23	4:C:913:VAL:HG21	1.97	0.46
4:C:1002:LEU:HD23	4:C:1007:LYS:CG	2.44	0.46
4:C:1132:LEU:HD22	4:C:1177:ARG:NH2	2.30	0.46
5:D:45:ASN:HB3	5:D:48:THR:O	2.14	0.46
5:D:51:PRO:HB2	5:D:57:PHE:O	2.15	0.46
5:D:127:LEU:HD21	5:D:234:PRO:HB3	1.95	0.46
5:D:170:GLU:N	5:D:170:GLU:OE1	2.48	0.46
5:D:559:ALA:HB3	5:D:562:GLU:CG	2.33	0.46
5:D:947:GLU:HG2	5:D:1020:TRP:CH2	2.50	0.46
5:D:1046:ILE:HG21	5:D:1059:LEU:HD23	1.97	0.46
7:F:324:LYS:O	7:F:328:GLU:HG2	2.16	0.46
2:I:148:TYR:HB2	2:I:151:SER:O	2.15	0.46
3:A:190:ALA:HB2	3:A:200:LYS:CG	2.45	0.46
4:C:78:PRO:HB3	4:C:93:SER:O	2.15	0.46
4:C:79:VAL:HG22	4:C:80:PHE:CD2	2.50	0.46
4:C:299:LYS:NZ	4:C:301:TYR:OH	2.41	0.46
4:C:805:MET:HE1	4:C:1221:PHE:CE2	2.50	0.46
5:D:85:CYS:O	5:D:89:GLY:HA2	2.15	0.46
5:D:550:VAL:HG23	5:D:552:ILE:HG23	1.98	0.46
5:D:1155:ILE:C	5:D:1156:LEU:HD22	2.41	0.46
8:G:54:DT:O2	8:G:55:DT:H1'	2.16	0.46
1:H:61:DG:H1'	1:H:62:DG:N7	2.30	0.46
2:I:169:PRO:HD2	2:I:208:ARG:HH22	1.80	0.46
3:A:85:LEU:HD21	3:A:130:ILE:HD13	1.96	0.46
3:A:92:VAL:HG12	3:A:121:VAL:HG22	1.97	0.46
3:B:85:LEU:HD23	3:B:85:LEU:HA	1.76	0.46
3:B:197:ASP:C	3:B:198:LEU:HD22	2.40	0.46
4:C:264:GLU:HB2	4:C:267:ARG:CD	2.42	0.46
4:C:1106:ARG:H	4:C:1106:ARG:HD2	1.81	0.46
5:D:298:MET:CE	7:F:406:GLN:HG3	2.43	0.46
5:D:688:ALA:O	5:D:692:ARG:HG3	2.15	0.46
5:D:868:TRP:CZ3	5:D:871:LEU:HD13	2.50	0.46
5:D:973:LEU:O	5:D:1003:LEU:HG	2.15	0.46
5:D:978:ARG:NH2	5:D:999:TYR:HB2	2.29	0.46
5:D:1067:ARG:HH22	5:D:1076:PRO:HD3	1.80	0.46
5:D:1082:ASP:OD1	5:D:1086:ASN:N	2.49	0.46
7:F:150:ARG:HB3	7:F:155:GLU:CB	2.45	0.46
1:H:14:DT:H2'	1:H:15:DG:O4'	2.15	0.46
2:J:88:LEU:HB2	2:J:156:LEU:HD23	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:113:LEU:HD23	2:J:132:LEU:CD1	2.43	0.46
4:C:67:GLU:O	4:C:102:LEU:HD12	2.15	0.46
4:C:100:LEU:CD1	4:C:122:VAL:HG11	2.44	0.46
4:C:260:LYS:HB3	4:C:262:TYR:HE1	1.80	0.46
4:C:935:THR:HG23	4:C:939:VAL:HG13	1.97	0.46
4:C:1022:LYS:HG3	4:C:1023:HIS:CD2	2.50	0.46
4:C:1105:SER:HB2	5:D:731:ARG:HG3	1.96	0.46
5:D:165:TYR:OH	5:D:169:LEU:HD22	2.15	0.46
5:D:665:GLN:O	5:D:669:GLN:HG2	2.15	0.46
5:D:722:ILE:O	5:D:722:ILE:HG12	2.15	0.46
7:F:414:LYS:O	7:F:418:LYS:HG3	2.16	0.46
7:F:575:GLU:HA	7:F:578:LYS:HZ1	1.80	0.46
3:K:254:LEU:HD12	3:K:254:LEU:H	1.81	0.46
3:A:197:ASP:OD1	3:A:197:ASP:N	2.47	0.46
4:C:270:THR:HG23	4:C:273:HIS:CE1	2.49	0.46
4:C:1157:GLN:HA	4:C:1157:GLN:HE21	1.81	0.46
5:D:34:SER:HA	5:D:102:MET:O	2.15	0.46
5:D:527:LEU:HB2	5:D:550:VAL:HG12	1.97	0.46
5:D:664:ILE:HD13	5:D:681:LYS:HG2	1.98	0.46
5:D:1167:LYS:HG3	5:D:1174:ARG:NE	2.29	0.46
5:D:1266:ILE:HD12	5:D:1274:PHE:H	1.78	0.46
7:F:414:LYS:HE3	7:F:434:TRP:CZ3	2.51	0.46
7:F:593:LYS:HB3	7:F:596:ARG:HH22	1.80	0.46
2:I:62:LEU:O	2:I:69:LEU:N	2.44	0.46
2:J:21:TYR:O	2:J:24:GLN:HB2	2.16	0.46
2:J:78:TYR:OH	2:J:82:ARG:NH1	2.43	0.46
3:A:187:VAL:CG2	3:A:199:ASP:HB3	2.45	0.46
4:C:38:PHE:CE1	4:C:461:GLU:HB2	2.50	0.46
4:C:214:ASN:OD1	4:C:359:ARG:HD2	2.16	0.46
4:C:544:GLY:N	4:C:546:GLU:OE2	2.48	0.46
4:C:882:ILE:HD11	4:C:919:ARG:NH2	2.31	0.46
5:D:62:PHE:O	5:D:98:ARG:HA	2.16	0.46
5:D:850:LYS:HD3	5:D:875:ASN:HD21	1.81	0.46
7:F:119:ILE:HG22	7:F:379:MET:HE2	1.98	0.46
7:F:292:VAL:HG21	7:F:299:LYS:CB	2.46	0.46
1:H:42:DG:C1'	1:H:43:DG:C1'	2.80	0.46
2:I:82:ARG:NH1	2:J:94:VAL:HG13	2.22	0.46
3:K:320:ASN:O	3:K:320:ASN:ND2	2.49	0.46
3:A:225:ALA:HB3	3:B:232:VAL:HG11	1.98	0.46
4:C:17:LYS:N	4:C:17:LYS:HD2	2.30	0.46
4:C:145:ILE:HD13	4:C:512:SER:HA	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:194:LEU:O	5:D:198:CYS:HB2	2.16	0.46
5:D:857:LEU:HD11	5:D:872:LEU:CD2	2.45	0.46
5:D:1314:LEU:HD23	5:D:1326:GLN:OE1	2.16	0.46
7:F:284:GLU:HA	7:F:287:ILE:HG13	1.97	0.46
7:F:320:ILE:HG12	7:F:330:LEU:HB2	1.97	0.46
2:I:8:ARG:NH1	2:I:8:ARG:HB2	2.31	0.46
2:I:170:GLN:HG3	2:I:171:LEU:HD23	1.97	0.46
2:J:116:THR:HA	2:J:120:GLY:HA3	1.98	0.46
3:A:98:VAL:C	3:A:99:ILE:HD12	2.40	0.46
3:B:123:ILE:HG22	3:B:125:LYS:H	1.80	0.46
4:C:472:GLU:HA	4:C:475:VAL:CG1	2.45	0.46
4:C:624:ASP:OD2	4:C:628:HIS:HB2	2.15	0.46
5:D:611:ILE:CG2	5:D:612:LEU:HD12	2.44	0.46
5:D:930:LEU:HD13	5:D:1244:GLN:HB2	1.97	0.46
5:D:972:LYS:HZ3	5:D:974:VAL:HA	1.80	0.46
5:D:1016:THR:OG1	5:D:1019:ASN:ND2	2.49	0.46
7:F:111:LEU:HG	7:F:112:THR:O	2.16	0.46
7:F:339:ARG:O	7:F:342:GLN:HB3	2.16	0.46
7:F:397:ARG:NH2	8:G:26:DT:O4	2.45	0.46
8:G:3:DT:H1'	8:G:4:DG:C5'	2.45	0.46
2:I:12:THR:O	2:I:63:VAL:N	2.49	0.46
2:I:110:TRP:HH2	2:I:139:ILE:HD13	1.79	0.46
2:J:194:ASP:HA	2:J:197:LEU:CB	2.46	0.46
4:C:189:ASP:OD1	4:C:189:ASP:N	2.45	0.46
4:C:270:THR:H	4:C:273:HIS:CG	2.33	0.46
4:C:309:LEU:HD23	4:C:309:LEU:H	1.80	0.46
4:C:632:ASP:OD1	4:C:633:LEU:HD23	2.15	0.46
4:C:734:ILE:HD12	4:C:777:VAL:HG21	1.98	0.46
4:C:840:SER:O	4:C:1047:LEU:HB2	2.16	0.46
4:C:1007:LYS:O	4:C:1011:LEU:HG	2.15	0.46
5:D:789:LYS:HG3	5:D:931:THR:HG22	1.98	0.46
7:F:320:ILE:CA	7:F:327:SER:HB2	2.37	0.46
7:F:503:GLU:HB2	7:F:504:PRO:HD2	1.98	0.46
7:F:506:SER:O	7:F:509:THR:HG22	2.15	0.46
7:F:551:LEU:HD22	7:F:551:LEU:HA	1.80	0.46
2:I:11:MET:SD	2:I:36:PHE:HA	2.56	0.46
4:C:981:ALA:O	4:C:1002:LEU:HD11	2.16	0.46
5:D:44:ILE:HD13	5:D:252:LEU:HD23	1.98	0.46
5:D:216:LYS:HD2	5:D:217:LEU:N	2.31	0.46
5:D:1012:ALA:HB3	5:D:1015:GLU:CB	2.46	0.46
5:D:1307:LEU:HG	5:D:1312:ALA:HB2	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:214:PRO:CB	7:F:218:ARG:HD3	2.46	0.46
7:F:232:ARG:NH1	7:F:233:ASP:HA	2.31	0.46
8:G:55:DT:H4'	8:G:56:DT:OP1	2.16	0.46
1:H:14:DT:OP2	7:F:584:ARG:NE	2.48	0.45
3:B:17:GLU:OE2	3:B:19:VAL:HG13	2.15	0.45
3:B:107:ILE:HG23	3:B:134:THR:O	2.15	0.45
4:C:21:VAL:HG11	4:C:592:ARG:HD2	1.98	0.45
4:C:206:ALA:O	4:C:209:ILE:HG22	2.16	0.45
4:C:477:GLU:O	4:C:481:LEU:HB3	2.15	0.45
4:C:545:PHE:CE1	5:D:781:LYS:HD3	2.51	0.45
4:C:1243:MET:HE3	5:D:445:LYS:HD3	1.98	0.45
5:D:154:LEU:HA	5:D:158:GLN:NE2	2.30	0.45
5:D:1062:LEU:HD13	5:D:1066:GLU:O	2.15	0.45
7:F:131:GLN:HB3	7:F:266:PHE:CZ	2.50	0.45
7:F:147:GLN:O	7:F:151:VAL:HG23	2.16	0.45
7:F:161:LEU:HG	7:F:162:ILE:HG23	1.98	0.45
7:F:298:PRO:HB2	7:F:301:ASN:ND2	2.30	0.45
2:I:82:ARG:NH2	7:F:578:LYS:HD2	2.31	0.45
3:A:187:VAL:HG23	3:A:199:ASP:HB3	1.98	0.45
4:C:494:ASN:HB3	4:C:497:PRO:HD2	1.97	0.45
4:C:689:ALA:HB1	4:C:1233:LEU:HD12	1.98	0.45
4:C:834:GLN:HE22	4:C:924:VAL:HG21	1.80	0.45
5:D:212:THR:O	5:D:216:LYS:HG3	2.16	0.45
5:D:253:VAL:HG11	7:F:523:ILE:HD12	1.99	0.45
5:D:390:LEU:CD2	5:D:407:VAL:HG11	2.46	0.45
5:D:398:LYS:HD3	7:F:532:LEU:HD21	1.98	0.45
5:D:872:LEU:HD23	5:D:872:LEU:HA	1.59	0.45
5:D:1167:LYS:HE3	5:D:1170:LYS:HD3	1.97	0.45
7:F:231:THR:HG21	7:F:252:LEU:CB	2.46	0.45
7:F:348:GLU:HB2	7:F:353:LEU:O	2.16	0.45
2:I:8:ARG:NH2	2:I:10:VAL:HB	2.32	0.45
3:B:59:VAL:HG23	3:B:171:LEU:HB2	1.99	0.45
4:C:255:ILE:CG2	4:C:263:VAL:H	2.28	0.45
4:C:368:ARG:O	4:C:368:ARG:HG3	2.15	0.45
4:C:1099:ASN:OD1	4:C:1100:PRO:HD2	2.16	0.45
5:D:114:ILE:O	5:D:114:ILE:HD13	2.16	0.45
5:D:423:LEU:HB3	5:D:466:MET:CE	2.46	0.45
5:D:959:LYS:CE	5:D:985:ILE:HG13	2.46	0.45
5:D:1161:GLY:HA3	5:D:1178:THR:O	2.16	0.45
1:H:37:DA:N6	7:F:420:GLU:HB3	2.21	0.45
3:B:103:ASN:HB2	3:B:141:SER:OG	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:119:GLU:HB2	4:C:489:PRO:HG2	1.98	0.45
5:D:700:ASN:O	5:D:704:GLU:HG2	2.16	0.45
5:D:1029:THR:OG1	5:D:1121:LEU:HD21	2.16	0.45
5:D:1080:ILE:O	5:D:1088:VAL:HG12	2.17	0.45
5:D:1103:GLY:O	5:D:1124:ILE:HG13	2.15	0.45
5:D:1159:ILE:HD12	5:D:1160:SER:H	1.81	0.45
5:D:1211:SER:OG	5:D:1212:ASP:N	2.49	0.45
6:E:8:ASP:HA	6:E:11:GLU:OE1	2.16	0.45
7:F:150:ARG:NH1	7:F:155:GLU:OE2	2.50	0.45
7:F:287:ILE:HG22	7:F:302:PHE:HE1	1.82	0.45
7:F:297:MET:CE	7:F:330:LEU:HD11	2.45	0.45
7:F:341:LEU:CB	7:F:344:LEU:HD21	2.45	0.45
7:F:354:THR:HG23	7:F:357:GLN:H	1.81	0.45
7:F:585:GLU:HG2	7:F:588:ARG:HD2	1.97	0.45
8:G:34:DT:H2''	8:G:35:DT:C5'	2.47	0.45
2:I:21:TYR:HB3	2:I:60:PRO:HD2	1.98	0.45
2:J:18:THR:HG23	2:J:207:MET:CE	2.47	0.45
2:J:129:ARG:HG3	2:J:173:ILE:HG12	1.98	0.45
2:J:137:LEU:HB3	2:J:179:GLY:CA	2.46	0.45
4:C:136:PHE:O	4:C:142:GLU:HA	2.17	0.45
4:C:1103:VAL:HG11	4:C:1112:ILE:HD11	1.99	0.45
4:C:1335:ILE:HD12	5:D:1336:ALA:CB	2.47	0.45
5:D:306:LEU:O	5:D:326:SER:HB2	2.16	0.45
5:D:706:VAL:HG12	5:D:715:LYS:CB	2.43	0.45
5:D:958:ILE:HG22	5:D:960:LEU:CD2	2.42	0.45
5:D:1032:SER:OG	5:D:1033:GLY:N	2.48	0.45
5:D:1084:GLN:OE1	5:D:1084:GLN:N	2.49	0.45
6:E:70:GLN:O	6:E:74:GLU:HG2	2.17	0.45
7:F:157:ARG:HG2	7:F:160:ASP:OD2	2.16	0.45
2:J:161:LEU:HA	2:J:164:LEU:HB3	1.98	0.45
4:C:284:LEU:HD12	4:C:285:ILE:H	1.81	0.45
4:C:591:TYR:OH	4:C:637:ARG:NH2	2.49	0.45
4:C:690:VAL:HG13	4:C:691:PRO:HD2	1.97	0.45
4:C:992:LEU:HD23	4:C:997:TRP:HE1	1.82	0.45
4:C:1336:ASN:HB3	5:D:23:ALA:O	2.16	0.45
7:F:228:TYR:CE2	7:F:229:VAL:HG13	2.52	0.45
2:I:50:LEU:O	2:I:54:ASN:HB3	2.17	0.45
2:I:126:ASP:HA	2:I:129:ARG:NH1	2.32	0.45
2:I:183:LEU:HG	2:I:187:MET:CE	2.46	0.45
3:A:112:ALA:O	3:A:115:ILE:HG13	2.17	0.45
3:B:47:LEU:HD21	3:B:220:ALA:CB	2.46	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:10:ARG:NH2	4:C:793:GLU:OE1	2.49	0.45
4:C:216:THR:OG1	4:C:217:THR:N	2.50	0.45
4:C:506:PHE:O	4:C:512:SER:OG	2.30	0.45
4:C:937:ASP:HB2	4:C:1039:GLY:HA3	1.98	0.45
5:D:24:LEU:HD12	5:D:24:LEU:HA	1.70	0.45
5:D:35:PHE:CD2	5:D:101:ARG:HD3	2.52	0.45
5:D:113:HIS:CE1	5:D:307:LEU:HD13	2.52	0.45
5:D:986:ASP:CG	5:D:992:LYS:HG2	2.41	0.45
5:D:1087:ASP:OD1	5:D:1087:ASP:N	2.43	0.45
7:F:151:VAL:CG2	7:F:156:ALA:HB3	2.46	0.45
8:G:30:DA:H3'	8:G:30:DA:P	2.57	0.45
2:I:46:PRO:HG2	2:I:51:ILE:CD1	2.42	0.45
2:J:23:HIS:CD2	2:J:27:ILE:HD11	2.51	0.45
4:C:223:LEU:HD13	4:C:426:ILE:HD13	1.99	0.45
4:C:841:ARG:HD3	4:C:1046:VAL:HG23	1.99	0.45
4:C:887:VAL:CG2	4:C:913:VAL:HG21	2.47	0.45
5:D:423:LEU:HB3	5:D:466:MET:HE3	1.99	0.45
7:F:141:ILE:O	7:F:141:ILE:HG22	2.17	0.45
7:F:586:ARG:NE	7:F:590:ILE:HG12	2.31	0.45
1:H:55:DG:C2'	1:H:56:DA:H5''	2.45	0.45
2:J:134:GLU:HA	2:J:137:LEU:HD11	1.98	0.45
2:J:190:VAL:HG13	2:J:191:PHE:HD1	1.81	0.45
3:A:62:ASP:OD1	3:A:63:GLY:N	2.50	0.45
4:C:232:ILE:CG2	4:C:237:LEU:HD23	2.45	0.45
4:C:672:GLU:HG2	4:C:673:HIS:HD2	1.82	0.45
4:C:699:LEU:HD22	4:C:699:LEU:HA	1.78	0.45
4:C:975:ILE:O	4:C:979:LEU:HB2	2.17	0.45
5:D:1168:GLU:HG3	5:D:1173:ARG:HG2	1.99	0.45
7:F:312:SER:OG	7:F:314:THR:HG23	2.16	0.45
7:F:512:GLY:O	7:F:513:ASP:HB2	2.17	0.45
1:H:62:DG:H1'	1:H:63:DG:H5'	1.98	0.45
2:I:44:ASP:OD1	2:I:45:ASN:N	2.50	0.45
3:A:12:ARG:HB3	3:A:12:ARG:HH11	1.82	0.45
4:C:34:SER:O	4:C:457:GLY:HA3	2.17	0.45
4:C:270:THR:H	4:C:273:HIS:HB2	1.81	0.45
4:C:299:LYS:NZ	4:C:301:TYR:CZ	2.84	0.45
4:C:609:ILE:HD12	4:C:610:GLU:N	2.31	0.45
5:D:317:THR:HG23	5:D:320:ASN:HB3	1.99	0.45
5:D:959:LYS:O	5:D:983:LYS:HB3	2.17	0.45
5:D:1156:LEU:HD12	5:D:1207:GLY:C	2.43	0.45
7:F:286:LEU:O	7:F:290:LEU:HB2	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:399:LEU:HD12	7:F:399:LEU:HA	1.79	0.45
7:F:493:LYS:O	7:F:497:VAL:HG23	2.17	0.45
2:J:112:THR:O	2:J:115:ASN:HB2	2.16	0.44
4:C:106:GLU:HG2	4:C:109:ALA:CB	2.40	0.44
4:C:321:LEU:O	4:C:325:LEU:N	2.49	0.44
4:C:759:SER:OG	4:C:760:ASN:N	2.48	0.44
4:C:1105:SER:HB2	5:D:731:ARG:HD2	1.99	0.44
5:D:839:VAL:CG2	5:D:882:VAL:HG11	2.47	0.44
7:F:139:GLU:CD	7:F:351:THR:HA	2.42	0.44
7:F:268:TYR:O	7:F:272:SER:N	2.50	0.44
7:F:602:SER:HA	7:F:605:GLU:HB2	1.98	0.44
1:H:18:DA:C4'	1:H:19:DA:H5'	2.47	0.44
2:J:201:THR:HG23	2:J:204:GLU:OE2	2.18	0.44
4:C:22:LEU:HB3	4:C:655:VAL:HG11	1.99	0.44
4:C:1002:LEU:CD2	4:C:1007:LYS:HD3	2.45	0.44
4:C:1004:ASP:CA	4:C:1008:GLN:HG2	2.36	0.44
5:D:977:SER:OG	5:D:978:ARG:N	2.50	0.44
5:D:981:GLU:HA	5:D:995:TYR:O	2.17	0.44
5:D:1327:GLU:HA	8:G:12:DG:OP1	2.16	0.44
7:F:113:ARG:HB2	7:F:426:LYS:CE	2.48	0.44
7:F:131:GLN:HG3	7:F:131:GLN:H	1.66	0.44
7:F:139:GLU:HA	7:F:142:THR:CG2	2.47	0.44
7:F:142:THR:HA	7:F:145:LEU:HD21	1.99	0.44
7:F:143:TYR:O	7:F:147:GLN:HG2	2.16	0.44
7:F:227:GLN:O	7:F:231:THR:HG23	2.18	0.44
7:F:275:VAL:HG13	7:F:278:ASP:OD2	2.17	0.44
7:F:299:LYS:O	7:F:303:ILE:HG23	2.18	0.44
7:F:309:ASN:O	7:F:355:ILE:HB	2.17	0.44
7:F:324:LYS:HB3	7:F:325:PRO:HD2	1.99	0.44
2:I:54:ASN:ND2	2:I:57:GLN:HA	2.32	0.44
2:I:165:LEU:HB3	2:I:191:PHE:HZ	1.82	0.44
2:J:23:HIS:HA	2:J:26:ARG:NH1	2.33	0.44
2:J:88:LEU:CB	2:J:156:LEU:HD23	2.48	0.44
2:J:191:PHE:HA	2:J:196:PHE:CD2	2.51	0.44
3:A:79:LEU:HD21	4:C:831:ILE:HD11	1.98	0.44
3:A:218:ARG:HG2	3:B:231:PHE:O	2.18	0.44
3:B:95:LYS:HE2	3:B:95:LYS:HB3	1.73	0.44
3:B:101:THR:O	3:B:116:THR:HG23	2.17	0.44
3:B:159:ILE:HA	3:B:162:GLU:HB2	1.99	0.44
4:C:102:LEU:O	4:C:116:ASP:HA	2.16	0.44
5:D:1080:ILE:HG22	5:D:1088:VAL:HG11	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:359:LYS:O	7:F:362:ASN:ND2	2.49	0.44
7:F:600:HIS:HB3	7:F:603:ARG:HH21	1.83	0.44
5:D:355:ILE:HG12	5:D:464:ASP:O	2.17	0.44
5:D:591:ILE:CG2	5:D:592:VAL:HG13	2.47	0.44
5:D:680:ASN:N	5:D:680:ASN:OD1	2.50	0.44
5:D:972:LYS:HZ1	5:D:1028:ILE:HD13	1.83	0.44
5:D:1144:LEU:CD2	5:D:1237:VAL:HG23	2.46	0.44
6:E:34:GLY:O	6:E:35:LYS:HD3	2.18	0.44
7:F:122:ARG:O	7:F:371:LYS:NZ	2.50	0.44
8:G:52:DC:H5'	8:G:52:DC:C6	2.49	0.44
1:H:60:DA:H2	8:G:3:DT:H3	1.64	0.44
1:H:63:DG:H4'	5:D:1170:LYS:HD2	2.00	0.44
2:I:54:ASN:HD21	2:I:58:SER:H	1.66	0.44
2:I:161:LEU:O	2:I:165:LEU:N	2.50	0.44
3:A:152:TYR:HD1	3:A:176:CYS:HB3	1.82	0.44
3:A:236:ASP:OD1	3:A:236:ASP:N	2.49	0.44
4:C:74:ARG:NH1	4:C:121:GLU:OE1	2.51	0.44
4:C:188:PHE:CE1	4:C:194:LEU:HD12	2.51	0.44
5:D:72:CYS:SG	5:D:74:LYS:HG3	2.58	0.44
5:D:655:SER:HA	5:D:658:GLU:HB3	1.99	0.44
5:D:843:VAL:CG2	5:D:883:ARG:HB2	2.48	0.44
5:D:1042:ASP:HB3	5:D:1048:ARG:CZ	2.47	0.44
7:F:346:GLN:O	7:F:350:GLU:HG3	2.17	0.44
1:H:53:DC:H2''	1:H:54:DG:C5'	2.47	0.44
2:J:10:VAL:CG1	2:J:65:ARG:HG2	2.47	0.44
3:A:175:ALA:HB1	3:A:177:TYR:CE1	2.52	0.44
4:C:490:GLN:HG3	7:F:472:GLN:HG2	2.00	0.44
4:C:496:LYS:HB3	4:C:497:PRO:HD3	1.99	0.44
4:C:730:SER:O	4:C:730:SER:OG	2.35	0.44
4:C:1042:LEU:HD13	4:C:1046:VAL:CG1	2.47	0.44
4:C:1225:VAL:HG13	5:D:638:SER:HB2	1.98	0.44
5:D:474:LEU:HD12	5:D:474:LEU:O	2.18	0.44
5:D:603:LYS:HE3	5:D:603:LYS:HB3	1.75	0.44
5:D:638:SER:OG	5:D:639:VAL:N	2.50	0.44
5:D:670:SER:HB2	5:D:672:LEU:CD1	2.48	0.44
5:D:872:LEU:HD22	5:D:877:VAL:HG12	1.99	0.44
5:D:1041:ILE:HB	5:D:1044:GLN:CD	2.42	0.44
7:F:272:SER:O	7:F:276:MET:HE2	2.18	0.44
7:F:278:ASP:HB3	7:F:281:ARG:HH12	1.82	0.44
2:I:31:GLU:HG3	2:I:195:SER:HB3	2.00	0.44
3:A:43:LEU:HA	3:A:43:LEU:HD23	1.71	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:103:ASN:OD1	3:B:141:SER:HB2	2.17	0.44
4:C:239:MET:HG2	4:C:287:VAL:HG11	1.98	0.44
4:C:849:GLU:OE1	4:C:851:THR:OG1	2.36	0.44
4:C:1230:MET:HE2	4:C:1230:MET:HB3	1.87	0.44
4:C:1339:LEU:HD13	5:D:17:PHE:CD2	2.53	0.44
5:D:279:LEU:O	5:D:283:LEU:HD13	2.17	0.44
5:D:721:SER:O	5:D:725:MET:HE3	2.18	0.44
5:D:1064:SER:OG	5:D:1192:LYS:O	2.28	0.44
7:F:136:GLU:OE2	7:F:361:ILE:HA	2.18	0.44
7:F:247:GLU:O	7:F:251:LYS:HG3	2.17	0.44
7:F:347:ILE:O	7:F:350:GLU:HB2	2.18	0.44
1:H:42:DG:H5'	7:F:385:ARG:HG2	1.99	0.44
2:J:174:GLU:HG3	2:J:175:PHE:N	2.33	0.44
3:K:262:LEU:HG	3:K:267:ALA:HB2	2.00	0.44
4:C:975:ILE:CG2	4:C:1010:GLN:HG2	2.46	0.44
5:D:1095:MET:SD	5:D:1096:PRO:HD2	2.57	0.44
5:D:1167:LYS:NZ	5:D:1170:LYS:HD3	2.33	0.44
8:G:51:DT:H2''	8:G:52:DC:H6	1.83	0.44
1:H:18:DA:H4'	1:H:19:DA:OP1	2.18	0.44
2:J:88:LEU:O	2:J:156:LEU:HB2	2.18	0.44
3:B:12:ARG:O	3:B:13:LEU:HB3	2.18	0.44
4:C:465:ARG:HG3	4:C:466:VAL:N	2.33	0.44
4:C:988:LYS:HA	4:C:991:LYS:CG	2.47	0.44
4:C:1002:LEU:HD12	4:C:1002:LEU:HA	1.79	0.44
4:C:1242:LYS:HD2	5:D:465:GLN:HE22	1.81	0.44
4:C:1275:VAL:O	4:C:1279:GLU:HG3	2.18	0.44
5:D:154:LEU:HA	5:D:158:GLN:CD	2.43	0.44
5:D:929:GLN:O	5:D:929:GLN:HG2	2.18	0.44
5:D:1029:THR:HG21	5:D:1117:SER:HA	2.00	0.44
5:D:1031:VAL:HG13	5:D:1080:ILE:CG2	2.42	0.44
7:F:296:LYS:O	7:F:296:LYS:HG3	2.17	0.44
7:F:588:ARG:H	7:F:588:ARG:HG2	1.53	0.44
2:I:8:ARG:HH22	2:I:10:VAL:HB	1.82	0.43
3:B:104:LYS:N	3:B:140:ILE:O	2.47	0.43
4:C:883:LEU:HD11	4:C:920:VAL:HG22	1.99	0.43
4:C:1211:ARG:HD3	4:C:1220:GLN:NE2	2.33	0.43
5:D:26:SER:HB3	5:D:236:TRP:CZ2	2.53	0.43
5:D:199:GLU:HA	5:D:202:ARG:CG	2.47	0.43
5:D:682:VAL:HA	5:D:685:ILE:HG22	1.99	0.43
5:D:816:THR:HG23	5:D:818:GLU:OE2	2.18	0.43
5:D:981:GLU:HB3	5:D:996:LYS:HE2	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:1138:LEU:HB3	5:D:1139:PRO:HD3	1.99	0.43
7:F:166:VAL:HG23	7:F:258:GLN:HG2	2.00	0.43
7:F:354:THR:HG23	7:F:356:GLU:H	1.83	0.43
7:F:576:VAL:O	7:F:579:GLN:HB3	2.18	0.43
8:G:5:DC:C2'	8:G:6:DA:H5'	2.43	0.43
1:H:63:DG:H5''	5:D:1170:LYS:CG	2.46	0.43
2:I:43:LYS:HD2	2:I:43:LYS:H	1.83	0.43
3:B:15:ASP:HB3	3:B:27:THR:HG23	1.99	0.43
4:C:61:SER:HG	4:C:65:ASN:H	1.64	0.43
4:C:296:VAL:HA	4:C:316:GLU:HA	2.00	0.43
4:C:478:ARG:NH1	4:C:487:LEU:HD13	2.33	0.43
4:C:906:PHE:CD2	7:F:611:LEU:HD11	2.53	0.43
4:C:1160:ASP:CG	4:C:1161:LEU:N	2.73	0.43
5:D:1080:ILE:HB	5:D:1097:ALA:HB3	1.99	0.43
5:D:1358:PRO:HB3	5:D:1366:HIS:CD2	2.53	0.43
6:E:73:GLN:O	6:E:76:GLU:HB3	2.18	0.43
7:F:275:VAL:HA	7:F:278:ASP:OD2	2.18	0.43
7:F:299:LYS:HA	7:F:302:PHE:CE2	2.52	0.43
7:F:530:LEU:HD22	7:F:532:LEU:HB3	1.99	0.43
1:H:44:DG:H2''	1:H:45:DA:C8	2.53	0.43
1:H:49:DG:C5	4:C:151:ARG:HD2	2.53	0.43
2:J:14:PHE:CG	2:J:50:LEU:HD13	2.53	0.43
2:J:137:LEU:HB3	2:J:179:GLY:HA3	1.98	0.43
3:A:44:ARG:O	3:A:44:ARG:HG2	2.17	0.43
3:A:234:LEU:HD23	3:A:234:LEU:HA	1.89	0.43
3:B:19:VAL:HG23	3:B:23:HIS:HD2	1.82	0.43
3:B:107:ILE:HD11	3:B:136:GLU:H	1.82	0.43
4:C:119:GLU:HG2	4:C:489:PRO:O	2.18	0.43
4:C:225:PHE:CZ	4:C:345:PRO:HA	2.54	0.43
4:C:836:LEU:HB3	4:C:918:LEU:HD21	2.00	0.43
4:C:898:GLU:OE1	4:C:898:GLU:N	2.51	0.43
5:D:208:THR:HG23	5:D:213:LYS:HE3	1.99	0.43
5:D:1280:VAL:HG11	5:D:1304:ARG:NH2	2.29	0.43
7:F:354:THR:CG2	7:F:357:GLN:HG3	2.47	0.43
2:J:175:PHE:HD2	2:J:184:LYS:HG2	1.82	0.43
3:B:65:LEU:HA	3:B:169:GLY:HA3	2.00	0.43
4:C:163:LYS:NZ	4:C:164:THR:HA	2.33	0.43
4:C:268:ARG:HD2	4:C:269:ILE:O	2.17	0.43
4:C:510:GLN:OE1	4:C:510:GLN:N	2.51	0.43
4:C:811:ASN:O	4:C:1099:ASN:ND2	2.51	0.43
1:H:11:DG:H2''	1:H:12:DA:O5'	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:47:PRO:HG2	2:I:50:LEU:HB2	2.01	0.43
2:I:113:LEU:CD2	2:I:132:LEU:HD13	2.49	0.43
2:J:200:LEU:HA	2:J:204:GLU:OE2	2.18	0.43
3:A:98:VAL:HG11	3:A:121:VAL:HG21	1.99	0.43
4:C:204:LEU:CG	4:C:369:MET:HE2	2.48	0.43
4:C:253:PHE:O	4:C:255:ILE:HD12	2.19	0.43
4:C:637:ARG:O	4:C:637:ARG:HG3	2.19	0.43
4:C:1022:LYS:HG3	4:C:1023:HIS:HD2	1.83	0.43
5:D:275:ARG:NE	7:F:403:ASP:OD2	2.48	0.43
5:D:789:LYS:HG3	5:D:931:THR:CG2	2.49	0.43
5:D:959:LYS:CD	5:D:985:ILE:HG13	2.48	0.43
5:D:1189:MET:HE2	5:D:1191:PRO:HD3	2.01	0.43
7:F:298:PRO:HB2	7:F:301:ASN:OD1	2.19	0.43
7:F:412:LEU:HB2	7:F:435:ILE:HD11	2.01	0.43
1:H:26:DT:H2"	1:H:27:DA:OP2	2.19	0.43
4:C:800:MET:HE2	4:C:800:MET:HB3	1.78	0.43
4:C:818:VAL:HG12	4:C:819:SER:O	2.18	0.43
4:C:1020:GLU:O	4:C:1024:GLU:CB	2.67	0.43
4:C:1319:MET:CG	4:C:1320:PRO:HD2	2.48	0.43
5:D:114:ILE:HB	5:D:304:ASP:CG	2.42	0.43
5:D:197:GLU:O	5:D:201:LEU:HB2	2.19	0.43
5:D:654:ILE:HD11	5:D:743:MET:SD	2.58	0.43
5:D:870:ASP:HA	5:D:873:GLU:CB	2.48	0.43
5:D:955:LYS:CG	5:D:1010:GLN:HB3	2.48	0.43
5:D:1031:VAL:O	5:D:1080:ILE:HG21	2.17	0.43
7:F:586:ARG:HE	7:F:590:ILE:HG12	1.84	0.43
2:I:17:PRO:HD3	2:I:41:VAL:O	2.19	0.43
2:I:98:GLU:C	2:I:101:LEU:H	2.27	0.43
2:I:116:THR:O	2:I:120:GLY:N	2.51	0.43
2:I:132:LEU:HD23	2:I:173:ILE:CD1	2.49	0.43
2:I:183:LEU:HD12	2:I:183:LEU:O	2.19	0.43
4:C:15:PHE:CD2	4:C:1190:ALA:HB2	2.53	0.43
4:C:198:ILE:CG2	4:C:199:ASP:N	2.73	0.43
4:C:299:LYS:HZ2	4:C:299:LYS:H	1.67	0.43
4:C:421:SER:OG	4:C:422:LYS:N	2.52	0.43
5:D:177:ASP:OD2	5:D:179:LYS:HE3	2.19	0.43
5:D:201:LEU:HA	5:D:204:GLU:OE1	2.19	0.43
5:D:552:ILE:HD11	5:D:570:LYS:CG	2.42	0.43
7:F:133:SER:C	7:F:136:GLU:HG2	2.44	0.43
2:I:27:ILE:HD11	2:I:163:PRO:CG	2.48	0.43
3:A:222:THR:HG22	3:B:232:VAL:HB	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:50:GLU:OE1	4:C:70:TYR:OH	2.37	0.43
4:C:1122:LYS:NZ	4:C:1178:LYS:O	2.29	0.43
5:D:17:PHE:CZ	5:D:1353:VAL:HG11	2.48	0.43
5:D:18:ASP:OD1	5:D:18:ASP:N	2.51	0.43
5:D:322:ARG:CG	5:D:323:PRO:HD2	2.39	0.43
5:D:552:ILE:HD12	5:D:589:TYR:CE1	2.53	0.43
5:D:861:ASN:N	5:D:861:ASN:OD1	2.52	0.43
5:D:869:CYS:O	5:D:873:GLU:N	2.52	0.43
5:D:999:TYR:CD2	5:D:1027:VAL:HA	2.54	0.43
5:D:1158:GLU:HG2	5:D:1186:TYR:OH	2.18	0.43
7:F:507:MET:SD	7:F:523:ILE:HD11	2.59	0.43
1:H:44:DG:C1'	1:H:45:DA:H5'	2.48	0.43
4:C:106:GLU:HB2	4:C:114:VAL:HG21	2.00	0.43
4:C:616:ILE:HA	4:C:652:TYR:O	2.19	0.43
4:C:1264:GLN:HA	4:C:1264:GLN:HE21	1.83	0.43
5:D:500:ILE:HG22	5:D:500:ILE:O	2.18	0.43
5:D:833:GLU:CG	5:D:838:ARG:HG3	2.49	0.43
5:D:1029:THR:N	5:D:1119:ASP:O	2.51	0.43
5:D:1268:ASN:HA	5:D:1274:PHE:CE1	2.53	0.43
7:F:306:PHE:HZ	7:F:341:LEU:HD22	1.84	0.43
7:F:373:ARG:O	7:F:377:LYS:HG3	2.18	0.43
7:F:572:THR:HB	7:F:575:GLU:HB2	2.01	0.43
1:H:20:DA:H2''	1:H:21:DA:H8	1.84	0.43
2:J:12:THR:O	2:J:62:LEU:HD12	2.18	0.43
2:J:133:ARG:CA	2:J:136:LEU:HG	2.45	0.43
2:J:139:ILE:C	2:J:142:VAL:HG13	2.43	0.43
2:J:190:VAL:HG13	2:J:191:PHE:CD1	2.54	0.43
4:C:22:LEU:HD12	4:C:23:ASP:H	1.84	0.43
4:C:272:ARG:O	4:C:276:GLN:HG3	2.18	0.43
4:C:1298:VAL:CG2	4:C:1321:GLU:HG3	2.48	0.43
5:D:140:TYR:CB	7:F:100:MET:HE1	2.29	0.43
5:D:929:GLN:C	5:D:930:LEU:HD23	2.44	0.43
5:D:1051:ASP:OD2	5:D:1057:SER:HA	2.19	0.43
7:F:213:ASP:HB2	7:F:216:LEU:HD11	2.00	0.43
4:C:4:SER:O	4:C:7:GLU:N	2.51	0.42
4:C:39:ILE:HG13	4:C:39:ILE:O	2.19	0.42
4:C:109:ALA:HB1	4:C:110:PRO:HD2	2.00	0.42
4:C:145:ILE:HB	4:C:456:VAL:HG22	2.00	0.42
4:C:241:LEU:HD21	4:C:246:LEU:HD11	1.99	0.42
5:D:527:LEU:CD2	5:D:548:VAL:HG21	2.49	0.42
5:D:596:LEU:HA	5:D:596:LEU:HD12	1.82	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:827:GLU:N	5:D:830:ASP:O	2.47	0.42
5:D:957:SER:O	5:D:985:ILE:HG12	2.19	0.42
5:D:1037:PHE:HD1	5:D:1037:PHE:HA	1.74	0.42
5:D:1044:GLN:OE1	5:D:1074:LEU:HD11	2.19	0.42
7:F:157:ARG:HG3	7:F:159:SER:H	1.83	0.42
7:F:287:ILE:HG22	7:F:302:PHE:CE1	2.54	0.42
7:F:495:ARG:O	7:F:499:LYS:HE3	2.19	0.42
8:G:12:DG:C2'	8:G:13:DA:H5'	2.49	0.42
2:J:48:GLN:O	2:J:51:ILE:HG23	2.19	0.42
3:B:83:LEU:HD21	5:D:526:VAL:CG2	2.48	0.42
3:B:83:LEU:HD13	5:D:528:THR:HB	2.01	0.42
4:C:210:LEU:HB3	4:C:220:ILE:HD12	2.01	0.42
4:C:268:ARG:CZ	4:C:270:THR:HA	2.49	0.42
4:C:637:ARG:HA	4:C:641:GLU:O	2.19	0.42
4:C:699:LEU:HB2	4:C:799:ASN:ND2	2.32	0.42
5:D:213:LYS:CA	5:D:216:LYS:HE3	2.42	0.42
5:D:487:THR:OG1	6:E:5:THR:HG22	2.19	0.42
5:D:793:SER:O	5:D:797:THR:HG22	2.19	0.42
7:F:142:THR:HA	7:F:145:LEU:CG	2.48	0.42
2:I:13:LEU:HD12	2:I:14:PHE:N	2.34	0.42
2:I:17:PRO:HB3	2:I:40:HIS:HB3	2.00	0.42
2:I:17:PRO:HA	2:I:40:HIS:ND1	2.34	0.42
2:I:170:GLN:HG3	2:I:171:LEU:HD22	2.00	0.42
2:J:16:GLY:H	2:J:22:SER:CB	2.32	0.42
2:J:29:LEU:O	2:J:34:VAL:HG12	2.20	0.42
3:A:8:PHE:HD1	3:A:8:PHE:HA	1.69	0.42
3:A:14:VAL:HG13	3:A:15:ASP:OD1	2.20	0.42
3:A:190:ALA:CB	3:A:200:LYS:HG3	2.47	0.42
4:C:144:VAL:HG21	4:C:515:MET:HG3	2.01	0.42
4:C:609:ILE:CD1	4:C:610:GLU:HG3	2.45	0.42
4:C:985:GLU:HA	4:C:988:LYS:CG	2.50	0.42
4:C:1020:GLU:O	4:C:1024:GLU:CG	2.67	0.42
4:C:1203:ASP:OD1	4:C:1203:ASP:N	2.50	0.42
5:D:228:VAL:HG13	5:D:229:GLN:H	1.83	0.42
5:D:582:ILE:HG23	5:D:623:GLN:HB3	2.00	0.42
5:D:759:ILE:CG2	5:D:771:GLN:HB3	2.49	0.42
5:D:883:ARG:NH2	5:D:898:CYS:SG	2.93	0.42
7:F:135:ALA:HB1	7:F:253:SER:HB2	2.01	0.42
7:F:141:ILE:HD11	7:F:252:LEU:HD11	2.01	0.42
7:F:160:ASP:OD1	7:F:160:ASP:N	2.52	0.42
8:G:27:DA:H1'	8:G:28:DG:H5'	2.00	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:22:DG:C2'	1:H:23:DT:H72	2.48	0.42
2:I:46:PRO:HB2	2:I:50:LEU:HD23	2.00	0.42
2:I:168:LEU:O	2:I:173:ILE:HB	2.20	0.42
4:C:17:LYS:NZ	4:C:1194:GLU:OE2	2.34	0.42
4:C:580:GLN:O	4:C:588:GLU:HG2	2.19	0.42
4:C:745:GLU:CD	4:C:1014:LEU:HA	2.44	0.42
5:D:999:TYR:CE2	5:D:1027:VAL:HA	2.54	0.42
5:D:999:TYR:HE2	5:D:1028:ILE:H	1.68	0.42
7:F:559:LEU:HD12	7:F:559:LEU:HA	1.74	0.42
2:J:110:TRP:O	2:J:113:LEU:HB3	2.20	0.42
3:A:192:VAL:HB	3:A:198:LEU:HD12	2.02	0.42
4:C:264:GLU:OE1	4:C:264:GLU:N	2.51	0.42
4:C:296:VAL:CG2	4:C:314:ASN:HA	2.49	0.42
4:C:373:GLY:CA	7:F:94:THR:HB	2.48	0.42
4:C:1157:GLN:HA	4:C:1157:GLN:NE2	2.33	0.42
4:C:1268:GLN:NE2	4:C:1268:GLN:HA	2.32	0.42
5:D:297:ARG:HH11	7:F:100:MET:HE2	1.85	0.42
5:D:1047:THR:O	5:D:1049:GLN:HG3	2.19	0.42
5:D:1053:LEU:HD22	5:D:1053:LEU:H	1.84	0.42
5:D:1062:LEU:HB3	5:D:1066:GLU:O	2.18	0.42
5:D:1156:LEU:HD13	5:D:1156:LEU:HA	1.89	0.42
6:E:60:ASN:OD1	6:E:63:ILE:HG13	2.20	0.42
7:F:160:ASP:C	7:F:262:VAL:HB	2.44	0.42
7:F:163:THR:OG1	7:F:260:ARG:HD3	2.20	0.42
1:H:38:DT:H4'	7:F:425:TYR:CE2	2.55	0.42
3:K:283:GLN:NE2	3:K:318:LEU:O	2.52	0.42
4:C:122:VAL:HG21	4:C:493:ILE:HG21	2.00	0.42
4:C:138:ILE:HD13	4:C:138:ILE:HA	1.74	0.42
4:C:255:ILE:HD13	4:C:263:VAL:C	2.44	0.42
4:C:672:GLU:HB3	4:C:1187:PHE:CE1	2.54	0.42
4:C:864:LYS:HD2	4:C:875:ALA:HB1	2.02	0.42
4:C:1134:GLN:C	4:C:1135:GLN:HG2	2.44	0.42
4:C:1210:ILE:HG22	4:C:1211:ARG:H	1.83	0.42
5:D:581:MET:HE3	5:D:581:MET:HB2	1.81	0.42
5:D:1031:VAL:HG21	5:D:1088:VAL:CG2	2.42	0.42
2:J:108:LYS:HE3	2:J:108:LYS:HB3	1.82	0.42
4:C:135:THR:OG1	4:C:142:GLU:HB3	2.19	0.42
4:C:473:ARG:HB2	4:C:473:ARG:CZ	2.49	0.42
4:C:590:PRO:HB2	4:C:655:VAL:HG21	2.02	0.42
4:C:877:VAL:HG21	4:C:920:VAL:HG21	2.01	0.42
4:C:1200:LYS:HE3	4:C:1200:LYS:HB2	1.87	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:72:GLN:O	6:E:76:GLU:N	2.52	0.42
7:F:150:ARG:HD2	7:F:155:GLU:CD	2.44	0.42
7:F:166:VAL:HG12	7:F:260:ARG:CZ	2.50	0.42
7:F:234:THR:OG1	7:F:245:ALA:HA	2.20	0.42
7:F:574:GLU:CD	7:F:588:ARG:HH12	2.28	0.42
7:F:589:GLN:HB3	7:F:593:LYS:NZ	2.35	0.42
7:F:593:LYS:HA	7:F:596:ARG:HH12	1.84	0.42
7:F:596:ARG:O	7:F:599:ARG:HB3	2.19	0.42
2:J:95:ALA:HA	2:J:98:GLU:CD	2.45	0.42
2:J:208:ARG:HG2	2:J:209:LEU:H	1.83	0.42
3:A:95:LYS:NZ	3:A:120:ASP:OD2	2.53	0.42
3:A:186:ASN:OD1	3:A:186:ASN:N	2.52	0.42
3:B:9:LEU:HD12	3:B:195:ARG:NH2	2.34	0.42
4:C:808:ASN:ND2	4:C:1216:ARG:HH22	2.18	0.42
4:C:1291:LEU:HD21	5:D:1351:VAL:HG22	2.01	0.42
5:D:573:THR:OG1	5:D:575:GLY:N	2.52	0.42
5:D:826:ILE:HD11	5:D:991:THR:HG21	2.00	0.42
6:E:38:LEU:HB3	6:E:58:LEU:HD23	2.02	0.42
7:F:111:LEU:HD21	7:F:115:GLY:C	2.45	0.42
7:F:286:LEU:CD2	7:F:290:LEU:HB2	2.50	0.42
7:F:354:THR:O	7:F:358:VAL:HG23	2.19	0.42
7:F:470:MET:CE	7:F:486:ARG:HD2	2.50	0.42
1:H:11:DG:H2"	1:H:12:DA:H5"	2.02	0.42
2:J:184:LYS:HA	2:J:187:MET:HE2	2.02	0.42
4:C:840:SER:O	4:C:840:SER:OG	2.31	0.42
5:D:133:ARG:HA	5:D:133:ARG:HD2	1.77	0.42
5:D:210:SER:CB	5:D:213:LYS:HB2	2.46	0.42
5:D:256:ASP:OD1	5:D:256:ASP:N	2.53	0.42
5:D:490:ILE:HD11	5:D:609:TYR:CE1	2.54	0.42
5:D:536:LEU:HD12	5:D:536:LEU:HA	1.84	0.42
5:D:655:SER:O	5:D:658:GLU:HB3	2.20	0.42
5:D:828:GLY:O	5:D:993:GLU:HB3	2.20	0.42
5:D:929:GLN:OE1	5:D:930:LEU:HG	2.20	0.42
7:F:297:MET:HG3	7:F:326:TRP:CE3	2.55	0.42
3:A:58:GLU:OE2	3:A:170:ARG:NH1	2.53	0.42
4:C:34:SER:O	4:C:34:SER:OG	2.37	0.42
4:C:194:LEU:HD23	4:C:206:ALA:CB	2.50	0.42
4:C:511:LEU:O	4:C:513:GLN:N	2.53	0.42
4:C:985:GLU:CB	4:C:989:LEU:HD13	2.50	0.42
4:C:1115:THR:HG22	4:C:1228:GLY:HA3	2.01	0.42
5:D:126:LEU:HD11	5:D:223:LEU:HD22	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:137:ARG:O	5:D:137:ARG:HG2	2.20	0.42
5:D:241:VAL:HG23	5:D:241:VAL:O	2.20	0.42
5:D:827:GLU:CG	5:D:832:LYS:HD3	2.50	0.42
5:D:885:VAL:CG2	5:D:894:VAL:HG11	2.50	0.42
5:D:955:LYS:HG2	5:D:1010:GLN:CB	2.50	0.42
5:D:1063:ASP:CG	5:D:1103:GLY:HA3	2.45	0.42
5:D:1190:ILE:HG22	5:D:1191:PRO:O	2.20	0.42
7:F:490:PRO:HD2	7:F:493:LYS:HB2	2.01	0.42
2:I:101:LEU:CD1	2:I:105:ARG:HD2	2.50	0.41
2:I:113:LEU:HD23	2:I:132:LEU:CB	2.41	0.41
2:J:13:LEU:HD12	2:J:14:PHE:N	2.35	0.41
2:J:67:LEU:HD12	2:J:67:LEU:HA	1.64	0.41
4:C:18:ARG:HD2	4:C:18:ARG:N	2.35	0.41
4:C:150:HIS:NE2	4:C:454:ARG:HG3	2.35	0.41
4:C:266:GLY:C	4:C:267:ARG:HD2	2.45	0.41
4:C:321:LEU:O	4:C:325:LEU:HB2	2.20	0.41
4:C:905:ILE:HG22	4:C:906:PHE:CD1	2.55	0.41
4:C:992:LEU:HD21	4:C:1000:LEU:HD12	2.01	0.41
4:C:1160:ASP:CG	4:C:1161:LEU:H	2.25	0.41
4:C:1293:VAL:CG2	4:C:1315:MET:HE3	2.50	0.41
5:D:1039:ASP:HB3	5:D:1074:LEU:CB	2.39	0.41
5:D:1067:ARG:NH2	5:D:1076:PRO:HG3	2.35	0.41
5:D:1140:ARG:HD3	5:D:1140:ARG:HA	1.80	0.41
5:D:1162:ILE:HD12	5:D:1202:GLU:O	2.20	0.41
6:E:3:ARG:HA	6:E:3:ARG:HH11	1.85	0.41
7:F:137:TYR:CZ	7:F:139:GLU:HB2	2.55	0.41
7:F:344:LEU:O	7:F:347:ILE:HB	2.20	0.41
7:F:530:LEU:HB3	7:F:533:ASP:HB2	2.02	0.41
2:I:50:LEU:O	2:I:50:LEU:HD12	2.21	0.41
2:J:97:GLY:O	2:J:101:LEU:HB2	2.20	0.41
3:A:33:ARG:HG3	3:A:34:GLY:N	2.35	0.41
3:A:193:GLU:OE2	3:A:194:GLN:HB3	2.20	0.41
4:C:242:VAL:CG2	4:C:245:ARG:HE	2.30	0.41
4:C:288:PRO:HG2	4:C:291:TYR:HB3	2.03	0.41
4:C:369:MET:HE3	4:C:369:MET:HB3	1.84	0.41
4:C:459:MET:HE1	4:C:511:LEU:HD13	2.02	0.41
4:C:768:MET:O	4:C:784:ALA:HA	2.20	0.41
4:C:1308:ILE:CG2	5:D:379:PRO:HB2	2.49	0.41
5:D:15:GLU:HG3	5:D:16:GLU:H	1.85	0.41
5:D:146:VAL:O	5:D:147:ILE:HD13	2.20	0.41
6:E:19:LEU:HD12	6:E:19:LEU:O	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:161:LEU:O	7:F:261:LEU:HA	2.19	0.41
7:F:354:THR:CG2	7:F:357:GLN:H	2.34	0.41
7:F:505:ILE:HD13	7:F:505:ILE:HA	1.89	0.41
2:I:23:HIS:CA	2:I:26:ARG:HG3	2.44	0.41
2:I:62:LEU:O	2:I:68:THR:HA	2.20	0.41
3:A:11:PRO:HA	3:A:30:PRO:HG2	2.01	0.41
4:C:34:SER:OG	4:C:455:SER:HB2	2.19	0.41
4:C:238:GLN:NE2	4:C:286:GLU:OE2	2.53	0.41
4:C:239:MET:HG2	4:C:287:VAL:CG1	2.50	0.41
4:C:1342:GLU:HG3	5:D:18:ASP:OD1	2.20	0.41
5:D:144:TYR:CD1	5:D:180:MET:HE3	2.55	0.41
5:D:305:ALA:O	5:D:309:ASN:HB2	2.20	0.41
5:D:954:ASN:HB2	5:D:984:LEU:CD2	2.51	0.41
5:D:1109:LEU:CD2	5:D:1115:ILE:HG21	2.50	0.41
5:D:1238:GLN:OE1	5:D:1238:GLN:HA	2.19	0.41
5:D:1342:ASP:OD1	5:D:1344:LEU:HD23	2.18	0.41
7:F:97:PRO:O	7:F:100:MET:N	2.53	0.41
7:F:371:LYS:O	7:F:371:LYS:HD3	2.20	0.41
7:F:404:LEU:HD22	7:F:439:ILE:CG2	2.49	0.41
7:F:479:THR:HB	7:F:480:PRO:HD2	2.02	0.41
8:G:52:DC:H2''	8:G:53:DA:O5'	2.20	0.41
2:I:14:PHE:HD2	2:I:50:LEU:HD13	1.86	0.41
2:J:11:MET:HE2	2:J:64:ASP:CB	2.48	0.41
2:J:134:GLU:OE1	2:J:134:GLU:HA	2.20	0.41
3:A:27:THR:HG23	3:A:201:LEU:O	2.20	0.41
3:B:11:PRO:O	3:B:12:ARG:NE	2.45	0.41
4:C:8:LYS:HE3	4:C:8:LYS:HB3	1.83	0.41
4:C:131:THR:OG1	4:C:135:THR:HG23	2.20	0.41
4:C:594:VAL:HB	4:C:651:ASP:O	2.21	0.41
4:C:1002:LEU:HD23	4:C:1007:LYS:CB	2.50	0.41
5:D:245:LEU:HG	5:D:246:PRO:HD2	2.03	0.41
5:D:320:ASN:C	5:D:321:LYS:HD3	2.45	0.41
5:D:350:SER:HA	5:D:468:VAL:O	2.20	0.41
5:D:816:THR:HG1	5:D:889:ASP:HB2	1.86	0.41
5:D:908:ILE:HG12	5:D:909:ILE:H	1.85	0.41
5:D:1000:GLY:O	5:D:1020:TRP:HA	2.20	0.41
5:D:1107:VAL:HG12	5:D:1122:ALA:HB2	2.01	0.41
6:E:41:GLU:HG3	6:E:43:ASN:H	1.85	0.41
7:F:94:THR:HG21	7:F:103:ARG:HH21	1.84	0.41
7:F:530:LEU:CD2	7:F:532:LEU:H	2.27	0.41
7:F:561:MET:HE2	7:F:576:VAL:CG2	2.35	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:42:DT:H6	8:G:42:DT:H2'	1.67	0.41
3:A:26:VAL:HG21	3:A:217:ILE:CD1	2.49	0.41
4:C:163:LYS:HG3	4:C:164:THR:N	2.35	0.41
4:C:268:ARG:NH1	4:C:270:THR:HG22	2.35	0.41
4:C:490:GLN:CG	7:F:472:GLN:HG2	2.50	0.41
4:C:660:VAL:HG21	5:D:769:VAL:HG11	2.03	0.41
4:C:1129:ASN:O	4:C:1133:LYS:HB2	2.21	0.41
4:C:1303:LYS:HD2	4:C:1303:LYS:HA	1.86	0.41
5:D:177:ASP:CG	5:D:179:LYS:HE3	2.45	0.41
5:D:200:GLN:O	5:D:204:GLU:HG3	2.19	0.41
5:D:801:VAL:HG23	5:D:917:VAL:HG13	2.02	0.41
5:D:1109:LEU:HA	5:D:1109:LEU:HD23	1.81	0.41
5:D:1140:ARG:NH1	5:D:1144:LEU:HD22	2.35	0.41
5:D:1159:ILE:HD12	5:D:1160:SER:N	2.35	0.41
7:F:162:ILE:HD12	7:F:216:LEU:HD13	2.02	0.41
7:F:471:LEU:CD1	7:F:477:GLU:HA	2.51	0.41
2:I:11:MET:CE	2:I:37:GLU:H	2.30	0.41
2:I:187:MET:HB3	2:I:191:PHE:CD2	2.56	0.41
2:J:12:THR:HA	2:J:37:GLU:O	2.21	0.41
2:J:76:MET:HE1	2:J:160:TYR:HE2	1.85	0.41
2:J:129:ARG:HB2	2:J:129:ARG:HH11	1.86	0.41
3:A:48:LEU:HD23	3:A:48:LEU:HA	1.93	0.41
3:A:111:THR:HG23	3:A:113:ALA:N	2.23	0.41
3:B:17:GLU:CD	3:B:19:VAL:HG13	2.46	0.41
3:B:31:LEU:O	3:B:198:LEU:HD12	2.20	0.41
3:B:59:VAL:HG11	3:B:85:LEU:HD12	2.01	0.41
4:C:13:LYS:HD2	4:C:14:ASP:N	2.36	0.41
4:C:239:MET:CB	4:C:287:VAL:HG11	2.51	0.41
4:C:782:VAL:C	4:C:783:LEU:HD23	2.45	0.41
4:C:935:THR:HG23	4:C:939:VAL:CG1	2.51	0.41
4:C:1158:LYS:HZ2	4:C:1158:LYS:HA	1.84	0.41
5:D:44:ILE:CG1	7:F:450:ILE:HG12	2.51	0.41
5:D:81:ARG:HH11	5:D:81:ARG:CB	2.29	0.41
5:D:291:ILE:HD13	7:F:409:ASN:HB3	2.02	0.41
5:D:797:THR:HB	5:D:924:GLY:HA3	2.02	0.41
5:D:1016:THR:HG21	5:D:1019:ASN:OD1	2.20	0.41
5:D:1027:VAL:O	5:D:1121:LEU:HG	2.20	0.41
5:D:1247:LYS:HB3	5:D:1247:LYS:HE2	1.79	0.41
7:F:152:GLU:H	7:F:152:GLU:HG2	1.56	0.41
7:F:351:THR:HG21	7:F:358:VAL:HG22	2.02	0.41
2:I:162:ALA:O	2:I:166:TRP:N	2.53	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:90:PRO:HG2	2:J:96:ARG:N	2.35	0.41
3:B:17:GLU:OE1	3:B:19:VAL:HG13	2.19	0.41
3:B:71:LYS:HB3	3:B:74:VAL:CG2	2.50	0.41
3:B:95:LYS:HZ3	3:B:98:VAL:HB	1.85	0.41
3:B:198:LEU:HD13	3:B:198:LEU:HA	1.86	0.41
4:C:540:ARG:H	4:C:540:ARG:HG3	1.57	0.41
4:C:883:LEU:HD23	4:C:883:LEU:HA	1.89	0.41
4:C:890:LYS:HE3	4:C:890:LYS:HB3	1.88	0.41
4:C:1170:MET:O	4:C:1174:GLU:HB2	2.21	0.41
5:D:107:LEU:HD13	5:D:111:THR:HG21	2.02	0.41
5:D:255:LEU:HA	5:D:255:LEU:HD13	1.86	0.41
5:D:703:THR:CG2	5:D:715:LYS:HD3	2.48	0.41
5:D:955:LYS:NZ	5:D:1012:ALA:HA	2.35	0.41
5:D:972:LYS:CG	5:D:1003:LEU:H	2.33	0.41
7:F:474:MET:HE3	7:F:474:MET:HB2	1.72	0.41
2:I:149:PHE:CD1	2:I:161:LEU:HD11	2.56	0.41
2:J:134:GLU:O	2:J:137:LEU:HD12	2.21	0.41
2:J:139:ILE:HG22	2:J:142:VAL:CG2	2.50	0.41
3:A:89:ALA:O	3:A:124:VAL:HG12	2.21	0.41
3:A:96:ASP:O	3:A:148:ARG:HG3	2.21	0.41
3:A:159:ILE:HD11	3:A:172:LEU:CD1	2.51	0.41
3:B:106:GLY:C	3:B:107:ILE:HG13	2.46	0.41
4:C:91:THR:HG21	4:C:503:LYS:HZ2	1.86	0.41
4:C:274:ILE:O	4:C:277:LEU:HG	2.21	0.41
4:C:1030:GLU:O	4:C:1034:ARG:N	2.54	0.41
4:C:1073:LYS:HE3	4:C:1073:LYS:HB2	1.90	0.41
4:C:1138:VAL:HG21	4:C:1166:ASP:HB3	2.02	0.41
4:C:1223:ARG:O	4:C:1223:ARG:HG3	2.21	0.41
5:D:520:ALA:HB3	5:D:546:ALA:HB2	2.03	0.41
5:D:653:ILE:HD13	5:D:692:ARG:O	2.21	0.41
5:D:1273:ASP:OD1	5:D:1275:LEU:HD12	2.21	0.41
7:F:288:MET:HE2	7:F:288:MET:HB3	1.97	0.41
7:F:338:HIS:O	7:F:341:LEU:HD12	2.20	0.41
7:F:402:LEU:HA	7:F:402:LEU:HD12	1.81	0.41
1:H:12:DA:H2''	1:H:13:DT:O5'	2.21	0.41
1:H:49:DG:C6	4:C:151:ARG:HD2	2.56	0.41
2:I:47:PRO:HG2	2:I:50:LEU:CB	2.51	0.41
2:I:126:ASP:OD1	2:I:130:LYS:HG3	2.21	0.41
3:A:59:VAL:HG12	3:A:60:GLU:N	2.36	0.41
3:A:132:HIS:C	3:A:133:LEU:HD22	2.46	0.41
3:A:191:ARG:HD3	3:A:191:ARG:HA	1.84	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:53:GLY:HA3	3:B:177:TYR:O	2.21	0.41
3:B:182:ARG:HG2	3:B:183:ILE:N	2.33	0.41
4:C:75:LEU:CD2	4:C:127:ILE:HD11	2.50	0.41
4:C:202:ARG:HG2	4:C:203:LYS:N	2.36	0.41
4:C:699:LEU:HD23	4:C:799:ASN:HD21	1.86	0.41
4:C:908:GLU:OE1	7:F:611:LEU:HD22	2.20	0.41
4:C:1028:LYS:HE2	4:C:1028:LYS:HB3	1.83	0.41
4:C:1158:LYS:HZ2	4:C:1158:LYS:N	2.17	0.41
4:C:1270:PHE:HZ	4:C:1278:LEU:HD12	1.85	0.41
4:C:1280:ALA:HA	5:D:918:ILE:HG22	2.02	0.41
5:D:201:LEU:HD22	5:D:217:LEU:HD11	2.03	0.41
5:D:377:PHE:CD2	5:D:416:ILE:HD11	2.55	0.41
5:D:666:GLU:O	5:D:669:GLN:HB2	2.21	0.41
5:D:909:ILE:HD11	5:D:913:GLU:HB3	2.02	0.41
5:D:1038:THR:OG1	5:D:1077:ALA:O	2.34	0.41
5:D:1161:GLY:HA2	5:D:1180:VAL:CG2	2.48	0.41
7:F:123:ILE:O	7:F:126:GLY:N	2.53	0.41
7:F:145:LEU:HD22	7:F:228:TYR:CE1	2.55	0.41
7:F:465:ARG:HH12	8:G:26:DT:H2''	1.85	0.41
2:I:191:PHE:HA	2:I:196:PHE:CD2	2.56	0.41
3:A:27:THR:HA	3:A:201:LEU:O	2.21	0.41
4:C:109:ALA:HB1	4:C:110:PRO:CD	2.51	0.41
4:C:200:ARG:HD3	4:C:200:ARG:HA	1.88	0.41
4:C:296:VAL:HG21	4:C:314:ASN:HA	2.02	0.41
4:C:965:GLN:HA	4:C:968:GLU:OE1	2.21	0.41
5:D:126:LEU:HD12	5:D:126:LEU:O	2.20	0.41
5:D:317:THR:HG22	5:D:322:ARG:O	2.21	0.41
5:D:860:ARG:HH11	5:D:861:ASN:H	1.69	0.41
5:D:1162:ILE:HD12	5:D:1162:ILE:HA	1.86	0.41
7:F:160:ASP:HB3	7:F:264:LYS:CG	2.37	0.41
7:F:235:ILE:HB	7:F:245:ALA:HB1	2.02	0.41
1:H:42:DG:C2'	1:H:43:DG:OP2	2.68	0.40
2:I:169:PRO:CD	2:I:208:ARG:HH22	2.33	0.40
2:J:116:THR:HA	2:J:120:GLY:CA	2.51	0.40
2:J:148:TYR:HA	2:J:186:TYR:HE1	1.85	0.40
3:B:92:VAL:HG23	3:B:120:ASP:O	2.20	0.40
3:B:104:LYS:HB3	3:B:140:ILE:CG2	2.52	0.40
4:C:97:ARG:HD2	4:C:97:ARG:HA	1.86	0.40
4:C:179:TYR:HB2	4:C:398:SER:HG	1.85	0.40
4:C:230:PHE:HE2	4:C:292:ILE:HG23	1.86	0.40
4:C:241:LEU:O	4:C:283:LYS:HA	2.20	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:270:THR:O	4:C:273:HIS:HB2	2.20	0.40
4:C:850:ILE:HG22	4:C:850:ILE:O	2.21	0.40
4:C:1146:GLN:NE2	4:C:1150:ASP:OD1	2.54	0.40
5:D:120:LEU:HD21	8:G:10:DG:C5'	2.51	0.40
5:D:825:VAL:HG11	5:D:832:LYS:HB2	2.02	0.40
5:D:841:GLY:CA	5:D:901:ARG:HD3	2.51	0.40
5:D:1247:LYS:O	5:D:1248:ILE:HG13	2.22	0.40
5:D:1281:GLU:O	5:D:1285:VAL:HG22	2.21	0.40
7:F:334:SER:HA	7:F:337:VAL:CG2	2.51	0.40
7:F:494:ILE:O	7:F:498:LEU:HG	2.21	0.40
7:F:592:ALA:O	7:F:595:LEU:HG	2.21	0.40
1:H:47:DC:H5''	1:H:47:DC:H6	1.85	0.40
2:I:46:PRO:HB3	2:I:50:LEU:HD23	2.02	0.40
2:J:139:ILE:O	2:J:142:VAL:HG22	2.21	0.40
3:A:140:ILE:HD11	3:A:142:MET:CE	2.52	0.40
3:A:226:GLU:HG2	3:B:10:LYS:HE2	2.03	0.40
3:B:80:GLU:CD	5:D:569:LEU:HD21	2.46	0.40
3:B:166:ARG:HB3	3:B:170:ARG:CG	2.43	0.40
4:C:579:ALA:C	4:C:580:GLN:HG3	2.45	0.40
4:C:885:GLY:HA2	4:C:917:SER:OG	2.22	0.40
4:C:1118:GLY:O	4:C:1229:TYR:HB2	2.20	0.40
5:D:94:GLN:H	5:D:94:GLN:HG2	1.68	0.40
5:D:996:LYS:HD3	5:D:996:LYS:HA	1.85	0.40
5:D:1081:VAL:HG12	5:D:1086:ASN:C	2.46	0.40
7:F:216:LEU:HD12	7:F:217:ALA:N	2.36	0.40
7:F:308:GLY:O	7:F:355:ILE:HG22	2.21	0.40
7:F:488:LEU:HD13	7:F:488:LEU:HA	1.90	0.40
7:F:600:HIS:CB	7:F:603:ARG:HH21	2.34	0.40
4:C:339:ASN:OD1	4:C:339:ASN:N	2.54	0.40
4:C:582:ASN:HB2	4:C:586:PHE:O	2.21	0.40
4:C:979:LEU:HA	4:C:1002:LEU:CD2	2.51	0.40
5:D:199:GLU:HA	5:D:202:ARG:HG2	2.03	0.40
5:D:889:ASP:O	5:D:1284:ARG:NH2	2.55	0.40
7:F:404:LEU:HD23	7:F:404:LEU:HA	1.83	0.40
7:F:470:MET:SD	7:F:486:ARG:HG3	2.61	0.40
1:H:30:DT:H2''	1:H:31:DT:O5'	2.21	0.40
2:I:41:VAL:CB	2:I:47:PRO:HD3	2.52	0.40
2:I:137:LEU:HD23	2:I:137:LEU:HA	1.98	0.40
2:J:75:ILE:O	2:J:78:TYR:HB3	2.21	0.40
2:J:166:TRP:CZ2	2:J:200:LEU:HD22	2.56	0.40
2:J:204:GLU:HA	2:J:207:MET:HE3	2.02	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:11:PRO:CA	3:A:30:PRO:HD2	2.49	0.40
3:B:190:ALA:O	3:B:198:LEU:HB2	2.21	0.40
4:C:9:LYS:HG3	4:C:1171:ARG:NH1	2.36	0.40
4:C:70:TYR:CZ	4:C:72:SER:HA	2.57	0.40
4:C:275:ARG:O	4:C:279:LYS:HG2	2.21	0.40
4:C:594:VAL:HB	4:C:651:ASP:C	2.46	0.40
5:D:411:ILE:HD13	5:D:411:ILE:HA	1.83	0.40
5:D:821:MET:HE2	5:D:821:MET:HB2	1.81	0.40
5:D:850:LYS:CD	5:D:875:ASN:HD21	2.33	0.40
5:D:884:SER:OG	5:D:886:VAL:HG12	2.22	0.40
5:D:1024:THR:HG22	5:D:1026:PRO:HD3	2.04	0.40
5:D:1069:ALA:O	5:D:1072:LYS:HG3	2.21	0.40
5:D:1164:SER:HA	5:D:1200:GLU:OE2	2.20	0.40
7:F:248:GLU:HA	7:F:251:LYS:HE3	2.02	0.40
7:F:253:SER:O	7:F:256:PHE:HB3	2.21	0.40
7:F:394:TYR:HE1	8:G:26:DT:H3	1.68	0.40
7:F:607:LEU:HA	7:F:607:LEU:HD23	1.77	0.40
2:J:146:LYS:HB3	2:J:151:SER:O	2.21	0.40
3:A:98:VAL:HG12	3:A:99:ILE:H	1.85	0.40
4:C:75:LEU:HD21	4:C:127:ILE:HD11	2.02	0.40
4:C:129:LEU:HD23	4:C:129:LEU:HA	1.90	0.40
4:C:284:LEU:HD12	4:C:285:ILE:N	2.37	0.40
4:C:804:PHE:O	5:D:638:SER:HB2	2.21	0.40
4:C:1257:GLN:HA	4:C:1258:PRO:HD3	1.94	0.40
5:D:615:LYS:HB2	5:D:615:LYS:HE2	1.92	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	I	204/212 (96%)	184 (90%)	19 (9%)	1 (0%)	24 56

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	J	199/212 (94%)	179 (90%)	19 (10%)	1 (0%)	24	56
3	A	228/329 (69%)	202 (89%)	26 (11%)	0	100	100
3	B	222/329 (68%)	191 (86%)	31 (14%)	0	100	100
3	K	63/329 (19%)	58 (92%)	5 (8%)	0	100	100
4	C	1338/1342 (100%)	1152 (86%)	183 (14%)	3 (0%)	43	71
5	D	1333/1407 (95%)	1159 (87%)	174 (13%)	0	100	100
6	E	77/91 (85%)	70 (91%)	6 (8%)	1 (1%)	9	38
7	F	466/613 (76%)	422 (91%)	44 (9%)	0	100	100
All	All	4130/4864 (85%)	3617 (88%)	507 (12%)	6 (0%)	49	78

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	C	200	ARG
2	J	72	SER
4	C	198	ILE
4	C	1164	PHE
2	I	72	SER
6	E	33	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	I	182/187 (97%)	163 (90%)	19 (10%)	7	28
2	J	179/187 (96%)	167 (93%)	12 (7%)	15	42
3	A	198/286 (69%)	177 (89%)	21 (11%)	6	27
3	B	194/286 (68%)	169 (87%)	25 (13%)	4	20
3	K	58/286 (20%)	50 (86%)	8 (14%)	3	18
4	C	1155/1157 (100%)	1009 (87%)	146 (13%)	4	21
5	D	1104/1168 (94%)	978 (89%)	126 (11%)	5	24

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	E	67/75 (89%)	60 (90%)	7 (10%)	7	28
7	F	420/540 (78%)	362 (86%)	58 (14%)	3	18
All	All	3557/4172 (85%)	3135 (88%)	422 (12%)	7	23

All (422) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	10	VAL
2	I	27	ILE
2	I	28	VAL
2	I	29	LEU
2	I	32	LYS
2	I	42	GLU
2	I	49	ASP
2	I	52	ASP
2	I	53	LEU
2	I	68	THR
2	I	98	GLU
2	I	101	LEU
2	I	111	TYR
2	I	118	ILE
2	I	189	ARG
2	I	190	VAL
2	I	192	GLU
2	I	200	LEU
2	I	207	MET
2	J	12	THR
2	J	38	ILE
2	J	106	ILE
2	J	116	THR
2	J	118	ILE
2	J	132	LEU
2	J	137	LEU
2	J	142	VAL
2	J	156	LEU
2	J	158	ASP
2	J	171	LEU
2	J	183	LEU
3	K	254	LEU
3	K	258	ASP
3	K	277	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	K	280	ASP
3	K	281	LEU
3	K	289	LEU
3	K	303	ILE
3	K	318	LEU
3	A	8	PHE
3	A	12	ARG
3	A	13	LEU
3	A	22	THR
3	A	26	VAL
3	A	54	CYS
3	A	61	ILE
3	A	70	THR
3	A	74	VAL
3	A	77	ASP
3	A	96	ASP
3	A	98	VAL
3	A	129	VAL
3	A	143	ARG
3	A	177	TYR
3	A	181	GLU
3	A	192	VAL
3	A	195	ARG
3	A	211	ILE
3	A	212	ASP
3	A	236	ASP
3	B	7	GLU
3	B	9	LEU
3	B	14	VAL
3	B	27	THR
3	B	29	GLU
3	B	33	ARG
3	B	38	THR
3	B	68	TYR
3	B	77	ASP
3	B	78	ILE
3	B	81	ILE
3	B	83	LEU
3	B	90	VAL
3	B	92	VAL
3	B	98	VAL
3	B	111	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	B	120	ASP
3	B	133	LEU
3	B	146	VAL
3	B	162	GLU
3	B	183	ILE
3	B	198	LEU
3	B	203	ILE
3	B	214	GLU
3	B	222	THR
4	C	6	THR
4	C	8	LYS
4	C	9	LYS
4	C	21	VAL
4	C	30	ILE
4	C	32	LEU
4	C	40	GLU
4	C	74	ARG
4	C	79	VAL
4	C	91	THR
4	C	111	GLU
4	C	113	THR
4	C	122	VAL
4	C	135	THR
4	C	141	THR
4	C	161	LYS
4	C	177	ILE
4	C	194	LEU
4	C	197	ARG
4	C	199	ASP
4	C	216	THR
4	C	231	GLU
4	C	263	VAL
4	C	264	GLU
4	C	274	ILE
4	C	279	LYS
4	C	281	ASP
4	C	285	ILE
4	C	286	GLU
4	C	287	VAL
4	C	290	GLU
4	C	299	LYS
4	C	320	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	C	331	LYS
4	C	335	THR
4	C	338	THR
4	C	347	ILE
4	C	364	VAL
4	C	366	ILE
4	C	377	THR
4	C	384	LEU
4	C	392	GLU
4	C	393	ASP
4	C	397	LEU
4	C	419	ILE
4	C	422	LYS
4	C	423	ASP
4	C	424	ASP
4	C	439	LYS
4	C	441	GLU
4	C	448	LEU
4	C	465	ARG
4	C	466	VAL
4	C	468	LEU
4	C	469	VAL
4	C	471	VAL
4	C	472	GLU
4	C	475	VAL
4	C	492	MET
4	C	522	SER
4	C	524	ILE
4	C	538	LEU
4	C	595	THR
4	C	598	VAL
4	C	615	VAL
4	C	622	ASN
4	C	626	GLU
4	C	632	ASP
4	C	659	GLN
4	C	663	VAL
4	C	672	GLU
4	C	681	MET
4	C	687	ARG
4	C	694	ARG
4	C	699	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	C	702	THR
4	C	704	MET
4	C	724	VAL
4	C	736	VAL
4	C	748	ILE
4	C	749	ASP
4	C	750	ILE
4	C	754	THR
4	C	759	SER
4	C	765	ILE
4	C	781	ASP
4	C	790	ASP
4	C	802	VAL
4	C	827	ARG
4	C	835	GLU
4	C	841	ARG
4	C	843	THR
4	C	844	LYS
4	C	850	ILE
4	C	865	LEU
4	C	877	VAL
4	C	881	ASP
4	C	882	ILE
4	C	895	LEU
4	C	905	ILE
4	C	915	ASP
4	C	919	ARG
4	C	924	VAL
4	C	935	THR
4	C	946	LEU
4	C	949	GLU
4	C	966	ILE
4	C	978	VAL
4	C	991	LYS
4	C	995	ASP
4	C	1017	GLN
4	C	1018	TYR
4	C	1019	ASP
4	C	1026	GLU
4	C	1033	ARG
4	C	1041	ASP
4	C	1046	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	C	1047	LEU
4	C	1057	LYS
4	C	1058	ARG
4	C	1060	ILE
4	C	1069	ARG
4	C	1096	ILE
4	C	1128	ILE
4	C	1134	GLN
4	C	1155	VAL
4	C	1158	LYS
4	C	1174	GLU
4	C	1198	LEU
4	C	1203	ASP
4	C	1217	THR
4	C	1220	GLN
4	C	1222	GLU
4	C	1227	VAL
4	C	1246	ARG
4	C	1254	VAL
4	C	1259	LEU
4	C	1262	LYS
4	C	1268	GLN
4	C	1274	GLU
4	C	1289	GLU
4	C	1292	THR
4	C	1302	THR
4	C	1316	GLU
4	C	1321	GLU
4	C	1337	ILE
5	D	24	LEU
5	D	39	LYS
5	D	46	TYR
5	D	48	THR
5	D	56	LEU
5	D	81	ARG
5	D	86	GLU
5	D	109	SER
5	D	111	THR
5	D	114	ILE
5	D	134	ASP
5	D	146	VAL
5	D	152	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	D	172	PHE
5	D	193	ASP
5	D	194	LEU
5	D	209	ASN
5	D	218	THR
5	D	228	VAL
5	D	232	ASN
5	D	237	MET
5	D	244	VAL
5	D	255	LEU
5	D	292	VAL
5	D	300	GLN
5	D	306	LEU
5	D	316	ILE
5	D	332	LYS
5	D	347	VAL
5	D	350	SER
5	D	353	SER
5	D	368	LEU
5	D	387	LEU
5	D	401	VAL
5	D	404	GLU
5	D	413	ASP
5	D	424	ASN
5	D	431	ARG
5	D	434	ILE
5	D	449	LEU
5	D	460	ASP
5	D	473	THR
5	D	489	ASN
5	D	506	VAL
5	D	526	VAL
5	D	527	LEU
5	D	528	THR
5	D	531	LYS
5	D	545	HIS
5	D	548	VAL
5	D	558	ASP
5	D	563	LEU
5	D	573	THR
5	D	594	GLN
5	D	617	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	D	618	VAL
5	D	619	ILE
5	D	634	ARG
5	D	654	ILE
5	D	661	VAL
5	D	666	GLU
5	D	674	THR
5	D	678	ARG
5	D	680	ASN
5	D	685	ILE
5	D	705	THR
5	D	707	ILE
5	D	710	ASP
5	D	713	GLU
5	D	722	ILE
5	D	724	MET
5	D	746	LEU
5	D	751	ASP
5	D	759	ILE
5	D	760	THR
5	D	765	GLU
5	D	769	VAL
5	D	797	THR
5	D	806	ASP
5	D	847	ASP
5	D	849	LEU
5	D	857	LEU
5	D	863	LEU
5	D	876	SER
5	D	905	ARG
5	D	907	HIS
5	D	909	ILE
5	D	918	ILE
5	D	925	GLU
5	D	929	GLN
5	D	986	ASP
5	D	999	TYR
5	D	1020	TRP
5	D	1023	HIS
5	D	1027	VAL
5	D	1034	PHE
5	D	1038	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	D	1045	THR
5	D	1052	GLU
5	D	1056	LEU
5	D	1081	VAL
5	D	1082	ASP
5	D	1156	LEU
5	D	1167	LYS
5	D	1180	VAL
5	D	1187	GLU
5	D	1200	GLU
5	D	1231	ARG
5	D	1234	VAL
5	D	1235	ASN
5	D	1246	VAL
5	D	1250	ASP
5	D	1253	ILE
5	D	1266	ILE
5	D	1275	LEU
5	D	1307	LEU
5	D	1309	ILE
5	D	1314	LEU
5	D	1317	GLU
5	D	1320	ILE
5	D	1325	PHE
5	D	1333	THR
5	D	1342	ASP
5	D	1351	VAL
5	D	1353	VAL
5	D	1365	TYR
6	E	4	VAL
6	E	39	VAL
6	E	41	GLU
6	E	46	THR
6	E	56	GLU
6	E	66	VAL
6	E	68	GLU
7	F	90	GLU
7	F	127	ILE
7	F	131	GLN
7	F	151	VAL
7	F	152	GLU
7	F	158	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	F	160	ASP
7	F	216	LEU
7	F	225	ARG
7	F	229	VAL
7	F	232	ARG
7	F	246	GLN
7	F	250	LEU
7	F	252	LEU
7	F	255	VAL
7	F	265	GLN
7	F	270	VAL
7	F	278	ASP
7	F	290	LEU
7	F	293	GLU
7	F	299	LYS
7	F	301	ASN
7	F	316	PHE
7	F	332	ASP
7	F	333	VAL
7	F	341	LEU
7	F	342	GLN
7	F	359	LYS
7	F	361	ILE
7	F	362	ASN
7	F	379	MET
7	F	384	LEU
7	F	390	ILE
7	F	405	ILE
7	F	412	LEU
7	F	429	THR
7	F	433	TRP
7	F	442	SER
7	F	446	GLN
7	F	452	ILE
7	F	472	GLN
7	F	488	LEU
7	F	489	MET
7	F	525	ASP
7	F	530	LEU
7	F	533	ASP
7	F	537	THR
7	F	540	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	F	547	VAL
7	F	551	LEU
7	F	554	ARG
7	F	558	VAL
7	F	566	ASP
7	F	573	LEU
7	F	579	GLN
7	F	589	GLN
7	F	591	GLU
7	F	604	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (54) such sidechains are listed below:

Mol	Chain	Res	Type
2	I	23	HIS
2	I	24	GLN
2	J	115	ASN
3	K	283	GLN
3	A	147	GLN
3	A	194	GLN
3	A	208	ASN
3	B	37	HIS
3	B	93	GLN
3	B	128	HIS
4	C	120	GLN
4	C	139	ASN
4	C	219	GLN
4	C	314	ASN
4	C	327	GLN
4	C	463	GLN
4	C	490	GLN
4	C	658	GLN
4	C	673	HIS
4	C	808	ASN
4	C	834	GLN
4	C	1008	GLN
4	C	1017	GLN
4	C	1023	HIS
4	C	1111	GLN
4	C	1220	GLN
4	C	1264	GLN
4	C	1268	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	C	1336	ASN
5	D	186	GLN
5	D	229	GLN
5	D	294	ASN
5	D	309	ASN
5	D	419	HIS
5	D	495	ASN
5	D	560	ASN
5	D	594	GLN
5	D	669	GLN
5	D	720	ASN
5	D	867	GLN
5	D	875	ASN
5	D	968	ASN
5	D	1010	GLN
5	D	1197	ASN
5	D	1235	ASN
6	E	31	GLN
6	E	75	GLN
7	F	128	ASN
7	F	131	GLN
7	F	258	GLN
7	F	283	GLN
7	F	362	ASN
7	F	455	HIS
7	F	464	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

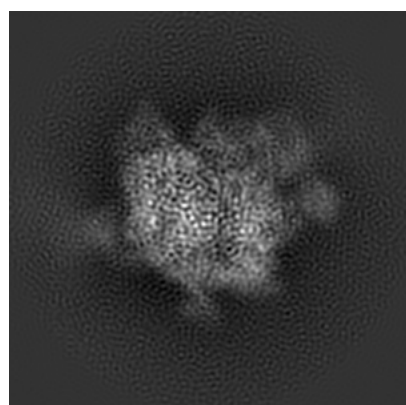
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30307. These allow visual inspection of the internal detail of the map and identification of artifacts.

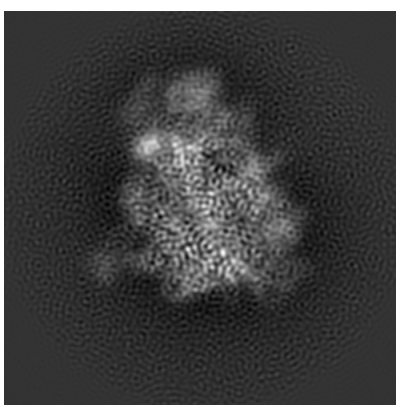
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

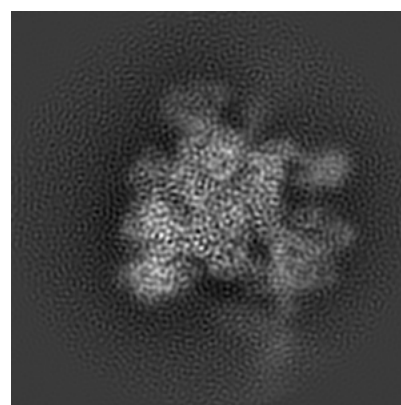
6.1.1 Primary map



X



Y

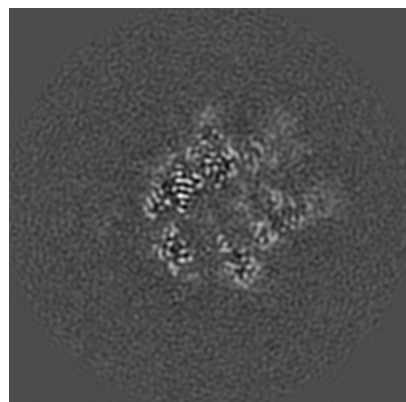


Z

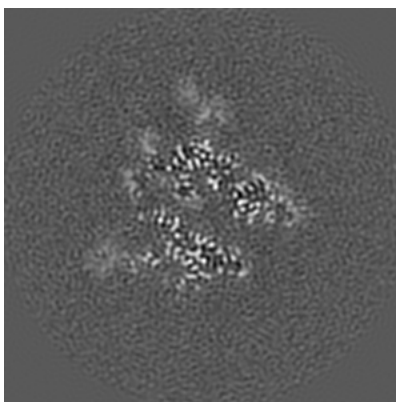
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

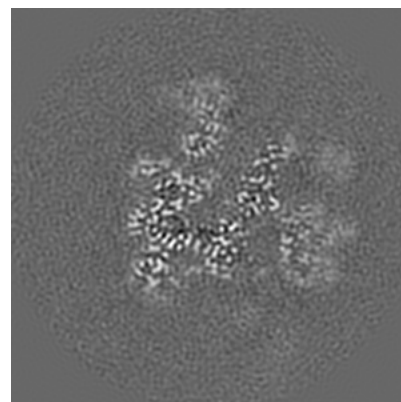
6.2.1 Primary map



X Index: 100



Y Index: 100

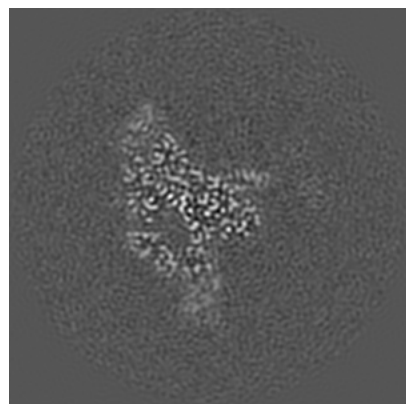


Z Index: 100

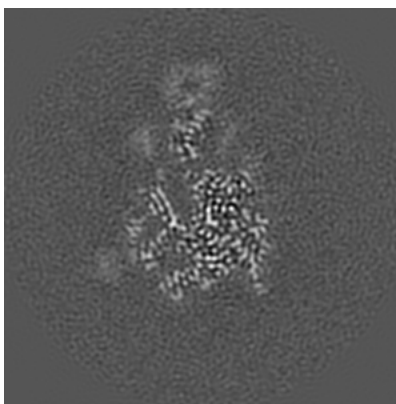
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

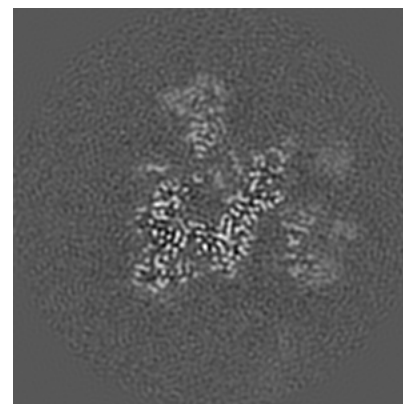
6.3.1 Primary map



X Index: 74



Y Index: 87

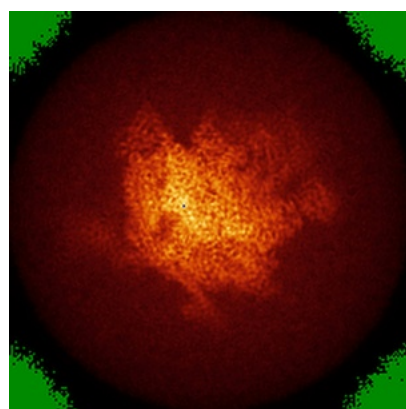


Z Index: 103

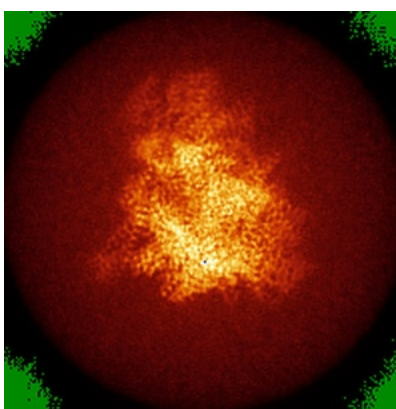
The images above show the largest variance slices of the map in three orthogonal directions.

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

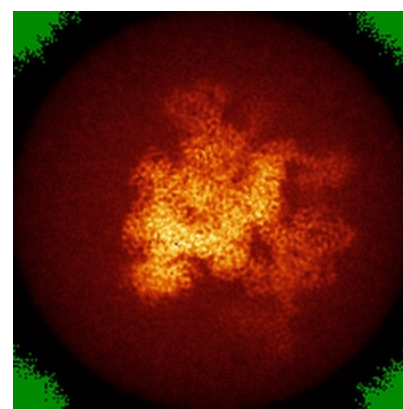
6.4.1 Primary map



X



Y

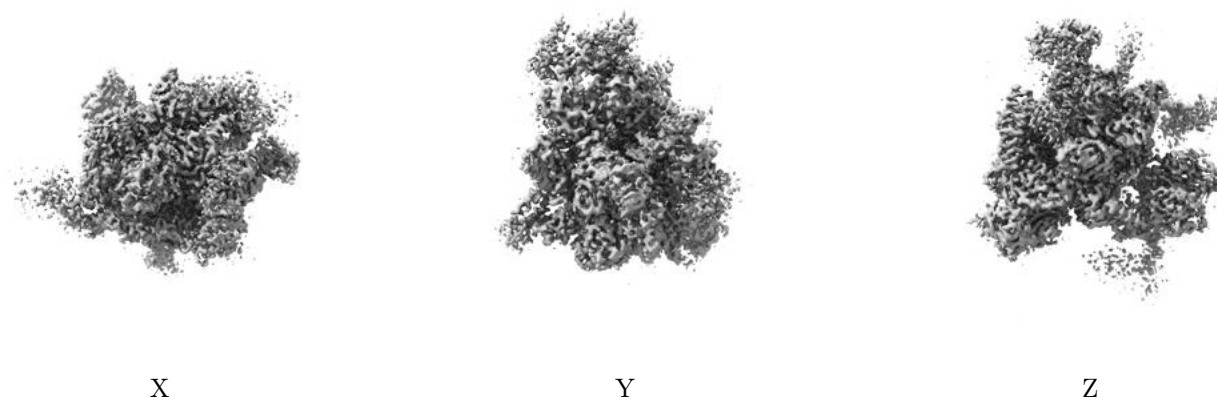


Z

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 0.026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

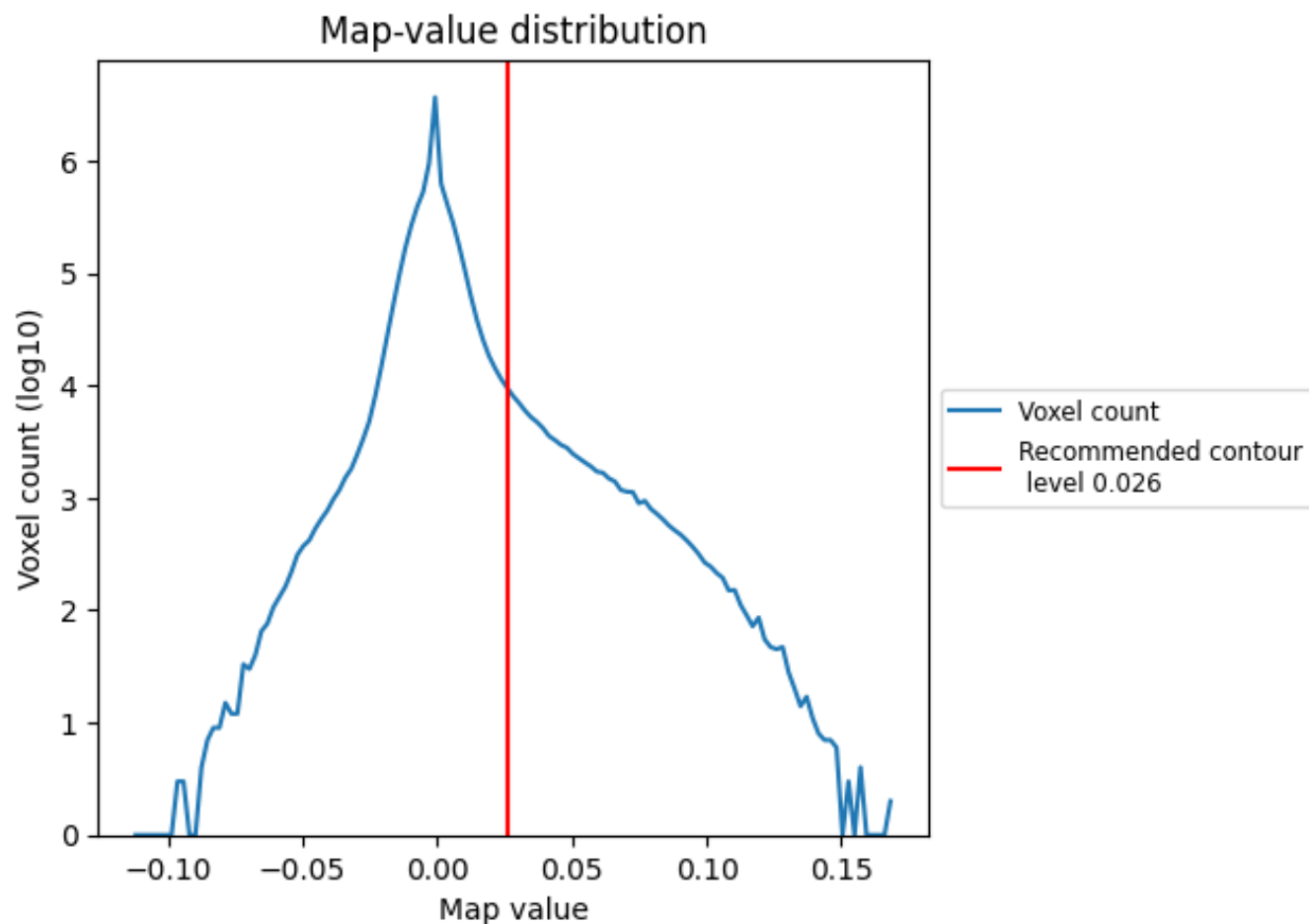
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

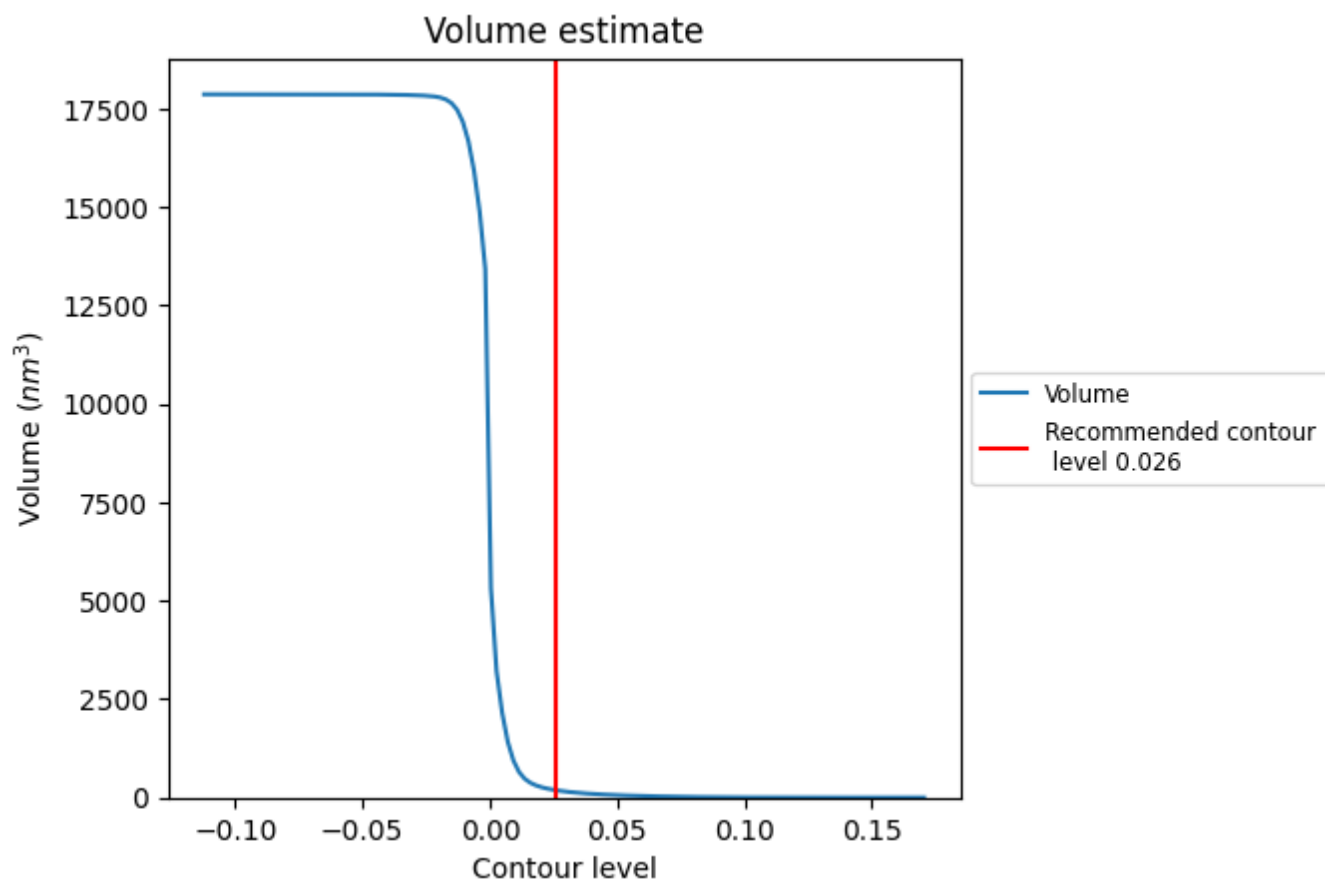
This section contains the results of statistical analysis of the map.

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.

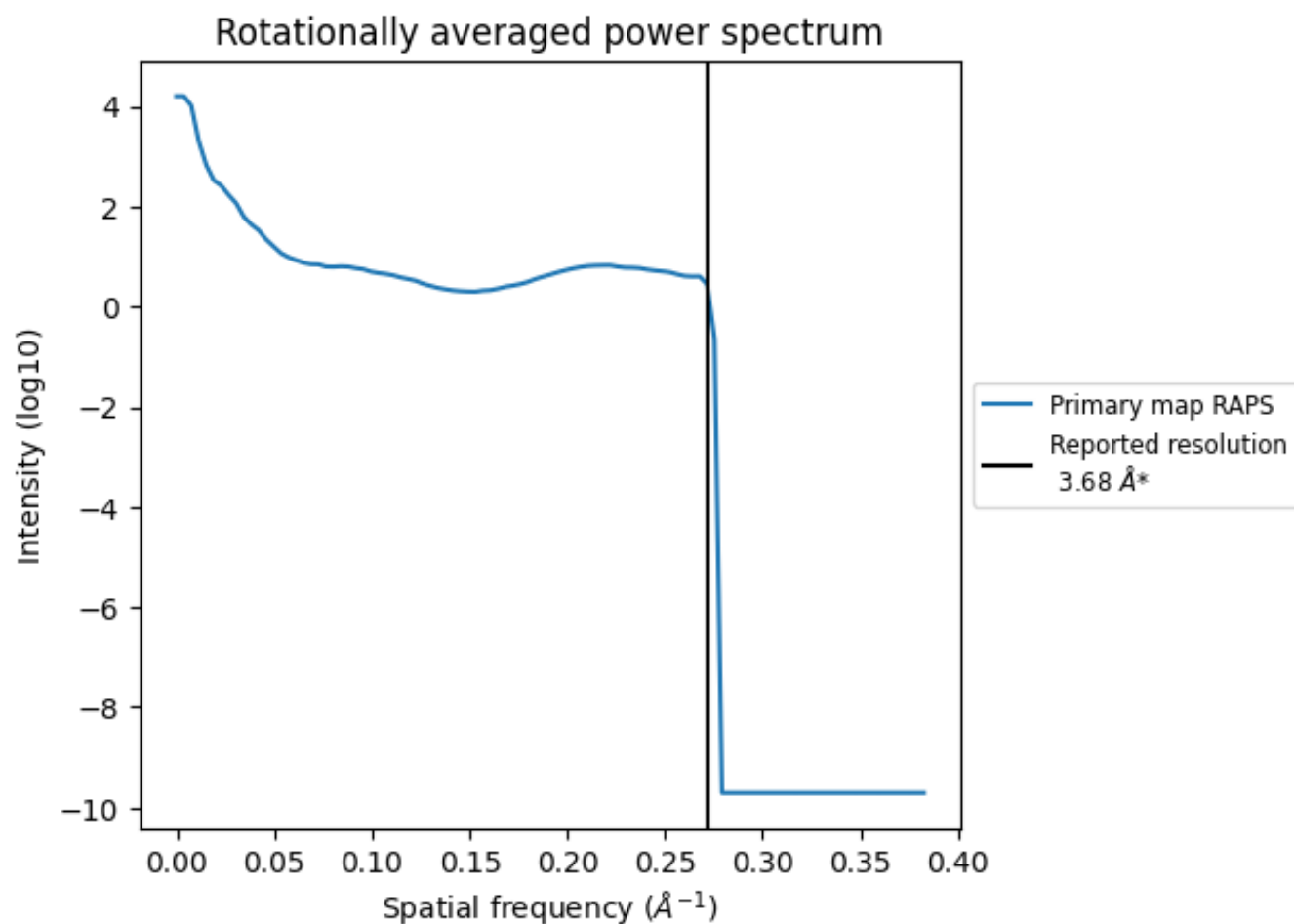
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 186 nm³; this corresponds to an approximate mass of 168 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 0.272 Å⁻¹

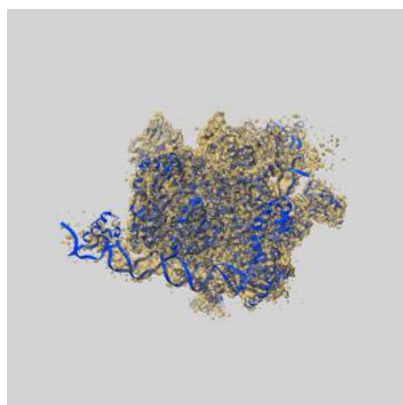
8 Fourier-Shell correlation

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

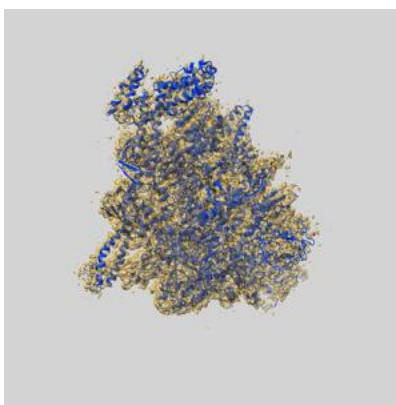
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30307 and PDB model 7C97. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

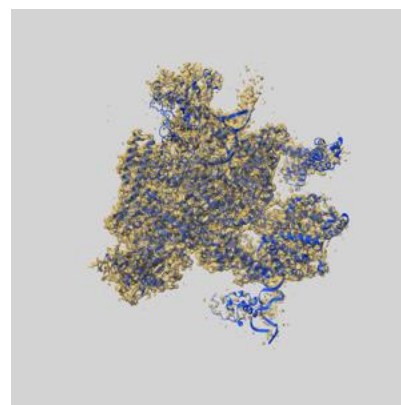
9.1 Map-model overlay [i](#)



X



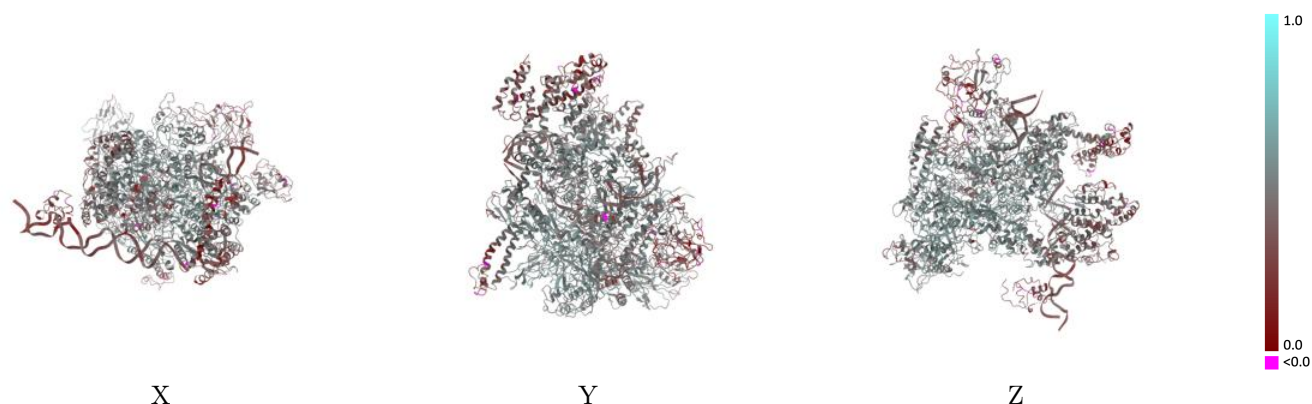
Y



Z

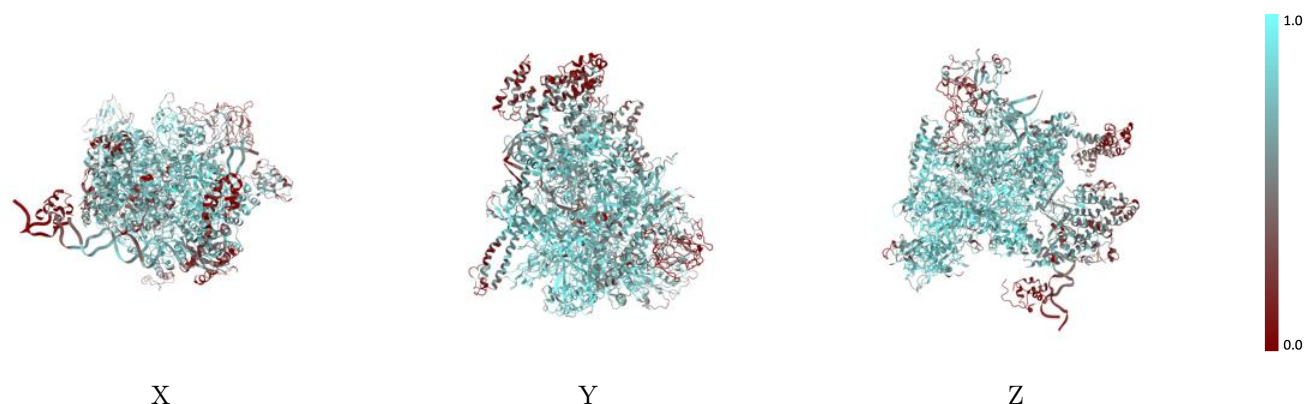
The images above show the 3D surface view of the map at the recommended contour level 0.026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



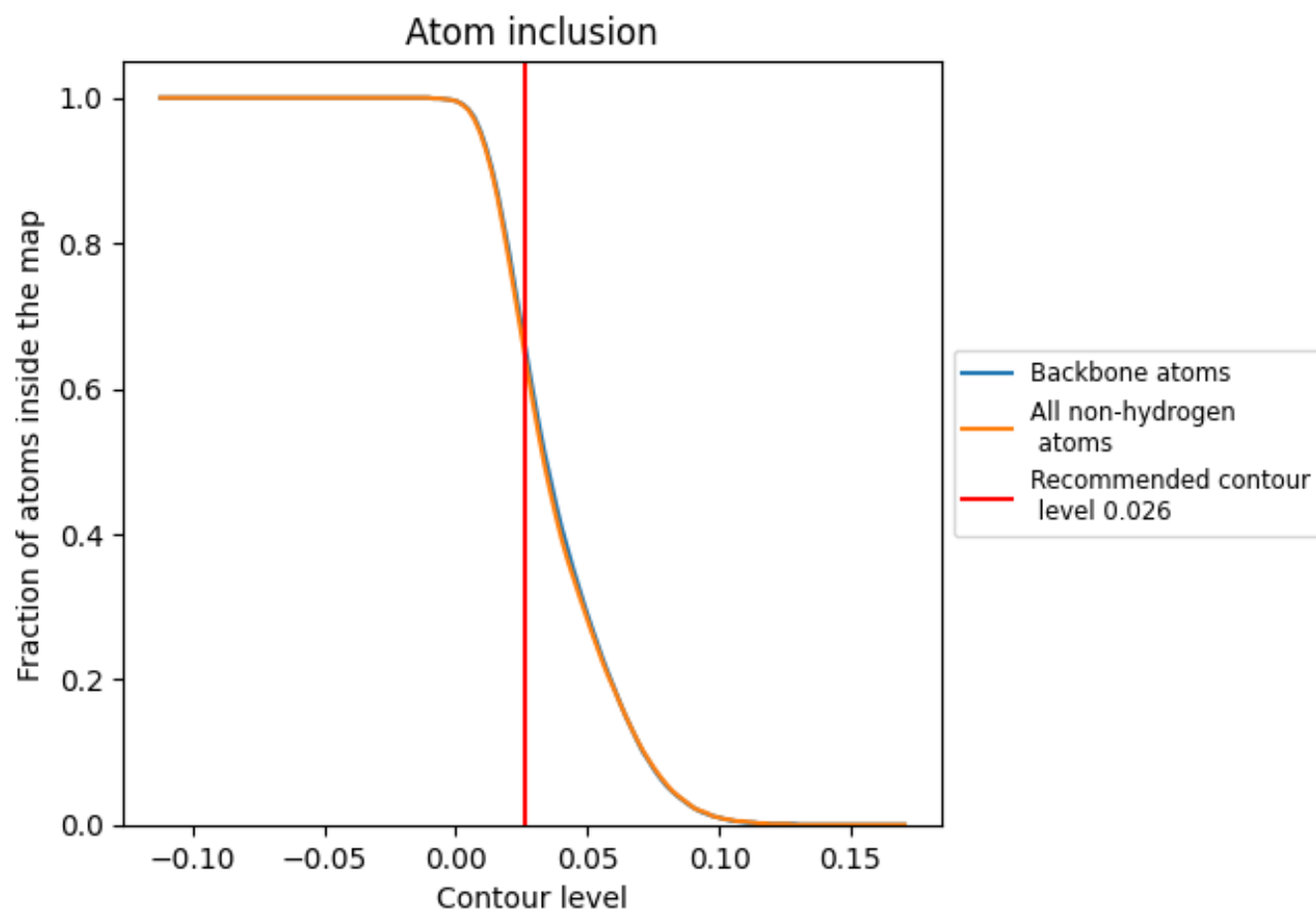
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.026).

9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 65% 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 (0.026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6510	 0.4610
A	 0.7700	 0.5210
B	 0.6850	 0.4780
C	 0.7430	 0.4990
D	 0.6900	 0.4800
E	 0.7330	 0.5020
F	 0.5090	 0.4020
G	 0.5280	 0.3400
H	 0.4940	 0.3570
I	 0.5170	 0.4190
J	 0.5270	 0.4150
K	 0.0630	 0.2430

