



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 09:46 AM UTC

PDB ID : 6PSR / pdb_00006psr
EMDB ID : EMD-20461
Title : Escherichia coli RNA polymerase promoter unwinding intermediate (TRPi1)
with TraR and rpsT P2 promoter
Authors : Chen, J.; Chiu, C.E.; Campbell, E.A.; Darst, S.A.
Deposited on : 2019-07-13
Resolution : 3.40 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:

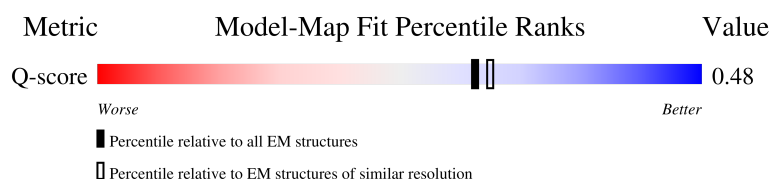
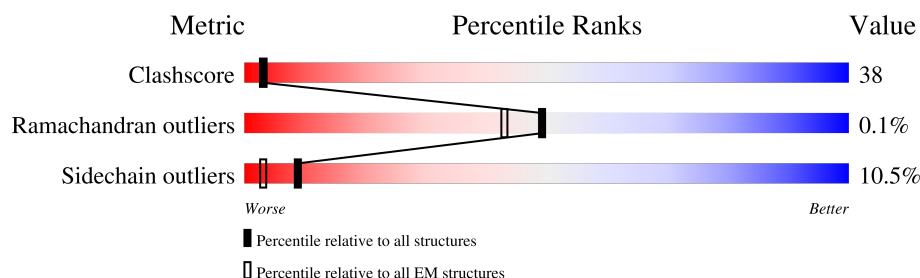
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	G	329	
1	H	329	
1	M	329	
2	I	1342	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	J	1430	10% 38% 50% 6% 6%
4	K	91	31% 46% 5% 18%
5	L	616	13% 32% 53% • 11%
6	N	72	51% 44% •
7	O	85	9% 33% 58%
8	P	85	• 39% 59%

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 32342 atoms, of which 156 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	G	230	Total	C	N	O	S	0	0
			1771	1106	314	345	6		
1	H	219	Total	C	N	O	S	0	0
			1678	1048	295	329	6		
1	M	73	Total	C	N	O	S	0	0
			572	362	100	108	2		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	1340	Total	C	N	O	S	0	0
			10559	6627	1841	2048	43		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	1345	Total	C	N	O	S	0	0
			10466	6577	1867	1972	50		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	1	VAL	-	expression tag	UNP P0A8T7
J	1408	LEU	-	expression tag	UNP P0A8T7
J	1409	GLU	-	expression tag	UNP P0A8T7
J	1410	LEU	-	expression tag	UNP P0A8T7
J	1411	GLU	-	expression tag	UNP P0A8T7
J	1412	VAL	-	expression tag	UNP P0A8T7
J	1413	LEU	-	expression tag	UNP P0A8T7
J	1414	PHE	-	expression tag	UNP P0A8T7
J	1415	GLN	-	expression tag	UNP P0A8T7
J	1416	GLY	-	expression tag	UNP P0A8T7
J	1417	PRO	-	expression tag	UNP P0A8T7

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
J	1418	SER	-	expression tag	UNP P0A8T7
J	1419	SER	-	expression tag	UNP P0A8T7
J	1420	GLY	-	expression tag	UNP P0A8T7
J	1421	HIS	-	expression tag	UNP P0A8T7
J	1422	HIS	-	expression tag	UNP P0A8T7
J	1423	HIS	-	expression tag	UNP P0A8T7
J	1424	HIS	-	expression tag	UNP P0A8T7
J	1425	HIS	-	expression tag	UNP P0A8T7
J	1426	HIS	-	expression tag	UNP P0A8T7
J	1427	HIS	-	expression tag	UNP P0A8T7
J	1428	HIS	-	expression tag	UNP P0A8T7
J	1429	HIS	-	expression tag	UNP P0A8T7
J	1430	HIS	-	expression tag	UNP P0A8T7

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	K	75	Total	C	N	O	S	0	0
			600	365	114	120	1		

- Molecule 5 is a protein called RNA polymerase sigma factor RpoD.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L	548	Total	C	N	O	S	0	0
			4407	2754	771	855	27		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	-2	SER	-	expression tag	UNP Q0P6L9
L	-1	GLU	-	expression tag	UNP Q0P6L9
L	0	PHE	-	expression tag	UNP Q0P6L9

- Molecule 6 is a protein called Protein TraR.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	72	Total	C	N	O	S	0	0
			565	350	102	108	5		

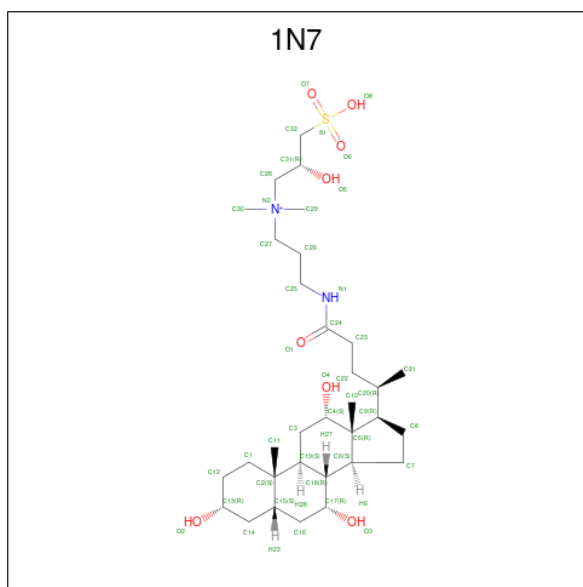
- Molecule 7 is a DNA chain called DNA (85-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	O	36	Total	C	N	O	P	0	0
			746	353	154	203	36		

- Molecule 8 is a DNA chain called DNA (85-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	35	Total	C	N	O	P	0	0
			710	342	111	222	35		

- Molecule 9 is CHAPSO (CCD ID: 1N7) (formula: C₃₂H₅₉N₂O₈S).



Mol	Chain	Residues	Atoms				AltConf
9	I	1	Total	C	H	O	0
			66	24	39	3	
9	J	1	Total	C	H	O	0
			66	24	39	3	
9	J	1	Total	C	H	O	0
			66	24	39	3	
9	L	1	Total	C	H	O	0
			66	24	39	3	

- Molecule 10 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
10	J	1	Total	Mg	0
			1	1	

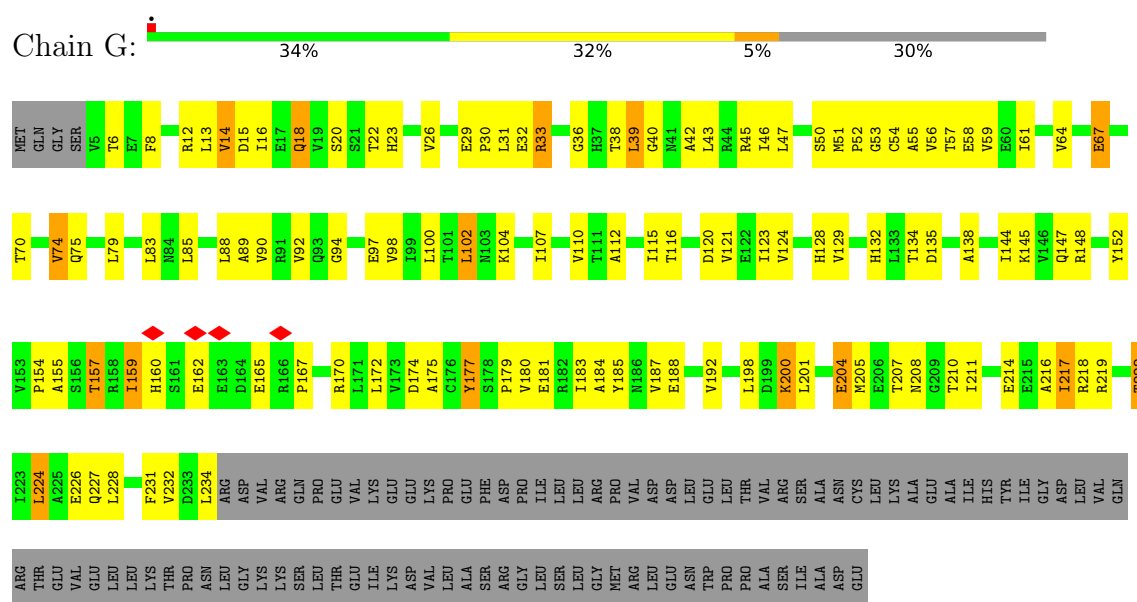
- Molecule 11 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
11	J	2	Total 2	Zn 2	0
11	N	1	Total 1	Zn 1	0

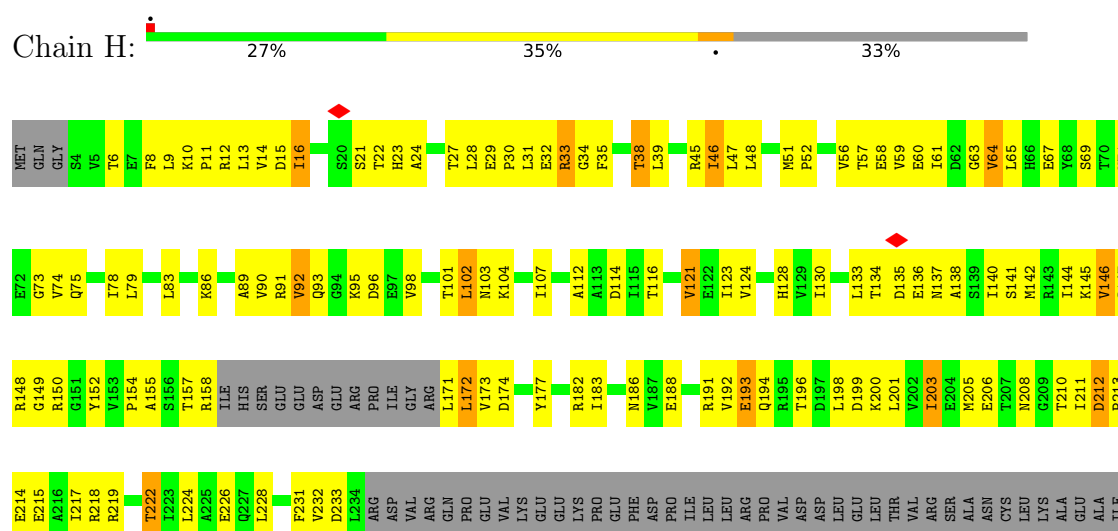
3 Residue-property plots

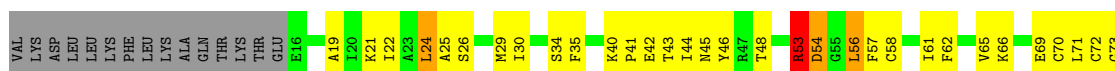
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

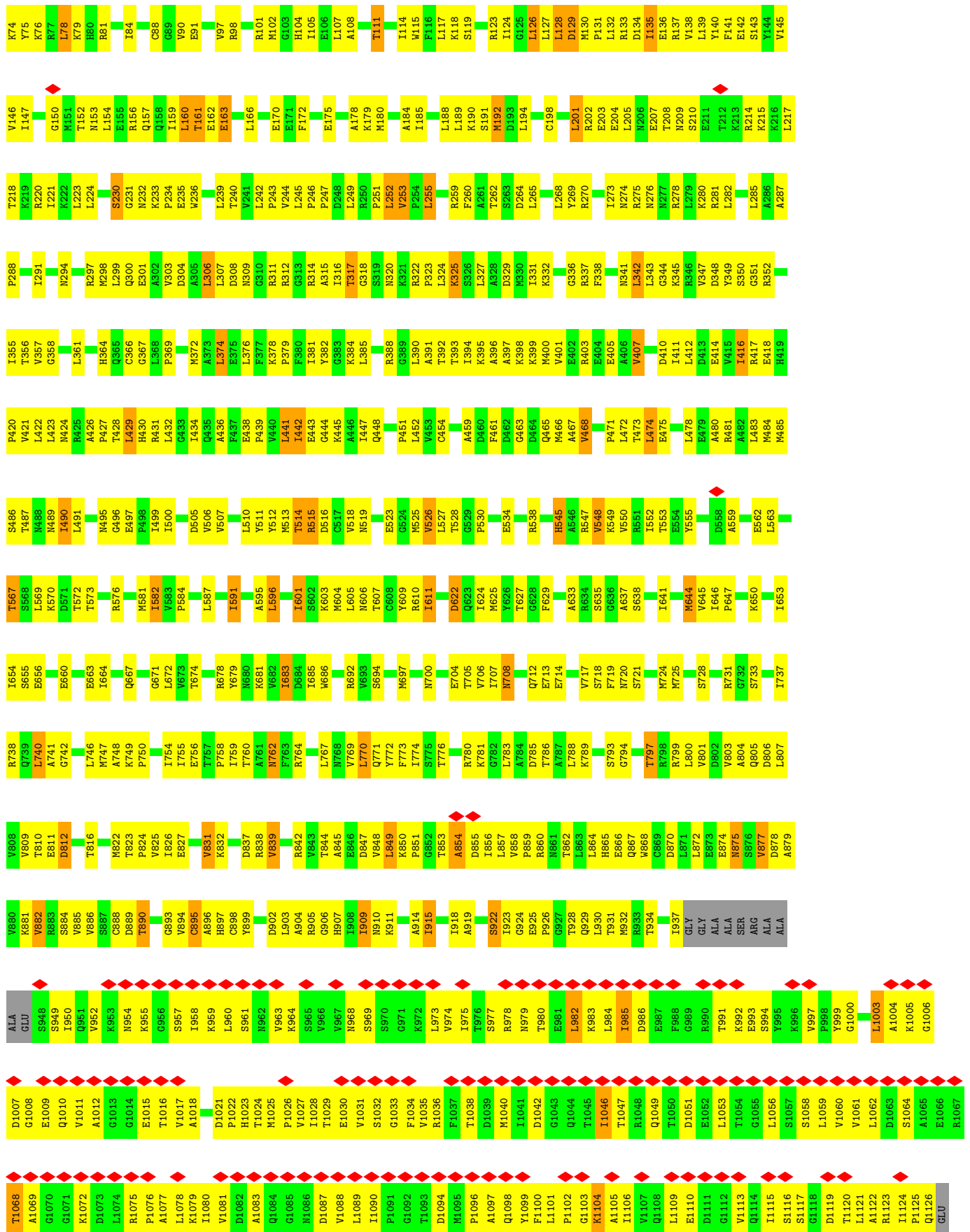
• Molecule 1: DNA-directed RNA polymerase subunit alpha

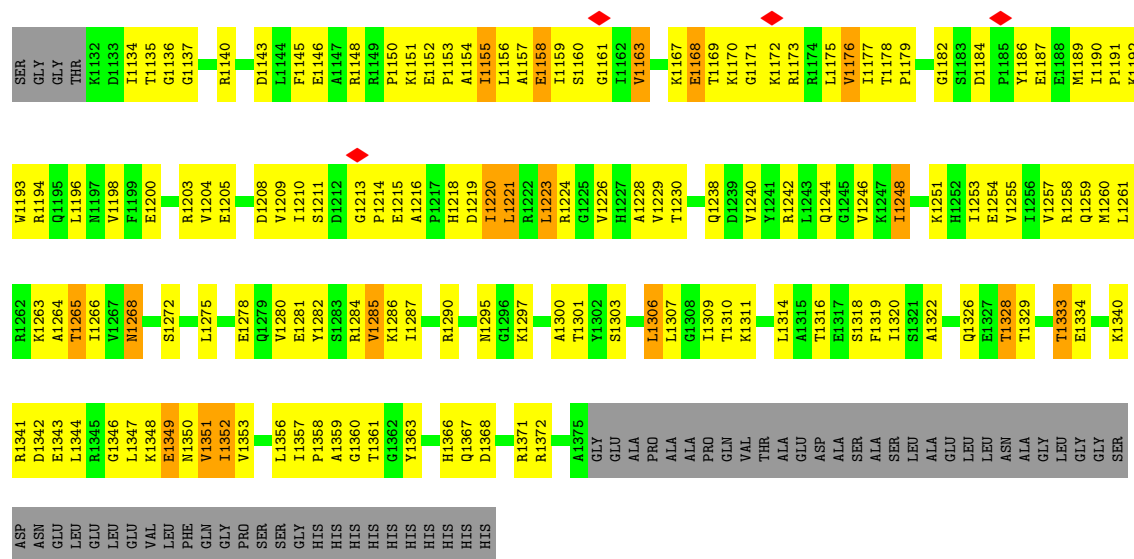


• Molecule 1: DNA-directed RNA polymerase subunit alpha

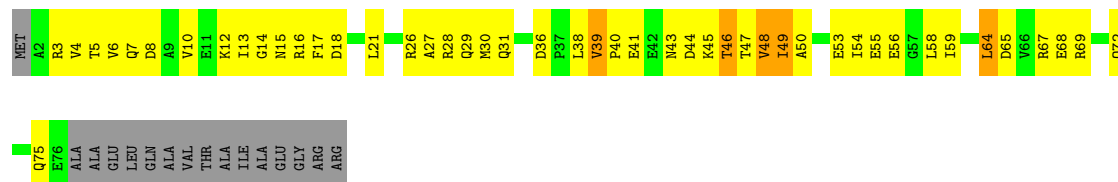




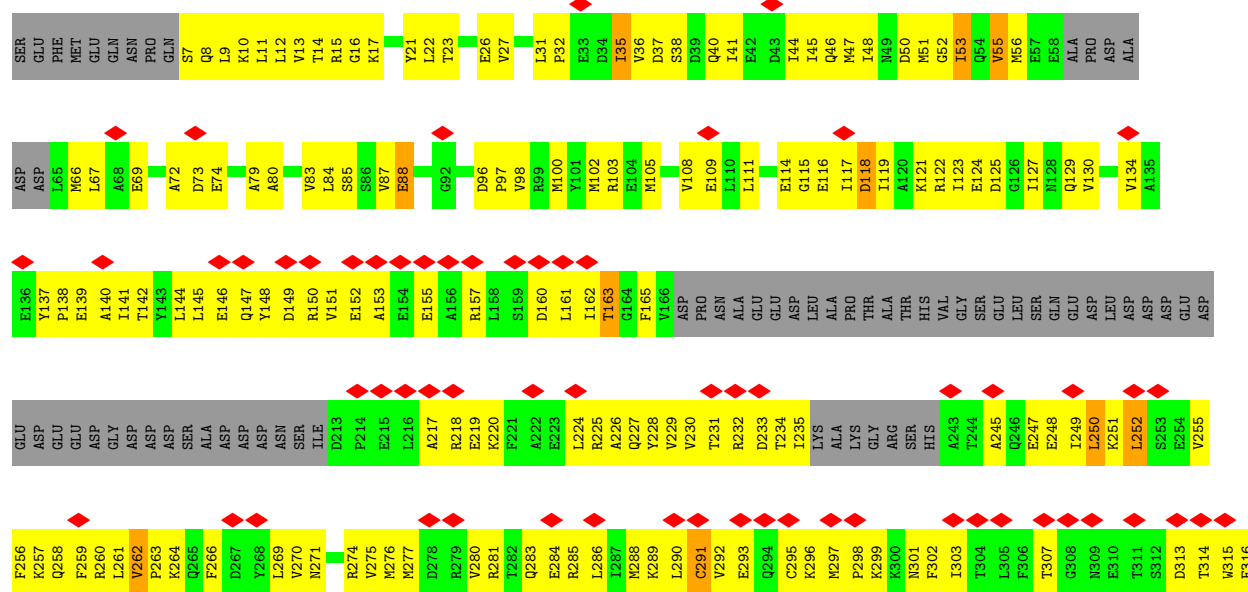


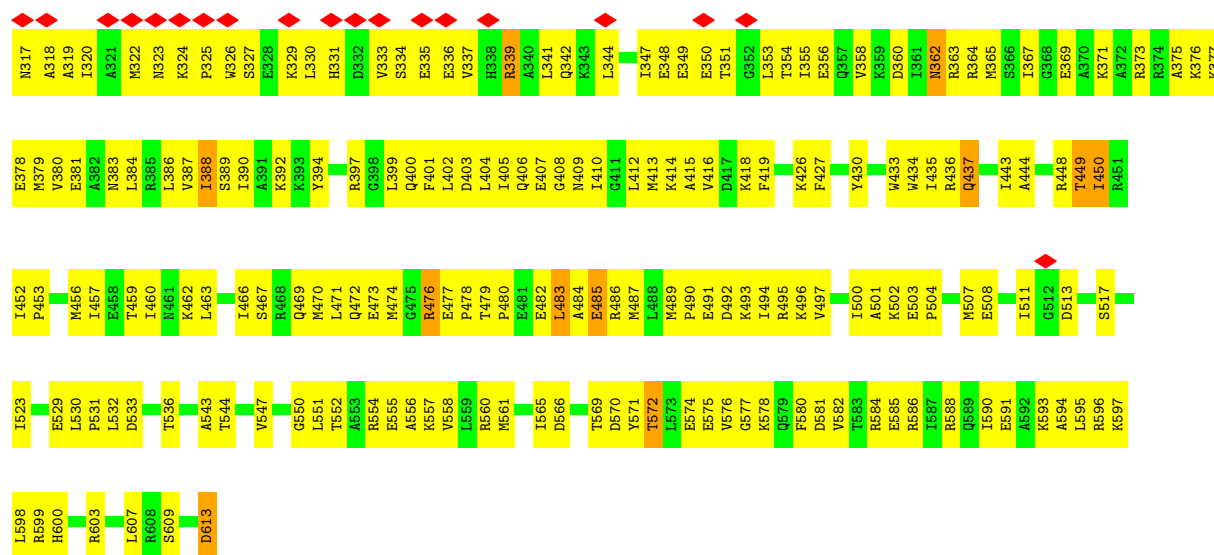


- Molecule 4: DNA-directed RNA polymerase subunit omega



- Molecule 5: RNA polymerase sigma factor RpoD





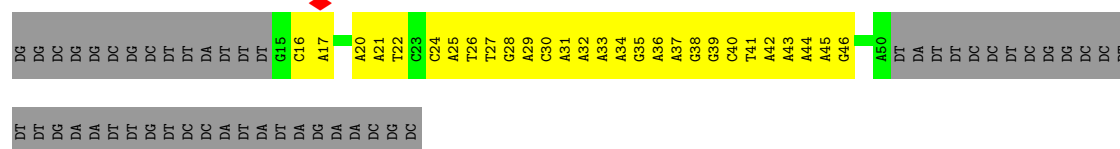
• Molecule 6: Protein TraR

Chain N: 51% 44%



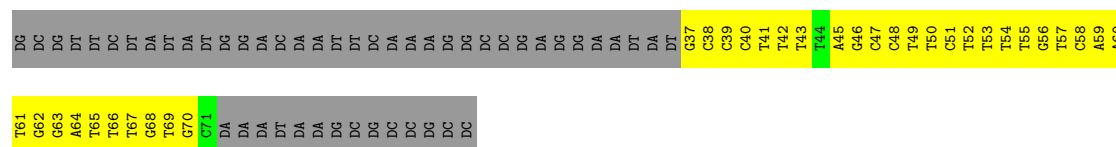
• Molecule 7: DNA (85-MER)

Chain O: 9% 33% 58%



• Molecule 8: DNA (85-MER)

Chain P: 39% 59%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	98324	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 ($e^-/\text{\AA}^2$)	80	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	0.223	Depositor
Minimum map value	-0.124	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	332.8, 332.8, 332.8	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3, 1.3, 1.3	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, 1N7

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	G	0.38	0/1793	0.55	0/2432
1	H	0.35	0/1697	0.54	0/2301
1	M	0.17	0/579	0.48	0/784
2	I	0.38	0/10728	0.55	2/14477 (0.0%)
3	J	0.36	0/10625	0.55	3/14345 (0.0%)
4	K	0.28	0/602	0.51	0/810
5	L	0.23	0/4461	0.51	0/6004
6	N	0.32	0/575	0.48	0/778
7	O	0.25	0/842	0.41	0/1297
8	P	0.25	0/790	0.47	0/1217
All	All	0.34	0/32692	0.53	5/44445 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	I	0	2
3	J	0	1
All	All	0	3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	9	LYS	N-CA-C	-6.20	104.78	112.72
3	J	53	ARG	CA-C-N	6.00	133.00	121.54
3	J	53	ARG	C-N-CA	6.00	133.00	121.54
3	J	839	VAL	N-CA-C	-5.91	107.37	113.10

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	I	162	GLY	N-CA-C	5.71	116.93	111.67

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	I	519	ASN	Peptide
2	I	897	PRO	Peptide
3	J	53	ARG	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	1771	0	1799	112	0
1	H	1678	0	1698	129	0
1	M	572	0	602	85	0
2	I	10559	0	10577	784	0
3	J	10466	0	10689	886	0
4	K	600	0	607	51	0
5	L	4407	0	4432	427	0
6	N	565	0	545	35	0
7	O	746	0	401	42	0
8	P	710	0	402	52	0
9	I	27	39	39	4	0
9	J	54	78	75	9	0
9	L	27	39	38	4	0
10	J	1	0	0	0	0
11	J	2	0	0	0	0
11	N	1	0	0	0	0
All	All	32186	156	31904	2439	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 38.

All (2439) 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)
9:L:701:1N7:C19	9:L:701:1N7:C3	1.82	1.58
9:I:1401:1N7:C3	9:I:1401:1N7:C19	1.82	1.56
9:J:1505:1N7:C3	9:J:1505:1N7:C19	1.81	1.54
9:J:1504:1N7:C19	9:J:1504:1N7:C3	1.84	1.50
3:J:1179:PRO:HD2	3:J:1184:ASP:HA	1.34	1.08
3:J:1025:MET:HB3	3:J:1124:ILE:HB	1.35	1.06
2:I:1002:LEU:HD21	2:I:1008:GLN:HB2	1.37	1.05
3:J:797:THR:HG22	3:J:924:GLY:HA3	1.39	1.04
2:I:985:GLU:HB2	2:I:989:LEU:HB2	1.36	1.04
5:L:45:ILE:HD11	5:L:55:VAL:HG11	1.36	1.03
3:J:1089:LEU:HA	3:J:1096:PRO:HA	1.39	1.01
5:L:37:ASP:HB2	5:L:40:GLN:HG2	1.37	1.01
5:L:394:TYR:HB3	5:L:397:ARG:HG3	1.43	1.00
2:I:745:GLU:HA	2:I:1017:GLN:HG2	1.43	0.99
2:I:207:THR:HA	2:I:210:LEU:HD12	1.42	0.99
3:J:1078:LEU:HD22	3:J:1121:LEU:HD11	1.44	0.98
5:L:105:MET:HE3	5:L:388:ILE:HD12	1.43	0.97
5:L:364:ARG:HA	5:L:367:ILE:HD12	1.43	0.97
2:I:839:VAL:HG12	2:I:1049:ILE:HG12	1.46	0.97
2:I:372:PRO:HG2	5:L:36:VAL:HG12	1.46	0.96
5:L:145:LEU:HD13	5:L:225:ARG:HG3	1.47	0.96
3:J:201:LEU:HD11	3:J:220:ARG:HD3	1.48	0.95
1:M:278:ILE:HG23	1:M:281:LEU:HD23	1.47	0.94
5:L:326:TRP:HA	5:L:329:LYS:HE2	1.49	0.94
2:I:254:ASP:HA	2:I:263:VAL:O	1.68	0.93
2:I:738:GLU:HA	2:I:741:MET:HE3	1.47	0.92
2:I:1243:MET:HE3	3:J:445:LYS:HD2	1.50	0.92
2:I:170:VAL:HG23	6:N:72:TYR:HB2	1.47	0.92
5:L:290:LEU:HB3	5:L:333:VAL:HG11	1.51	0.92
5:L:145:LEU:HB3	5:L:225:ARG:HD3	1.53	0.91
3:J:1198:VAL:HG11	3:J:1210:ILE:HD12	1.49	0.91
3:J:975:ILE:HD13	3:J:980:THR:HB	1.50	0.91
3:J:79:LYS:HB2	5:L:569:THR:HB	1.53	0.91
3:J:338:PHE:HA	3:J:342:LEU:HD22	1.53	0.90
3:J:1038:THR:O	3:J:1077:ALA:HB3	1.72	0.90
3:J:1061:VAL:HG21	3:J:1101:LEU:HG	1.51	0.90
3:J:1081:VAL:HG12	3:J:1087:ASP:HA	1.52	0.90
5:L:456:MET:HE3	5:L:497:VAL:HG22	1.53	0.90
2:I:94:ALA:HB2	2:I:129:LEU:HD11	1.55	0.89
3:J:705:THR:HG22	3:J:707:ILE:HD11	1.53	0.89
3:J:955:LYS:HA	3:J:1012:ALA:HA	1.55	0.89
5:L:119:ILE:HG23	5:L:375:ALA:HB1	1.54	0.88

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:470:MET:HE1	5:L:482:GLU:HB3	1.55	0.88
3:J:129:ASP:HB2	3:J:220:ARG:HH21	1.39	0.88
3:J:809:VAL:HG21	3:J:909:ILE:HG21	1.54	0.88
7:O:40:DC:H2"	7:O:41:DT:H5"	1.55	0.88
5:L:72:ALA:HB1	5:L:73:ASP:HB2	1.56	0.88
2:I:898:GLU:HG3	5:L:565:ILE:HG12	1.56	0.88
2:I:1333:LEU:HD23	3:J:307:LEU:HD22	1.55	0.88
3:J:958:ILE:HG23	3:J:982:LEU:HD21	1.56	0.88
3:J:1307:LEU:HD23	3:J:1311:LYS:HD2	1.54	0.87
3:J:759:ILE:HG23	3:J:771:GLN:HB3	1.56	0.87
1:G:167:PRO:HG2	1:G:170:ARG:HD2	1.56	0.87
2:I:1103:VAL:HG22	2:I:1111:GLN:HE21	1.40	0.87
5:L:130:VAL:HG12	5:L:365:MET:HG3	1.56	0.87
1:H:61:ILE:HD13	1:H:142:MET:HB3	1.57	0.87
4:K:26:ARG:HD3	4:K:59:ILE:HD12	1.56	0.86
5:L:32:PRO:HB2	5:L:35:ILE:HG13	1.55	0.86
5:L:9:LEU:HD11	5:L:32:PRO:HD3	1.57	0.86
2:I:633:LEU:HD13	2:I:644:LEU:HB3	1.58	0.86
3:J:1104:LYS:HG3	3:J:1124:ILE:HG23	1.58	0.86
1:H:58:GLU:HG3	1:H:145:LYS:HB3	1.57	0.86
2:I:979:LEU:HD23	2:I:989:LEU:HD11	1.55	0.86
2:I:471:VAL:HG11	2:I:498:ILE:HD11	1.59	0.85
3:J:251:PRO:HG2	5:L:507:MET:HE1	1.57	0.85
3:J:964:LYS:HB3	3:J:977:SER:HB3	1.58	0.85
2:I:106:GLU:HB2	2:I:115:LYS:HG3	1.57	0.85
3:J:398:LYS:HD2	5:L:532:LEU:HD21	1.58	0.85
2:I:1267:GLY:HA3	3:J:347:VAL:O	1.77	0.85
3:J:957:SER:HA	3:J:1010:GLN:HA	1.58	0.85
3:J:163:GLU:HA	3:J:166:LEU:HD12	1.58	0.84
5:L:247:GLU:HA	5:L:250:LEU:HD23	1.58	0.84
3:J:291:ILE:HD13	5:L:409:ASN:HB3	1.58	0.84
3:J:438:GLU:HG3	3:J:485:MET:HE1	1.59	0.84
5:L:109:GLU:HG3	5:L:111:LEU:HD12	1.59	0.84
2:I:538:LEU:HD21	2:I:547:VAL:HG11	1.57	0.84
5:L:38:SER:HA	5:L:41:ILE:HD12	1.59	0.84
3:J:1135:THR:OG1	3:J:1140:ARG:HG2	1.77	0.83
2:I:993:PRO:HG2	2:I:996:ARG:HB2	1.57	0.83
4:K:39:VAL:HG22	4:K:40:PRO:HD2	1.59	0.83
2:I:69:GLN:HE21	2:I:101:ARG:HD2	1.43	0.83
2:I:298:ALA:HB3	2:I:334:GLU:HG2	1.61	0.83
2:I:103:VAL:HG12	2:I:117:ILE:HG13	1.61	0.83

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1079:LYS:HD3	3:J:1098:GLN:HB3	1.61	0.82
1:M:260:LEU:HD11	1:M:310:ARG:HH11	1.43	0.82
5:L:390:ILE:HG21	5:L:435:ILE:HG21	1.61	0.82
1:M:313:SER:HB3	1:M:316:MET:HE3	1.59	0.82
1:H:201:LEU:HD21	1:H:203:ILE:HD11	1.61	0.82
3:J:123:ARG:HA	3:J:126:LEU:HD23	1.62	0.82
4:K:5:THR:HG22	4:K:7:GLN:H	1.44	0.82
2:I:1326:LEU:HD22	3:J:342:LEU:HD21	1.62	0.81
3:J:1109:LEU:HD12	3:J:1121:LEU:HD13	1.61	0.81
5:L:10:LYS:HE2	5:L:85:SER:HB3	1.63	0.81
3:J:53:ARG:HE	3:J:54:ASP:HB2	1.43	0.81
2:I:9:LYS:HG2	2:I:1171:ARG:HH12	1.45	0.81
3:J:857:LEU:HG	3:J:858:VAL:HG23	1.63	0.81
5:L:557:LYS:HG3	5:L:561:MET:HE2	1.62	0.81
3:J:553:THR:HG22	3:J:567:THR:HB	1.63	0.80
3:J:823:THR:HG22	3:J:879:ALA:HA	1.62	0.80
2:I:957:LYS:HB2	2:I:1029:LEU:HD11	1.64	0.80
2:I:996:ARG:HA	2:I:996:ARG:HH11	1.46	0.80
2:I:210:LEU:HD21	2:I:429:MET:HE1	1.64	0.80
3:J:1177:ILE:HB	3:J:1186:TYR:HD2	1.47	0.80
2:I:898:GLU:HG2	5:L:544:THR:HG21	1.63	0.80
2:I:1257:GLN:HE22	3:J:341:ASN:HB2	1.47	0.80
3:J:986:ASP:HB2	3:J:992:LYS:HD3	1.62	0.80
1:H:107:ILE:HG12	1:H:135:ASP:HA	1.62	0.80
3:J:317:THR:H	3:J:318:GLY:HA2	1.45	0.80
2:I:811:ASN:HA	2:I:815:SER:HB2	1.64	0.79
3:J:1176:VAL:HG13	3:J:1187:GLU:HB3	1.63	0.79
9:L:701:1N7:C3	9:L:701:1N7:C18	2.59	0.79
3:J:983:LYS:HE3	3:J:994:SER:HB3	1.64	0.79
2:I:196:VAL:HG23	2:I:206:ALA:HA	1.64	0.79
5:L:118:ASP:N	5:L:118:ASP:OD1	2.15	0.79
1:G:102:LEU:HD11	1:G:110:VAL:HG11	1.62	0.79
2:I:142:GLU:HG2	2:I:515:MET:HE2	1.65	0.79
3:J:550:VAL:HG23	3:J:552:ILE:HG23	1.63	0.78
2:I:39:ILE:HD11	2:I:75:LEU:HG	1.64	0.78
2:I:303:ASP:HB3	2:I:308:GLU:HB2	1.64	0.78
2:I:746:ALA:HB2	2:I:974:ARG:HD2	1.65	0.78
3:J:278:ARG:HG3	3:J:281:ARG:HH21	1.48	0.78
5:L:316:PHE:HE2	5:L:334:SER:HA	1.48	0.78
1:M:289:LEU:HD13	1:M:300:LEU:HD21	1.65	0.78
5:L:341:LEU:HA	5:L:344:LEU:HD12	1.65	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:242:VAL:HB	2:I:245:ARG:HD3	1.66	0.78
5:L:288:MET:O	5:L:292:VAL:N	2.17	0.78
2:I:528:ARG:NH2	2:I:576:SER:O	2.16	0.78
3:J:1170:LYS:HD3	3:J:1172:LYS:HE3	1.66	0.78
5:L:266:PHE:HA	5:L:269:LEU:HD12	1.63	0.78
1:M:260:LEU:HD23	1:M:306:VAL:HG22	1.65	0.78
5:L:596:ARG:HA	5:L:599:ARG:HD2	1.65	0.77
2:I:300:ASP:HA	2:I:312:ALA:HA	1.65	0.77
3:J:1110:GLU:HB2	3:J:1113:VAL:HG21	1.67	0.77
1:H:64:VAL:HG11	1:H:78:ILE:HD13	1.67	0.77
2:I:538:LEU:HD13	2:I:543:ALA:HB2	1.67	0.77
5:L:588:ARG:NH2	8:P:58:DC:OP2	2.16	0.77
8:P:42:DT:H1'	8:P:43:DT:H5'	1.67	0.77
1:M:269:CYS:HB3	1:M:295:LEU:HD12	1.67	0.76
2:I:826:ASP:OD1	2:I:829:THR:OG1	2.03	0.76
2:I:802:VAL:HG21	2:I:1098:LEU:HD22	1.68	0.76
3:J:973:LEU:HG	3:J:1006:GLY:HA3	1.68	0.76
3:J:804:ALA:HA	3:J:1259:GLN:HG3	1.67	0.76
3:J:888:CYS:SG	3:J:890:THR:OG1	2.44	0.76
1:H:86:LYS:HD3	1:H:174:ASP:HB2	1.68	0.76
3:J:959:LYS:HB3	3:J:983:LYS:HB2	1.68	0.76
1:G:8:PHE:HE1	1:H:150:ARG:HD3	1.51	0.76
3:J:1061:VAL:HG11	3:J:1101:LEU:HB3	1.67	0.76
3:J:108:ALA:H	3:J:276:ASN:HD21	1.30	0.75
5:L:476:ARG:NH2	5:L:482:GLU:OE2	2.20	0.75
2:I:1119:MET:HG2	2:I:1204:LEU:HD13	1.67	0.75
2:I:877:VAL:HG11	2:I:920:VAL:HG21	1.69	0.75
2:I:1242:LYS:HB3	3:J:465:GLN:HE21	1.52	0.75
3:J:288:PRO:HG2	3:J:291:ILE:HD12	1.69	0.75
3:J:1230:THR:HG22	3:J:1257:VAL:HG11	1.68	0.75
1:G:179:PRO:HB3	1:G:210:THR:HG23	1.69	0.75
1:G:14:VAL:HG21	1:G:29:GLU:HB2	1.69	0.75
2:I:341:LEU:HD11	6:N:67:ARG:HD2	1.68	0.75
5:L:449:THR:HG23	5:L:450:ILE:HD13	1.67	0.75
1:G:45:ARG:HG2	1:H:38:THR:HB	1.69	0.74
3:J:1005:LYS:HE3	3:J:1009:GLU:HB3	1.66	0.74
1:G:45:ARG:HH21	2:I:1216:ARG:HA	1.52	0.74
8:P:38:DC:H2''	8:P:39:DC:H5''	1.69	0.74
2:I:484:LEU:HB3	2:I:486:THR:HG22	1.69	0.74
3:J:142:GLU:OE2	5:L:103:ARG:NH2	2.21	0.74
3:J:1172:LYS:HB2	3:J:1189:MET:HB3	1.68	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1329:GLU:OE1	3:J:337:ARG:NH1	2.21	0.74
3:J:811:GLU:O	3:J:896:ALA:N	2.20	0.74
3:J:412:LEU:HG	3:J:441:LEU:HD11	1.70	0.73
3:J:390:LEU:HD23	3:J:407:VAL:HG21	1.71	0.73
3:J:844:THR:OG1	3:J:860:ARG:O	2.05	0.73
3:J:960:LEU:HD11	3:J:1007:ASP:HA	1.71	0.73
1:H:64:VAL:HG21	1:H:78:ILE:HD11	1.70	0.73
2:I:146:VAL:HG21	2:I:513:GLN:HE21	1.51	0.73
2:I:148:GLN:OE1	2:I:454:ARG:NH1	2.21	0.73
3:J:97:VAL:HG12	3:J:101:ARG:HD2	1.70	0.73
3:J:1046:ILE:HD12	3:J:1059:LEU:HD13	1.70	0.73
5:L:324:LYS:N	5:L:327:SER:OG	2.21	0.73
3:J:153:ASN:HB2	3:J:172:PHE:HE2	1.54	0.73
1:G:18:GLN:NE2	1:G:20:SER:O	2.21	0.73
4:K:3:ARG:NH1	4:K:5:THR:O	2.21	0.73
5:L:217:ALA:HA	5:L:220:LYS:HE2	1.69	0.73
8:P:48:DC:H2"	8:P:49:DT:H71	1.70	0.73
3:J:1161:GLY:O	3:J:1204:VAL:N	2.22	0.73
2:I:1288:GLN:HG2	2:I:1315:MET:HE1	1.71	0.73
2:I:988:LYS:HA	2:I:991:LYS:HG3	1.71	0.73
1:H:24:ALA:HB3	1:H:213:PRO:HB2	1.70	0.72
2:I:8:LYS:O	2:I:1171:ARG:NH2	2.22	0.72
3:J:895:CYS:SG	3:J:898:CYS:N	2.61	0.72
5:L:401:PHE:HA	5:L:404:LEU:HD12	1.69	0.72
3:J:697:MET:HE3	3:J:741:ALA:HB3	1.70	0.72
1:G:31:LEU:HD13	1:G:36:GLY:HA2	1.72	0.72
2:I:716:ALA:HB3	2:I:784:ALA:HB3	1.70	0.72
3:J:230:SER:OG	3:J:232:ASN:ND2	2.23	0.72
1:H:61:ILE:HG22	1:H:63:GLY:H	1.55	0.72
3:J:893:GLY:O	3:J:1258:ARG:NH2	2.22	0.72
8:P:64:DA:H1'	8:P:65:DT:H5"	1.72	0.72
1:H:47:LEU:HA	1:H:51:MET:HG3	1.71	0.72
2:I:936:ARG:N	2:I:1047:LEU:O	2.23	0.71
2:I:363:LEU:HB3	2:I:381:ALA:HB1	1.71	0.71
2:I:897:PRO:O	2:I:899:GLU:N	2.23	0.71
5:L:550:GLY:O	5:L:603:ARG:NH2	2.22	0.71
2:I:142:GLU:HG2	2:I:515:MET:CE	2.21	0.71
3:J:264:ASP:HB3	3:J:324:LEU:HD22	1.72	0.71
3:J:1081:VAL:HA	3:J:1088:VAL:HG23	1.72	0.71
2:I:301:TYR:N	2:I:311:CYS:O	2.22	0.71
2:I:1106:ARG:HE	3:J:731:ARG:HH22	1.39	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:53:ARG:HB3	3:J:54:ASP:CB	2.21	0.71
2:I:803:ALA:HB2	2:I:1094:VAL:HG11	1.72	0.71
2:I:990:ASP:N	2:I:990:ASP:OD1	2.22	0.71
5:L:386:LEU:O	5:L:389:SER:OG	2.03	0.71
3:J:809:VAL:HG12	3:J:911:LYS:HA	1.73	0.71
9:J:1505:1N7:C3	9:J:1505:1N7:C18	2.65	0.71
3:J:853:THR:O	3:J:855:ASP:N	2.24	0.71
5:L:463:LEU:HD11	5:L:483:LEU:HD23	1.72	0.71
2:I:204:LEU:HD11	2:I:369:MET:HE2	1.73	0.70
3:J:1030:GLU:HG3	3:J:1090:ILE:HG23	1.73	0.70
5:L:119:ILE:HA	5:L:122:ARG:HD3	1.72	0.70
2:I:870:ILE:HG21	2:I:931:VAL:HG11	1.74	0.70
5:L:533:ASP:HA	5:L:536:THR:HG22	1.72	0.70
2:I:933:VAL:HG22	2:I:1050:VAL:HG22	1.73	0.70
2:I:1060:ILE:HD12	2:I:1234:LYS:HD2	1.73	0.70
3:J:1265:THR:OG1	3:J:1303:SER:O	2.09	0.70
5:L:146:GLU:OE2	5:L:150:ARG:NH1	2.24	0.70
5:L:320:ILE:HD11	5:L:331:HIS:HB3	1.73	0.70
3:J:325:LYS:HD2	5:L:508:GLU:HG3	1.73	0.70
5:L:555:GLU:OE2	5:L:597:LYS:NZ	2.24	0.70
3:J:117:LEU:HG	3:J:124:ILE:HD12	1.72	0.70
5:L:152:GLU:HB3	5:L:218:ARG:HD3	1.74	0.70
5:L:405:ILE:O	5:L:409:ASN:ND2	2.23	0.70
1:H:46:ILE:HD12	1:H:224:LEU:HB2	1.74	0.70
2:I:998:LEU:HG	2:I:1015:ALA:HA	1.74	0.70
3:J:977:SER:OG	3:J:980:THR:OG1	2.09	0.70
1:M:270:LEU:O	1:M:275:ILE:N	2.24	0.70
3:J:1157:ALA:N	3:J:1208:ASP:O	2.25	0.69
3:J:1064:SER:HB3	3:J:1072:LYS:HB2	1.74	0.69
5:L:123:ILE:HD11	5:L:379:MET:HE1	1.72	0.69
2:I:211:ARG:NH1	2:I:357:ASN:O	2.25	0.69
2:I:253:PHE:CA	2:I:265:LYS:HB3	2.22	0.69
1:G:90:VAL:HG22	1:G:123:ILE:HD13	1.72	0.69
3:J:262:THR:HG23	5:L:504:PRO:HB2	1.74	0.69
2:I:714:VAL:HB	2:I:787:PRO:HD2	1.75	0.69
3:J:961:SER:O	3:J:980:THR:HA	1.92	0.69
5:L:584:ARG:NH2	8:P:56:DG:N7	2.40	0.69
1:G:104:LYS:HG2	1:G:110:VAL:HG22	1.75	0.69
2:I:118:LYS:HD3	2:I:488:MET:HG2	1.74	0.69
5:L:319:ALA:HA	5:L:322:MET:HG3	1.75	0.69
2:I:241:LEU:N	2:I:283:LYS:O	2.25	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:O:26:DT:H2'	7:O:27:DT:H71	1.72	0.69
2:I:685:MET:SD	2:I:1073:LYS:HG2	2.33	0.69
3:J:252:LEU:HD12	3:J:262:THR:HG22	1.75	0.69
3:J:849:LEU:HD12	3:J:856:ILE:HA	1.75	0.69
2:I:517:GLN:HB3	2:I:759:SER:OG	1.93	0.69
2:I:1117:LEU:HD12	2:I:1195:ILE:HG12	1.73	0.69
3:J:749:LYS:HG2	3:J:755:ILE:HD11	1.74	0.69
3:J:1101:LEU:HD12	3:J:1102:PRO:HD2	1.74	0.69
3:J:596:LEU:HD11	3:J:604:MET:HE1	1.75	0.69
2:I:520:PRO:HG3	2:I:714:VAL:HG21	1.75	0.68
2:I:637:ARG:HA	2:I:642:SER:HA	1.74	0.68
5:L:150:ARG:HB3	5:L:155:GLU:HB2	1.73	0.68
9:L:701:1N7:C3	9:L:701:1N7:C2	2.69	0.68
2:I:1116:HIS:HE1	3:J:641:ILE:H	1.39	0.68
2:I:1288:GLN:O	2:I:1292:THR:HG22	1.93	0.68
5:L:555:GLU:HG2	5:L:594:ALA:HB2	1.74	0.68
1:H:205:MET:HE1	1:H:217:ILE:HG13	1.75	0.68
5:L:383:ASN:O	5:L:387:VAL:HG23	1.94	0.68
1:G:51:MET:HE3	1:G:211:ILE:HD13	1.75	0.68
3:J:491:LEU:HB2	3:J:904:ALA:HB1	1.74	0.68
3:J:1160:SER:OG	3:J:1205:GLU:OE1	2.11	0.68
2:I:361:SER:HA	2:I:364:VAL:HG22	1.75	0.68
1:G:100:LEU:HD23	1:G:115:ILE:HG21	1.76	0.68
3:J:809:VAL:HG23	3:J:915:ILE:HG21	1.74	0.68
2:I:151:ARG:HH11	2:I:445:ILE:HG21	1.59	0.67
2:I:253:PHE:CE2	2:I:255:ILE:HG12	2.28	0.67
2:I:565:GLU:HB3	2:I:680:LEU:HD21	1.73	0.67
5:L:387:VAL:HA	5:L:390:ILE:HG22	1.74	0.67
2:I:1072:ASN:ND2	2:I:1111:GLN:OE1	2.27	0.67
3:J:823:THR:HB	3:J:824:PRO:HD2	1.76	0.67
3:J:1175:LEU:HD13	3:J:1190:ILE:HD11	1.76	0.67
5:L:348:GLU:HG2	5:L:355:ILE:HG23	1.75	0.67
2:I:255:ILE:HD12	2:I:263:VAL:HG21	1.76	0.67
3:J:369:PRO:HD2	3:J:372:MET:HE2	1.77	0.67
5:L:316:PHE:CE2	5:L:334:SER:HA	2.28	0.67
3:J:426:ALA:HB3	3:J:427:PRO:HD3	1.76	0.67
3:J:534:GLU:O	3:J:538:ARG:HG2	1.94	0.67
5:L:72:ALA:CB	5:L:73:ASP:HB2	2.25	0.67
1:M:270:LEU:HB3	1:M:275:ILE:HB	1.76	0.67
3:J:700:ASN:O	3:J:704:GLU:HB2	1.95	0.67
8:P:39:DC:H2''	8:P:40:DC:H5'	1.77	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:182:ARG:NH1	3:J:534:GLU:OE1	2.27	0.67
2:I:253:PHE:HA	2:I:265:LYS:HD2	1.77	0.67
2:I:966:ILE:HG12	9:I:1401:1N7:H26	1.75	0.67
3:J:801:VAL:O	3:J:805:GLN:HB2	1.94	0.67
3:J:950:ILE:HD12	3:J:1017:VAL:HG23	1.75	0.67
4:K:38:LEU:N	4:K:53:GLU:OE2	2.27	0.67
5:L:296:LYS:HE2	5:L:296:LYS:HA	1.77	0.67
3:J:253:VAL:HG21	5:L:523:ILE:HD13	1.77	0.67
3:J:842:ARG:HB2	3:J:882:VAL:HG21	1.76	0.67
1:M:307:LEU:O	1:M:311:GLY:N	2.28	0.67
3:J:968:ASN:HD21	3:J:974:VAL:HG13	1.60	0.66
3:J:1357:ILE:HD12	3:J:1359:ALA:HB3	1.76	0.66
2:I:1275:VAL:O	2:I:1279:GLU:HG3	1.95	0.66
5:L:554:ARG:NH2	7:O:25:DA:OP2	2.28	0.66
2:I:982:GLY:O	2:I:1002:LEU:HB2	1.95	0.66
2:I:1151:LEU:HD21	2:I:1198:LEU:HA	1.76	0.66
2:I:1269:ARG:NH2	3:J:344:GLY:O	2.27	0.66
5:L:277:MET:HE2	5:L:281:ARG:HH22	1.60	0.66
5:L:381:GLU:O	5:L:384:LEU:HG	1.95	0.66
1:M:294:ASN:N	8:P:69:DT:OP1	2.28	0.66
3:J:1051:ASP:HB2	3:J:1056:LEU:H	1.61	0.66
5:L:577:GLY:O	5:L:581:ASP:N	2.29	0.66
2:I:74:ARG:NH1	2:I:121:GLU:OE2	2.28	0.66
2:I:971:LEU:HD11	2:I:1017:GLN:HG3	1.76	0.66
3:J:314:ARG:H	3:J:314:ARG:HD2	1.61	0.66
3:J:865:HIS:CE1	3:J:867:GLN:HB2	2.31	0.66
3:J:886:VAL:HG11	3:J:1230:THR:HG21	1.76	0.66
5:L:335:GLU:O	5:L:339:ARG:HD3	1.96	0.66
3:J:810:THR:OG1	3:J:1363:TYR:OH	2.11	0.66
5:L:297:MET:HE2	5:L:302:PHE:HD1	1.60	0.66
5:L:466:ILE:HD11	5:L:486:ARG:HH11	1.61	0.66
5:L:148:TYR:HE1	5:L:218:ARG:HG2	1.59	0.66
3:J:518:VAL:HG11	3:J:707:ILE:HB	1.78	0.66
3:J:1069:ALA:HA	3:J:1072:LYS:HG2	1.76	0.66
5:L:46:GLN:O	5:L:50:ASP:HB2	1.96	0.66
1:M:253:LEU:HD22	1:M:282:VAL:HG21	1.77	0.66
5:L:324:LYS:HB3	5:L:325:PRO:HD2	1.77	0.66
2:I:519:ASN:HB3	2:I:522:SER:H	1.60	0.66
2:I:700:VAL:HG13	2:I:1117:LEU:HD22	1.78	0.66
9:J:1505:1N7:C3	9:J:1505:1N7:C2	2.69	0.66
2:I:120:GLN:NE2	2:I:490:GLN:OE1	2.29	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1346:GLY:O	3:J:1350:ASN:ND2	2.25	0.65
5:L:448:ARG:NH1	5:L:501:ALA:O	2.28	0.65
1:M:270:LEU:HD22	1:M:275:ILE:HD12	1.78	0.65
2:I:233:ARG:HA	2:I:233:ARG:HE	1.61	0.65
2:I:671:LEU:HB3	2:I:1186:VAL:HG12	1.77	0.65
2:I:977:ALA:HA	2:I:980:VAL:HG23	1.77	0.65
2:I:1065:LYS:HD3	2:I:1235:LEU:HD12	1.77	0.65
2:I:1294:LYS:HD2	3:J:349:TYR:HD2	1.61	0.65
3:J:724:MET:O	3:J:728:SER:OG	2.13	0.65
3:J:803:VAL:HG11	3:J:1309:ILE:HG22	1.77	0.65
5:L:9:LEU:O	5:L:13:VAL:HG23	1.96	0.65
2:I:133:ASN:ND2	2:I:713:GLY:HA3	2.12	0.65
3:J:288:PRO:HG3	5:L:380:VAL:HG21	1.78	0.65
3:J:489:ASN:HD21	3:J:905:ARG:HH11	1.45	0.65
5:L:231:THR:HA	5:L:248:GLU:HG3	1.79	0.65
9:I:1401:1N7:C3	9:I:1401:1N7:C18	2.72	0.65
3:J:198:CYS:O	3:J:202:ARG:HG3	1.95	0.65
8:P:40:DC:H1'	8:P:41:DT:H5'	1.79	0.65
1:G:45:ARG:HD3	2:I:1083:GLU:HG3	1.78	0.65
2:I:253:PHE:HA	2:I:265:LYS:HB3	1.77	0.65
3:J:1215:GLU:OE1	3:J:1224:ARG:NH2	2.27	0.65
3:J:141:PHE:HD1	3:J:180:MET:HE3	1.60	0.65
1:M:299:SER:O	1:M:303:ILE:HG13	1.96	0.65
2:I:861:ALA:HB1	2:I:882:ILE:HD11	1.78	0.65
5:L:419:PHE:HA	5:L:430:TYR:HE2	1.60	0.65
3:J:822:MET:SD	3:J:838:ARG:NH2	2.70	0.65
1:G:42:ALA:HB1	1:G:224:LEU:HD11	1.78	0.64
2:I:841:ARG:HA	2:I:1046:VAL:HA	1.79	0.64
9:I:1401:1N7:C3	9:I:1401:1N7:C2	2.71	0.64
1:H:57:THR:OG1	1:H:147:GLN:HB3	1.97	0.64
3:J:308:ASP:OD2	3:J:311:ARG:NH1	2.29	0.64
3:J:137:ARG:HG2	3:J:143:SER:OG	1.97	0.64
5:L:125:ASP:OD2	5:L:371:LYS:NZ	2.31	0.64
5:L:231:THR:HA	5:L:248:GLU:CG	2.27	0.64
1:H:71:LYS:HB3	1:H:74:VAL:HG22	1.78	0.64
2:I:14:ASP:H	2:I:1157:GLN:HG2	1.62	0.64
5:L:460:ILE:HG22	5:L:497:VAL:HG13	1.79	0.64
2:I:813:GLU:HB2	3:J:461:PHE:HD2	1.63	0.64
2:I:886:LYS:H	2:I:917:SER:HB3	1.62	0.64
3:J:1064:SER:CB	3:J:1072:LYS:HB2	2.28	0.64
1:H:33:ARG:NH2	2:I:820:GLU:OE2	2.30	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:57:PHE:CD2	2:I:70:TYR:HB2	2.33	0.64
3:J:937:ILE:HD11	3:J:1134:ILE:HB	1.78	0.64
2:I:529:ARG:HD3	2:I:572:ILE:HG22	1.80	0.64
2:I:742:TYR:HB3	2:I:743:PRO:HD2	1.80	0.64
3:J:364:HIS:HB3	3:J:487:THR:CG2	2.28	0.64
6:N:20:ILE:O	6:N:24:ARG:HG2	1.98	0.64
3:J:518:VAL:O	3:J:547:ARG:NH2	2.31	0.64
3:J:1143:ASP:OD1	5:L:67:LEU:HD22	1.97	0.64
5:L:487:MET:HE2	5:L:489:MET:HE3	1.80	0.64
2:I:299:LYS:HG2	2:I:334:GLU:OE1	1.98	0.64
3:J:759:ILE:HD12	3:J:771:GLN:HB3	1.80	0.64
3:J:925:GLU:HB3	3:J:926:PRO:HD3	1.79	0.64
5:L:490:PRO:HG3	5:L:493:LYS:HE3	1.79	0.64
2:I:27:LEU:HD13	2:I:524:ILE:HD11	1.79	0.63
2:I:231:GLU:O	2:I:238:GLN:HG3	1.98	0.63
3:J:417:ARG:NH1	4:K:43:ASN:OD1	2.31	0.63
7:O:25:DA:H2'	7:O:26:DT:H71	1.79	0.63
1:H:215:GLU:OE2	1:H:219:ARG:NH2	2.31	0.63
2:I:130:MET:SD	2:I:134:GLY:HA2	2.38	0.63
2:I:241:LEU:HD21	2:I:277:LEU:HD11	1.80	0.63
5:L:257:LYS:HE2	5:L:258:GLN:HE22	1.63	0.63
5:L:490:PRO:HG2	5:L:493:LYS:HG2	1.80	0.63
1:M:262:LEU:HD11	1:M:306:VAL:HG11	1.79	0.63
2:I:1154:ASP:N	2:I:1154:ASP:OD1	2.31	0.63
3:J:596:LEU:HD11	3:J:604:MET:CE	2.28	0.63
5:L:150:ARG:HB3	5:L:155:GLU:CB	2.28	0.63
5:L:377:LYS:O	5:L:381:GLU:HG3	1.98	0.63
1:H:193:GLU:OE1	1:H:194:GLN:N	2.24	0.63
2:I:27:LEU:O	2:I:528:ARG:NH1	2.32	0.63
3:J:73:GLY:O	3:J:76:LYS:NZ	2.24	0.63
3:J:679:TYR:OH	3:J:754:ILE:O	2.12	0.63
1:M:262:LEU:HD11	1:M:306:VAL:CG1	2.28	0.63
1:M:280:ASP:HA	1:M:283:GLN:HG3	1.79	0.63
1:H:59:VAL:O	1:H:171:LEU:HB2	1.98	0.63
2:I:470:ARG:CD	2:I:497:PRO:HB3	2.28	0.63
3:J:826:ILE:HD13	3:J:831:VAL:HG12	1.79	0.63
5:L:266:PHE:O	5:L:270:VAL:HG23	1.97	0.63
3:J:870:ASP:O	3:J:874:GLU:HG2	1.98	0.63
1:H:104:LYS:HG3	1:H:114:ASP:OD1	1.99	0.63
3:J:1075:ARG:HB2	3:J:1100:PHE:HD1	1.64	0.63
3:J:1175:LEU:HD22	3:J:1190:ILE:HD11	1.81	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:552:THR:OG1	5:L:555:GLU:OE1	2.16	0.63
1:G:8:PHE:CE1	1:H:150:ARG:HD3	2.34	0.63
1:H:228:LEU:O	1:H:232:VAL:HG23	1.97	0.63
2:I:178:PRO:HG3	2:I:395:TYR:CE1	2.33	0.63
1:G:222:THR:OG1	1:H:233:ASP:OD1	2.17	0.63
2:I:1005:GLU:HG2	2:I:1006:GLU:H	1.62	0.63
3:J:252:LEU:HD12	3:J:262:THR:CG2	2.29	0.63
3:J:1329:THR:O	3:J:1333:THR:OG1	2.16	0.63
5:L:484:ALA:HB1	5:L:491:GLU:HG3	1.81	0.63
2:I:12:ARG:HG3	2:I:1181:PRO:HB2	1.79	0.62
2:I:303:ASP:CB	2:I:308:GLU:HB2	2.29	0.62
3:J:1358:PRO:HB3	3:J:1366:HIS:CD2	2.34	0.62
2:I:180:ARG:NH2	2:I:393:ASP:O	2.32	0.62
2:I:924:VAL:HG13	2:I:1056:VAL:HG11	1.80	0.62
3:J:510:LEU:O	3:J:514:THR:HG23	1.99	0.62
3:J:525:MET:O	3:J:548:VAL:HG22	1.99	0.62
3:J:1035:VAL:HB	3:J:1109:LEU:HD13	1.79	0.62
2:I:216:THR:OG1	2:I:219:GLN:OE1	2.14	0.62
2:I:469:VAL:O	2:I:472:GLU:HG3	2.00	0.62
2:I:1120:ALA:O	2:I:1124:ILE:HG12	1.99	0.62
2:I:1212:LEU:HD22	2:I:1225:VAL:CG2	2.30	0.62
3:J:681:LYS:O	3:J:685:ILE:HG13	1.99	0.62
2:I:225:PHE:HE2	2:I:347:ILE:HB	1.63	0.62
2:I:302:ILE:HG22	2:I:309:LEU:HA	1.80	0.62
2:I:724:VAL:HG11	2:I:727:VAL:HG22	1.81	0.62
3:J:1011:VAL:HG12	3:J:1012:ALA:H	1.63	0.62
5:L:271:ASN:O	5:L:275:VAL:HG23	1.99	0.62
1:M:280:ASP:HB2	1:M:284:ARG:HH21	1.64	0.62
1:G:14:VAL:HG12	1:G:15:ASP:H	1.63	0.62
1:H:73:GLY:CA	1:H:134:THR:HB	2.29	0.62
2:I:796:LEU:HB2	2:I:1233:LEU:HD22	1.81	0.62
3:J:955:LYS:CA	3:J:1012:ALA:HA	2.28	0.62
3:J:1022:PRO:HB2	3:J:1126:GLN:HG2	1.80	0.62
3:J:1079:LYS:HD3	3:J:1098:GLN:CB	2.28	0.62
3:J:1238:GLN:HB3	3:J:1242:ARG:NH2	2.14	0.62
5:L:148:TYR:HE2	5:L:225:ARG:HH21	1.44	0.62
1:G:185:TYR:HB2	1:G:201:LEU:HD11	1.81	0.62
2:I:444:ASP:OD1	2:I:551:HIS:NE2	2.28	0.62
3:J:150:GLY:HA3	3:J:175:GLU:O	1.99	0.62
3:J:609:TYR:HD2	3:J:610:ARG:HD3	1.65	0.62
3:J:664:ILE:HG22	3:J:678:ARG:HG3	1.82	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1156:LEU:HD23	3:J:1219:ASP:HB3	1.81	0.62
5:L:119:ILE:O	5:L:123:ILE:HG13	2.00	0.62
5:L:444:ALA:HB1	5:L:457:ILE:HD12	1.81	0.62
1:M:278:ILE:HA	1:M:281:LEU:HB3	1.82	0.62
2:I:103:VAL:HG12	2:I:117:ILE:CG1	2.30	0.62
3:J:84:ILE:HD12	3:J:91:GLU:HB2	1.80	0.62
1:G:154:PRO:HG2	1:G:157:THR:HG23	1.81	0.62
1:H:152:TYR:HE2	1:H:154:PRO:HG3	1.65	0.62
2:I:1062:PRO:HA	2:I:1076:ILE:O	2.00	0.62
3:J:625:MET:HE3	3:J:629:PHE:HE2	1.64	0.62
5:L:109:GLU:HG3	5:L:111:LEU:CD1	2.30	0.62
5:L:409:ASN:O	5:L:413:MET:HG3	1.99	0.62
5:L:551:LEU:HD21	5:L:597:LYS:HD2	1.81	0.62
3:J:930:LEU:HD22	3:J:1244:GLN:HG3	1.80	0.62
3:J:1040:MET:HG2	3:J:1076:PRO:HA	1.82	0.62
3:J:1272:SER:HB2	3:J:1300:ALA:HB2	1.81	0.62
2:I:378:ARG:O	2:I:382:GLU:HG2	1.99	0.61
2:I:1130:ALA:O	2:I:1134:GLN:HG2	2.00	0.61
3:J:1163:VAL:HG13	3:J:1200:GLU:HA	1.82	0.61
2:I:759:SER:OG	2:I:760:ASN:N	2.33	0.61
3:J:337:ARG:HD3	3:J:341:ASN:OD1	2.00	0.61
3:J:816:THR:CG2	3:J:889:ASP:HB2	2.29	0.61
5:L:281:ARG:HG2	5:L:285:ARG:HE	1.64	0.61
5:L:613:ASP:N	5:L:613:ASP:OD1	2.32	0.61
1:G:224:LEU:HD22	1:G:228:LEU:HD23	1.81	0.61
2:I:118:LYS:HD3	2:I:488:MET:HA	1.82	0.61
3:J:848:VAL:CG1	3:J:858:VAL:HB	2.30	0.61
3:J:1156:LEU:HD12	3:J:1209:VAL:HG22	1.81	0.61
1:G:112:ALA:HB1	1:G:123:ILE:HG21	1.82	0.61
2:I:1113:LEU:HD13	3:J:641:ILE:HD13	1.82	0.61
3:J:140:TYR:HB3	5:L:100:MET:HE1	1.82	0.61
3:J:519:ASN:HA	3:J:523:GLU:OE1	2.00	0.61
3:J:1172:LYS:HD3	3:J:1189:MET:HG3	1.82	0.61
5:L:591:GLU:O	5:L:595:LEU:HG	2.01	0.61
6:N:3:ASP:OD1	6:N:3:ASP:N	2.33	0.61
2:I:262:TYR:O	2:I:273:HIS:NE2	2.32	0.61
2:I:347:ILE:HA	2:I:350:THR:HG22	1.83	0.61
2:I:817:LEU:HD11	2:I:1080:ASN:ND2	2.14	0.61
3:J:859:PRO:HD2	3:J:862:THR:HG21	1.81	0.61
3:J:399:LYS:O	3:J:403:ARG:HG2	2.01	0.61
3:J:423:LEU:HB3	3:J:466:MET:HE1	1.82	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:427:PRO:O	3:J:429:LEU:HD22	2.01	0.61
5:L:479:THR:HG23	5:L:482:GLU:H	1.65	0.61
1:G:45:ARG:NH2	2:I:1216:ARG:HA	2.15	0.61
2:I:590:PRO:HG3	2:I:605:TYR:CE1	2.36	0.61
2:I:905:ILE:HD11	5:L:598:LEU:HD12	1.81	0.61
9:J:1504:1N7:C3	9:J:1504:1N7:C2	2.73	0.61
5:L:10:LYS:O	5:L:14:THR:HG22	2.01	0.61
5:L:115:GLY:O	5:L:119:ILE:HG13	2.01	0.61
5:L:147:GLN:CG	5:L:161:LEU:HD13	2.31	0.61
5:L:283:GLN:OE1	5:L:344:LEU:HG	2.01	0.61
1:H:73:GLY:HA2	1:H:134:THR:HB	1.82	0.61
3:J:111:THR:HG23	3:J:300:GLN:OE1	2.00	0.61
3:J:452:LEU:HD13	3:J:500:ILE:CG2	2.30	0.61
5:L:51:MET:HB3	5:L:80:ALA:HB3	1.83	0.61
5:L:544:THR:HA	5:L:547:VAL:HG22	1.82	0.61
2:I:1148:ALA:HA	2:I:1201:LEU:HD21	1.82	0.61
3:J:1316:THR:CG2	3:J:1322:ALA:HB2	2.30	0.61
4:K:26:ARG:NH1	4:K:29:GLN:OE1	2.33	0.61
1:G:155:ALA:N	1:G:174:ASP:OD1	2.27	0.60
2:I:246:LEU:O	2:I:274:ILE:HD11	2.01	0.60
2:I:1289:GLU:OE1	3:J:473:THR:HG22	2.00	0.60
3:J:1275:LEU:HB2	3:J:1278:GLU:HB2	1.83	0.60
1:H:214:GLU:O	1:H:218:ARG:NE	2.33	0.60
2:I:1077:SER:HB2	3:J:356:THR:HB	1.82	0.60
3:J:44:ILE:HG13	5:L:450:ILE:HG22	1.82	0.60
3:J:337:ARG:HE	3:J:341:ASN:HD21	1.49	0.60
3:J:1319:PHE:CE1	3:J:1342:ASP:HB2	2.36	0.60
1:G:234:LEU:HD22	1:H:14:VAL:HG11	1.82	0.60
2:I:1263:ALA:N	2:I:1264:GLN:HA	2.16	0.60
3:J:1347:LEU:HD11	3:J:1359:ALA:HB2	1.83	0.60
5:L:51:MET:HB3	5:L:80:ALA:CB	2.31	0.60
5:L:466:ILE:HD11	5:L:486:ARG:HG2	1.83	0.60
2:I:69:GLN:NE2	2:I:101:ARG:HD2	2.15	0.60
2:I:962:GLU:O	2:I:966:ILE:HG13	2.01	0.60
2:I:1070:HIS:NE2	2:I:1114:GLU:OE1	2.28	0.60
2:I:1257:GLN:NE2	3:J:341:ASN:HB2	2.15	0.60
3:J:147:ILE:HD11	3:J:179:LYS:HB2	1.83	0.60
3:J:986:ASP:HB2	3:J:992:LYS:CD	2.31	0.60
3:J:1361:THR:O	4:K:21:LEU:HD11	2.01	0.60
1:M:269:CYS:CB	1:M:295:LEU:HD12	2.30	0.60
8:P:59:DA:H2''	8:P:60:DA:O5'	2.01	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:818:VAL:HG21	2:I:1066:MET:HE1	1.84	0.60
3:J:74:LYS:HG2	3:J:75:TYR:CE2	2.36	0.60
3:J:301:GLU:OE1	5:L:97:PRO:HG2	2.02	0.60
3:J:1023:HIS:HA	3:J:1125:PRO:HA	1.83	0.60
5:L:503:GLU:CD	5:L:504:PRO:HD2	2.26	0.60
5:L:554:ARG:HD2	5:L:580:PHE:HE1	1.65	0.60
7:O:25:DA:H2'	7:O:26:DT:C6	2.37	0.60
7:O:33:DA:H2''	7:O:34:DA:H5'	1.82	0.60
2:I:471:VAL:HG11	2:I:498:ILE:CD1	2.29	0.60
2:I:903:ARG:HG2	2:I:908:GLU:O	2.02	0.60
3:J:123:ARG:NH2	3:J:1334:GLU:HG2	2.17	0.60
3:J:418:GLU:O	3:J:420:PRO:HD3	2.01	0.60
3:J:1005:LYS:HE2	3:J:1011:VAL:CG2	2.32	0.60
5:L:17:LYS:HG3	5:L:53:ILE:HD11	1.83	0.60
5:L:314:THR:HA	5:L:318:ALA:HB3	1.84	0.60
2:I:204:LEU:H	2:I:204:LEU:HD12	1.67	0.60
2:I:230:PHE:HE1	2:I:239:MET:HG3	1.66	0.60
2:I:240:GLU:HG2	2:I:284:LEU:CD1	2.32	0.60
3:J:147:ILE:CD1	3:J:179:LYS:HB2	2.31	0.60
3:J:954:ASN:HB2	3:J:992:LYS:NZ	2.17	0.60
9:J:1505:1N7:H31	9:J:1505:1N7:H5	1.84	0.60
1:M:264:VAL:O	1:M:268:ASN:ND2	2.35	0.60
2:I:118:LYS:HG2	2:I:488:MET:HG2	1.82	0.60
2:I:246:LEU:O	2:I:269:ILE:HG21	2.02	0.60
2:I:817:LEU:CD1	2:I:1085:MET:HE1	2.32	0.60
2:I:896:THR:O	2:I:900:LYS:HB2	2.01	0.60
5:L:139:GLU:O	5:L:142:THR:OG1	2.16	0.60
5:L:277:MET:HE3	5:L:362:ASN:HD21	1.65	0.60
1:G:183:ILE:HD12	1:G:205:MET:HB2	1.84	0.60
2:I:622:ASN:ND2	2:I:631:GLU:OE2	2.34	0.60
3:J:124:ILE:O	3:J:128:LEU:HD12	2.02	0.60
3:J:268:LEU:HB3	3:J:306:LEU:HD23	1.83	0.60
1:M:283:GLN:OE1	1:M:317:ARG:HA	2.02	0.60
2:I:975:ILE:HG13	2:I:1014:LEU:HD23	1.82	0.60
3:J:194:LEU:HD22	3:J:224:LEU:HD22	1.84	0.60
5:L:229:VAL:HB	5:L:232:ARG:NH2	2.16	0.60
5:L:419:PHE:HA	5:L:430:TYR:CE2	2.36	0.60
1:H:215:GLU:HA	1:H:218:ARG:HG2	1.84	0.59
2:I:14:ASP:HA	2:I:1183:ALA:HB3	1.84	0.59
2:I:249:GLU:HB2	2:I:269:ILE:HD13	1.83	0.59
3:J:1171:GLY:O	3:J:1191:PRO:HA	2.02	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:79:ALA:O	5:L:83:VAL:HG23	2.02	0.59
2:I:118:LYS:CG	2:I:488:MET:HG2	2.32	0.59
3:J:140:TYR:CB	5:L:100:MET:HE1	2.32	0.59
3:J:1173:ARG:HH21	3:J:1192:LYS:HB2	1.66	0.59
5:L:280:VAL:O	5:L:283:GLN:HG3	2.01	0.59
7:O:20:DA:H2''	7:O:21:DA:C8	2.37	0.59
1:G:79:LEU:HD21	2:I:693:LEU:HD11	1.85	0.59
2:I:104:ILE:HD11	2:I:116:ASP:HB2	1.85	0.59
2:I:136:PHE:CZ	2:I:456:VAL:HG21	2.36	0.59
2:I:230:PHE:HB2	2:I:333:ILE:HB	1.83	0.59
2:I:1082:ILE:H	2:I:1082:ILE:HD12	1.65	0.59
3:J:899:TYR:CE2	3:J:909:ILE:HD12	2.37	0.59
5:L:298:PRO:HB2	5:L:301:ASN:OD1	2.01	0.59
1:M:253:LEU:HD21	1:M:312:LEU:HD13	1.83	0.59
1:H:89:ALA:HB3	1:H:124:VAL:HG22	1.82	0.59
3:J:656:GLU:O	3:J:660:GLU:HG3	2.01	0.59
3:J:748:ALA:CB	6:N:16:THR:HG22	2.32	0.59
3:J:982:LEU:HB2	3:J:997:VAL:HG21	1.84	0.59
5:L:387:VAL:HG22	5:L:435:ILE:HD13	1.83	0.59
8:P:62:DG:H2''	8:P:63:DG:H2'	1.85	0.59
1:H:47:LEU:HA	1:H:51:MET:CG	2.32	0.59
2:I:227:LYS:HE3	2:I:298:ALA:HB1	1.84	0.59
3:J:826:ILE:O	3:J:994:SER:OG	2.17	0.59
3:J:1064:SER:OG	3:J:1168:GLU:OE2	2.14	0.59
5:L:235:ILE:HA	5:L:245:ALA:HB2	1.84	0.59
5:L:582:VAL:HG11	5:L:586:ARG:HG2	1.83	0.59
2:I:988:LYS:HA	2:I:991:LYS:CG	2.32	0.59
2:I:1062:PRO:HD3	2:I:1079:ILE:HD13	1.83	0.59
2:I:1103:VAL:HB	2:I:1104:PRO:HD3	1.84	0.59
3:J:418:GLU:HG3	4:K:45:LYS:H	1.66	0.59
3:J:707:ILE:HG22	3:J:708:ASN:H	1.67	0.59
3:J:1061:VAL:O	3:J:1062:LEU:HD23	2.03	0.59
3:J:1284:ARG:O	3:J:1287:ILE:HG13	2.02	0.59
2:I:868:SER:OG	2:I:942:ASP:OD2	2.19	0.59
3:J:491:LEU:O	3:J:904:ALA:HB2	2.03	0.59
2:I:1119:MET:HE2	2:I:1204:LEU:HB3	1.85	0.59
3:J:423:LEU:HB3	3:J:466:MET:CE	2.32	0.59
3:J:527:LEU:HB2	3:J:550:VAL:HG12	1.85	0.59
5:L:224:LEU:HD22	5:L:259:PHE:CE2	2.37	0.59
5:L:450:ILE:HD11	5:L:504:PRO:HD3	1.84	0.59
2:I:68:LEU:HD11	2:I:100:LEU:HD13	1.84	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1121:ALA:HB2	2:I:1182:ILE:HD12	1.84	0.59
3:J:40:LYS:HE3	3:J:42:GLU:HG3	1.84	0.59
3:J:217:LEU:O	3:J:221:ILE:HG13	2.03	0.59
5:L:416:VAL:HG22	5:L:427:PHE:HZ	1.68	0.59
3:J:338:PHE:HA	3:J:342:LEU:CD2	2.30	0.59
3:J:530:PRO:HB2	3:J:581:MET:HG2	1.85	0.59
5:L:256:PHE:CZ	5:L:261:LEU:HD21	2.38	0.59
1:H:222:THR:O	1:H:226:GLU:HG2	2.02	0.58
2:I:349:GLU:OE2	2:I:352:ARG:NH1	2.36	0.58
2:I:808:ASN:H	3:J:633:ALA:HB2	1.66	0.58
3:J:70:CYS:SG	3:J:71:LEU:N	2.76	0.58
1:H:107:ILE:HG23	1:H:135:ASP:HA	1.84	0.58
2:I:227:LYS:HE2	2:I:334:GLU:HB2	1.85	0.58
3:J:937:ILE:HG13	3:J:1134:ILE:H	1.67	0.58
3:J:1155:ILE:HD11	3:J:1211:SER:HB3	1.85	0.58
5:L:283:GLN:HE22	5:L:344:LEU:HD21	1.68	0.58
1:M:282:VAL:O	1:M:316:MET:N	2.35	0.58
1:H:58:GLU:HA	1:H:173:VAL:HG12	1.84	0.58
2:I:1340:GLU:OE1	3:J:1341:ARG:HD2	2.02	0.58
3:J:201:LEU:CD1	3:J:220:ARG:HD3	2.30	0.58
3:J:1080:ILE:HB	3:J:1097:ALA:O	2.03	0.58
1:M:251:PRO:HA	1:M:254:LEU:HD11	1.83	0.58
1:M:285:THR:O	1:M:289:LEU:HD12	2.03	0.58
2:I:298:ALA:HB3	2:I:334:GLU:CG	2.32	0.58
2:I:303:ASP:N	2:I:308:GLU:O	2.29	0.58
2:I:1117:LEU:HD12	2:I:1195:ILE:CG1	2.33	0.58
3:J:1069:ALA:HA	3:J:1072:LYS:HB3	1.85	0.58
5:L:292:VAL:HA	5:L:297:MET:HB3	1.84	0.58
1:G:16:ILE:CD1	1:G:214:GLU:HB2	2.34	0.58
2:I:210:LEU:HD21	2:I:429:MET:CE	2.32	0.58
2:I:1112:ILE:HD11	3:J:644:MET:HE1	1.85	0.58
2:I:1308:ILE:HG21	3:J:379:PRO:HB2	1.85	0.58
3:J:19:ALA:HB2	3:J:1343:GLU:HA	1.85	0.58
3:J:515:ARG:O	3:J:545:HIS:HB3	2.04	0.58
3:J:865:HIS:HE1	3:J:867:GLN:HB2	1.69	0.58
5:L:511:ILE:CG2	5:L:513:ASP:HB2	2.34	0.58
1:M:287:VAL:O	1:M:291:LYS:HG2	2.02	0.58
7:O:40:DC:C2'	7:O:41:DT:H5''	2.33	0.58
1:G:97:GLU:HG3	1:G:145:LYS:HZ3	1.69	0.58
2:I:582:ASN:HA	2:I:588:GLU:OE2	2.03	0.58
2:I:1291:LEU:CD2	3:J:1351:VAL:HG13	2.33	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:557:LYS:HG3	5:L:561:MET:CE	2.34	0.58
1:M:283:GLN:C	1:M:315:GLY:HA2	2.29	0.58
7:O:21:DA:H1'	7:O:22:DT:H5'	1.86	0.58
1:H:35:PHE:HA	1:H:38:THR:CG2	2.33	0.58
2:I:1212:LEU:HD22	2:I:1225:VAL:HG21	1.86	0.58
2:I:1260:GLY:HA3	2:I:1266:GLY:N	2.18	0.58
5:L:401:PHE:CZ	5:L:405:ILE:HD11	2.38	0.58
2:I:5:TYR:CE2	2:I:776:PRO:HD2	2.38	0.58
2:I:157:PHE:O	2:I:442:VAL:HB	2.04	0.58
2:I:452:ARG:NH2	2:I:458:GLU:OE2	2.18	0.58
2:I:1124:ILE:HG13	2:I:1198:LEU:HD11	1.86	0.58
3:J:918:ILE:O	3:J:922:SER:OG	2.18	0.58
1:G:135:ASP:HB3	1:G:138:ALA:CB	2.33	0.58
2:I:245:ARG:HH21	2:I:337:PHE:HB2	1.68	0.58
2:I:892:GLU:OE2	2:I:894:GLN:N	2.34	0.58
2:I:1153:ALA:O	2:I:1155:VAL:HG13	2.03	0.58
3:J:282:LEU:HD21	5:L:410:ILE:HG12	1.86	0.58
5:L:493:LYS:HA	5:L:496:LYS:CD	2.34	0.58
7:O:45:DA:H8	7:O:45:DA:H5''	1.68	0.58
2:I:466:VAL:O	2:I:469:VAL:HG12	2.04	0.58
3:J:607:THR:O	3:J:611:ILE:HG13	2.03	0.58
5:L:144:LEU:HD23	5:L:145:LEU:HD23	1.85	0.58
3:J:1116:SER:H	3:J:1119:ASP:HB2	1.69	0.57
5:L:145:LEU:HB3	5:L:225:ARG:CD	2.31	0.57
5:L:257:LYS:HE2	5:L:258:GLN:NE2	2.19	0.57
6:N:37:CYS:SG	6:N:39:ALA:N	2.67	0.57
5:L:378:GLU:N	5:L:378:GLU:OE2	2.38	0.57
3:J:201:LEU:HB3	3:J:221:ILE:HG12	1.86	0.57
3:J:350:SER:HA	3:J:468:VAL:O	2.04	0.57
3:J:474:LEU:CD1	4:K:47:THR:HG22	2.34	0.57
3:J:514:THR:OG1	3:J:596:LEU:HB2	2.04	0.57
3:J:958:ILE:HG21	3:J:1006:GLY:O	2.04	0.57
1:M:266:SER:O	1:M:270:LEU:HG	2.04	0.57
1:G:12:ARG:H	1:G:30:PRO:HD2	1.69	0.57
1:H:192:VAL:HG12	1:H:193:GLU:H	1.70	0.57
2:I:255:ILE:HB	2:I:263:VAL:HB	1.85	0.57
2:I:1151:LEU:HD13	2:I:1201:LEU:HD22	1.86	0.57
3:J:205:LEU:HB2	3:J:217:LEU:HD11	1.87	0.57
3:J:397:ALA:O	3:J:401:VAL:HG23	2.05	0.57
3:J:978:ARG:HA	3:J:999:TYR:HD1	1.69	0.57
3:J:1036:ARG:HE	3:J:1081:VAL:HG21	1.70	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:266:PHE:HA	5:L:269:LEU:CD1	2.34	0.57
5:L:322:MET:HB2	5:L:327:SER:CB	2.35	0.57
2:I:866:ASP:OD2	2:I:944:ARG:HG3	2.04	0.57
3:J:842:ARG:HB2	3:J:882:VAL:CG2	2.35	0.57
3:J:1190:ILE:HD13	3:J:1196:LEU:HD11	1.87	0.57
5:L:117:ILE:O	5:L:121:LYS:HG3	2.04	0.57
2:I:289:VAL:HG12	2:I:319:LEU:CD2	2.35	0.57
2:I:1271:GLY:O	2:I:1275:VAL:HG23	2.05	0.57
3:J:474:LEU:HD11	4:K:47:THR:HG22	1.87	0.57
3:J:848:VAL:HG12	3:J:858:VAL:HB	1.86	0.57
5:L:339:ARG:O	5:L:342:GLN:HG3	2.04	0.57
1:M:278:ILE:O	1:M:282:VAL:HG22	2.04	0.57
1:G:208:ASN:OD1	1:G:210:THR:HG22	2.04	0.57
1:H:48:LEU:HD13	1:H:183:ILE:CD1	2.35	0.57
3:J:203:GLU:O	3:J:207:GLU:HB2	2.05	0.57
3:J:393:THR:HG23	3:J:395:LYS:H	1.70	0.57
3:J:514:THR:OG1	3:J:514:THR:O	2.20	0.57
3:J:772:TYR:O	3:J:776:THR:HG23	2.05	0.57
3:J:975:ILE:N	3:J:1000:GLY:HA2	2.19	0.57
3:J:1251:LYS:O	3:J:1255:VAL:HG23	2.05	0.57
5:L:543:ALA:O	5:L:547:VAL:HG13	2.04	0.57
7:O:46:DG:H3'	7:O:46:DG:OP2	2.04	0.57
2:I:360:LEU:O	2:I:364:VAL:HG13	2.04	0.57
2:I:835:GLU:HB2	2:I:1053:TYR:CD1	2.39	0.57
3:J:416:ILE:HG13	3:J:441:LEU:HD21	1.85	0.57
3:J:850:LYS:HG2	3:J:851:PRO:HD2	1.87	0.57
3:J:1367:GLN:O	3:J:1371:ARG:HG3	2.05	0.57
5:L:225:ARG:O	5:L:229:VAL:HG13	2.05	0.57
8:P:56:DG:H2'	8:P:57:DT:H71	1.86	0.57
1:G:135:ASP:HB3	1:G:138:ALA:HB3	1.87	0.57
2:I:168:GLY:O	6:N:72:TYR:HB3	2.05	0.57
2:I:429:MET:O	2:I:433:ILE:HG13	2.05	0.57
2:I:964:LEU:HD13	2:I:1025:PHE:CD2	2.40	0.57
3:J:1109:LEU:HD12	3:J:1121:LEU:CD1	2.33	0.57
3:J:1194:ARG:HD3	3:J:1211:SER:OG	2.05	0.57
3:J:1221:LEU:HD23	3:J:1229:VAL:HG11	1.86	0.57
1:G:155:ALA:O	1:G:159:ILE:HG22	2.04	0.57
2:I:225:PHE:CE2	2:I:347:ILE:HB	2.40	0.57
2:I:930:ASP:HB3	2:I:1053:TYR:HD2	1.70	0.57
3:J:132:LEU:O	3:J:136:GLU:HG2	2.05	0.57
3:J:514:THR:O	3:J:595:ALA:HA	2.05	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1003:LEU:HA	3:J:1018:ALA:CB	2.35	0.57
3:J:1021:ASP:HB3	3:J:1024:THR:HG23	1.86	0.57
1:G:45:ARG:CD	2:I:1083:GLU:HG3	2.35	0.56
1:H:134:THR:HG22	1:H:138:ALA:HB3	1.88	0.56
2:I:770:CYS:HB3	2:I:785:ASP:OD2	2.05	0.56
2:I:1314:GLN:HB2	4:K:28:ARG:HH11	1.70	0.56
5:L:123:ILE:HD11	5:L:379:MET:CE	2.34	0.56
5:L:144:LEU:HD13	5:L:256:PHE:CZ	2.40	0.56
5:L:460:ILE:HG22	5:L:497:VAL:CG1	2.35	0.56
5:L:580:PHE:O	5:L:582:VAL:HG23	2.04	0.56
2:I:231:GLU:HA	2:I:331:LYS:O	2.06	0.56
2:I:271:ALA:O	2:I:275:ARG:HG3	2.04	0.56
2:I:403:MET:HE2	2:I:584:TYR:CD2	2.40	0.56
2:I:444:ASP:O	2:I:447:HIS:HB2	2.06	0.56
2:I:660:VAL:HG11	3:J:769:VAL:HG13	1.86	0.56
2:I:848:GLU:OE1	2:I:886:LYS:NZ	2.29	0.56
2:I:949:GLU:O	2:I:953:LEU:HG	2.05	0.56
3:J:111:THR:HG21	3:J:303:VAL:HG11	1.86	0.56
3:J:849:LEU:CD1	3:J:856:ILE:HA	2.35	0.56
5:L:9:LEU:HD11	5:L:32:PRO:CD	2.34	0.56
5:L:138:PRO:O	5:L:142:THR:HG23	2.05	0.56
5:L:249:ILE:HG23	5:L:252:LEU:HD22	1.87	0.56
5:L:467:SER:OG	5:L:478:PRO:HG3	2.06	0.56
1:H:102:LEU:HD13	1:H:142:MET:HE3	1.88	0.56
2:I:242:VAL:CB	2:I:245:ARG:HD3	2.34	0.56
2:I:820:GLU:HB2	2:I:1080:ASN:O	2.05	0.56
2:I:861:ALA:HB1	2:I:882:ILE:CD1	2.35	0.56
2:I:1103:VAL:HG11	2:I:1112:ILE:HD13	1.86	0.56
2:I:1113:LEU:HD13	3:J:641:ILE:CD1	2.35	0.56
3:J:105:ILE:HD13	3:J:273:ILE:HG13	1.87	0.56
3:J:582:ILE:HD12	3:J:627:THR:HG21	1.86	0.56
3:J:809:VAL:HG21	3:J:909:ILE:CG2	2.32	0.56
4:K:41:GLU:HB2	4:K:49:ILE:HD11	1.87	0.56
5:L:137:TYR:CE2	5:L:139:GLU:HB3	2.39	0.56
5:L:493:LYS:O	5:L:496:LYS:HG2	2.05	0.56
5:L:600:HIS:CE1	1:M:259:ASP:HA	2.40	0.56
1:G:89:ALA:O	1:G:124:VAL:HG22	2.05	0.56
1:H:205:MET:CE	1:H:217:ILE:HG13	2.36	0.56
3:J:975:ILE:H	3:J:1000:GLY:HA2	1.70	0.56
7:O:40:DC:H2'	7:O:41:DT:H71	1.87	0.56
1:H:31:LEU:O	1:H:198:LEU:HD22	2.05	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:148:GLN:HB2	2:I:511:LEU:HD11	1.87	0.56
2:I:165:HIS:ND1	2:I:167:SER:HB3	2.21	0.56
2:I:320:ASP:N	2:I:320:ASP:OD1	2.38	0.56
3:J:79:LYS:CB	5:L:569:THR:HB	2.31	0.56
3:J:937:ILE:HG12	3:J:1134:ILE:O	2.06	0.56
1:G:107:ILE:HG23	1:G:134:THR:HA	1.88	0.56
1:H:103:ASN:HA	1:H:140:ILE:O	2.06	0.56
3:J:511:TYR:CG	3:J:728:SER:HB3	2.40	0.56
3:J:825:VAL:HG22	3:J:827:GLU:HG3	1.88	0.56
5:L:84:LEU:HA	5:L:87:VAL:HG12	1.88	0.56
1:G:207:THR:HG21	1:G:211:ILE:HG22	1.88	0.56
1:H:14:VAL:HG13	1:H:28:LEU:HD13	1.88	0.56
2:I:197:ARG:HH22	2:I:203:LYS:HD2	1.70	0.56
3:J:126:LEU:HD11	3:J:223:LEU:HD22	1.87	0.56
3:J:156:ARG:NH2	3:J:191:SER:OG	2.39	0.56
3:J:255:LEU:HB2	3:J:259:ARG:O	2.05	0.56
3:J:603:LYS:O	3:J:607:THR:HG23	2.06	0.56
3:J:1287:ILE:HG22	3:J:1290:ARG:HH21	1.70	0.56
4:K:26:ARG:HE	4:K:30:MET:HE3	1.70	0.56
2:I:36:GLN:O	2:I:40:GLU:HB2	2.06	0.56
2:I:185:ASP:HB3	2:I:187:GLU:OE2	2.06	0.56
2:I:817:LEU:HB3	2:I:1097:VAL:HB	1.87	0.56
3:J:390:LEU:HD23	3:J:407:VAL:CG2	2.36	0.56
3:J:660:GLU:HB2	3:J:685:ILE:HD13	1.87	0.56
5:L:27:VAL:O	5:L:31:LEU:HG	2.06	0.56
5:L:119:ILE:CG2	5:L:375:ALA:HB1	2.32	0.56
5:L:152:GLU:CB	5:L:218:ARG:HD3	2.36	0.56
5:L:256:PHE:HZ	5:L:261:LEU:HD21	1.69	0.56
1:M:255:ARG:O	1:M:278:ILE:HG12	2.06	0.56
1:M:298:LYS:HB2	8:P:67:DT:H3'	1.86	0.56
6:N:48:ARG:HH11	6:N:59:VAL:HG22	1.71	0.56
7:O:34:DA:H4'	7:O:35:DG:OP1	2.06	0.56
2:I:210:LEU:O	2:I:215:TYR:HB2	2.05	0.56
2:I:551:HIS:ND1	2:I:553:THR:HG23	2.21	0.56
3:J:233:LYS:HD2	3:J:235:GLU:OE2	2.06	0.56
4:K:6:VAL:O	4:K:10:VAL:HG23	2.06	0.56
5:L:469:GLN:O	5:L:473:GLU:HG3	2.06	0.56
2:I:484:LEU:HG	2:I:485:ASP:H	1.71	0.56
5:L:479:THR:CG2	5:L:482:GLU:H	2.19	0.56
2:I:118:LYS:CD	2:I:488:MET:HG2	2.36	0.55
2:I:196:VAL:CG2	2:I:206:ALA:HA	2.36	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:231:GLU:HB2	2:I:238:GLN:NE2	2.20	0.55
2:I:1119:MET:HE3	2:I:1210:ILE:HD11	1.88	0.55
3:J:22:ILE:HG22	3:J:1340:LYS:O	2.06	0.55
3:J:1177:ILE:O	3:J:1179:PRO:HD3	2.06	0.55
4:K:26:ARG:HD3	4:K:59:ILE:CD1	2.33	0.55
5:L:419:PHE:CE1	5:L:427:PHE:HA	2.41	0.55
1:G:58:GLU:OE1	1:G:170:ARG:NH1	2.36	0.55
2:I:107:ARG:NH2	2:I:108:GLU:HA	2.21	0.55
2:I:227:LYS:HE3	2:I:298:ALA:CB	2.36	0.55
3:J:516:ASP:HA	3:J:545:HIS:HB2	1.88	0.55
3:J:664:ILE:CG2	3:J:678:ARG:HG3	2.35	0.55
3:J:914:ALA:O	3:J:918:ILE:HG13	2.06	0.55
3:J:1272:SER:CB	3:J:1300:ALA:HB2	2.36	0.55
5:L:96:ASP:OD1	5:L:98:VAL:HG12	2.05	0.55
1:M:283:GLN:O	1:M:315:GLY:HA2	2.05	0.55
7:O:21:DA:H1'	7:O:22:DT:C5'	2.36	0.55
1:H:71:LYS:HB3	1:H:74:VAL:CG2	2.36	0.55
2:I:6:THR:O	2:I:6:THR:OG1	2.24	0.55
2:I:76:GLY:N	2:I:95:PRO:O	2.33	0.55
2:I:270:THR:HG22	6:N:42:ASN:HD21	1.72	0.55
2:I:629:PHE:HB2	2:I:647:ARG:HD2	1.88	0.55
2:I:1332:SER:CB	3:J:245:LEU:HD13	2.36	0.55
3:J:123:ARG:HA	3:J:126:LEU:CD2	2.35	0.55
3:J:140:TYR:O	3:J:297:ARG:NH1	2.39	0.55
3:J:511:TYR:CE2	3:J:724:MET:HG2	2.41	0.55
3:J:1177:ILE:N	3:J:1186:TYR:O	2.26	0.55
1:G:22:THR:HB	1:G:207:THR:O	2.07	0.55
2:I:192:ASP:OD2	2:I:436:ARG:NH2	2.39	0.55
2:I:1033:ARG:O	2:I:1037:THR:HG22	2.07	0.55
3:J:645:VAL:HG22	3:J:700:ASN:HD21	1.70	0.55
5:L:41:ILE:O	5:L:45:ILE:HG22	2.05	0.55
5:L:406:GLN:O	5:L:410:ILE:HG13	2.06	0.55
5:L:572:THR:O	5:L:576:VAL:HG23	2.07	0.55
1:H:182:ARG:O	1:H:205:MET:HA	2.07	0.55
2:I:559:CYS:HB2	2:I:662:SER:HB3	1.88	0.55
2:I:690:VAL:HG23	2:I:763:THR:HG21	1.89	0.55
2:I:697:LYS:HD2	2:I:1181:PRO:HG3	1.87	0.55
3:J:683:ILE:HD12	6:N:23:ILE:HD13	1.89	0.55
3:J:816:THR:HG23	3:J:889:ASP:HB2	1.88	0.55
5:L:375:ALA:O	5:L:379:MET:HG2	2.06	0.55
8:P:42:DT:H1'	8:P:43:DT:C5'	2.35	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:65:ASN:HB3	2:I:105:TYR:CB	2.37	0.55
2:I:231:GLU:HB2	2:I:238:GLN:HE21	1.71	0.55
2:I:1127:LYS:O	2:I:1131:MET:HG3	2.06	0.55
3:J:127:LEU:CD2	3:J:234:PRO:HB3	2.37	0.55
3:J:975:ILE:HB	3:J:1000:GLY:H	1.70	0.55
4:K:8:ASP:HB2	4:K:55:GLU:HG3	1.88	0.55
5:L:141:ILE:O	5:L:145:LEU:HG	2.07	0.55
5:L:387:VAL:HG22	5:L:435:ILE:CD1	2.37	0.55
5:L:511:ILE:HG23	5:L:513:ASP:HB2	1.89	0.55
1:H:208:ASN:N	1:H:208:ASN:OD1	2.39	0.55
2:I:70:TYR:HA	2:I:100:LEU:CD2	2.37	0.55
2:I:232:ILE:HG13	2:I:237:LEU:HD23	1.87	0.55
2:I:359:ARG:O	2:I:363:LEU:HD12	2.07	0.55
2:I:470:ARG:HD2	2:I:497:PRO:HB3	1.88	0.55
2:I:618:GLN:HE22	3:J:770:LEU:HD23	1.72	0.55
3:J:381:ILE:HD11	3:J:412:LEU:HD13	1.89	0.55
3:J:1116:SER:N	3:J:1119:ASP:HB2	2.21	0.55
3:J:1163:VAL:O	3:J:1200:GLU:HG2	2.07	0.55
3:J:1194:ARG:HD3	3:J:1211:SER:CB	2.37	0.55
3:J:239:LEU:HD11	3:J:307:LEU:HD11	1.87	0.55
5:L:270:VAL:O	5:L:274:ARG:HG2	2.06	0.55
2:I:75:LEU:HD11	2:I:127:ILE:HD11	1.89	0.55
2:I:411:ARG:NH2	2:I:424:ASP:OD1	2.39	0.55
2:I:728:ASP:OD1	2:I:729:ALA:N	2.39	0.55
3:J:130:MET:HE2	3:J:134:ASP:C	2.31	0.55
3:J:385:LEU:CD2	3:J:411:ILE:HG13	2.37	0.55
3:J:454:CYS:HB3	3:J:459:ALA:O	2.07	0.55
3:J:872:LEU:O	3:J:877:VAL:HG23	2.07	0.55
2:I:829:THR:HG22	2:I:1057:LYS:HG2	1.89	0.55
3:J:124:ILE:HG22	3:J:135:ILE:HD13	1.89	0.55
3:J:259:ARG:HH21	5:L:502:LYS:HD3	1.72	0.55
3:J:388:ARG:HB2	3:J:390:LEU:HD13	1.88	0.55
3:J:391:ALA:HB2	3:J:400:MET:SD	2.47	0.55
2:I:1067:ALA:HB3	2:I:1235:LEU:HD21	1.89	0.54
2:I:1104:PRO:HG2	3:J:725:MET:SD	2.47	0.54
3:J:1198:VAL:CG1	3:J:1210:ILE:HG23	2.37	0.54
5:L:565:ILE:HG22	5:L:566:ASP:OD2	2.07	0.54
1:H:107:ILE:HA	1:H:134:THR:O	2.07	0.54
2:I:71:VAL:HB	2:I:99:LYS:O	2.07	0.54
2:I:800:MET:HE1	2:I:822:VAL:HG22	1.88	0.54
3:J:1061:VAL:HG11	3:J:1101:LEU:CB	2.37	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:289:LYS:HA	5:L:293:GLU:CB	2.36	0.54
5:L:574:GLU:O	5:L:578:LYS:HG3	2.07	0.54
8:P:38:DC:C2'	8:P:39:DC:H5''	2.36	0.54
2:I:303:ASP:HB2	2:I:310:ILE:HD11	1.90	0.54
2:I:453:ILE:HG22	2:I:585:GLY:O	2.07	0.54
2:I:479:LEU:HG	2:I:492:MET:HE1	1.90	0.54
2:I:508:SER:O	2:I:508:SER:OG	2.25	0.54
2:I:898:GLU:CG	5:L:544:THR:HG21	2.35	0.54
2:I:1304:MET:CE	2:I:1315:MET:HB3	2.38	0.54
3:J:559:ALA:HB3	3:J:562:GLU:O	2.07	0.54
3:J:985:ILE:HD13	3:J:991:THR:HA	1.89	0.54
4:K:72:GLN:HA	4:K:75:GLN:OE1	2.07	0.54
5:L:570:ASP:OD1	5:L:570:ASP:N	2.40	0.54
1:M:318:LEU:HD23	1:M:321:TRP:CG	2.42	0.54
2:I:84:GLU:O	2:I:88:ARG:HG3	2.07	0.54
2:I:170:VAL:HG23	6:N:72:TYR:CB	2.30	0.54
2:I:539:THR:HG22	2:I:541:GLU:H	1.72	0.54
2:I:548:ARG:HD2	2:I:569:ILE:O	2.06	0.54
3:J:491:LEU:HB2	3:J:904:ALA:CB	2.37	0.54
3:J:1023:HIS:O	3:J:1125:PRO:HA	2.08	0.54
2:I:475:VAL:HG22	2:I:492:MET:HE2	1.90	0.54
2:I:877:VAL:HG13	2:I:881:ASP:HB2	1.90	0.54
3:J:146:VAL:HA	3:J:178:ALA:HA	1.88	0.54
3:J:646:ILE:HD11	3:J:762:ASN:HD21	1.73	0.54
4:K:50:ALA:O	4:K:54:ILE:HG13	2.07	0.54
5:L:130:VAL:CG1	5:L:365:MET:HG3	2.34	0.54
1:H:107:ILE:CG2	1:H:135:ASP:HA	2.37	0.54
2:I:194:LEU:HB3	2:I:206:ALA:CB	2.38	0.54
2:I:594:VAL:HG11	2:I:650:VAL:HG23	1.89	0.54
3:J:789:LYS:NZ	3:J:928:THR:O	2.22	0.54
3:J:826:ILE:HD11	3:J:992:LYS:O	2.08	0.54
3:J:1027:VAL:CG2	3:J:1122:ALA:HB3	2.38	0.54
3:J:1090:ILE:HG12	3:J:1097:ALA:HA	1.89	0.54
3:J:1310:THR:O	3:J:1314:LEU:HD13	2.07	0.54
5:L:9:LEU:CD2	5:L:44:ILE:HD11	2.38	0.54
5:L:137:TYR:OH	5:L:351:THR:HA	2.08	0.54
5:L:228:TYR:CD1	5:L:252:LEU:HD12	2.43	0.54
5:L:379:MET:HE3	5:L:416:VAL:CG1	2.38	0.54
5:L:554:ARG:HD2	5:L:580:PHE:CE1	2.41	0.54
1:M:283:GLN:NE2	1:M:318:LEU:HB2	2.22	0.54
2:I:153:PRO:HB2	2:I:401:GLY:HA3	1.88	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:478:ARG:HH22	2:I:483:ASP:HB2	1.73	0.54
2:I:661:VAL:HG11	2:I:671:LEU:CD2	2.37	0.54
2:I:961:SER:O	2:I:965:GLN:HG3	2.07	0.54
3:J:385:LEU:HD23	3:J:411:ILE:HG13	1.89	0.54
3:J:511:TYR:HE2	3:J:724:MET:HG2	1.72	0.54
3:J:952:VAL:CG2	3:J:984:LEU:HD22	2.38	0.54
3:J:1178:THR:HA	3:J:1184:ASP:O	2.08	0.54
3:J:1268:ASN:HB3	3:J:1301:THR:OG1	2.07	0.54
2:I:136:PHE:HB3	2:I:138:ILE:HD13	1.88	0.54
2:I:268:ARG:HB3	6:N:40:CYS:CB	2.37	0.54
2:I:556:GLY:HA2	2:I:659:GLN:O	2.07	0.54
2:I:1340:GLU:HG3	3:J:21:LYS:HB2	1.89	0.54
3:J:697:MET:CE	3:J:741:ALA:HB3	2.37	0.54
3:J:1152:GLU:O	3:J:1214:PRO:HD2	2.08	0.54
5:L:459:THR:HG23	5:L:489:MET:HE1	1.90	0.54
1:G:40:GLY:HA2	1:G:201:LEU:HD21	1.90	0.54
2:I:11:ILE:O	2:I:1149:TYR:OH	2.24	0.54
2:I:268:ARG:HB3	6:N:40:CYS:HB2	1.89	0.54
2:I:494:ASN:HB3	2:I:497:PRO:HD2	1.90	0.54
2:I:958:LYS:HD3	2:I:962:GLU:OE2	2.07	0.54
3:J:762:ASN:N	3:J:762:ASN:OD1	2.39	0.54
3:J:1023:HIS:CA	3:J:1125:PRO:HA	2.38	0.54
5:L:415:ALA:O	5:L:419:PHE:N	2.41	0.54
1:M:275:ILE:HG12	1:M:284:ARG:HH12	1.73	0.54
1:M:296:GLY:N	8:P:68:DG:OP1	2.40	0.54
6:N:58:CYS:SG	6:N:60:GLU:HG2	2.48	0.54
7:O:44:DA:H4'	7:O:45:DA:OP1	2.08	0.54
1:G:152:TYR:CD2	1:G:154:PRO:HD3	2.43	0.54
1:H:56:VAL:HG22	1:H:146:VAL:HG23	1.90	0.54
2:I:448:LEU:HB2	2:I:553:THR:OG1	2.08	0.54
2:I:753:LEU:HD11	2:I:769:PRO:HG3	1.90	0.54
2:I:846:GLY:O	2:I:889:PRO:HG3	2.07	0.54
2:I:1141:LEU:HD21	2:I:1173:ALA:HB1	1.90	0.54
3:J:1170:LYS:CD	3:J:1172:LYS:HE3	2.36	0.54
3:J:1368:ASP:O	3:J:1372:ARG:HG2	2.08	0.54
7:O:40:DC:H2''	7:O:41:DT:C6	2.43	0.54
2:I:204:LEU:CD1	2:I:369:MET:HE2	2.37	0.53
3:J:1049:GLN:O	3:J:1058:SER:HB2	2.08	0.53
5:L:322:MET:HB3	5:L:324:LYS:HG2	1.90	0.53
5:L:376:LYS:O	5:L:380:VAL:HG22	2.08	0.53
2:I:529:ARG:HD3	2:I:572:ILE:CG2	2.38	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:854:ILE:HG22	2:I:855:PRO:HD2	1.91	0.53
2:I:1132:LEU:HD13	2:I:1177:ARG:NH1	2.23	0.53
2:I:1192:GLU:O	2:I:1196:LYS:HG2	2.07	0.53
2:I:1275:VAL:HG13	2:I:1287:LEU:HD21	1.89	0.53
3:J:325:LYS:HE2	3:J:329:ASP:OD2	2.08	0.53
3:J:1175:LEU:HD13	3:J:1190:ILE:CD1	2.37	0.53
5:L:228:TYR:HD1	5:L:252:LEU:HD12	1.73	0.53
5:L:571:TYR:HB3	5:L:575:GLU:HB3	1.89	0.53
8:P:59:DA:H2''	8:P:60:DA:C5'	2.38	0.53
2:I:559:CYS:SG	2:I:662:SER:OG	2.51	0.53
2:I:883:LEU:HG	2:I:920:VAL:HG23	1.89	0.53
3:J:1109:LEU:HD22	3:J:1113:VAL:HB	1.90	0.53
1:H:29:GLU:HG2	1:H:30:PRO:CA	2.39	0.53
3:J:179:LYS:HB3	3:J:184:ALA:HB2	1.89	0.53
3:J:331:ILE:HG22	3:J:1328:THR:HG21	1.90	0.53
3:J:1035:VAL:N	3:J:1113:VAL:O	2.32	0.53
5:L:232:ARG:O	5:L:235:ILE:HG23	2.08	0.53
5:L:493:LYS:O	5:L:497:VAL:HG23	2.08	0.53
5:L:593:LYS:HG2	5:L:596:ARG:HH21	1.74	0.53
1:M:253:LEU:HD22	1:M:282:VAL:HG11	1.90	0.53
2:I:39:ILE:CD1	2:I:75:LEU:HG	2.37	0.53
3:J:844:THR:CG2	3:J:864:LEU:HD11	2.38	0.53
5:L:9:LEU:HD13	5:L:88:GLU:HG2	1.90	0.53
2:I:246:LEU:HD22	2:I:249:GLU:OE1	2.08	0.53
2:I:519:ASN:OD1	2:I:796:LEU:HD22	2.09	0.53
2:I:671:LEU:CB	2:I:1186:VAL:HG12	2.38	0.53
2:I:813:GLU:HB2	3:J:461:PHE:CD2	2.43	0.53
2:I:877:VAL:CG1	2:I:920:VAL:HG21	2.37	0.53
3:J:422:LEU:HD13	3:J:471:PRO:HG3	1.89	0.53
3:J:1167:LYS:O	3:J:1173:ARG:HA	2.09	0.53
5:L:108:VAL:HG21	5:L:381:GLU:CD	2.34	0.53
5:L:297:MET:HE3	5:L:326:TRP:CZ3	2.43	0.53
5:L:383:ASN:HA	5:L:386:LEU:HB3	1.90	0.53
8:P:64:DA:C1'	8:P:65:DT:H5''	2.38	0.53
1:H:23:HIS:ND1	1:H:206:GLU:HG2	2.24	0.53
2:I:241:LEU:HD21	2:I:277:LEU:CD1	2.39	0.53
2:I:598:VAL:HA	2:I:627:GLY:O	2.08	0.53
3:J:205:LEU:HB2	3:J:217:LEU:CD1	2.38	0.53
3:J:553:THR:HG22	3:J:567:THR:CB	2.36	0.53
3:J:827:GLU:HB2	3:J:832:LYS:HE2	1.90	0.53
3:J:842:ARG:NH2	3:J:1254:GLU:OE1	2.28	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1011:VAL:HG11	3:J:1015:GLU:CD	2.33	0.53
5:L:37:ASP:HB2	5:L:40:GLN:CG	2.25	0.53
5:L:162:ILE:N	5:L:262:VAL:HG23	2.24	0.53
6:N:44:ILE:O	6:N:49:ARG:NH2	2.33	0.53
2:I:221:LEU:HD23	2:I:336:LEU:HD21	1.91	0.53
8:P:53:DT:H2''	8:P:54:DT:H5'	1.91	0.53
2:I:253:PHE:CE2	2:I:287:VAL:HG12	2.43	0.53
2:I:255:ILE:HG23	2:I:285:ILE:HD12	1.90	0.53
2:I:454:ARG:HD2	2:I:459:MET:HG2	1.91	0.53
2:I:1085:MET:HE2	2:I:1085:MET:HA	1.89	0.53
2:I:1107:MET:HG2	3:J:740:LEU:HD13	1.91	0.53
3:J:481:ARG:NH1	4:K:3:ARG:O	2.42	0.53
3:J:495:ASN:OD1	3:J:497:GLU:HB2	2.09	0.53
3:J:705:THR:OG1	3:J:718:SER:HA	2.09	0.53
3:J:1021:ASP:HB3	3:J:1024:THR:CG2	2.39	0.53
3:J:1226:VAL:HG23	3:J:1261:LEU:CD2	2.39	0.53
5:L:600:HIS:HB3	1:M:261:GLU:OE2	2.09	0.53
1:G:13:LEU:HD21	1:G:26:VAL:HG13	1.90	0.53
1:G:51:MET:CE	1:G:211:ILE:HD13	2.39	0.53
2:I:192:ASP:HB3	2:I:346:TYR:CD1	2.44	0.53
2:I:349:GLU:O	2:I:353:VAL:HG23	2.09	0.53
3:J:40:LYS:HE2	3:J:53:ARG:HG3	1.91	0.53
3:J:138:VAL:HG21	3:J:145:VAL:HG12	1.91	0.53
3:J:388:ARG:NH2	3:J:414:GLU:OE1	2.39	0.53
3:J:1150:PRO:O	3:J:1153:PRO:HG3	2.09	0.53
3:J:1157:ALA:HB1	3:J:1204:VAL:CG1	2.39	0.53
1:G:183:ILE:CD1	1:G:205:MET:HB2	2.39	0.52
1:H:205:MET:HE3	1:H:213:PRO:HB3	1.89	0.52
2:I:812:PHE:CD2	2:I:813:GLU:HG2	2.43	0.52
3:J:438:GLU:OE2	3:J:481:ARG:NH2	2.21	0.52
5:L:369:GLU:O	5:L:373:ARG:HG3	2.09	0.52
1:M:270:LEU:CB	1:M:275:ILE:HB	2.37	0.52
1:G:207:THR:HG21	1:G:211:ILE:CG2	2.39	0.52
1:H:134:THR:HG23	1:H:136:GLU:N	2.23	0.52
5:L:229:VAL:HB	5:L:232:ARG:HH21	1.72	0.52
2:I:356:THR:HG23	2:I:361:SER:HB2	1.90	0.52
3:J:124:ILE:HG22	3:J:135:ILE:CD1	2.39	0.52
3:J:523:GLU:OE2	3:J:547:ARG:NH2	2.42	0.52
3:J:781:LYS:HE3	3:J:785:ASP:OD1	2.08	0.52
5:L:125:ASP:O	5:L:129:GLN:HG3	2.10	0.52
7:O:39:DG:H5''	7:O:39:DG:C8	2.45	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:32:GLU:HB3	1:H:35:PHE:CD1	2.45	0.52
1:H:95:LYS:HD2	1:H:96:ASP:H	1.74	0.52
2:I:520:PRO:HB2	2:I:794:LEU:HD13	1.92	0.52
2:I:803:ALA:HB2	2:I:1227:VAL:HG12	1.92	0.52
3:J:56:LEU:HD21	3:J:269:TYR:HB2	1.91	0.52
3:J:201:LEU:HB3	3:J:221:ILE:CD1	2.39	0.52
3:J:361:LEU:HD13	3:J:366:CYS:HA	1.90	0.52
3:J:647:PRO:HG3	3:J:697:MET:HB3	1.92	0.52
3:J:1178:THR:HG23	3:J:1184:ASP:HB3	1.90	0.52
5:L:102:MET:O	5:L:105:MET:HG3	2.10	0.52
5:L:285:ARG:O	5:L:289:LYS:HG2	2.10	0.52
5:L:400:GLN:HB2	5:L:403:ASP:OD1	2.08	0.52
7:O:41:DT:H1'	7:O:42:DA:H5'	1.90	0.52
2:I:95:PRO:HG3	2:I:126:GLU:OE2	2.10	0.52
2:I:228:VAL:HB	2:I:335:THR:OG1	2.10	0.52
2:I:240:GLU:HG2	2:I:284:LEU:HD11	1.92	0.52
3:J:331:ILE:CG2	3:J:1328:THR:HG21	2.39	0.52
3:J:341:ASN:O	3:J:345:LYS:HE2	2.10	0.52
3:J:518:VAL:CG1	3:J:707:ILE:HB	2.37	0.52
3:J:686:TRP:CD2	3:J:758:PRO:HG3	2.44	0.52
3:J:807:LEU:HD11	3:J:1259:GLN:HG2	1.90	0.52
3:J:1348:LYS:O	3:J:1352:ILE:HD12	2.09	0.52
5:L:247:GLU:O	5:L:250:LEU:HG	2.09	0.52
5:L:313:ASP:O	5:L:317:ASN:N	2.41	0.52
1:M:264:VAL:HG22	1:M:268:ASN:HD21	1.74	0.52
2:I:459:MET:HE1	2:I:511:LEU:HD13	1.91	0.52
2:I:1145:ILE:HG22	2:I:1161:LEU:HD11	1.92	0.52
2:I:1304:MET:O	2:I:1308:ILE:HG12	2.10	0.52
3:J:43:THR:HG21	5:L:449:THR:OG1	2.09	0.52
3:J:163:GLU:HA	3:J:166:LEU:CD1	2.36	0.52
3:J:654:ILE:HD13	3:J:760:THR:HB	1.92	0.52
3:J:975:ILE:HD13	3:J:980:THR:CB	2.32	0.52
4:K:44:ASP:HB3	4:K:48:VAL:HG23	1.91	0.52
1:M:270:LEU:CA	1:M:275:ILE:HB	2.40	0.52
1:G:23:HIS:HE1	1:G:204:GLU:HG3	1.74	0.52
2:I:61:SER:HB3	2:I:65:ASN:N	2.24	0.52
2:I:1185:PRO:HB2	2:I:1188:ASP:HB3	1.92	0.52
2:I:1325:VAL:O	2:I:1329:GLU:HG3	2.09	0.52
3:J:71:LEU:HB2	3:J:90:VAL:HG21	1.90	0.52
3:J:320:ASN:HD22	3:J:322:ARG:HH21	1.58	0.52
3:J:491:LEU:HD22	3:J:496:GLY:O	2.09	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:660:GLU:CB	3:J:685:ILE:HD13	2.39	0.52
3:J:1034:PHE:CD2	3:J:1083:ALA:HA	2.45	0.52
5:L:226:ALA:O	5:L:230:VAL:HG22	2.09	0.52
5:L:285:ARG:HA	5:L:289:LYS:HE2	1.92	0.52
8:P:51:DC:H2''	8:P:52:DT:H71	1.90	0.52
2:I:246:LEU:HA	2:I:249:GLU:CD	2.35	0.52
2:I:292:ILE:HG22	2:I:317:LEU:HD12	1.90	0.52
2:I:1148:ALA:HA	2:I:1201:LEU:CD2	2.39	0.52
3:J:984:LEU:HB3	3:J:993:GLU:HB2	1.92	0.52
3:J:1155:ILE:HD12	3:J:1155:ILE:O	2.10	0.52
1:G:45:ARG:HH22	2:I:1216:ARG:HG2	1.75	0.52
2:I:205:PRO:O	2:I:208:ILE:HG22	2.10	0.52
2:I:218:GLU:CD	2:I:299:LYS:HB2	2.35	0.52
2:I:958:LYS:O	2:I:962:GLU:HG3	2.09	0.52
3:J:53:ARG:HB3	3:J:54:ASP:HB3	1.92	0.52
3:J:268:LEU:CB	3:J:306:LEU:HD23	2.39	0.52
3:J:275:ARG:NH2	5:L:403:ASP:OD1	2.40	0.52
3:J:349:TYR:CD2	3:J:472:LEU:HD11	2.44	0.52
3:J:812:ASP:O	3:J:897:HIS:ND1	2.37	0.52
3:J:1221:LEU:HD23	3:J:1229:VAL:CG1	2.39	0.52
8:P:46:DG:H2''	8:P:47:DC:C6	2.45	0.52
1:G:226:GLU:OE2	1:H:10:LYS:NZ	2.35	0.52
2:I:230:PHE:O	2:I:231:GLU:HG3	2.10	0.52
2:I:596:ASP:OD1	2:I:596:ASP:N	2.42	0.52
2:I:1289:GLU:O	2:I:1294:LYS:HG3	2.10	0.52
3:J:443:GLU:OE2	3:J:444:GLY:N	2.43	0.52
3:J:653:ILE:HG12	3:J:692:ARG:NH2	2.25	0.52
3:J:799:ARG:HD3	3:J:1310:THR:CG2	2.40	0.52
3:J:934:THR:HA	3:J:1137:GLY:HA3	1.91	0.52
3:J:1040:MET:CE	3:J:1078:LEU:HG	2.39	0.52
5:L:381:GLU:HA	5:L:384:LEU:CD2	2.39	0.52
5:L:503:GLU:OE2	5:L:504:PRO:HD2	2.10	0.52
1:M:270:LEU:HD22	1:M:275:ILE:CD1	2.39	0.52
1:M:280:ASP:O	1:M:283:GLN:HB2	2.09	0.52
7:O:38:DG:H1'	7:O:39:DG:H5''	1.92	0.52
2:I:470:ARG:HD3	2:I:497:PRO:HB3	1.91	0.51
2:I:736:VAL:HG12	2:I:737:ASN:O	2.10	0.51
3:J:66:LYS:HE2	3:J:69:GLU:OE1	2.09	0.51
3:J:421:VAL:HG13	3:J:439:PRO:HG3	1.92	0.51
3:J:1005:LYS:HG3	3:J:1009:GLU:HB2	1.91	0.51
3:J:1104:LYS:O	3:J:1124:ILE:HA	2.11	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:65:ASP:O	4:K:69:ARG:HG2	2.10	0.51
2:I:136:PHE:CE2	2:I:456:VAL:HG21	2.46	0.51
2:I:198:ILE:HG22	2:I:199:ASP:OD1	2.09	0.51
3:J:596:LEU:HD13	3:J:601:ILE:HG13	1.91	0.51
3:J:847:ASP:OD1	3:J:860:ARG:N	2.43	0.51
3:J:919:ALA:O	3:J:923:ILE:HG13	2.11	0.51
3:J:973:LEU:HB3	3:J:1003:LEU:HD12	1.92	0.51
3:J:1260:MET:HE3	3:J:1307:LEU:O	2.10	0.51
5:L:363:ARG:O	5:L:367:ILE:HG13	2.10	0.51
2:I:21:VAL:HG21	2:I:592:ARG:CZ	2.40	0.51
2:I:347:ILE:HA	2:I:350:THR:CG2	2.39	0.51
2:I:754:THR:O	2:I:766:ASN:HA	2.10	0.51
3:J:343:LEU:HD21	3:J:1352:ILE:HD11	1.91	0.51
3:J:1009:GLU:O	3:J:1011:VAL:HG23	2.11	0.51
5:L:124:GLU:O	5:L:127:ILE:HG13	2.10	0.51
5:L:137:TYR:HE1	5:L:351:THR:HB	1.75	0.51
5:L:484:ALA:CB	5:L:491:GLU:HG3	2.41	0.51
2:I:237:LEU:HD12	2:I:322:LEU:HD23	1.92	0.51
2:I:905:ILE:HG22	2:I:906:PHE:CD1	2.46	0.51
2:I:993:PRO:HB2	2:I:995:ASP:OD2	2.10	0.51
2:I:1066:MET:HE2	2:I:1076:ILE:CG2	2.40	0.51
2:I:1305:TYR:CE1	3:J:379:PRO:HG3	2.45	0.51
3:J:123:ARG:HH22	3:J:1334:GLU:HG2	1.76	0.51
3:J:483:LEU:CD2	4:K:16:ARG:HG2	2.41	0.51
5:L:140:ALA:HB1	5:L:269:LEU:CD2	2.39	0.51
5:L:147:GLN:HG2	5:L:161:LEU:HD13	1.92	0.51
5:L:234:THR:OG1	5:L:248:GLU:HG2	2.10	0.51
5:L:479:THR:HG22	5:L:482:GLU:CG	2.41	0.51
2:I:65:ASN:O	2:I:105:TYR:HB2	2.11	0.51
2:I:131:THR:HG23	2:I:135:THR:O	2.09	0.51
2:I:360:LEU:HA	2:I:363:LEU:HD12	1.93	0.51
2:I:618:GLN:NE2	3:J:770:LEU:HD23	2.26	0.51
2:I:1242:LYS:HB3	3:J:465:GLN:NE2	2.24	0.51
2:I:1293:VAL:HG11	2:I:1304:MET:SD	2.51	0.51
3:J:53:ARG:HB3	3:J:54:ASP:CA	2.40	0.51
3:J:194:LEU:HD22	3:J:224:LEU:CD2	2.41	0.51
3:J:650:LYS:O	3:J:654:ILE:HG13	2.10	0.51
3:J:1004:ALA:H	3:J:1018:ALA:HA	1.75	0.51
3:J:1175:LEU:HB2	3:J:1190:ILE:HG13	1.92	0.51
1:G:98:VAL:HG21	1:G:121:VAL:HG21	1.92	0.51
2:I:264:GLU:O	2:I:267:ARG:HB2	2.09	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:424:ASP:O	2:I:428:VAL:HG23	2.11	0.51
2:I:582:ASN:N	2:I:586:PHE:O	2.28	0.51
2:I:1008:GLN:NE2	2:I:1008:GLN:O	2.43	0.51
2:I:1222:GLU:OE1	3:J:512:TYR:OH	2.22	0.51
2:I:1327:LEU:HD21	2:I:1339:LEU:HD21	1.92	0.51
3:J:1226:VAL:HG23	3:J:1261:LEU:HD22	1.93	0.51
8:P:41:DT:H2''	8:P:42:DT:OP2	2.10	0.51
1:G:179:PRO:HB3	1:G:210:THR:CG2	2.38	0.51
3:J:162:GLU:O	3:J:166:LEU:HG	2.11	0.51
3:J:969:SER:HB2	3:J:1116:SER:HB2	1.93	0.51
5:L:248:GLU:OE2	5:L:251:LYS:HD2	2.10	0.51
1:G:54:CYS:HB3	1:G:90:VAL:O	2.10	0.51
2:I:1076:ILE:HD11	2:I:1079:ILE:HD11	1.93	0.51
3:J:133:ARG:HD2	3:J:136:GLU:OE1	2.11	0.51
3:J:436:ALA:HB1	3:J:480:ALA:HB1	1.91	0.51
3:J:1257:VAL:HA	3:J:1260:MET:HB2	1.93	0.51
3:J:1314:LEU:HA	3:J:1326:GLN:NE2	2.26	0.51
1:G:6:THR:CG2	1:H:148:ARG:HD3	2.41	0.51
1:H:158:ARG:HB2	1:H:172:LEU:HD23	1.92	0.51
2:I:270:THR:HA	6:N:60:GLU:OE1	2.11	0.51
2:I:816:ILE:HG23	2:I:1098:LEU:HD12	1.92	0.51
2:I:877:VAL:CG1	2:I:881:ASP:HB2	2.41	0.51
3:J:490:ILE:HB	3:J:500:ILE:HG13	1.92	0.51
5:L:251:LYS:O	5:L:255:VAL:HG22	2.11	0.51
5:L:456:MET:O	5:L:460:ILE:HG23	2.11	0.51
2:I:110:PRO:HD2	2:I:113:THR:HB	1.93	0.51
2:I:1002:LEU:HG	2:I:1003:THR:O	2.11	0.51
2:I:1027:LYS:HE2	2:I:1027:LYS:HA	1.93	0.51
3:J:105:ILE:N	3:J:242:LEU:O	2.36	0.51
3:J:1264:ALA:HB3	3:J:1285:VAL:HG11	1.91	0.51
5:L:235:ILE:C	5:L:245:ALA:HB2	2.36	0.51
1:G:192:VAL:HG11	1:G:198:LEU:HD12	1.93	0.50
2:I:303:ASP:CB	2:I:310:ILE:HD11	2.41	0.50
2:I:479:LEU:CD1	2:I:492:MET:HE1	2.41	0.50
3:J:1025:MET:CB	3:J:1124:ILE:HB	2.25	0.50
1:M:253:LEU:O	1:M:279:GLY:N	2.44	0.50
7:O:30:DC:H2''	7:O:31:DA:C8	2.46	0.50
8:P:41:DT:H2'	8:P:42:DT:H72	1.93	0.50
1:H:14:VAL:HG13	1:H:28:LEU:CD1	2.40	0.50
2:I:699:LEU:HD13	2:I:1121:ALA:HB3	1.92	0.50
3:J:78:LEU:O	3:J:81:ARG:HB2	2.11	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:233:LYS:HB3	3:J:235:GLU:OE1	2.11	0.50
3:J:309:ASN:OD1	3:J:315:ALA:HA	2.11	0.50
3:J:719:PHE:HA	3:J:724:MET:HE2	1.92	0.50
3:J:885:VAL:HG23	3:J:894:VAL:CG1	2.42	0.50
4:K:45:LYS:O	4:K:49:ILE:HG13	2.11	0.50
5:L:11:LEU:HA	5:L:14:THR:CG2	2.41	0.50
5:L:477:GLU:CD	5:L:478:PRO:HD2	2.37	0.50
1:M:260:LEU:HD23	1:M:306:VAL:CG2	2.39	0.50
2:I:228:VAL:CG2	2:I:337:PHE:HB2	2.40	0.50
2:I:840:SER:O	2:I:840:SER:OG	2.26	0.50
2:I:1314:GLN:HB2	4:K:28:ARG:NH1	2.26	0.50
3:J:451:PRO:HG2	3:J:625:MET:HE3	1.93	0.50
3:J:844:THR:HG22	3:J:864:LEU:HD11	1.93	0.50
3:J:888:CYS:HB2	3:J:898:CYS:CB	2.41	0.50
3:J:1000:GLY:O	3:J:1026:PRO:HG3	2.11	0.50
5:L:299:LYS:O	5:L:303:ILE:HG12	2.11	0.50
1:H:73:GLY:O	1:H:134:THR:N	2.44	0.50
2:I:297:VAL:HG13	2:I:313:ALA:HA	1.94	0.50
2:I:1246:ARG:HG2	2:I:1247:SER:N	2.27	0.50
3:J:201:LEU:HB3	3:J:221:ILE:HD11	1.92	0.50
4:K:58:LEU:HD23	4:K:58:LEU:H	1.76	0.50
1:G:13:LEU:CD1	1:G:217:ILE:HD11	2.42	0.50
1:G:13:LEU:HD22	1:G:16:ILE:HD11	1.94	0.50
1:G:184:ALA:HB2	2:I:1091:GLY:HA3	1.94	0.50
3:J:56:LEU:HD21	3:J:269:TYR:CB	2.42	0.50
3:J:322:ARG:HG3	3:J:323:PRO:HD2	1.94	0.50
5:L:474:MET:HE2	5:L:486:ARG:NH2	2.27	0.50
8:P:64:DA:C2'	8:P:65:DT:H5''	2.41	0.50
1:H:212:ASP:OD1	1:H:212:ASP:N	2.35	0.50
2:I:127:ILE:HG13	2:I:127:ILE:O	2.11	0.50
2:I:478:ARG:HD2	2:I:492:MET:HB3	1.92	0.50
2:I:631:GLU:OE1	2:I:631:GLU:N	2.45	0.50
2:I:696:ASP:O	2:I:795:ALA:HB1	2.12	0.50
2:I:971:LEU:HD13	2:I:1018:TYR:HB2	1.93	0.50
3:J:1061:VAL:O	3:J:1103:GLY:HA2	2.11	0.50
5:L:145:LEU:O	5:L:149:ASP:OD1	2.30	0.50
5:L:150:ARG:O	5:L:155:GLU:N	2.42	0.50
5:L:381:GLU:HA	5:L:384:LEU:HD23	1.94	0.50
5:L:405:ILE:HG22	5:L:409:ASN:HD21	1.76	0.50
5:L:492:ASP:O	5:L:495:ARG:HB2	2.12	0.50
2:I:81:ASP:HB3	2:I:84:GLU:OE1	2.12	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:726:TYR:OH	2:I:728:ASP:OD2	2.26	0.50
3:J:138:VAL:HG21	3:J:145:VAL:CG1	2.41	0.50
3:J:364:HIS:HB3	3:J:487:THR:HG21	1.94	0.50
3:J:398:LYS:HD2	5:L:532:LEU:CD2	2.35	0.50
3:J:748:ALA:HB3	6:N:16:THR:HG22	1.92	0.50
3:J:1064:SER:OG	3:J:1072:LYS:HB2	2.12	0.50
5:L:286:LEU:HD23	5:L:290:LEU:HD22	1.93	0.50
1:M:252:ILE:CG2	1:M:312:LEU:HD11	2.42	0.50
1:M:284:ARG:HD2	1:M:288:GLU:OE2	2.12	0.50
2:I:339:ASN:ND2	2:I:343:HIS:HB2	2.27	0.50
2:I:724:VAL:CG1	2:I:727:VAL:HG22	2.41	0.50
2:I:803:ALA:CB	2:I:1227:VAL:HG12	2.42	0.50
2:I:911:SER:OG	2:I:913:VAL:HG12	2.11	0.50
2:I:1167:GLU:O	2:I:1171:ARG:HG3	2.11	0.50
3:J:436:ALA:N	3:J:484:MET:O	2.37	0.50
3:J:528:THR:O	3:J:528:THR:OG1	2.29	0.50
3:J:858:VAL:HG22	3:J:868:TRP:CE3	2.47	0.50
3:J:999:TYR:HB3	3:J:1025:MET:HE3	1.93	0.50
3:J:1040:MET:HG2	3:J:1076:PRO:CA	2.42	0.50
3:J:1110:GLU:HB2	3:J:1113:VAL:CG2	2.38	0.50
5:L:116:GLU:OE1	5:L:116:GLU:N	2.45	0.50
1:G:59:VAL:HG21	1:G:85:LEU:HD12	1.94	0.50
1:H:29:GLU:HG2	1:H:30:PRO:N	2.26	0.50
2:I:496:LYS:O	2:I:500:ALA:CB	2.60	0.50
2:I:1201:LEU:O	2:I:1201:LEU:HD12	2.12	0.50
2:I:1247:SER:O	3:J:348:ASP:HB3	2.12	0.50
3:J:1229:VAL:HG21	3:J:1306:LEU:CD1	2.41	0.50
3:J:1229:VAL:HG21	3:J:1306:LEU:HD13	1.94	0.50
5:L:403:ASP:O	5:L:407:GLU:HG2	2.12	0.50
1:M:285:THR:HG22	1:M:286:GLU:H	1.77	0.50
2:I:82:VAL:HG13	2:I:83:GLN:HG3	1.94	0.49
2:I:136:PHE:HB3	2:I:138:ILE:CD1	2.42	0.49
2:I:314:ASN:ND2	2:I:351:LEU:HB2	2.26	0.49
2:I:319:LEU:HA	2:I:322:LEU:HB2	1.94	0.49
2:I:488:MET:HB3	2:I:489:PRO:HD2	1.94	0.49
2:I:1107:MET:HG2	3:J:740:LEU:CD1	2.42	0.49
2:I:1323:PHE:CZ	3:J:1353:VAL:HG12	2.47	0.49
3:J:107:LEU:HA	3:J:276:ASN:ND2	2.27	0.49
3:J:473:THR:OG1	3:J:475:GLU:OE1	2.20	0.49
3:J:572:THR:OG1	3:J:573:THR:N	2.45	0.49
3:J:1123:ARG:O	3:J:1125:PRO:HD3	2.11	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:12:LEU:HD11	5:L:22:LEU:HD13	1.94	0.49
8:P:59:DA:H4'	8:P:60:DA:OP1	2.11	0.49
1:G:39:LEU:O	1:G:43:LEU:HG	2.12	0.49
1:H:31:LEU:HD11	1:H:39:LEU:HD12	1.94	0.49
1:H:48:LEU:HD13	1:H:183:ILE:HD13	1.92	0.49
1:H:112:ALA:N	1:H:128:HIS:O	2.45	0.49
2:I:788:SER:O	2:I:795:ALA:N	2.29	0.49
3:J:127:LEU:HD21	3:J:234:PRO:HB3	1.94	0.49
3:J:452:LEU:HD13	3:J:500:ILE:HG23	1.93	0.49
3:J:1307:LEU:HD23	3:J:1311:LYS:CD	2.34	0.49
6:N:36:LEU:HA	6:N:43:PRO:HA	1.94	0.49
6:N:56:THR:HG23	6:N:57:LEU:HG	1.93	0.49
1:H:34:GLY:N	1:H:199:ASP:OD2	2.45	0.49
1:H:101:THR:HG22	1:H:116:THR:OG1	2.12	0.49
2:I:1340:GLU:OE1	3:J:21:LYS:HD3	2.13	0.49
3:J:812:ASP:HA	3:J:896:ALA:HB3	1.93	0.49
3:J:978:ARG:HG3	3:J:979:ASN:CG	2.38	0.49
3:J:1322:ALA:O	3:J:1326:GLN:HB2	2.12	0.49
4:K:38:LEU:HD11	4:K:67:ARG:HH12	1.77	0.49
5:L:36:VAL:HG23	5:L:37:ASP:OD1	2.11	0.49
5:L:456:MET:CE	5:L:497:VAL:HG22	2.35	0.49
7:O:38:DG:H2''	7:O:39:DG:OP2	2.13	0.49
1:G:14:VAL:HG21	1:G:29:GLU:HG3	1.95	0.49
1:G:165:GLU:OE2	1:G:172:LEU:HD11	2.12	0.49
1:H:52:PRO:HG3	1:H:150:ARG:NH1	2.26	0.49
2:I:833:ILE:HA	2:I:1054:LEU:O	2.12	0.49
3:J:143:SER:HB2	3:J:160:LEU:O	2.13	0.49
3:J:337:ARG:O	3:J:342:LEU:HD13	2.12	0.49
3:J:1061:VAL:HG21	3:J:1101:LEU:CG	2.34	0.49
3:J:1061:VAL:HG22	3:J:1105:ALA:O	2.12	0.49
3:J:1151:LYS:C	3:J:1153:PRO:HD3	2.38	0.49
4:K:38:LEU:HD11	4:K:67:ARG:HH22	1.77	0.49
5:L:449:THR:HG21	5:L:504:PRO:HG3	1.93	0.49
1:M:292:THR:OG1	1:M:295:LEU:HB3	2.12	0.49
2:I:287:VAL:HB	2:I:288:PRO:HD2	1.93	0.49
2:I:672:GLU:HG3	2:I:673:HIS:CD2	2.47	0.49
2:I:754:THR:N	2:I:767:GLN:OE1	2.24	0.49
2:I:1112:ILE:CD1	3:J:644:MET:HE1	2.43	0.49
2:I:1151:LEU:HD21	2:I:1198:LEU:CA	2.42	0.49
2:I:1326:LEU:HD21	3:J:338:PHE:CZ	2.47	0.49
3:J:115:TRP:O	3:J:119:SER:HB3	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:117:LEU:CD1	3:J:139:LEU:HD11	2.42	0.49
3:J:610:ARG:HG3	3:J:866:GLU:OE2	2.11	0.49
5:L:314:THR:HG23	5:L:318:ALA:HB3	1.94	0.49
5:L:507:MET:SD	5:L:523:ILE:HD12	2.52	0.49
2:I:455:SER:O	2:I:459:MET:HG3	2.13	0.49
2:I:660:VAL:HG11	3:J:769:VAL:CG1	2.43	0.49
3:J:214:ARG:HA	3:J:217:LEU:HB3	1.94	0.49
3:J:276:ASN:O	3:J:280:LYS:HG3	2.12	0.49
3:J:646:ILE:HG23	3:J:647:PRO:HD2	1.94	0.49
3:J:1023:HIS:C	3:J:1125:PRO:HA	2.37	0.49
5:L:105:MET:O	5:L:108:VAL:HG12	2.13	0.49
1:M:250:ASP:OD1	1:M:251:PRO:HD2	2.12	0.49
7:O:28:DG:H2''	7:O:29:DA:H8	1.78	0.49
1:G:98:VAL:HG21	1:G:121:VAL:CG2	2.42	0.49
1:H:14:VAL:HG22	1:H:28:LEU:HD12	1.95	0.49
2:I:60:GLN:HB3	2:I:67:GLU:OE2	2.13	0.49
2:I:65:ASN:HB3	2:I:105:TYR:HB3	1.95	0.49
2:I:232:ILE:HG12	2:I:237:LEU:H	1.77	0.49
2:I:237:LEU:CD1	2:I:322:LEU:HD23	2.43	0.49
2:I:690:VAL:HG12	2:I:1234:LYS:O	2.12	0.49
2:I:805:MET:HB2	2:I:805:MET:HE3	1.61	0.49
2:I:995:ASP:O	2:I:996:ARG:NH1	2.46	0.49
3:J:189:LEU:HA	3:J:192:MET:HE3	1.95	0.49
3:J:318:GLY:N	3:J:322:ARG:O	2.45	0.49
3:J:1036:ARG:NE	3:J:1081:VAL:HG21	2.28	0.49
3:J:1061:VAL:HG11	3:J:1101:LEU:HD23	1.95	0.49
4:K:5:THR:HG22	4:K:7:GLN:N	2.21	0.49
5:L:286:LEU:O	5:L:290:LEU:HD22	2.13	0.49
1:M:280:ASP:O	1:M:284:ARG:NE	2.45	0.49
3:J:46:TYR:CE1	5:L:453:PRO:HD3	2.47	0.49
3:J:750:PRO:HB3	3:J:781:LYS:HD3	1.95	0.49
3:J:955:LYS:NZ	3:J:986:ASP:OD1	2.26	0.49
3:J:1047:THR:HG22	3:J:1060:VAL:O	2.13	0.49
2:I:145:ILE:HA	2:I:511:LEU:O	2.13	0.49
2:I:1296:ASP:OD2	2:I:1322:SER:HB3	2.13	0.49
3:J:201:LEU:HB3	3:J:221:ILE:CG1	2.42	0.49
3:J:372:MET:O	3:J:376:LEU:HG	2.13	0.49
5:L:148:TYR:CE1	5:L:218:ARG:HG2	2.45	0.49
5:L:249:ILE:HD13	5:L:353:LEU:HD11	1.94	0.49
5:L:530:LEU:O	5:L:533:ASP:N	2.36	0.49
1:M:269:CYS:SG	1:M:295:LEU:HB2	2.53	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:852:ALA:HB2	2:I:869:GLY:HA2	1.95	0.49
3:J:316:ILE:O	3:J:316:ILE:HG13	2.13	0.49
3:J:957:SER:OG	3:J:1010:GLN:HB3	2.13	0.49
3:J:1005:LYS:CE	3:J:1009:GLU:HB3	2.39	0.49
5:L:235:ILE:O	5:L:245:ALA:HB2	2.12	0.49
5:L:482:GLU:O	5:L:485:GLU:HB3	2.13	0.49
1:H:11:PRO:HG3	1:H:28:LEU:HD21	1.95	0.48
1:H:92:VAL:HG12	1:H:121:VAL:HG22	1.95	0.48
2:I:207:THR:CG2	2:I:350:THR:HG23	2.43	0.48
2:I:545:PHE:HE2	3:J:788:LEU:HD11	1.77	0.48
2:I:812:PHE:CE2	2:I:813:GLU:HG2	2.48	0.48
2:I:975:ILE:CG1	2:I:1014:LEU:HD23	2.42	0.48
3:J:104:HIS:HA	3:J:243:PRO:HA	1.95	0.48
3:J:622:ASP:OD2	3:J:622:ASP:N	2.46	0.48
3:J:793:SER:OG	3:J:794:GLY:N	2.46	0.48
3:J:959:LYS:O	3:J:982:LEU:HA	2.13	0.48
3:J:1075:ARG:HB2	3:J:1100:PHE:CD1	2.45	0.48
5:L:157:ARG:O	5:L:160:ASP:HB2	2.12	0.48
5:L:277:MET:HG2	5:L:281:ARG:HH12	1.77	0.48
5:L:383:ASN:O	5:L:386:LEU:HB3	2.13	0.48
1:M:251:PRO:HA	1:M:254:LEU:CG	2.42	0.48
8:P:60:DA:C8	8:P:61:DT:H72	2.48	0.48
1:G:31:LEU:HD11	1:G:201:LEU:HB2	1.95	0.48
2:I:221:LEU:HD23	2:I:336:LEU:CD2	2.43	0.48
2:I:264:GLU:HB3	2:I:267:ARG:HG3	1.94	0.48
2:I:689:ALA:HB3	2:I:796:LEU:HB3	1.94	0.48
3:J:215:LYS:O	3:J:218:THR:HG22	2.13	0.48
3:J:748:ALA:HB2	6:N:16:THR:HG22	1.95	0.48
3:J:1053:LEU:O	3:J:1053:LEU:HD23	2.13	0.48
3:J:1069:ALA:CA	3:J:1072:LYS:HG2	2.44	0.48
3:J:1177:ILE:HB	3:J:1186:TYR:CD2	2.38	0.48
5:L:415:ALA:HB2	5:L:434:TRP:CB	2.43	0.48
1:M:255:ARG:HD2	1:M:256:PRO:HD3	1.95	0.48
1:G:52:PRO:HG2	1:G:219:ARG:NH1	2.28	0.48
2:I:875:ALA:O	2:I:877:VAL:HG23	2.14	0.48
3:J:204:GLU:O	3:J:208:THR:HB	2.13	0.48
3:J:954:ASN:O	3:J:984:LEU:HD21	2.13	0.48
2:I:66:SER:HB3	2:I:479:LEU:HD22	1.95	0.48
2:I:130:MET:HE1	2:I:456:VAL:HG11	1.93	0.48
2:I:247:ARG:HH12	2:I:271:ALA:HA	1.78	0.48
2:I:490:GLN:NE2	5:L:472:GLN:O	2.47	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:978:ARG:HA	3:J:999:TYR:CD1	2.47	0.48
3:J:1046:ILE:CD1	3:J:1059:LEU:HD13	2.40	0.48
3:J:1176:VAL:HA	3:J:1187:GLU:HA	1.93	0.48
5:L:147:GLN:HB3	5:L:161:LEU:HD13	1.94	0.48
5:L:288:MET:HA	5:L:292:VAL:HG23	1.95	0.48
5:L:292:VAL:HG22	5:L:297:MET:HB3	1.94	0.48
2:I:58:PRO:HB3	2:I:69:GLN:CB	2.44	0.48
2:I:1234:LYS:HE3	2:I:1238:LEU:HD21	1.94	0.48
2:I:1262:LYS:HE2	2:I:1262:LYS:HA	1.96	0.48
4:K:64:LEU:HD23	4:K:64:LEU:HA	1.68	0.48
5:L:247:GLU:HA	5:L:250:LEU:CD2	2.39	0.48
1:M:260:LEU:HB3	1:M:306:VAL:HG21	1.95	0.48
1:M:264:VAL:HG22	1:M:268:ASN:ND2	2.28	0.48
2:I:238:GLN:HB2	2:I:285:ILE:O	2.14	0.48
2:I:254:ASP:CA	2:I:263:VAL:O	2.53	0.48
2:I:478:ARG:HH22	2:I:483:ASP:CB	2.27	0.48
2:I:538:LEU:HD13	2:I:543:ALA:CB	2.41	0.48
2:I:866:ASP:HB3	2:I:872:TYR:CE1	2.49	0.48
2:I:1340:GLU:CD	3:J:1341:ARG:HD2	2.39	0.48
3:J:436:ALA:CB	3:J:480:ALA:HB1	2.43	0.48
3:J:978:ARG:HG3	3:J:979:ASN:OD1	2.13	0.48
3:J:1172:LYS:HB2	3:J:1189:MET:CB	2.39	0.48
5:L:163:THR:CG2	5:L:263:PRO:HD3	2.44	0.48
5:L:289:LYS:HA	5:L:293:GLU:HB3	1.94	0.48
1:M:251:PRO:HA	1:M:254:LEU:CD1	2.42	0.48
2:I:230:PHE:CE2	2:I:292:ILE:HG23	2.49	0.48
2:I:781:ASP:OD2	2:I:782:VAL:N	2.47	0.48
3:J:1220:ILE:HG22	3:J:1228:ALA:HB1	1.95	0.48
5:L:415:ALA:HB2	5:L:434:TRP:HB2	1.95	0.48
7:O:44:DA:H1'	7:O:45:DA:C8	2.49	0.48
1:G:90:VAL:HG22	1:G:123:ILE:CD1	2.43	0.48
2:I:7:GLU:OE1	2:I:7:GLU:HA	2.12	0.48
2:I:619:ALA:HB2	2:I:654:ASP:HB2	1.95	0.48
2:I:883:LEU:HD11	2:I:1054:LEU:HD11	1.95	0.48
3:J:357:VAL:HG13	3:J:358:GLY:H	1.78	0.48
3:J:507:VAL:HA	3:J:601:ILE:CD1	2.44	0.48
3:J:1260:MET:HB3	3:J:1260:MET:HE2	1.71	0.48
5:L:109:GLU:HB2	5:L:111:LEU:HG	1.95	0.48
2:I:545:PHE:CE2	3:J:788:LEU:HD11	2.49	0.48
2:I:548:ARG:O	3:J:780:ARG:HD3	2.13	0.48
2:I:865:LEU:HD22	2:I:869:GLY:O	2.14	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:553:THR:CG2	3:J:567:THR:HB	2.40	0.48
3:J:954:ASN:HB2	3:J:992:LYS:CE	2.44	0.48
5:L:152:GLU:HG3	5:L:218:ARG:HG2	1.96	0.48
5:L:316:PHE:CE2	5:L:337:VAL:HB	2.49	0.48
8:P:55:DT:H2''	8:P:56:DG:H8	1.78	0.48
1:G:94:GLY:H	1:G:120:ASP:HB3	1.78	0.48
1:H:192:VAL:HG23	1:H:198:LEU:CD1	2.44	0.48
2:I:993:PRO:HG2	2:I:996:ARG:CB	2.36	0.48
3:J:955:LYS:CB	3:J:1012:ALA:HA	2.44	0.48
3:J:958:ILE:HB	3:J:1008:GLY:N	2.29	0.48
3:J:968:ASN:HD21	3:J:974:VAL:CG1	2.26	0.48
3:J:1226:VAL:O	3:J:1230:THR:HG23	2.14	0.48
3:J:1263:LYS:HB2	3:J:1307:LEU:HD11	1.96	0.48
5:L:277:MET:HE2	5:L:281:ARG:NH2	2.28	0.48
5:L:295:CYS:HB3	5:L:329:LYS:HB3	1.96	0.48
5:L:437:GLN:HG3	8:P:37:DG:O6	2.14	0.48
5:L:560:ARG:HD3	5:L:566:ASP:OD2	2.14	0.48
1:M:257:VAL:HG13	1:M:276:HIS:C	2.39	0.48
7:O:41:DT:H4'	7:O:41:DT:OP1	2.13	0.48
1:G:8:PHE:HB3	1:G:32:GLU:HG3	1.94	0.47
2:I:231:GLU:O	2:I:238:GLN:N	2.47	0.47
2:I:272:ARG:O	2:I:276:GLN:HG2	2.14	0.47
2:I:324:LYS:HA	2:I:327:GLN:HG2	1.95	0.47
2:I:1010:GLN:O	2:I:1014:LEU:HD13	2.14	0.47
3:J:1047:THR:CG2	3:J:1060:VAL:HB	2.44	0.47
9:J:1504:1N7:C3	9:J:1504:1N7:C18	2.76	0.47
5:L:130:VAL:O	5:L:134:VAL:HG23	2.14	0.47
5:L:316:PHE:CD1	5:L:337:VAL:HG11	2.49	0.47
5:L:317:ASN:O	5:L:320:ILE:HG22	2.14	0.47
2:I:53:PHE:CD1	2:I:468:LEU:HD11	2.49	0.47
2:I:255:ILE:CB	2:I:263:VAL:HB	2.44	0.47
2:I:1032:LYS:O	2:I:1036:ILE:HG13	2.14	0.47
3:J:298:MET:HE1	5:L:406:GLN:HG3	1.97	0.47
3:J:591:ILE:HD12	3:J:591:ILE:HA	1.74	0.47
3:J:1030:GLU:HG3	3:J:1090:ILE:CG2	2.43	0.47
4:K:65:ASP:O	4:K:68:GLU:HB2	2.14	0.47
5:L:9:LEU:HD22	5:L:44:ILE:HD11	1.95	0.47
5:L:118:ASP:O	5:L:122:ARG:HG3	2.14	0.47
5:L:251:LYS:O	5:L:255:VAL:HG13	2.13	0.47
8:P:45:DA:H2''	8:P:46:DG:H8	1.79	0.47
2:I:8:LYS:HB3	2:I:11:ILE:HD11	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:133:ASN:HD21	2:I:713:GLY:HA3	1.78	0.47
2:I:182:SER:HB2	2:I:199:ASP:OD1	2.14	0.47
2:I:521:LEU:HD23	2:I:521:LEU:HA	1.72	0.47
3:J:45:ASN:HB3	3:J:48:THR:O	2.13	0.47
3:J:1318:SER:HB3	3:J:1342:ASP:OD2	2.14	0.47
1:G:67:GLU:H	1:G:67:GLU:HG2	1.45	0.47
1:H:107:ILE:HG12	1:H:135:ASP:CA	2.38	0.47
1:H:140:ILE:HD12	1:H:141:SER:H	1.80	0.47
2:I:360:LEU:O	2:I:360:LEU:HD23	2.13	0.47
2:I:1212:LEU:HD21	2:I:1227:VAL:HG11	1.96	0.47
3:J:126:LEU:CD1	3:J:223:LEU:HD22	2.44	0.47
3:J:474:LEU:HD23	4:K:31:GLN:NE2	2.30	0.47
3:J:646:ILE:CD1	3:J:762:ASN:HD21	2.28	0.47
3:J:1069:ALA:HA	3:J:1072:LYS:CG	2.44	0.47
4:K:53:GLU:O	4:K:58:LEU:HD23	2.14	0.47
5:L:123:ILE:O	5:L:127:ILE:HG23	2.14	0.47
5:L:142:THR:HG22	5:L:228:TYR:HE2	1.78	0.47
5:L:419:PHE:HD1	5:L:430:TYR:HD2	1.62	0.47
6:N:14:GLN:O	6:N:18:THR:HG22	2.14	0.47
1:H:149:GLY:HA3	1:H:177:TYR:CD1	2.50	0.47
1:H:152:TYR:CE2	1:H:154:PRO:HG3	2.45	0.47
2:I:972:PHE:CE2	2:I:994:ARG:HB3	2.50	0.47
2:I:1086:PRO:HB3	2:I:1221:PHE:HE2	1.80	0.47
3:J:875:ASN:N	3:J:875:ASN:OD1	2.46	0.47
3:J:1115:ILE:HB	3:J:1119:ASP:HB3	1.97	0.47
5:L:47:MET:HE2	5:L:47:MET:HB2	1.58	0.47
5:L:449:THR:HG23	5:L:450:ILE:CD1	2.41	0.47
5:L:551:LEU:HD13	5:L:555:GLU:HB3	1.94	0.47
5:L:560:ARG:NH1	5:L:566:ASP:OD2	2.45	0.47
1:G:14:VAL:HG21	1:G:29:GLU:CB	2.41	0.47
1:G:53:GLY:O	1:G:148:ARG:HA	2.15	0.47
1:H:52:PRO:HA	1:H:150:ARG:HA	1.95	0.47
1:H:75:GLN:OE1	1:H:75:GLN:N	2.43	0.47
2:I:197:ARG:HG3	2:I:201:ARG:O	2.15	0.47
2:I:669:PRO:HG3	2:I:1069:ARG:NH2	2.30	0.47
2:I:890:LYS:HD2	2:I:890:LYS:O	2.14	0.47
2:I:1210:ILE:HG22	2:I:1211:ARG:O	2.15	0.47
2:I:1282:GLY:HA3	4:K:17:PHE:CE1	2.50	0.47
3:J:209:ASN:HA	3:J:214:ARG:HD3	1.95	0.47
3:J:1026:PRO:HB2	3:J:1028:ILE:HG23	1.97	0.47
5:L:286:LEU:HD23	5:L:286:LEU:O	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:529:GLU:OE1	5:L:529:GLU:HA	2.14	0.47
5:L:560:ARG:HA	5:L:565:ILE:HB	1.95	0.47
1:G:13:LEU:HD21	1:G:26:VAL:CG1	2.44	0.47
1:G:234:LEU:HD22	1:H:14:VAL:CG1	2.45	0.47
1:H:158:ARG:HB2	1:H:172:LEU:CD2	2.45	0.47
2:I:195:PHE:CE2	2:I:203:LYS:HE2	2.50	0.47
2:I:629:PHE:HB2	2:I:647:ARG:CD	2.44	0.47
2:I:849:GLU:O	2:I:886:LYS:HG3	2.14	0.47
2:I:1043:ALA:HB1	2:I:1044:PRO:HD2	1.97	0.47
2:I:1282:GLY:CA	3:J:1360:GLY:HA3	2.44	0.47
3:J:298:MET:HE1	5:L:406:GLN:CG	2.44	0.47
3:J:322:ARG:HB3	3:J:322:ARG:CZ	2.44	0.47
3:J:357:VAL:CG2	3:J:451:PRO:HG3	2.45	0.47
3:J:952:VAL:HG11	3:J:1017:VAL:HG13	1.97	0.47
3:J:1059:LEU:HD12	3:J:1059:LEU:O	2.15	0.47
3:J:1140:ARG:HA	3:J:1140:ARG:HD2	1.54	0.47
3:J:1257:VAL:O	3:J:1260:MET:N	2.48	0.47
4:K:10:VAL:O	4:K:14:GLY:N	2.45	0.47
5:L:9:LEU:CD1	5:L:88:GLU:HG2	2.44	0.47
5:L:16:GLY:HA3	5:L:22:LEU:HG	1.96	0.47
5:L:23:THR:HA	5:L:56:MET:O	2.14	0.47
5:L:163:THR:OG1	5:L:261:LEU:O	2.28	0.47
5:L:281:ARG:O	5:L:285:ARG:HG2	2.14	0.47
5:L:348:GLU:OE1	5:L:355:ILE:HG12	2.14	0.47
5:L:412:LEU:O	5:L:416:VAL:HG23	2.15	0.47
7:O:32:DA:H2"	7:O:33:DA:C8	2.49	0.47
2:I:102:LEU:N	2:I:118:LYS:O	2.40	0.47
2:I:197:ARG:NH2	2:I:203:LYS:HB3	2.30	0.47
2:I:755:LYS:NZ	2:I:767:GLN:O	2.41	0.47
3:J:128:LEU:O	3:J:157:GLN:NE2	2.45	0.47
3:J:264:ASP:CB	3:J:324:LEU:HD22	2.41	0.47
3:J:697:MET:HE2	3:J:697:MET:HB2	1.84	0.47
3:J:1005:LYS:HE3	3:J:1009:GLU:CB	2.40	0.47
3:J:1101:LEU:HD12	3:J:1102:PRO:CD	2.42	0.47
1:H:92:VAL:HG23	1:H:93:GLN:O	2.15	0.47
1:H:191:ARG:NH1	1:H:193:GLU:O	2.48	0.47
2:I:346:TYR:O	2:I:350:THR:HG22	2.14	0.47
2:I:887:VAL:CG2	2:I:913:VAL:HG21	2.44	0.47
2:I:1073:LYS:H	2:I:1073:LYS:HG3	1.38	0.47
2:I:1103:VAL:HG22	2:I:1111:GLN:NE2	2.20	0.47
2:I:1120:ALA:HB1	2:I:1198:LEU:HG	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:349:TYR:CE2	3:J:472:LEU:HD11	2.50	0.47
5:L:326:TRP:O	5:L:329:LYS:HB2	2.15	0.47
1:G:218:ARG:HG3	1:H:231:PHE:O	2.15	0.47
1:H:16:ILE:HD12	1:H:214:GLU:HB3	1.96	0.47
2:I:178:PRO:HB3	2:I:397:LEU:CD1	2.45	0.47
2:I:719:LYS:H	2:I:751:TYR:HH	1.63	0.47
2:I:829:THR:CG2	2:I:1057:LYS:HG2	2.45	0.47
2:I:1117:LEU:HD21	2:I:1182:ILE:HG21	1.96	0.47
2:I:1129:ASN:OD1	2:I:1177:ARG:NE	2.48	0.47
3:J:141:PHE:HA	3:J:180:MET:CG	2.44	0.47
3:J:797:THR:O	3:J:801:VAL:HG23	2.15	0.47
3:J:803:VAL:HG11	3:J:1309:ILE:CG2	2.45	0.47
3:J:810:THR:O	3:J:811:GLU:HG2	2.15	0.47
3:J:1061:VAL:HG12	3:J:1076:PRO:CG	2.45	0.47
3:J:1136:GLY:HA2	3:J:1240:VAL:HG23	1.97	0.47
5:L:551:LEU:HD23	5:L:551:LEU:HA	1.69	0.47
1:G:38:THR:OG1	1:H:45:ARG:HD3	2.15	0.46
2:I:10:ARG:HD2	2:I:697:LYS:HD3	1.96	0.46
2:I:106:GLU:O	2:I:115:LYS:HE2	2.15	0.46
2:I:453:ILE:HD11	2:I:530:ILE:CD1	2.44	0.46
3:J:1036:ARG:CD	3:J:1081:VAL:HG21	2.46	0.46
5:L:227:GLN:NE2	5:L:255:VAL:HG11	2.30	0.46
2:I:67:GLU:HB3	2:I:103:VAL:CG2	2.45	0.46
2:I:230:PHE:CE2	2:I:292:ILE:HG12	2.49	0.46
2:I:230:PHE:CE1	2:I:239:MET:HG3	2.49	0.46
2:I:1323:PHE:CE2	3:J:1353:VAL:HG12	2.49	0.46
3:J:442:ILE:HD13	3:J:448:GLN:HG3	1.98	0.46
3:J:584:PRO:HG2	3:J:587:LEU:CD1	2.46	0.46
3:J:1146:GLU:OE2	3:J:1310:THR:OG1	2.12	0.46
3:J:1198:VAL:HG12	3:J:1210:ILE:HG23	1.97	0.46
3:J:1295:ASN:OD1	3:J:1297:LYS:HE3	2.15	0.46
5:L:137:TYR:HD2	5:L:140:ALA:HB2	1.80	0.46
5:L:490:PRO:CG	5:L:493:LYS:HG2	2.44	0.46
1:H:60:GLU:OE1	1:H:171:LEU:N	2.48	0.46
2:I:106:GLU:CB	2:I:115:LYS:HG3	2.37	0.46
2:I:144:VAL:HG23	2:I:515:MET:HB2	1.98	0.46
2:I:453:ILE:HD11	2:I:530:ILE:HD12	1.97	0.46
2:I:542:ARG:HD3	2:I:543:ALA:N	2.30	0.46
2:I:680:LEU:HD13	3:J:783:LEU:HD12	1.97	0.46
2:I:964:LEU:HB2	2:I:1025:PHE:CD2	2.51	0.46
2:I:1119:MET:CE	2:I:1210:ILE:HD11	2.44	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:759:ILE:HD12	3:J:771:GLN:CB	2.45	0.46
3:J:1034:PHE:CE2	3:J:1083:ALA:HA	2.50	0.46
3:J:1040:MET:HE2	3:J:1078:LEU:HG	1.97	0.46
5:L:15:ARG:NH2	5:L:26:GLU:OE2	2.49	0.46
5:L:291:CYS:O	5:L:297:MET:N	2.41	0.46
5:L:533:ASP:HA	5:L:536:THR:CG2	2.42	0.46
1:M:257:VAL:HB	1:M:270:LEU:HD12	1.98	0.46
2:I:814:ASP:O	2:I:1074:GLY:HA3	2.14	0.46
3:J:98:ARG:O	3:J:247:PRO:HD2	2.15	0.46
3:J:516:ASP:HA	3:J:545:HIS:CB	2.45	0.46
3:J:952:VAL:HG22	3:J:984:LEU:HD22	1.97	0.46
8:P:65:DT:H1'	8:P:66:DT:H5'	1.97	0.46
1:H:79:LEU:HD12	3:J:526:VAL:HG11	1.98	0.46
2:I:122:VAL:HG21	2:I:493:ILE:HG21	1.98	0.46
2:I:146:VAL:CG2	2:I:513:GLN:HE21	2.24	0.46
2:I:1328:LYS:HD3	2:I:1328:LYS:HA	1.61	0.46
3:J:26:SER:HB2	3:J:236:TRP:CZ2	2.51	0.46
3:J:128:LEU:HD21	3:J:189:LEU:HD23	1.98	0.46
3:J:205:LEU:HD12	3:J:217:LEU:CD1	2.46	0.46
3:J:510:LEU:HD11	3:J:624:ILE:HG23	1.97	0.46
3:J:644:MET:HB2	3:J:764:ARG:HD2	1.97	0.46
3:J:1003:LEU:HA	3:J:1018:ALA:HB1	1.97	0.46
3:J:1023:HIS:HA	3:J:1126:GLN:N	2.31	0.46
3:J:1221:LEU:O	3:J:1221:LEU:HD22	2.16	0.46
5:L:84:LEU:O	5:L:87:VAL:HG12	2.16	0.46
5:L:144:LEU:HD13	5:L:256:PHE:HZ	1.78	0.46
8:P:64:DA:H2''	8:P:65:DT:H5''	1.97	0.46
2:I:478:ARG:O	2:I:478:ARG:NH1	2.46	0.46
2:I:479:LEU:HG	2:I:492:MET:CE	2.46	0.46
3:J:500:ILE:HG22	3:J:500:ILE:O	2.15	0.46
3:J:664:ILE:HD11	3:J:681:LYS:HG2	1.97	0.46
3:J:708:ASN:N	3:J:708:ASN:OD1	2.49	0.46
3:J:756:GLU:O	3:J:758:PRO:HD3	2.15	0.46
3:J:895:CYS:SG	3:J:897:HIS:N	2.88	0.46
3:J:1031:VAL:HG21	3:J:1088:VAL:HG11	1.96	0.46
5:L:556:ALA:O	5:L:560:ARG:HG3	2.16	0.46
7:O:29:DA:H2''	7:O:30:DC:O5'	2.15	0.46
1:G:192:VAL:HG21	1:G:198:LEU:HD13	1.97	0.46
2:I:46:GLN:OE1	2:I:47:TYR:N	2.47	0.46
2:I:1138:VAL:O	2:I:1142:ARG:HB3	2.15	0.46
2:I:1298:VAL:HB	2:I:1321:GLU:CD	2.41	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:510:LEU:HB2	3:J:601:ILE:HD11	1.98	0.46
3:J:1005:LYS:HE2	3:J:1011:VAL:HG22	1.97	0.46
3:J:1179:PRO:HD2	3:J:1184:ASP:CA	2.24	0.46
3:J:1275:LEU:HD23	3:J:1278:GLU:OE1	2.16	0.46
8:P:50:DT:H5'	8:P:50:DT:C6	2.51	0.46
2:I:144:VAL:CG2	2:I:515:MET:HB2	2.46	0.46
2:I:1182:ILE:HD11	2:I:1198:LEU:HD21	1.98	0.46
3:J:318:GLY:H	3:J:322:ARG:H	1.63	0.46
3:J:355:ILE:HG21	3:J:466:MET:HG3	1.98	0.46
3:J:663:GLU:O	3:J:667:GLN:HG3	2.15	0.46
3:J:848:VAL:O	3:J:857:LEU:HB3	2.16	0.46
3:J:1104:LYS:O	3:J:1124:ILE:HG23	2.16	0.46
3:J:1137:GLY:O	3:J:1140:ARG:N	2.47	0.46
3:J:1169:THR:HG22	3:J:1169:THR:O	2.16	0.46
5:L:52:GLY:HA2	5:L:53:ILE:C	2.40	0.46
5:L:344:LEU:O	5:L:348:GLU:HG3	2.16	0.46
5:L:360:ASP:HA	5:L:363:ARG:HB3	1.97	0.46
5:L:586:ARG:O	5:L:590:ILE:HG13	2.15	0.46
8:P:55:DT:H2''	8:P:56:DG:C8	2.50	0.46
1:H:155:ALA:HA	1:H:158:ARG:HG2	1.97	0.46
2:I:14:ASP:HB3	2:I:1157:GLN:HB2	1.98	0.46
2:I:27:LEU:HD22	2:I:663:VAL:HG21	1.97	0.46
2:I:835:GLU:HB2	2:I:1053:TYR:HD1	1.80	0.46
2:I:1096:ILE:HG22	2:I:1098:LEU:HD13	1.97	0.46
2:I:1148:ALA:CA	2:I:1201:LEU:HD21	2.45	0.46
3:J:320:ASN:HD22	3:J:322:ARG:NH2	2.13	0.46
3:J:378:LYS:HE3	3:J:382:TYR:OH	2.16	0.46
3:J:1357:ILE:HG13	3:J:1357:ILE:O	2.16	0.46
5:L:108:VAL:HG21	5:L:381:GLU:OE1	2.16	0.46
7:O:42:DA:H2''	7:O:43:DA:C8	2.51	0.46
2:I:256:GLU:HB2	2:I:261:VAL:HA	1.98	0.46
2:I:359:ARG:O	2:I:362:ALA:HB3	2.15	0.46
2:I:371:ARG:HB3	2:I:374:GLU:OE2	2.16	0.46
2:I:819:SER:HB2	2:I:1085:MET:CG	2.46	0.46
2:I:839:VAL:HG12	2:I:1049:ILE:CG1	2.31	0.46
3:J:278:ARG:HG3	3:J:281:ARG:NH2	2.23	0.46
3:J:526:VAL:HG12	3:J:549:LYS:HB2	1.97	0.46
5:L:123:ILE:CD1	5:L:379:MET:HE1	2.42	0.46
5:L:511:ILE:HG21	5:L:517:SER:HB3	1.97	0.46
1:H:46:ILE:CD1	1:H:224:LEU:HB2	2.44	0.45
2:I:9:LYS:HG2	2:I:1171:ARG:NH1	2.23	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:58:CYS:SG	3:J:61:ILE:HG13	2.56	0.45
3:J:859:PRO:HB2	3:J:862:THR:HG23	1.97	0.45
2:I:148:GLN:NE2	2:I:535:PRO:O	2.45	0.45
2:I:255:ILE:HG23	2:I:285:ILE:CD1	2.46	0.45
2:I:336:LEU:H	2:I:336:LEU:HG	1.56	0.45
2:I:1141:LEU:HD21	2:I:1173:ALA:CB	2.47	0.45
3:J:114:ILE:HD12	3:J:304:ASP:HB3	1.97	0.45
5:L:594:ALA:O	5:L:598:LEU:HG	2.16	0.45
1:G:74:VAL:HA	1:G:132:HIS:O	2.16	0.45
1:G:162:GLU:CD	1:G:165:GLU:HB3	2.41	0.45
2:I:15:PHE:CD2	2:I:1190:ALA:HB2	2.52	0.45
2:I:122:VAL:HG21	2:I:493:ILE:CG2	2.46	0.45
2:I:816:ILE:HG23	2:I:1098:LEU:CD1	2.45	0.45
3:J:146:VAL:HA	3:J:178:ALA:CB	2.46	0.45
3:J:552:ILE:HG12	3:J:570:LYS:HG3	1.98	0.45
3:J:1003:LEU:HD23	3:J:1018:ALA:CB	2.46	0.45
3:J:1361:THR:CG2	4:K:21:LEU:HD21	2.46	0.45
5:L:323:ASN:N	5:L:327:SER:OG	2.50	0.45
2:I:130:MET:HE3	2:I:130:MET:HB2	1.73	0.45
2:I:356:THR:HG23	2:I:361:SER:CB	2.46	0.45
2:I:715:THR:HG21	2:I:782:VAL:HG12	1.98	0.45
2:I:854:ILE:HB	2:I:857:VAL:HG21	1.99	0.45
2:I:1128:ILE:HG23	2:I:1141:LEU:HD11	1.98	0.45
3:J:128:LEU:HD11	3:J:189:LEU:HD21	1.98	0.45
3:J:141:PHE:CD1	3:J:180:MET:HE3	2.45	0.45
3:J:201:LEU:HD12	3:J:221:ILE:HG12	1.98	0.45
3:J:816:THR:HG21	3:J:889:ASP:HB2	1.98	0.45
3:J:1068:THR:HG22	3:J:1069:ALA:H	1.81	0.45
5:L:401:PHE:CE2	5:L:405:ILE:HD11	2.51	0.45
7:O:21:DA:C8	7:O:21:DA:H5'	2.51	0.45
2:I:69:GLN:O	2:I:100:LEU:HD22	2.17	0.45
2:I:233:ARG:HB3	2:I:238:GLN:HG2	1.99	0.45
2:I:388:LEU:HD12	2:I:388:LEU:HA	1.79	0.45
2:I:446:ASP:OD2	2:I:551:HIS:HB2	2.17	0.45
2:I:727:VAL:HG12	2:I:728:ASP:H	1.82	0.45
2:I:882:ILE:H	2:I:882:ILE:HD12	1.80	0.45
3:J:474:LEU:HD23	4:K:31:GLN:HE22	1.82	0.45
3:J:515:ARG:C	3:J:545:HIS:HB3	2.42	0.45
3:J:1170:LYS:CE	3:J:1172:LYS:HE3	2.47	0.45
1:H:211:ILE:HD12	1:H:212:ASP:H	1.81	0.45
2:I:1245:ALA:HA	3:J:351:GLY:HA2	1.97	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:53:ARG:HB3	3:J:54:ASP:C	2.41	0.45
3:J:56:LEU:HD12	3:J:56:LEU:HA	1.62	0.45
3:J:466:MET:HE2	3:J:466:MET:HB3	1.69	0.45
3:J:932:MET:HE3	3:J:932:MET:HB2	1.92	0.45
3:J:1027:VAL:HG21	3:J:1122:ALA:HB3	1.98	0.45
3:J:1105:ALA:HB1	3:J:1122:ALA:HB1	1.99	0.45
5:L:313:ASP:HB3	5:L:317:ASN:OD1	2.15	0.45
1:M:252:ILE:HG21	1:M:312:LEU:HD11	1.98	0.45
1:M:253:LEU:CD2	1:M:282:VAL:HG11	2.46	0.45
8:P:45:DA:H2''	8:P:46:DG:OP2	2.16	0.45
1:H:9:LEU:HD21	1:H:192:VAL:HG21	1.98	0.45
2:I:75:LEU:HD12	2:I:94:ALA:HB3	1.98	0.45
2:I:804:PHE:HZ	2:I:1230:MET:HE1	1.81	0.45
3:J:420:PRO:O	3:J:471:PRO:HD2	2.17	0.45
3:J:490:ILE:HB	3:J:500:ILE:CG1	2.46	0.45
3:J:925:GLU:HB3	3:J:926:PRO:CD	2.47	0.45
3:J:1047:THR:HB	3:J:1062:LEU:CD1	2.47	0.45
3:J:1191:PRO:HB3	3:J:1193:TRP:CZ3	2.52	0.45
5:L:73:ASP:OD1	5:L:74:GLU:N	2.50	0.45
8:P:67:DT:H2''	8:P:68:DG:O5'	2.16	0.45
2:I:255:ILE:HG13	2:I:263:VAL:HG11	1.98	0.45
2:I:1284:ALA:HB1	3:J:1356:LEU:HD23	1.98	0.45
2:I:1298:VAL:HB	2:I:1321:GLU:OE2	2.17	0.45
3:J:1029:THR:HA	3:J:1099:TYR:OH	2.16	0.45
5:L:22:LEU:HD23	5:L:22:LEU:HA	1.78	0.45
5:L:38:SER:CA	5:L:41:ILE:HD12	2.41	0.45
5:L:230:VAL:HA	5:L:233:ASP:HB2	1.99	0.45
5:L:349:GLU:OE2	5:L:350:GLU:HG3	2.17	0.45
5:L:414:LYS:O	5:L:418:LYS:HG3	2.17	0.45
2:I:107:ARG:CZ	2:I:108:GLU:HA	2.46	0.45
2:I:251:ALA:CB	2:I:265:LYS:HA	2.47	0.45
3:J:985:ILE:HD13	3:J:991:THR:CB	2.47	0.45
3:J:1120:THR:HB	3:J:1123:ARG:HD3	1.98	0.45
5:L:532:LEU:O	5:L:536:THR:HB	2.16	0.45
1:M:289:LEU:HD13	1:M:300:LEU:CD2	2.40	0.45
1:G:159:ILE:O	1:G:159:ILE:HG23	2.17	0.45
1:H:211:ILE:HD12	1:H:212:ASP:OD1	2.16	0.45
2:I:277:LEU:CD2	2:I:282:VAL:HB	2.47	0.45
2:I:719:LYS:HB2	2:I:719:LYS:HE3	1.76	0.45
2:I:815:SER:HB3	2:I:1077:SER:HB3	1.99	0.45
2:I:1064:ASP:OD1	2:I:1239:VAL:HG12	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:137:ARG:O	3:J:142:GLU:HB2	2.17	0.45
3:J:959:LYS:CB	3:J:983:LYS:HB2	2.43	0.45
3:J:974:VAL:HB	3:J:1028:ILE:HD13	1.99	0.45
3:J:1060:VAL:HG13	3:J:1106:ILE:HA	1.99	0.45
1:G:152:TYR:CE2	1:G:154:PRO:HD3	2.52	0.44
2:I:361:SER:O	2:I:364:VAL:HG22	2.17	0.44
3:J:107:LEU:HA	3:J:276:ASN:HD21	1.82	0.44
3:J:958:ILE:HG22	3:J:960:LEU:HD12	1.99	0.44
3:J:1346:GLY:HA3	3:J:1349:GLU:OE2	2.18	0.44
5:L:31:LEU:HD23	5:L:31:LEU:HA	1.76	0.44
5:L:141:ILE:CD1	5:L:252:LEU:HD11	2.46	0.44
5:L:162:ILE:HD12	5:L:165:PHE:CE2	2.51	0.44
5:L:320:ILE:HD13	5:L:330:LEU:HD12	1.97	0.44
1:M:298:LYS:HB2	8:P:67:DT:C3'	2.47	0.44
7:O:45:DA:H5''	7:O:45:DA:C8	2.50	0.44
1:G:50:SER:HB3	1:H:8:PHE:CZ	2.52	0.44
2:I:34:SER:O	2:I:37:LYS:HB2	2.17	0.44
2:I:902:LEU:HD12	5:L:607:LEU:HB3	1.99	0.44
3:J:849:LEU:HG	3:J:853:THR:HG23	2.00	0.44
4:K:26:ARG:NH2	4:K:36:ASP:O	2.50	0.44
5:L:53:ILE:H	5:L:53:ILE:HD12	1.82	0.44
5:L:277:MET:CE	5:L:362:ASN:HD21	2.30	0.44
1:M:253:LEU:HD22	1:M:282:VAL:CG2	2.47	0.44
1:H:205:MET:HE3	1:H:213:PRO:CB	2.48	0.44
2:I:10:ARG:HD2	2:I:697:LYS:CD	2.47	0.44
2:I:58:PRO:HB3	2:I:69:GLN:HB3	2.00	0.44
2:I:59:ILE:CD1	2:I:472:GLU:HB2	2.47	0.44
2:I:196:VAL:O	2:I:203:LYS:HA	2.18	0.44
2:I:341:LEU:HD22	6:N:64:TYR:HD1	1.81	0.44
2:I:561:ILE:HG21	3:J:772:TYR:HE2	1.83	0.44
2:I:1078:LYS:C	2:I:1079:ILE:HD12	2.42	0.44
3:J:141:PHE:CD1	3:J:180:MET:HG2	2.52	0.44
3:J:516:ASP:HB3	3:J:573:THR:HG21	1.99	0.44
3:J:931:THR:OG1	3:J:1244:GLN:NE2	2.45	0.44
3:J:975:ILE:HB	3:J:1000:GLY:N	2.32	0.44
3:J:1060:VAL:HG22	3:J:1106:ILE:HG23	2.00	0.44
5:L:324:LYS:N	5:L:327:SER:HG	2.12	0.44
5:L:416:VAL:HG22	5:L:427:PHE:CZ	2.50	0.44
1:G:231:PHE:CE2	1:H:28:LEU:HD22	2.52	0.44
3:J:161:THR:OG1	3:J:162:GLU:N	2.50	0.44
3:J:396:ALA:O	3:J:400:MET:HG3	2.18	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:606:ASN:OD1	3:J:610:ARG:NH1	2.49	0.44
3:J:825:VAL:CG2	3:J:827:GLU:HG3	2.46	0.44
3:J:968:ASN:HA	3:J:1117:SER:O	2.17	0.44
3:J:1023:HIS:CD2	3:J:1126:GLN:HG3	2.52	0.44
5:L:463:LEU:HD12	5:L:487:MET:SD	2.57	0.44
5:L:551:LEU:HD13	5:L:555:GLU:CB	2.47	0.44
1:M:280:ASP:CB	1:M:284:ARG:HH21	2.29	0.44
7:O:16:DC:H2''	7:O:17:DA:OP2	2.18	0.44
1:H:69:SER:HB2	1:H:78:ILE:CD1	2.47	0.44
1:H:133:LEU:HD12	1:H:133:LEU:HA	1.79	0.44
3:J:152:THR:OG1	3:J:153:ASN:N	2.50	0.44
3:J:203:GLU:HG2	3:J:207:GLU:OE2	2.17	0.44
3:J:707:ILE:HG22	3:J:708:ASN:N	2.32	0.44
3:J:1170:LYS:HE2	3:J:1172:LYS:HE3	2.00	0.44
1:M:275:ILE:HG12	1:M:284:ARG:NH1	2.31	0.44
1:M:298:LYS:HB2	8:P:68:DG:P	2.57	0.44
1:H:91:ARG:HD2	1:H:124:VAL:CG1	2.47	0.44
2:I:66:SER:O	2:I:479:LEU:HD13	2.17	0.44
2:I:270:THR:OG1	2:I:273:HIS:N	2.46	0.44
2:I:594:VAL:HG11	2:I:650:VAL:CG2	2.47	0.44
2:I:891:GLY:HA2	2:I:892:GLU:HA	1.70	0.44
3:J:975:ILE:HG22	3:J:977:SER:O	2.18	0.44
5:L:147:GLN:CB	5:L:161:LEU:HD13	2.48	0.44
7:O:22:DT:O2	8:P:64:DA:N1	2.51	0.44
1:G:16:ILE:HG12	1:G:26:VAL:HG13	1.98	0.44
1:G:75:GLN:HE21	1:G:132:HIS:CB	2.31	0.44
2:I:240:GLU:HG2	2:I:284:LEU:HD12	1.99	0.44
2:I:255:ILE:HG13	2:I:263:VAL:CG1	2.47	0.44
2:I:672:GLU:H	2:I:672:GLU:HG2	1.51	0.44
2:I:1322:SER:HB2	3:J:342:LEU:HD12	2.00	0.44
3:J:136:GLU:HA	3:J:139:LEU:HB2	1.98	0.44
3:J:204:GLU:O	3:J:204:GLU:HG2	2.17	0.44
3:J:265:LEU:HD11	3:J:327:LEU:HD23	1.99	0.44
3:J:707:ILE:N	3:J:707:ILE:HD12	2.33	0.44
3:J:721:SER:O	3:J:725:MET:HG3	2.18	0.44
3:J:999:TYR:O	3:J:1026:PRO:HD2	2.17	0.44
3:J:1190:ILE:CG2	3:J:1196:LEU:HD21	2.48	0.44
5:L:149:ASP:O	5:L:153:ALA:CB	2.66	0.44
1:M:298:LYS:O	1:M:301:THR:HG22	2.18	0.44
1:G:227:GLN:HB3	1:H:39:LEU:HD11	1.99	0.44
2:I:70:TYR:HA	2:I:100:LEU:HD23	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:93:SER:HB3	2:I:126:GLU:HB3	2.00	0.44
2:I:148:GLN:HB2	2:I:511:LEU:CD1	2.46	0.44
2:I:231:GLU:O	2:I:237:LEU:HA	2.18	0.44
2:I:239:MET:HE2	2:I:241:LEU:HA	1.99	0.44
2:I:538:LEU:HD22	2:I:547:VAL:HG21	2.00	0.44
2:I:724:VAL:HG22	2:I:734:ILE:HD11	2.00	0.44
2:I:877:VAL:HG11	2:I:920:VAL:CG2	2.44	0.44
2:I:896:THR:HB	2:I:897:PRO:HD2	2.00	0.44
3:J:245:LEU:HD12	3:J:245:LEU:HA	1.87	0.44
3:J:352:ARG:HA	3:J:466:MET:O	2.17	0.44
3:J:1155:ILE:HD11	3:J:1211:SER:CB	2.47	0.44
3:J:1158:GLU:HG3	3:J:1186:TYR:OH	2.17	0.44
3:J:1358:PRO:HB3	3:J:1366:HIS:CG	2.53	0.44
4:K:26:ARG:NE	4:K:30:MET:HE3	2.31	0.44
5:L:137:TYR:CE2	5:L:276:MET:HE1	2.53	0.44
5:L:313:ASP:HB3	5:L:317:ASN:HB2	1.99	0.44
5:L:453:PRO:HG2	7:O:44:DA:OP2	2.17	0.44
1:M:280:ASP:HA	1:M:283:GLN:CG	2.46	0.44
1:G:33:ARG:HB3	1:G:33:ARG:CZ	2.48	0.44
1:G:50:SER:HB3	1:H:8:PHE:HZ	1.83	0.44
2:I:4:SER:OG	2:I:7:GLU:HB2	2.18	0.44
2:I:360:LEU:HD23	2:I:364:VAL:HG13	1.99	0.44
2:I:563:THR:OG1	2:I:564:PRO:HD2	2.18	0.44
2:I:1125:GLY:HA3	2:I:1179:GLY:HA2	1.99	0.44
2:I:1131:MET:HE1	2:I:1141:LEU:HA	2.00	0.44
3:J:118:LYS:NZ	3:J:312:ARG:HB2	2.32	0.44
3:J:929:GLN:HB2	3:J:1246:VAL:HG21	2.00	0.44
5:L:235:ILE:CA	5:L:245:ALA:HB2	2.45	0.44
1:H:16:ILE:CD1	1:H:214:GLU:HB3	2.48	0.43
1:H:35:PHE:HA	1:H:38:THR:HG22	1.98	0.43
2:I:228:VAL:HG22	2:I:245:ARG:HH21	1.82	0.43
2:I:459:MET:HE1	2:I:511:LEU:CD1	2.48	0.43
2:I:974:ARG:HG2	2:I:1014:LEU:HD21	1.99	0.43
3:J:201:LEU:CD1	3:J:221:ILE:HG12	2.48	0.43
3:J:347:VAL:HG12	3:J:348:ASP:O	2.18	0.43
3:J:783:LEU:HD23	3:J:783:LEU:HA	1.70	0.43
3:J:1361:THR:HG22	4:K:21:LEU:HD21	1.99	0.43
5:L:336:GLU:HA	5:L:339:ARG:NE	2.33	0.43
1:G:55:ALA:HB3	1:G:177:TYR:CD1	2.54	0.43
1:H:103:ASN:HB3	1:H:141:SER:HB2	1.99	0.43
2:I:61:SER:HB3	2:I:65:ASN:H	1.83	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:318:SER:OG	2:I:320:ASP:OD1	2.35	0.43
2:I:611:GLU:O	2:I:611:GLU:HG2	2.18	0.43
3:J:25:ALA:HB3	3:J:30:ILE:HD11	1.99	0.43
3:J:163:GLU:CD	3:J:163:GLU:H	2.25	0.43
3:J:705:THR:CG2	3:J:707:ILE:HD11	2.37	0.43
3:J:706:VAL:HG12	3:J:713:GLU:HG2	2.00	0.43
3:J:747:MET:CG	3:J:774:ILE:HG22	2.47	0.43
7:O:35:DG:H2''	7:O:36:DA:OP2	2.17	0.43
8:P:42:DT:OP2	8:P:42:DT:H2'	2.17	0.43
1:G:234:LEU:HB2	1:H:218:ARG:NH2	2.34	0.43
2:I:600:THR:CG2	2:I:602:GLU:HG2	2.49	0.43
2:I:1107:MET:HE2	2:I:1107:MET:HB2	1.62	0.43
3:J:140:TYR:HB2	5:L:100:MET:HE1	2.01	0.43
3:J:645:VAL:CG2	3:J:700:ASN:HD21	2.31	0.43
3:J:1005:LYS:HE2	3:J:1011:VAL:HG21	1.98	0.43
5:L:137:TYR:CZ	5:L:139:GLU:HB3	2.54	0.43
5:L:405:ILE:HG22	5:L:409:ASN:ND2	2.33	0.43
5:L:462:LYS:HE3	5:L:489:MET:CE	2.47	0.43
6:N:3:ASP:OD1	6:N:6:ASP:HB2	2.19	0.43
1:G:79:LEU:HD11	2:I:1057:LYS:NZ	2.33	0.43
1:H:102:LEU:HD12	1:H:144:ILE:HD11	1.99	0.43
2:I:74:ARG:NH2	2:I:97:ARG:HG3	2.33	0.43
2:I:219:GLN:HA	2:I:222:ASP:HB2	2.00	0.43
2:I:865:LEU:HD21	2:I:882:ILE:O	2.18	0.43
2:I:1072:ASN:OD1	2:I:1072:ASN:N	2.51	0.43
3:J:41:PRO:HG3	3:J:274:ASN:OD1	2.18	0.43
3:J:108:ALA:N	3:J:276:ASN:HD21	2.08	0.43
3:J:432:LEU:HD21	3:J:489:ASN:HB3	2.01	0.43
3:J:500:ILE:HG23	3:J:500:ILE:HD12	1.82	0.43
3:J:507:VAL:HA	3:J:601:ILE:HD12	2.00	0.43
3:J:664:ILE:CD1	3:J:681:LYS:HG2	2.48	0.43
3:J:1078:LEU:CD2	3:J:1121:LEU:HD11	2.32	0.43
3:J:1172:LYS:CB	3:J:1189:MET:HB3	2.45	0.43
5:L:147:GLN:OE1	5:L:151:VAL:HG23	2.19	0.43
5:L:152:GLU:CG	5:L:218:ARG:HD3	2.47	0.43
5:L:476:ARG:HE	5:L:476:ARG:HB3	1.47	0.43
5:L:511:ILE:CG2	5:L:517:SER:HB3	2.48	0.43
2:I:153:PRO:HA	2:I:177:ILE:O	2.18	0.43
2:I:957:LYS:CB	2:I:1029:LEU:HD11	2.42	0.43
3:J:131:PRO:HG2	3:J:134:ASP:OD2	2.18	0.43
3:J:596:LEU:HD22	3:J:596:LEU:HA	1.73	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:707:ILE:O	3:J:714:GLU:N	2.52	0.43
3:J:1216:ALA:O	3:J:1220:ILE:HG12	2.18	0.43
5:L:586:ARG:NE	7:O:24:DC:H2'	2.33	0.43
1:M:257:VAL:HG11	1:M:275:ILE:HG22	2.01	0.43
1:M:294:ASN:HA	8:P:68:DG:O3'	2.18	0.43
1:G:167:PRO:CG	1:G:170:ARG:HD2	2.39	0.43
1:H:134:THR:HG23	1:H:136:GLU:H	1.83	0.43
2:I:57:PHE:HD1	2:I:59:ILE:HG13	1.83	0.43
2:I:66:SER:CB	2:I:479:LEU:HD22	2.49	0.43
2:I:468:LEU:HA	2:I:471:VAL:HG22	2.00	0.43
2:I:618:GLN:O	2:I:621:SER:OG	2.17	0.43
2:I:1286:THR:HG22	2:I:1290:MET:HE2	2.01	0.43
3:J:57:PHE:HB3	3:J:98:ARG:HH22	1.84	0.43
3:J:137:ARG:HG3	3:J:142:GLU:HB2	2.01	0.43
3:J:190:LYS:HE3	3:J:190:LYS:HB2	1.67	0.43
3:J:809:VAL:HG23	3:J:915:ILE:CG2	2.43	0.43
3:J:974:VAL:HB	3:J:1028:ILE:CD1	2.49	0.43
3:J:1143:ASP:OD1	3:J:1148:ARG:NH1	2.43	0.43
3:J:1223:LEU:HD13	3:J:1223:LEU:HA	1.80	0.43
4:K:64:LEU:O	4:K:68:GLU:HG2	2.18	0.43
5:L:72:ALA:CA	5:L:73:ASP:HB2	2.49	0.43
5:L:121:LYS:HA	5:L:124:GLU:OE1	2.19	0.43
5:L:281:ARG:O	5:L:284:GLU:HB2	2.18	0.43
2:I:218:GLU:OE1	2:I:299:LYS:HB2	2.18	0.43
2:I:241:LEU:HD12	2:I:242:VAL:H	1.84	0.43
2:I:667:LEU:CD1	2:I:794:LEU:HD23	2.49	0.43
3:J:146:VAL:HG13	3:J:156:ARG:O	2.18	0.43
3:J:188:LEU:HA	3:J:188:LEU:HD23	1.79	0.43
3:J:672:LEU:CD2	6:N:47:ALA:HB1	2.48	0.43
3:J:812:ASP:HA	3:J:896:ALA:CB	2.48	0.43
3:J:868:TRP:O	3:J:872:LEU:HG	2.19	0.43
3:J:1159:ILE:HD12	3:J:1186:TYR:CG	2.54	0.43
9:J:1505:1N7:C19	9:J:1505:1N7:C4	2.85	0.43
5:L:399:LEU:HD12	5:L:399:LEU:HA	1.86	0.43
6:N:48:ARG:NH1	6:N:59:VAL:HG22	2.34	0.43
6:N:56:THR:O	6:N:57:LEU:HD23	2.18	0.43
1:G:88:LEU:HD12	1:G:128:HIS:CD2	2.54	0.43
2:I:100:LEU:HD23	2:I:100:LEU:HA	1.61	0.43
2:I:223:LEU:HD23	2:I:223:LEU:HA	1.84	0.43
3:J:512:TYR:CD2	3:J:635:SER:HB2	2.53	0.43
3:J:1189:MET:N	3:J:1189:MET:SD	2.91	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:15:ASN:HB2	4:K:18:ASP:HB2	1.99	0.43
4:K:15:ASN:CB	4:K:18:ASP:HB2	2.49	0.43
5:L:45:ILE:O	5:L:48:ILE:HG22	2.19	0.43
5:L:449:THR:HG23	5:L:450:ILE:H	1.84	0.43
1:G:175:ALA:HB1	1:G:177:TYR:CZ	2.53	0.43
1:H:186:ASN:O	1:H:188:GLU:HG2	2.19	0.43
2:I:57:PHE:HD2	2:I:70:TYR:HB2	1.81	0.43
2:I:253:PHE:O	2:I:263:VAL:HG12	2.19	0.43
2:I:448:LEU:HA	2:I:448:LEU:HD23	1.70	0.43
2:I:903:ARG:NH1	2:I:910:ALA:HA	2.33	0.43
3:J:264:ASP:CG	3:J:324:LEU:HD22	2.44	0.43
3:J:530:PRO:CB	3:J:581:MET:HG2	2.48	0.43
3:J:857:LEU:HD22	3:J:875:ASN:HD22	1.83	0.43
3:J:958:ILE:HG12	3:J:1009:GLU:O	2.19	0.43
3:J:1029:THR:OG1	3:J:1030:GLU:N	2.49	0.43
4:K:41:GLU:HG3	4:K:41:GLU:O	2.18	0.43
6:N:64:TYR:O	6:N:68:GLN:HG2	2.19	0.43
1:G:188:GLU:HG2	1:G:200:LYS:HD2	2.01	0.43
2:I:18:ARG:HD3	2:I:18:ARG:HA	1.75	0.43
2:I:1301:ARG:HG3	2:I:1302:THR:N	2.33	0.43
3:J:317:THR:N	3:J:318:GLY:HA2	2.16	0.43
3:J:432:LEU:CD2	3:J:489:ASN:HB3	2.49	0.43
3:J:474:LEU:HA	3:J:474:LEU:HD13	1.77	0.43
3:J:800:LEU:HA	3:J:803:VAL:HG12	2.01	0.43
3:J:850:LYS:HD3	3:J:854:ALA:CB	2.49	0.43
3:J:888:CYS:HB2	3:J:898:CYS:HB3	2.01	0.43
3:J:1172:LYS:HD2	3:J:1172:LYS:O	2.19	0.43
5:L:40:GLN:O	5:L:44:ILE:HG22	2.18	0.43
5:L:148:TYR:O	5:L:152:GLU:HG2	2.19	0.43
1:M:256:PRO:O	1:M:278:ILE:HD11	2.19	0.43
8:P:58:DC:H2''	8:P:59:DA:H8	1.83	0.43
8:P:62:DG:H2''	8:P:63:DG:H5'	2.01	0.43
1:H:16:ILE:O	1:H:16:ILE:HG12	2.16	0.42
2:I:213:LEU:HD23	2:I:385:PHE:HE2	1.83	0.42
2:I:215:TYR:HB3	2:I:220:ILE:HG13	2.00	0.42
2:I:223:LEU:HD13	2:I:426:ILE:HG21	2.01	0.42
2:I:233:ARG:CB	2:I:238:GLN:HG2	2.49	0.42
2:I:277:LEU:HD23	2:I:277:LEU:HA	1.81	0.42
2:I:516:ASP:HB3	2:I:522:SER:HB3	2.01	0.42
2:I:800:MET:CE	2:I:822:VAL:HG22	2.49	0.42
2:I:1211:ARG:O	2:I:1212:LEU:HD12	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:189:LEU:HD13	3:J:234:PRO:O	2.19	0.42
3:J:332:LYS:O	3:J:336:GLY:HA3	2.19	0.42
3:J:694:SER:HA	3:J:697:MET:HG3	2.01	0.42
3:J:1089:LEU:CD2	3:J:1094:ASP:HA	2.48	0.42
1:G:13:LEU:CD2	1:G:16:ILE:HD11	2.49	0.42
2:I:398:SER:OG	2:I:399:ALA:N	2.53	0.42
2:I:745:GLU:HA	2:I:1017:GLN:CG	2.31	0.42
3:J:153:ASN:HB2	3:J:172:PHE:CE2	2.43	0.42
3:J:382:TYR:HB3	3:J:394:ILE:CD1	2.49	0.42
3:J:400:MET:HB3	3:J:405:GLU:HG3	2.00	0.42
3:J:671:GLY:C	3:J:672:LEU:HD12	2.44	0.42
3:J:747:MET:HA	3:J:747:MET:HE3	1.99	0.42
3:J:1163:VAL:HG13	3:J:1200:GLU:O	2.19	0.42
3:J:1286:LYS:HD2	3:J:1286:LYS:HA	1.76	0.42
1:H:211:ILE:HD11	1:H:215:GLU:CD	2.45	0.42
2:I:39:ILE:O	2:I:39:ILE:HG23	2.19	0.42
2:I:314:ASN:ND2	2:I:352:ARG:HG2	2.34	0.42
2:I:361:SER:CA	2:I:364:VAL:HG22	2.48	0.42
2:I:561:ILE:CD1	2:I:661:VAL:HG12	2.50	0.42
2:I:804:PHE:O	3:J:638:SER:HB2	2.19	0.42
2:I:817:LEU:CD2	2:I:1078:LYS:HB3	2.49	0.42
2:I:871:VAL:CG1	2:I:928:VAL:HG11	2.50	0.42
2:I:1287:LEU:O	2:I:1291:LEU:HG	2.20	0.42
3:J:29:MET:HA	3:J:29:MET:HE2	2.01	0.42
3:J:316:ILE:HA	3:J:317:THR:HA	1.59	0.42
3:J:374:LEU:HD23	3:J:381:ILE:CD1	2.49	0.42
3:J:839:VAL:HG12	3:J:864:LEU:HD12	2.00	0.42
3:J:1320:ILE:HG12	3:J:1342:ASP:OD2	2.19	0.42
1:M:255:ARG:HD2	1:M:256:PRO:CD	2.49	0.42
8:P:46:DG:OP2	8:P:46:DG:H2'	2.19	0.42
1:G:192:VAL:HG11	1:G:198:LEU:CD1	2.49	0.42
1:H:39:LEU:HA	1:H:39:LEU:HD23	1.71	0.42
2:I:920:VAL:HG13	2:I:921:PRO:HD2	2.01	0.42
2:I:1151:LEU:CD2	2:I:1198:LEU:HD13	2.49	0.42
3:J:35:PHE:C	3:J:61:ILE:HG23	2.45	0.42
3:J:185:ILE:O	3:J:189:LEU:HG	2.19	0.42
5:L:316:PHE:CE1	5:L:330:LEU:HD13	2.53	0.42
2:I:39:ILE:HG13	2:I:75:LEU:CD2	2.49	0.42
2:I:1016:GLU:N	2:I:1016:GLU:OE1	2.51	0.42
2:I:1100:PRO:HG2	3:J:637:ALA:O	2.20	0.42
3:J:287:ALA:HB1	3:J:288:PRO:HD2	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:357:VAL:HG13	3:J:358:GLY:N	2.34	0.42
3:J:748:ALA:HB2	3:J:754:ILE:HD13	2.00	0.42
3:J:844:THR:HA	3:J:882:VAL:HA	2.02	0.42
5:L:114:GLU:HA	5:L:114:GLU:OE1	2.19	0.42
5:L:227:GLN:HE21	5:L:255:VAL:HG11	1.84	0.42
5:L:584:ARG:HG3	5:L:585:GLU:OE2	2.20	0.42
7:O:39:DG:H5''	7:O:39:DG:H8	1.84	0.42
8:P:69:DT:H2''	8:P:70:DG:C8	2.53	0.42
1:H:11:PRO:CG	1:H:28:LEU:HD11	2.49	0.42
1:H:90:VAL:HG22	1:H:123:ILE:CD1	2.50	0.42
2:I:12:ARG:CZ	2:I:1181:PRO:HB3	2.49	0.42
2:I:231:GLU:C	2:I:237:LEU:HA	2.45	0.42
2:I:324:LYS:HA	2:I:327:GLN:CG	2.49	0.42
2:I:324:LYS:O	2:I:327:GLN:HG3	2.20	0.42
2:I:475:VAL:HG22	2:I:492:MET:CE	2.49	0.42
2:I:638:SER:HB2	2:I:645:PHE:CZ	2.55	0.42
2:I:1255:THR:O	2:I:1255:THR:OG1	2.32	0.42
3:J:581:MET:HE2	3:J:581:MET:HB3	1.85	0.42
3:J:949:SER:HB3	3:J:1016:THR:HG21	2.01	0.42
3:J:1021:ASP:OD1	3:J:1023:HIS:N	2.49	0.42
3:J:1061:VAL:HG12	3:J:1076:PRO:HG3	2.01	0.42
5:L:45:ILE:HA	5:L:48:ILE:HG22	2.01	0.42
5:L:264:LYS:H	5:L:264:LYS:HZ3	1.68	0.42
5:L:387:VAL:HG11	5:L:408:GLY:HA3	2.00	0.42
5:L:582:VAL:HG13	7:O:25:DA:H5'	2.01	0.42
1:M:262:LEU:HD13	1:M:302:GLU:OE1	2.20	0.42
1:M:284:ARG:HB2	1:M:289:LEU:HD11	2.02	0.42
1:M:307:LEU:CD2	1:M:312:LEU:HD12	2.50	0.42
7:O:40:DC:C2'	7:O:41:DT:H71	2.48	0.42
8:P:53:DT:H2'	8:P:54:DT:H71	2.02	0.42
1:G:75:GLN:O	2:I:729:ALA:HB2	2.20	0.42
1:G:228:LEU:HD13	1:G:228:LEU:HA	1.91	0.42
2:I:533:LEU:HD21	2:I:571:LEU:CD1	2.50	0.42
2:I:720:ARG:NH2	2:I:749:ASP:OD1	2.53	0.42
2:I:988:LYS:O	2:I:992:LEU:HG	2.20	0.42
2:I:992:LEU:HB3	2:I:993:PRO:HD2	2.02	0.42
2:I:1211:ARG:HD3	2:I:1220:GLN:OE1	2.20	0.42
3:J:259:ARG:HD2	9:J:1504:1N7:O2	2.19	0.42
3:J:374:LEU:O	3:J:378:LYS:HG3	2.20	0.42
3:J:930:LEU:CD2	3:J:1244:GLN:HG3	2.48	0.42
3:J:1061:VAL:HG23	3:J:1103:GLY:HA2	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:8:GLN:OE1	5:L:11:LEU:HD13	2.20	0.42
5:L:21:TYR:HD1	5:L:66:MET:HE1	1.84	0.42
5:L:554:ARG:O	5:L:558:VAL:HG23	2.20	0.42
6:N:34:VAL:CG2	6:N:44:ILE:HD12	2.49	0.42
1:G:42:ALA:CB	1:G:224:LEU:HD11	2.48	0.42
1:H:136:GLU:HG2	1:H:137:ASN:H	1.85	0.42
2:I:498:ILE:H	2:I:498:ILE:HD12	1.85	0.42
2:I:616:ILE:HG13	2:I:652:TYR:HB2	2.02	0.42
2:I:870:ILE:H	2:I:870:ILE:HD12	1.84	0.42
3:J:78:LEU:O	3:J:78:LEU:HD23	2.19	0.42
3:J:166:LEU:O	3:J:170:GLU:HG2	2.19	0.42
4:K:12:LYS:HA	4:K:12:LYS:HD3	1.86	0.42
1:H:67:GLU:HG3	1:H:171:LEU:HD22	2.01	0.42
2:I:53:PHE:CE1	2:I:468:LEU:HD11	2.54	0.42
2:I:83:GLN:HG3	2:I:83:GLN:H	1.73	0.42
2:I:107:ARG:NH1	2:I:108:GLU:O	2.52	0.42
3:J:424:ASN:HB2	3:J:434:ILE:HG12	2.02	0.42
3:J:910:ASN:HB2	4:K:15:ASN:OD1	2.19	0.42
5:L:227:GLN:HG2	5:L:255:VAL:HG21	2.00	0.42
5:L:313:ASP:O	5:L:317:ASN:HB2	2.20	0.42
5:L:327:SER:HA	5:L:330:LEU:CD2	2.50	0.42
5:L:457:ILE:O	5:L:460:ILE:HG12	2.20	0.42
5:L:600:HIS:NE2	1:M:259:ASP:O	2.53	0.42
1:G:51:MET:HE1	1:G:216:ALA:HA	2.02	0.42
1:G:54:CYS:SG	1:G:92:VAL:HG22	2.59	0.42
1:G:102:LEU:HD11	1:G:110:VAL:CG1	2.40	0.42
1:H:46:ILE:HD11	1:H:224:LEU:HD13	2.01	0.42
1:H:90:VAL:HG21	1:H:146:VAL:HG21	2.01	0.42
2:I:561:ILE:O	2:I:680:LEU:HA	2.20	0.42
2:I:797:GLY:C	2:I:798:GLN:HG2	2.44	0.42
2:I:1080:ASN:CB	2:I:1085:MET:HE3	2.50	0.42
2:I:1303:LYS:HB2	2:I:1303:LYS:HE3	1.57	0.42
2:I:1331:ARG:HA	2:I:1335:ILE:O	2.19	0.42
3:J:324:LEU:HD23	3:J:324:LEU:HA	1.76	0.42
3:J:337:ARG:O	3:J:342:LEU:HB2	2.20	0.42
3:J:603:LYS:HE2	3:J:603:LYS:HB2	1.51	0.42
3:J:1282:TYR:HA	3:J:1285:VAL:HG13	2.02	0.42
5:L:316:PHE:CZ	5:L:337:VAL:HB	2.55	0.42
5:L:413:MET:HG3	5:L:413:MET:H	1.68	0.42
6:N:35:TYR:O	6:N:43:PRO:HA	2.19	0.42
1:G:135:ASP:HB3	1:G:138:ALA:HB2	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:185:ASP:OD1	2:I:185:ASP:N	2.52	0.41
2:I:192:ASP:HB3	2:I:346:TYR:CE1	2.55	0.41
2:I:233:ARG:HA	2:I:233:ARG:NE	2.29	0.41
2:I:299:LYS:HB2	2:I:299:LYS:HE3	1.80	0.41
2:I:560:PRO:HG3	3:J:773:PHE:CD1	2.55	0.41
2:I:562:GLU:HG3	2:I:683:ALA:HB1	2.02	0.41
2:I:590:PRO:HB2	2:I:655:VAL:HG21	2.01	0.41
2:I:616:ILE:O	2:I:636:CYS:HB3	2.19	0.41
2:I:1017:GLN:NE2	2:I:1021:LEU:HG	2.35	0.41
3:J:84:ILE:CD1	3:J:91:GLU:HB2	2.48	0.41
3:J:111:THR:HG21	3:J:303:VAL:CG1	2.50	0.41
3:J:245:LEU:HD12	3:J:246:PRO:HD3	2.01	0.41
3:J:367:GLY:O	3:J:447:ILE:HG23	2.20	0.41
3:J:672:LEU:HD21	6:N:47:ALA:HB1	2.02	0.41
3:J:705:THR:HG22	3:J:707:ILE:CD1	2.37	0.41
3:J:1179:PRO:HB2	3:J:1182:GLY:H	1.85	0.41
5:L:102:MET:HA	5:L:105:MET:CG	2.50	0.41
5:L:347:ILE:HA	5:L:350:GLU:OE1	2.19	0.41
1:H:188:GLU:HB2	1:H:200:LYS:HB3	2.02	0.41
2:I:49:LEU:HD23	2:I:49:LEU:HA	1.87	0.41
2:I:130:MET:CG	2:I:134:GLY:HA2	2.50	0.41
2:I:153:PRO:HG2	2:I:400:VAL:HG12	2.01	0.41
2:I:155:VAL:HA	2:I:175:ARG:O	2.20	0.41
2:I:156:PHE:CE2	2:I:177:ILE:HD12	2.56	0.41
2:I:192:ASP:HB3	2:I:346:TYR:HD1	1.86	0.41
2:I:406:ASN:ND2	2:I:413:GLU:O	2.31	0.41
2:I:496:LYS:O	2:I:500:ALA:HB2	2.20	0.41
2:I:1124:ILE:HD11	2:I:1198:LEU:HD12	2.02	0.41
2:I:1131:MET:CE	2:I:1141:LEU:HA	2.50	0.41
2:I:1255:THR:O	2:I:1257:GLN:N	2.54	0.41
2:I:1268:GLN:HG3	3:J:467:ALA:HB1	2.00	0.41
3:J:117:LEU:HD23	3:J:117:LEU:HA	1.71	0.41
3:J:224:LEU:HA	3:J:224:LEU:HD23	1.73	0.41
3:J:1266:ILE:HD13	3:J:1266:ILE:HA	1.87	0.41
5:L:341:LEU:O	5:L:344:LEU:HB2	2.20	0.41
5:L:466:ILE:HG21	5:L:487:MET:SD	2.60	0.41
1:M:268:ASN:HA	1:M:271:LYS:NZ	2.35	0.41
1:M:314:LEU:O	1:M:316:MET:HE2	2.20	0.41
8:P:47:DC:H2"	8:P:48:DC:C6	2.56	0.41
1:G:47:LEU:O	1:G:180:VAL:HG21	2.19	0.41
1:G:57:THR:HB	1:G:147:GLN:HE21	1.84	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:24:ALA:N	1:H:213:PRO:HG2	2.35	0.41
1:H:61:ILE:HD13	1:H:142:MET:CB	2.39	0.41
2:I:296:VAL:HG21	2:I:352:ARG:HH22	1.85	0.41
2:I:974:ARG:HD3	2:I:1014:LEU:HD11	2.02	0.41
3:J:24:LEU:HB2	3:J:232:ASN:OD1	2.19	0.41
3:J:35:PHE:CD2	3:J:101:ARG:HG2	2.56	0.41
3:J:203:GLU:HA	3:J:207:GLU:OE1	2.20	0.41
3:J:260:PHE:O	5:L:504:PRO:HA	2.19	0.41
3:J:410:ASP:O	3:J:414:GLU:HG3	2.20	0.41
3:J:510:LEU:HD23	3:J:513:MET:CE	2.50	0.41
3:J:738:ARG:O	3:J:742:GLY:N	2.50	0.41
3:J:911:LYS:HB2	3:J:911:LYS:HE3	1.80	0.41
3:J:1121:LEU:O	3:J:1123:ARG:NH1	2.53	0.41
3:J:1192:LYS:HB2	3:J:1192:LYS:HE2	1.84	0.41
5:L:21:TYR:CD1	5:L:66:MET:HE1	2.56	0.41
5:L:470:MET:SD	5:L:483:LEU:HD12	2.60	0.41
7:O:36:DA:H2''	7:O:37:DA:O5'	2.19	0.41
1:G:47:LEU:HD12	1:G:183:ILE:HG21	2.01	0.41
2:I:53:PHE:HE1	2:I:468:LEU:HD21	1.85	0.41
2:I:173:ASN:CB	2:I:187:GLU:HG3	2.51	0.41
2:I:463:GLN:HG3	2:I:505:PHE:HB2	2.02	0.41
2:I:839:VAL:HG21	2:I:841:ARG:NH1	2.35	0.41
2:I:1225:VAL:HA	3:J:638:SER:HB3	2.01	0.41
3:J:62:PHE:CD1	3:J:247:PRO:HD3	2.54	0.41
3:J:245:LEU:HD12	3:J:246:PRO:CD	2.50	0.41
3:J:878:ASP:OD2	3:J:991:THR:HG22	2.21	0.41
3:J:1154:ALA:HB2	3:J:1213:GLY:C	2.46	0.41
3:J:1155:ILE:H	3:J:1155:ILE:HG13	1.68	0.41
3:J:1311:LYS:O	3:J:1311:LYS:HG2	2.21	0.41
5:L:298:PRO:HG2	5:L:326:TRP:CD1	2.55	0.41
1:H:91:ARG:HD2	1:H:124:VAL:HG12	2.03	0.41
2:I:76:GLY:O	2:I:94:ALA:HB1	2.21	0.41
2:I:270:THR:HG22	6:N:42:ASN:ND2	2.35	0.41
2:I:311:CYS:SG	2:I:315:MET:HB3	2.60	0.41
2:I:544:GLY:O	2:I:548:ARG:HG2	2.20	0.41
2:I:551:HIS:CG	2:I:552:PRO:HD2	2.55	0.41
2:I:741:MET:SD	2:I:974:ARG:NH2	2.91	0.41
2:I:832:HIS:HB2	2:I:1056:VAL:HG23	2.02	0.41
2:I:1248:THR:HG21	2:I:1305:TYR:CD1	2.56	0.41
2:I:1291:LEU:HD21	3:J:1351:VAL:HG13	2.02	0.41
2:I:1332:SER:HB2	3:J:245:LEU:HD13	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:294:ASN:ND2	5:L:406:GLN:HE21	2.17	0.41
3:J:672:LEU:O	6:N:48:ARG:HG3	2.20	0.41
3:J:694:SER:O	3:J:697:MET:HG3	2.20	0.41
3:J:1104:LYS:HD2	3:J:1104:LYS:HA	1.61	0.41
3:J:1172:LYS:HB2	3:J:1189:MET:CG	2.51	0.41
3:J:1177:ILE:O	3:J:1186:TYR:HB3	2.21	0.41
5:L:149:ASP:OD1	5:L:149:ASP:N	2.52	0.41
5:L:387:VAL:HG11	5:L:408:GLY:C	2.45	0.41
5:L:399:LEU:HD22	5:L:443:ILE:HA	2.02	0.41
5:L:401:PHE:O	5:L:405:ILE:HG13	2.20	0.41
7:O:26:DT:H2'	7:O:27:DT:C6	2.55	0.41
1:G:57:THR:CB	1:G:147:GLN:HE21	2.34	0.41
1:H:215:GLU:HA	1:H:218:ARG:CG	2.50	0.41
2:I:83:GLN:O	2:I:87:ILE:HD13	2.21	0.41
2:I:135:THR:HG21	2:I:142:GLU:OE2	2.21	0.41
2:I:702:THR:O	2:I:702:THR:OG1	2.39	0.41
2:I:1002:LEU:HG	2:I:1003:THR:C	2.45	0.41
2:I:1223:ARG:NH1	2:I:1223:ARG:HB3	2.36	0.41
3:J:550:VAL:HG22	3:J:572:THR:CG2	2.51	0.41
3:J:1115:ILE:HD12	3:J:1115:ILE:O	2.20	0.41
3:J:1145:PHE:CE1	3:J:1253:ILE:HG23	2.55	0.41
3:J:1218:HIS:CD2	3:J:1218:HIS:H	2.39	0.41
5:L:297:MET:HE2	5:L:302:PHE:CD1	2.47	0.41
5:L:354:THR:HB	5:L:356:GLU:OE2	2.21	0.41
5:L:412:LEU:HB2	5:L:435:ILE:HD11	2.02	0.41
1:M:284:ARG:CB	1:M:289:LEU:HG	2.51	0.41
8:P:38:DC:OP1	8:P:38:DC:H3'	2.20	0.41
8:P:39:DC:C2'	8:P:40:DC:H5'	2.48	0.41
8:P:66:DT:H2''	8:P:67:DT:C6	2.55	0.41
1:G:180:VAL:HA	1:G:207:THR:HA	2.03	0.41
1:H:69:SER:HB2	1:H:78:ILE:HD12	2.01	0.41
1:H:95:LYS:CG	1:H:98:VAL:HG22	2.51	0.41
2:I:296:VAL:HA	2:I:316:GLU:HA	2.02	0.41
2:I:998:LEU:HG	2:I:1015:ALA:CA	2.45	0.41
2:I:1042:LEU:HD13	2:I:1049:ILE:HG13	2.02	0.41
2:I:1101:LEU:HD23	3:J:725:MET:SD	2.60	0.41
2:I:1302:THR:O	2:I:1306:LYS:HG3	2.20	0.41
3:J:506:VAL:HG11	3:J:625:MET:HA	2.01	0.41
3:J:572:THR:OG1	3:J:576:ARG:HB2	2.21	0.41
3:J:1151:LYS:O	3:J:1153:PRO:HD3	2.21	0.41
5:L:430:TYR:O	5:L:433:TRP:HB3	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:253:LEU:CD2	1:M:312:LEU:HD13	2.50	0.41
8:P:41:DT:H2''	8:P:42:DT:C6	2.55	0.41
1:G:98:VAL:HG11	1:G:121:VAL:HG22	2.03	0.41
1:G:134:THR:HB	2:I:773:LEU:HD12	2.02	0.41
1:H:12:ARG:CG	1:H:13:LEU:HD23	2.51	0.41
2:I:101:ARG:HA	2:I:118:LYS:O	2.20	0.41
2:I:149:LEU:HD21	2:I:451:ARG:CZ	2.50	0.41
2:I:346:TYR:HE2	2:I:437:ASN:HD21	1.68	0.41
2:I:816:ILE:HG22	2:I:1096:ILE:HG23	2.03	0.41
2:I:1262:LYS:HB2	2:I:1265:PHE:HB2	2.02	0.41
3:J:454:CYS:HG	3:J:461:PHE:HZ	1.65	0.41
3:J:858:VAL:HG22	3:J:868:TRP:HE3	1.85	0.41
3:J:923:ILE:HA	3:J:1248:ILE:HD12	2.02	0.41
3:J:1046:ILE:HG21	3:J:1059:LEU:HD13	2.02	0.41
5:L:151:VAL:HG13	5:L:157:ARG:O	2.20	0.41
5:L:163:THR:HG21	5:L:263:PRO:HD3	2.02	0.41
1:G:79:LEU:O	1:G:83:LEU:HG	2.21	0.41
2:I:5:TYR:HB3	2:I:778:GLU:OE1	2.20	0.41
2:I:13:LYS:O	2:I:13:LYS:HG3	2.20	0.41
2:I:199:ASP:O	2:I:200:ARG:HD3	2.21	0.41
2:I:297:VAL:HG22	2:I:298:ALA:H	1.86	0.41
2:I:410:LEU:HD23	2:I:410:LEU:HA	1.82	0.41
2:I:467:GLY:O	2:I:471:VAL:HG22	2.21	0.41
2:I:598:VAL:HG12	2:I:628:HIS:CD2	2.56	0.41
2:I:854:ILE:HD12	2:I:862:LEU:HD21	2.02	0.41
2:I:901:LEU:O	2:I:905:ILE:HG13	2.21	0.41
2:I:998:LEU:HG	2:I:1015:ALA:CB	2.51	0.41
2:I:1106:ARG:O	2:I:1108:ASN:N	2.53	0.41
2:I:1254:VAL:HG13	2:I:1255:THR:H	1.85	0.41
3:J:34:SER:HA	3:J:102:MET:O	2.21	0.41
3:J:253:VAL:HG21	5:L:523:ILE:CD1	2.49	0.41
3:J:364:HIS:HB3	3:J:487:THR:HG23	2.02	0.41
3:J:806:ASP:OD1	3:J:806:ASP:N	2.54	0.41
3:J:1032:SER:OG	3:J:1116:SER:HA	2.21	0.41
3:J:1109:LEU:HD23	3:J:1109:LEU:HA	1.88	0.41
3:J:1198:VAL:HG11	3:J:1210:ILE:HG23	2.03	0.41
3:J:1220:ILE:CG2	3:J:1228:ALA:HB1	2.51	0.41
5:L:7:SER:CB	5:L:88:GLU:HG3	2.50	0.41
5:L:148:TYR:CE1	5:L:152:GLU:HG3	2.56	0.41
5:L:162:ILE:HA	5:L:261:LEU:HA	2.02	0.41
5:L:478:PRO:HB3	5:L:483:LEU:HD11	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:490:PRO:HD2	5:L:493:LYS:CG	2.50	0.41
1:M:257:VAL:CG1	1:M:275:ILE:HG22	2.51	0.41
6:N:33:PRO:HB2	6:N:35:TYR:CE2	2.55	0.41
6:N:36:LEU:HA	6:N:42:ASN:O	2.20	0.41
6:N:48:ARG:HH11	6:N:48:ARG:HG3	1.86	0.41
2:I:98:VAL:HG21	2:I:124:MET:SD	2.61	0.41
2:I:178:PRO:HG3	2:I:395:TYR:CZ	2.56	0.41
2:I:607:SER:HB3	2:I:610:GLU:OE2	2.21	0.41
2:I:757:THR:HG23	2:I:765:ILE:HB	2.02	0.41
2:I:841:ARG:H	2:I:841:ARG:HG2	1.46	0.41
2:I:975:ILE:CD1	2:I:998:LEU:HD12	2.51	0.41
3:J:270:ARG:O	3:J:274:ASN:ND2	2.54	0.41
3:J:300:GLN:NE2	3:J:304:ASP:OD1	2.54	0.41
3:J:438:GLU:HG3	3:J:485:MET:CE	2.42	0.41
3:J:487:THR:OG1	4:K:4:VAL:O	2.28	0.41
3:J:826:ILE:O	3:J:826:ILE:HG23	2.21	0.41
3:J:1029:THR:HA	3:J:1099:TYR:CE2	2.56	0.41
3:J:1036:ARG:NH2	3:J:1079:LYS:HG3	2.36	0.41
1:H:193:GLU:H	1:H:193:GLU:HG3	1.58	0.40
2:I:561:ILE:HD11	2:I:665:ALA:HB1	2.03	0.40
2:I:715:THR:HG21	2:I:782:VAL:CG1	2.51	0.40
2:I:717:VAL:HG12	2:I:782:VAL:HG12	2.03	0.40
2:I:887:VAL:HB	2:I:913:VAL:CG2	2.51	0.40
2:I:1075:VAL:HG11	3:J:463:GLY:HA2	2.02	0.40
3:J:249:LEU:C	3:J:251:PRO:HD3	2.46	0.40
3:J:393:THR:HG22	5:L:609:SER:OG	2.21	0.40
3:J:845:ALA:HB3	3:J:881:LYS:HD3	2.03	0.40
3:J:1158:GLU:H	3:J:1158:GLU:HG2	1.54	0.40
3:J:1161:GLY:C	3:J:1203:ARG:HG3	2.46	0.40
4:K:6:VAL:O	4:K:6:VAL:HG23	2.21	0.40
5:L:17:LYS:HB3	5:L:17:LYS:HE2	1.92	0.40
5:L:224:LEU:HD21	5:L:256:PHE:CD1	2.57	0.40
5:L:327:SER:HA	5:L:330:LEU:HD23	2.03	0.40
5:L:390:ILE:HD11	5:L:436:ARG:NH2	2.37	0.40
8:P:47:DC:H4'	8:P:48:DC:OP1	2.21	0.40
8:P:51:DC:C2'	8:P:52:DT:H71	2.51	0.40
1:G:58:GLU:OE1	1:G:145:LYS:HD2	2.20	0.40
1:H:21:SER:OG	1:H:22:THR:HG23	2.21	0.40
2:I:561:ILE:HD11	2:I:665:ALA:CB	2.51	0.40
2:I:724:VAL:HG23	2:I:777:VAL:HG13	2.03	0.40
2:I:1322:SER:CB	3:J:342:LEU:HD12	2.50	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:230:SER:OG	3:J:231:GLY:N	2.54	0.40
3:J:510:LEU:CD1	3:J:601:ILE:HD11	2.51	0.40
3:J:1033:GLY:O	3:J:1115:ILE:HG13	2.21	0.40
4:K:27:ALA:HB1	4:K:46:THR:HB	2.03	0.40
5:L:470:MET:CE	5:L:482:GLU:HB3	2.38	0.40
1:M:251:PRO:HA	1:M:254:LEU:HG	2.03	0.40
2:I:170:VAL:HG12	2:I:171:LEU:O	2.20	0.40
2:I:347:ILE:CA	2:I:350:THR:HG22	2.49	0.40
2:I:400:VAL:HG22	2:I:584:TYR:HB3	2.03	0.40
2:I:615:VAL:HB	2:I:650:VAL:HA	2.02	0.40
2:I:885:GLY:HA2	2:I:917:SER:CB	2.51	0.40
3:J:105:ILE:HG13	3:J:244:VAL:CG1	2.52	0.40
3:J:300:GLN:HG3	3:J:312:ARG:HH12	1.86	0.40
3:J:733:SER:O	3:J:737:ILE:HG12	2.22	0.40
3:J:809:VAL:HG11	3:J:909:ILE:HG23	2.02	0.40
3:J:1025:MET:HB3	3:J:1124:ILE:CB	2.27	0.40
3:J:1038:THR:HB	3:J:1079:LYS:HG2	2.03	0.40
4:K:15:ASN:HB3	4:K:18:ASP:H	1.86	0.40
5:L:11:LEU:HA	5:L:14:THR:HG22	2.03	0.40
5:L:165:PHE:HE1	5:L:260:ARG:H	1.69	0.40
5:L:354:THR:O	5:L:358:VAL:HG22	2.21	0.40
5:L:426:LYS:HB2	5:L:426:LYS:HE2	1.84	0.40
7:O:37:DA:H2''	7:O:38:DG:O5'	2.21	0.40
1:H:90:VAL:HG22	1:H:123:ILE:HD13	2.03	0.40
2:I:27:LEU:HD13	2:I:524:ILE:CD1	2.48	0.40
2:I:179:TYR:HB3	2:I:396:ASP:O	2.21	0.40
2:I:629:PHE:O	2:I:647:ARG:HD2	2.21	0.40
2:I:896:THR:HB	2:I:897:PRO:CD	2.52	0.40
2:I:1225:VAL:HG12	3:J:638:SER:HB3	2.04	0.40
3:J:62:PHE:O	3:J:98:ARG:HA	2.22	0.40
3:J:72:CYS:SG	3:J:73:GLY:N	2.93	0.40
3:J:137:ARG:HG3	3:J:142:GLU:CB	2.51	0.40
3:J:605:LEU:HA	3:J:605:LEU:HD23	1.90	0.40
3:J:707:ILE:O	3:J:713:GLU:HA	2.22	0.40
3:J:982:LEU:HB2	3:J:997:VAL:CG2	2.49	0.40
3:J:1042:ASP:OD2	3:J:1046:ILE:HG13	2.22	0.40
3:J:1280:VAL:HG13	3:J:1285:VAL:HG12	2.03	0.40
1:M:255:ARG:HD3	1:M:255:ARG:HA	1.73	0.40
7:O:21:DA:H2''	7:O:22:DT:H71	2.04	0.40
1:G:217:ILE:HG13	1:G:218:ARG:N	2.35	0.40
2:I:43:PRO:O	2:I:44:GLU:HG3	2.22	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:230:PHE:HD1	2:I:239:MET:HA	1.86	0.40
2:I:277:LEU:HD22	2:I:282:VAL:HB	2.04	0.40
2:I:533:LEU:HD21	2:I:571:LEU:HD13	2.03	0.40
2:I:578:TYR:HD2	2:I:659:GLN:HG3	1.87	0.40
2:I:606:LEU:HD21	2:I:652:TYR:CE2	2.57	0.40
2:I:849:GLU:HB3	2:I:851:THR:HG23	2.03	0.40
2:I:1066:MET:HE3	2:I:1066:MET:HB2	1.94	0.40
2:I:1096:ILE:HD12	2:I:1232:MET:SD	2.61	0.40
2:I:1243:MET:HE3	3:J:445:LYS:HB3	2.01	0.40
2:I:1305:TYR:CG	5:L:531:PRO:HB2	2.56	0.40
3:J:265:LEU:HD23	3:J:265:LEU:HA	1.93	0.40
3:J:393:THR:OG1	3:J:394:ILE:N	2.54	0.40
3:J:418:GLU:CD	4:K:48:VAL:HG21	2.46	0.40
3:J:505:ASP:HB2	3:J:629:PHE:HE1	1.85	0.40
3:J:555:TYR:HB3	3:J:563:LEU:HB3	2.03	0.40
3:J:904:ALA:O	3:J:906:GLY:N	2.55	0.40
5:L:479:THR:OG1	5:L:480:PRO:HD2	2.21	0.40
5:L:511:ILE:HD11	9:L:701:1N7:C10	2.51	0.40
7:O:35:DG:H2"	7:O:36:DA:H8	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	228/329 (69%)	205 (90%)	23 (10%)	0	100	100
1	H	215/329 (65%)	189 (88%)	26 (12%)	0	100	100
1	M	71/329 (22%)	68 (96%)	3 (4%)	0	100	100
2	I	1338/1342 (100%)	1179 (88%)	157 (12%)	2 (0%)	48	78
3	J	1339/1430 (94%)	1197 (89%)	141 (10%)	1 (0%)	48	78

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	K	73/91 (80%)	68 (93%)	5 (7%)	0	100	100
5	L	540/616 (88%)	500 (93%)	40 (7%)	0	100	100
6	N	70/72 (97%)	65 (93%)	5 (7%)	0	100	100
All	All	3874/4538 (85%)	3471 (90%)	400 (10%)	3 (0%)	49	78

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	I	898	GLU
3	J	854	ALA
2	I	897	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	195/286 (68%)	168 (86%)	27 (14%)	3	14
1	H	184/286 (64%)	161 (88%)	23 (12%)	4	18
1	M	65/286 (23%)	62 (95%)	3 (5%)	24	50
2	I	1153/1157 (100%)	1020 (88%)	133 (12%)	5	20
3	J	1128/1189 (95%)	1010 (90%)	118 (10%)	6	23
4	K	65/75 (87%)	58 (89%)	7 (11%)	6	22
5	L	479/543 (88%)	448 (94%)	31 (6%)	15	42
6	N	60/61 (98%)	52 (87%)	8 (13%)	4	15
All	All	3329/3883 (86%)	2979 (90%)	350 (10%)	9	23

All (350) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	14	VAL
1	G	18	GLN
1	G	33	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	39	LEU
1	G	46	ILE
1	G	56	VAL
1	G	61	ILE
1	G	64	VAL
1	G	67	GLU
1	G	70	THR
1	G	74	VAL
1	G	102	LEU
1	G	116	THR
1	G	129	VAL
1	G	144	ILE
1	G	157	THR
1	G	159	ILE
1	G	160	HIS
1	G	177	TYR
1	G	181	GLU
1	G	187	VAL
1	G	200	LYS
1	G	204	GLU
1	G	217	ILE
1	G	222	THR
1	G	224	LEU
1	G	232	VAL
1	H	6	THR
1	H	15	ASP
1	H	16	ILE
1	H	27	THR
1	H	33	ARG
1	H	38	THR
1	H	46	ILE
1	H	64	VAL
1	H	65	LEU
1	H	83	LEU
1	H	92	VAL
1	H	102	LEU
1	H	121	VAL
1	H	130	ILE
1	H	146	VAL
1	H	157	THR
1	H	172	LEU
1	H	193	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	H	196	THR
1	H	203	ILE
1	H	210	THR
1	H	212	ASP
1	H	222	THR
2	I	6	THR
2	I	8	LYS
2	I	39	ILE
2	I	55	SER
2	I	56	VAL
2	I	60	GLN
2	I	75	LEU
2	I	77	GLU
2	I	79	VAL
2	I	91	THR
2	I	104	ILE
2	I	138	ILE
2	I	144	VAL
2	I	147	SER
2	I	149	LEU
2	I	160	ASP
2	I	161	LYS
2	I	189	ASP
2	I	194	LEU
2	I	198	ILE
2	I	208	ILE
2	I	220	ILE
2	I	250	THR
2	I	261	VAL
2	I	273	HIS
2	I	277	LEU
2	I	301	TYR
2	I	320	ASP
2	I	321	LEU
2	I	322	LEU
2	I	336	LEU
2	I	347	ILE
2	I	393	ASP
2	I	397	LEU
2	I	422	LYS
2	I	435	ILE
2	I	443	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	I	444	ASP
2	I	453	ILE
2	I	472	GLU
2	I	475	VAL
2	I	493	ILE
2	I	508	SER
2	I	513	GLN
2	I	514	PHE
2	I	521	LEU
2	I	524	ILE
2	I	525	THR
2	I	550	VAL
2	I	558	VAL
2	I	561	ILE
2	I	562	GLU
2	I	565	GLU
2	I	571	LEU
2	I	573	ASN
2	I	575	LEU
2	I	577	VAL
2	I	606	LEU
2	I	609	ILE
2	I	615	VAL
2	I	630	VAL
2	I	633	LEU
2	I	662	SER
2	I	672	GLU
2	I	692	THR
2	I	699	LEU
2	I	702	THR
2	I	717	VAL
2	I	727	VAL
2	I	731	ARG
2	I	748	ILE
2	I	750	ILE
2	I	754	THR
2	I	757	THR
2	I	759	SER
2	I	766	ASN
2	I	777	VAL
2	I	789	THR
2	I	791	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	I	799	ASN
2	I	800	MET
2	I	815	SER
2	I	816	ILE
2	I	819	SER
2	I	823	VAL
2	I	826	ASP
2	I	841	ARG
2	I	845	LEU
2	I	850	ILE
2	I	854	ILE
2	I	856	ASN
2	I	857	VAL
2	I	873	ILE
2	I	878	THR
2	I	888	THR
2	I	902	LEU
2	I	948	ILE
2	I	951	MET
2	I	960	LEU
2	I	978	VAL
2	I	979	LEU
2	I	984	VAL
2	I	990	ASP
2	I	996	ARG
2	I	1002	LEU
2	I	1003	THR
2	I	1011	LEU
2	I	1016	GLU
2	I	1046	VAL
2	I	1054	LEU
2	I	1056	VAL
2	I	1060	ILE
2	I	1073	LYS
2	I	1076	ILE
2	I	1082	ILE
2	I	1092	THR
2	I	1096	ILE
2	I	1107	MET
2	I	1109	ILE
2	I	1163	THR
2	I	1167	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	I	1186	VAL
2	I	1211	ARG
2	I	1222	GLU
2	I	1226	THR
2	I	1235	LEU
2	I	1253	LEU
2	I	1254	VAL
2	I	1259	LEU
2	I	1269	ARG
2	I	1287	LEU
2	I	1296	ASP
2	I	1301	ARG
3	J	24	LEU
3	J	54	ASP
3	J	56	LEU
3	J	65	VAL
3	J	78	LEU
3	J	88	CYS
3	J	111	THR
3	J	126	LEU
3	J	128	LEU
3	J	129	ASP
3	J	135	ILE
3	J	154	LEU
3	J	159	ILE
3	J	160	LEU
3	J	161	THR
3	J	163	GLU
3	J	192	MET
3	J	201	LEU
3	J	210	SER
3	J	230	SER
3	J	240	THR
3	J	252	LEU
3	J	253	VAL
3	J	255	LEU
3	J	285	LEU
3	J	299	LEU
3	J	306	LEU
3	J	317	THR
3	J	325	LYS
3	J	342	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	J	374	LEU
3	J	384	LYS
3	J	392	THR
3	J	407	VAL
3	J	416	ILE
3	J	428	THR
3	J	429	LEU
3	J	430	HIS
3	J	431	ARG
3	J	441	LEU
3	J	442	ILE
3	J	468	VAL
3	J	474	LEU
3	J	478	LEU
3	J	486	SER
3	J	490	ILE
3	J	499	ILE
3	J	514	THR
3	J	515	ARG
3	J	526	VAL
3	J	545	HIS
3	J	548	VAL
3	J	567	THR
3	J	569	LEU
3	J	582	ILE
3	J	591	ILE
3	J	596	LEU
3	J	601	ILE
3	J	611	ILE
3	J	622	ASP
3	J	644	MET
3	J	655	SER
3	J	674	THR
3	J	683	ILE
3	J	708	ASN
3	J	712	GLN
3	J	717	VAL
3	J	720	ASN
3	J	740	LEU
3	J	746	LEU
3	J	762	ASN
3	J	767	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	J	770	LEU
3	J	786	THR
3	J	797	THR
3	J	812	ASP
3	J	831	VAL
3	J	837	ASP
3	J	849	LEU
3	J	875	ASN
3	J	877	VAL
3	J	882	VAL
3	J	884	SER
3	J	890	THR
3	J	895	CYS
3	J	902	ASP
3	J	903	LEU
3	J	907	HIS
3	J	909	ILE
3	J	915	ILE
3	J	922	SER
3	J	963	VAL
3	J	982	LEU
3	J	985	ILE
3	J	1003	LEU
3	J	1046	ILE
3	J	1068	THR
3	J	1104	LYS
3	J	1155	ILE
3	J	1158	GLU
3	J	1163	VAL
3	J	1168	GLU
3	J	1176	VAL
3	J	1220	ILE
3	J	1221	LEU
3	J	1223	LEU
3	J	1248	ILE
3	J	1265	THR
3	J	1268	ASN
3	J	1281	GLU
3	J	1285	VAL
3	J	1306	LEU
3	J	1328	THR
3	J	1333	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	J	1344	LEU
3	J	1349	GLU
3	J	1351	VAL
3	J	1352	ILE
4	K	13	ILE
4	K	39	VAL
4	K	46	THR
4	K	48	VAL
4	K	49	ILE
4	K	56	GLU
4	K	64	LEU
5	L	35	ILE
5	L	53	ILE
5	L	55	VAL
5	L	69	GLU
5	L	88	GLU
5	L	118	ASP
5	L	163	THR
5	L	219	GLU
5	L	250	LEU
5	L	252	LEU
5	L	262	VAL
5	L	291	CYS
5	L	307	THR
5	L	315	TRP
5	L	339	ARG
5	L	362	ASN
5	L	388	ILE
5	L	392	LYS
5	L	402	LEU
5	L	437	GLN
5	L	449	THR
5	L	450	ILE
5	L	452	ILE
5	L	471	LEU
5	L	476	ARG
5	L	483	LEU
5	L	485	GLU
5	L	494	ILE
5	L	500	ILE
5	L	572	THR
5	L	613	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	M	281	LEU
1	M	285	THR
1	M	318	LEU
6	N	2	SER
6	N	3	ASP
6	N	7	GLU
6	N	12	THR
6	N	27	ILE
6	N	34	VAL
6	N	48	ARG
6	N	55	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (56) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	23	HIS
1	G	147	GLN
1	H	37	HIS
1	H	93	GLN
1	H	227	GLN
2	I	69	GLN
2	I	120	GLN
2	I	327	GLN
2	I	437	ASN
2	I	513	GLN
2	I	554	HIS
2	I	573	ASN
2	I	618	GLN
2	I	659	GLN
2	I	799	ASN
2	I	1009	ASN
2	I	1080	ASN
2	I	1116	HIS
2	I	1244	HIS
2	I	1257	GLN
2	I	1268	GLN
2	I	1313	HIS
3	J	45	ASN
3	J	80	HIS
3	J	164	GLN
3	J	276	ASN
3	J	294	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	J	320	ASN
3	J	340	GLN
3	J	364	HIS
3	J	465	GLN
3	J	477	GLN
3	J	489	ASN
3	J	680	ASN
3	J	700	ASN
3	J	792	ASN
3	J	817	HIS
3	J	962	ASN
3	J	1108	GLN
3	J	1114	GLN
3	J	1218	HIS
3	J	1235	ASN
3	J	1279	GLN
3	J	1289	ASN
4	K	7	GLN
4	K	31	GLN
5	L	54	GLN
5	L	227	GLN
5	L	246	GLN
5	L	258	GLN
5	L	362	ASN
5	L	437	GLN
5	L	464	ASN
1	M	268	ASN
1	M	276	HIS
6	N	68	GLN

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 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	1N7	J	1505	-	30,30,46	4.93	15 (50%)	47,48,72	2.12	15 (31%)
9	1N7	L	701	-	30,30,46	5.00	15 (50%)	47,48,72	2.48	20 (42%)
9	1N7	J	1504	-	30,30,46	5.20	16 (53%)	47,48,72	2.39	17 (36%)
9	1N7	I	1401	-	30,30,46	5.07	16 (53%)	47,48,72	2.09	10 (21%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	1N7	J	1505	-	-	0/7/72/92	0/4/4/4
9	1N7	L	701	-	-	5/7/72/92	0/4/4/4
9	1N7	J	1504	-	-	7/7/72/92	0/4/4/4
9	1N7	I	1401	-	-	5/7/72/92	0/4/4/4

All (62) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	J	1504	1N7	C3-C19	18.71	1.84	1.53
9	I	1401	1N7	C3-C19	17.97	1.82	1.53
9	L	701	1N7	C3-C19	17.48	1.82	1.53
9	J	1505	1N7	C3-C19	17.39	1.81	1.53
9	J	1504	1N7	C3-C4	12.37	1.73	1.53
9	I	1401	1N7	C3-C4	12.08	1.73	1.53
9	J	1505	1N7	C3-C4	11.63	1.72	1.53
9	L	701	1N7	C3-C4	11.30	1.71	1.53
9	L	701	1N7	C5-C4	-9.47	1.40	1.54
9	J	1504	1N7	C5-C4	-9.39	1.40	1.54
9	I	1401	1N7	C5-C4	-9.22	1.40	1.54

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	J	1505	1N7	C5-C4	-8.70	1.41	1.54
9	J	1505	1N7	C2-C19	-7.95	1.42	1.56
9	L	701	1N7	C2-C19	-7.68	1.42	1.56
9	J	1504	1N7	C2-C19	-7.49	1.43	1.56
9	I	1401	1N7	C2-C19	-7.47	1.43	1.56
9	L	701	1N7	C8-C7	6.42	1.71	1.54
9	J	1505	1N7	C8-C7	6.01	1.70	1.54
9	J	1504	1N7	C8-C7	5.86	1.70	1.54
9	I	1401	1N7	C8-C7	5.80	1.69	1.54
9	J	1505	1N7	C5-C9	4.41	1.62	1.55
9	L	701	1N7	O4-C4	-4.36	1.36	1.43
9	J	1504	1N7	O4-C4	-4.31	1.36	1.43
9	J	1505	1N7	O4-C4	-4.24	1.36	1.43
9	I	1401	1N7	O4-C4	-4.07	1.36	1.43
9	L	701	1N7	C5-C9	3.99	1.62	1.55
9	J	1504	1N7	C5-C6	-3.90	1.49	1.55
9	I	1401	1N7	C5-C6	-3.83	1.49	1.55
9	L	701	1N7	C5-C6	-3.75	1.49	1.55
9	L	701	1N7	C7-C6	3.73	1.62	1.54
9	I	1401	1N7	C5-C9	3.71	1.61	1.55
9	J	1504	1N7	C2-C15	3.70	1.61	1.55
9	I	1401	1N7	C7-C6	3.57	1.61	1.54
9	I	1401	1N7	C18-C6	-3.52	1.47	1.53
9	J	1505	1N7	C5-C6	-3.52	1.49	1.55
9	J	1504	1N7	C5-C9	3.52	1.61	1.55
9	J	1504	1N7	C7-C6	3.45	1.61	1.54
9	J	1504	1N7	C10-C5	3.37	1.59	1.54
9	J	1505	1N7	C18-C6	-3.14	1.47	1.53
9	L	701	1N7	C2-C15	3.13	1.60	1.55
9	L	701	1N7	C14-C15	-3.09	1.48	1.53
9	J	1504	1N7	C18-C6	-3.06	1.48	1.53
9	I	1401	1N7	C14-C15	-3.05	1.49	1.53
9	I	1401	1N7	C2-C15	3.00	1.60	1.55
9	J	1505	1N7	C14-C15	-2.95	1.49	1.53
9	L	701	1N7	C18-C6	-2.90	1.48	1.53
9	J	1505	1N7	C2-C15	2.87	1.59	1.55
9	J	1505	1N7	C7-C6	2.81	1.60	1.54
9	L	701	1N7	C10-C5	2.81	1.58	1.54
9	I	1401	1N7	C10-C5	2.69	1.58	1.54
9	I	1401	1N7	C1-C2	2.58	1.58	1.54
9	J	1504	1N7	C14-C15	-2.53	1.49	1.53
9	J	1504	1N7	C1-C2	2.40	1.58	1.54

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	J	1505	1N7	O2-C13	-2.37	1.36	1.43
9	J	1504	1N7	C14-C13	2.29	1.56	1.52
9	J	1505	1N7	C10-C5	2.21	1.57	1.54
9	L	701	1N7	C1-C2	2.19	1.58	1.54
9	I	1401	1N7	O2-C13	-2.18	1.37	1.43
9	J	1504	1N7	O2-C13	-2.18	1.37	1.43
9	I	1401	1N7	C14-C13	2.18	1.55	1.52
9	L	701	1N7	O2-C13	-2.16	1.37	1.43
9	J	1505	1N7	C14-C13	2.05	1.55	1.52

All (62) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	L	701	1N7	C9-C5-C4	-7.86	110.59	117.67
9	J	1504	1N7	C9-C5-C4	-7.73	110.71	117.67
9	I	1401	1N7	C9-C5-C4	-6.76	111.58	117.67
9	L	701	1N7	C3-C19-C18	-6.29	101.58	110.89
9	J	1505	1N7	C19-C3-C4	-4.99	107.77	114.29
9	J	1505	1N7	C7-C6-C18	-4.74	111.86	118.36
9	J	1505	1N7	C9-C5-C4	-4.70	113.44	117.67
9	I	1401	1N7	C6-C5-C4	4.66	111.68	107.42
9	J	1504	1N7	C7-C6-C18	-4.66	111.97	118.36
9	J	1504	1N7	C14-C13-C12	-4.55	105.06	110.62
9	L	701	1N7	C6-C5-C4	4.55	111.58	107.42
9	L	701	1N7	C2-C19-C18	4.54	116.90	111.84
9	J	1504	1N7	C19-C18-C17	-4.49	106.21	111.86
9	J	1504	1N7	C21-C20-C22	-4.16	103.90	110.34
9	I	1401	1N7	C7-C6-C18	-4.12	112.70	118.36
9	J	1505	1N7	C3-C19-C18	-4.12	104.80	110.89
9	I	1401	1N7	C21-C20-C9	-4.03	106.83	112.88
9	I	1401	1N7	C19-C18-C17	-3.99	106.84	111.86
9	J	1505	1N7	C2-C19-C18	3.88	116.16	111.84
9	J	1505	1N7	C6-C5-C4	3.82	110.91	107.42
9	I	1401	1N7	C19-C3-C4	-3.60	109.59	114.29
9	J	1504	1N7	C6-C5-C4	3.54	110.65	107.42
9	L	701	1N7	C19-C3-C4	-3.50	109.72	114.29
9	L	701	1N7	C16-C15-C2	-3.48	108.95	112.66
9	L	701	1N7	C14-C13-C12	-3.47	106.38	110.62
9	L	701	1N7	C21-C20-C22	-3.35	105.15	110.34
9	J	1504	1N7	C16-C15-C14	-3.35	107.40	111.23
9	J	1504	1N7	C22-C20-C9	3.31	117.20	110.33
9	J	1504	1N7	C16-C17-C18	-3.20	108.00	111.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	J	1505	1N7	C21-C20-C22	-3.09	105.55	110.34
9	J	1504	1N7	C1-C12-C13	-3.06	106.42	110.48
9	J	1505	1N7	C16-C15-C2	-3.04	109.43	112.66
9	L	701	1N7	C5-C6-C18	3.03	118.56	114.72
9	L	701	1N7	C7-C6-C18	-2.93	114.33	118.36
9	J	1505	1N7	C5-C6-C18	2.92	118.42	114.72
9	J	1505	1N7	C11-C2-C1	-2.90	103.70	108.31
9	J	1504	1N7	C5-C9-C20	-2.88	115.99	119.48
9	I	1401	1N7	C16-C15-C14	-2.84	107.98	111.23
9	L	701	1N7	C1-C12-C13	-2.82	106.75	110.48
9	I	1401	1N7	C1-C12-C13	-2.78	106.80	110.48
9	J	1505	1N7	C9-C5-C6	2.64	102.76	100.11
9	J	1505	1N7	C16-C17-C18	2.61	114.34	111.50
9	I	1401	1N7	C2-C19-C18	2.60	114.74	111.84
9	L	701	1N7	C9-C5-C6	2.57	102.69	100.11
9	L	701	1N7	C11-C2-C1	-2.55	104.25	108.31
9	L	701	1N7	C8-C9-C20	2.53	116.01	112.18
9	J	1505	1N7	C22-C20-C9	2.50	115.51	110.33
9	J	1504	1N7	C8-C9-C20	2.49	115.95	112.18
9	L	701	1N7	C5-C9-C20	-2.40	116.58	119.48
9	J	1504	1N7	C11-C2-C15	-2.36	106.50	110.44
9	L	701	1N7	C19-C2-C15	2.35	111.78	108.51
9	L	701	1N7	C22-C20-C9	2.34	115.18	110.33
9	J	1504	1N7	C9-C5-C6	2.32	102.44	100.11
9	I	1401	1N7	C8-C9-C20	2.21	115.53	112.18
9	J	1505	1N7	C8-C7-C6	-2.20	100.83	105.14
9	J	1504	1N7	C21-C20-C9	-2.17	109.63	112.88
9	J	1504	1N7	C14-C15-C2	2.16	114.96	112.66
9	L	701	1N7	C11-C2-C15	-2.14	106.86	110.44
9	L	701	1N7	C8-C9-C5	-2.06	101.54	103.54
9	J	1505	1N7	C11-C2-C19	2.06	113.94	111.18
9	J	1504	1N7	C7-C8-C9	-2.05	101.13	105.14
9	L	701	1N7	C15-C14-C13	-2.03	109.64	112.71

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	J	1504	1N7	C21-C20-C9-C5
9	J	1504	1N7	C21-C20-C9-C8
9	I	1401	1N7	C21-C20-C9-C5
9	I	1401	1N7	C21-C20-C9-C8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
9	I	1401	1N7	C22-C20-C9-C5
9	J	1504	1N7	C22-C20-C9-C5
9	J	1504	1N7	C22-C20-C9-C8
9	I	1401	1N7	C22-C20-C9-C8
9	J	1504	1N7	C9-C20-C22-C23
9	L	701	1N7	C20-C22-C23-C24
9	J	1504	1N7	C21-C20-C22-C23
9	I	1401	1N7	C20-C22-C23-C24
9	L	701	1N7	C21-C20-C9-C5
9	J	1504	1N7	C20-C22-C23-C24
9	L	701	1N7	C21-C20-C9-C8
9	L	701	1N7	C22-C20-C9-C5
9	L	701	1N7	C22-C20-C9-C8

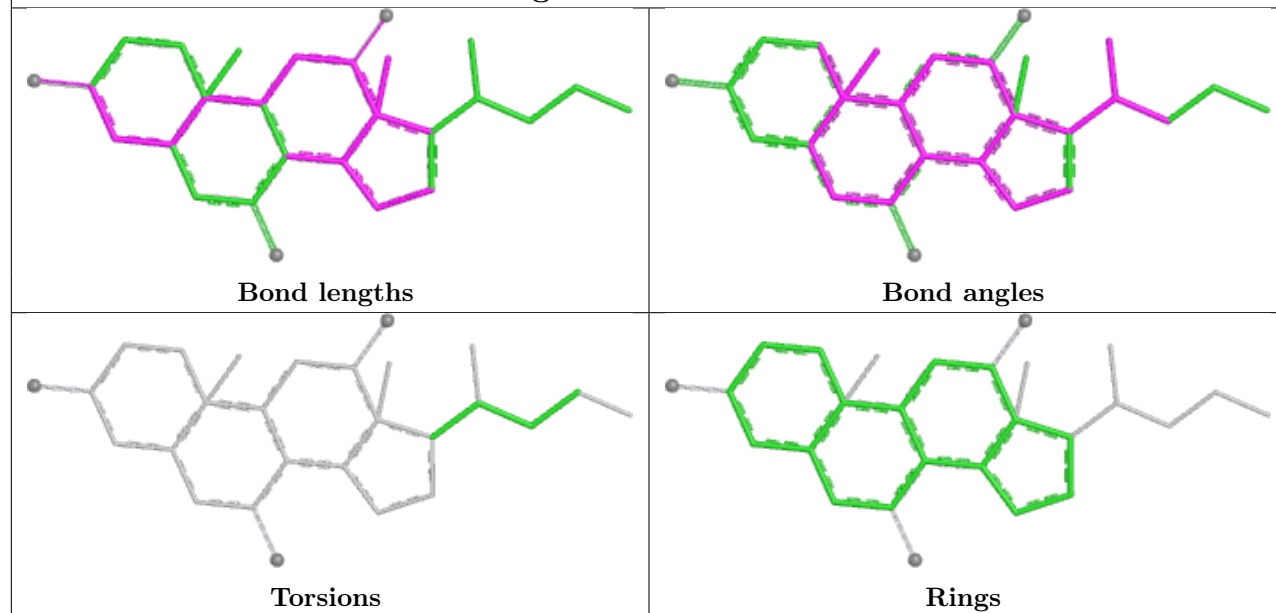
There are no ring outliers.

4 monomers are involved in 17 short contacts:

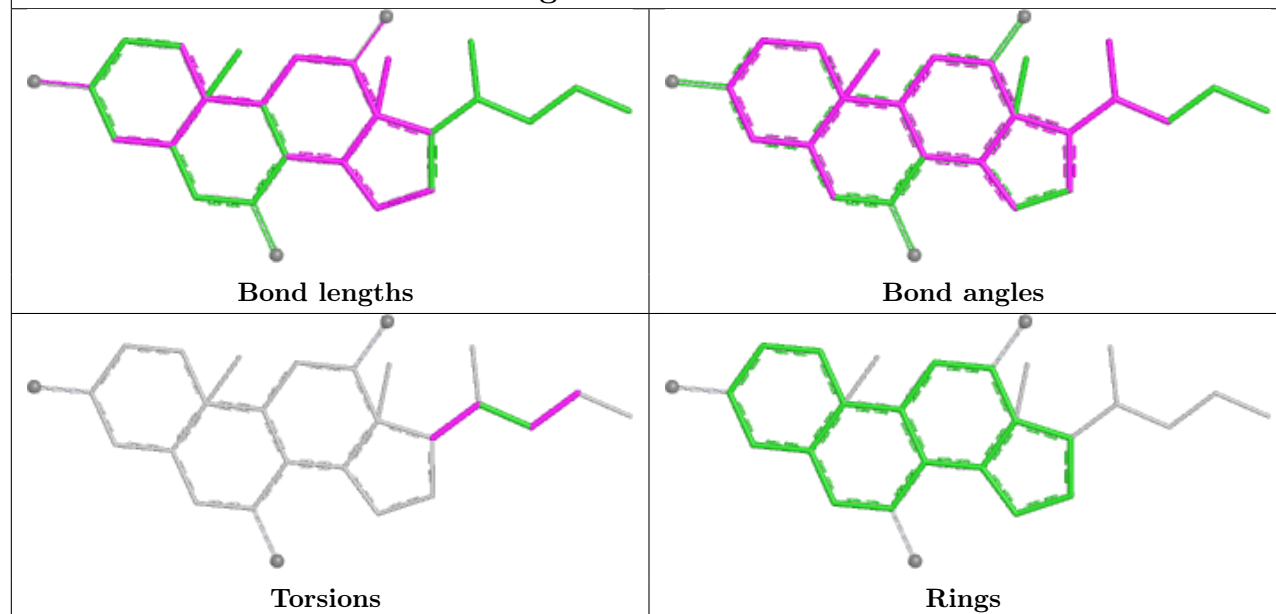
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	J	1505	1N7	5	0
9	L	701	1N7	4	0
9	J	1504	1N7	4	0
9	I	1401	1N7	4	0

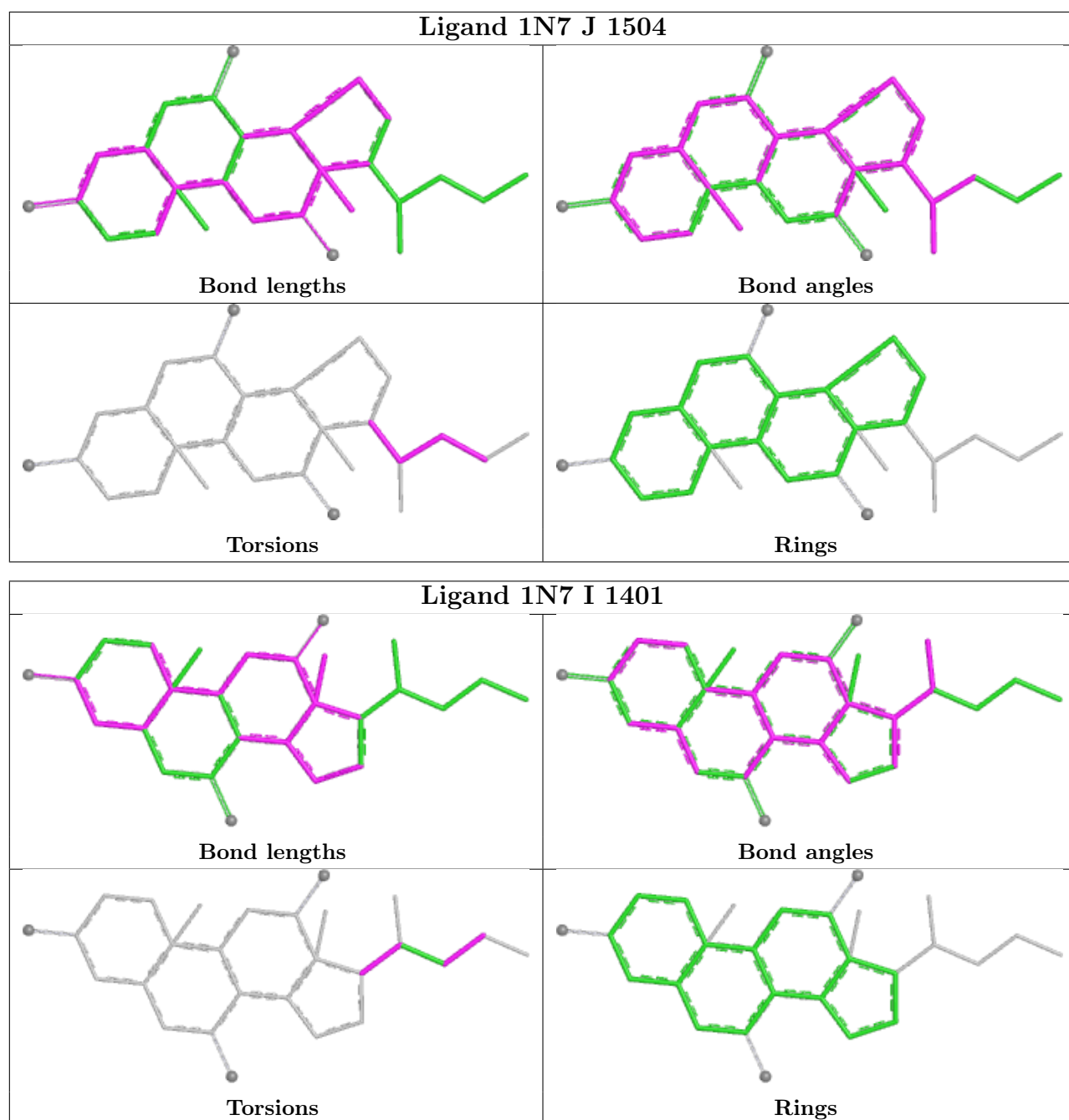
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand 1N7 J 1505



Ligand 1N7 L 701





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

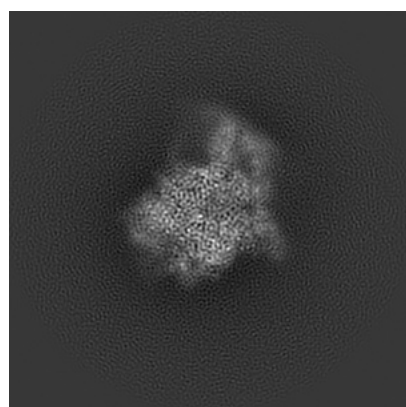
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20461. These allow visual inspection of the internal detail of the map and identification of artifacts.

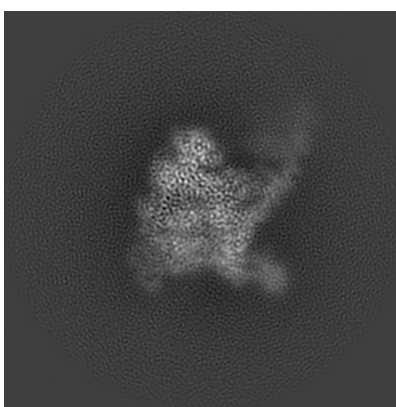
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

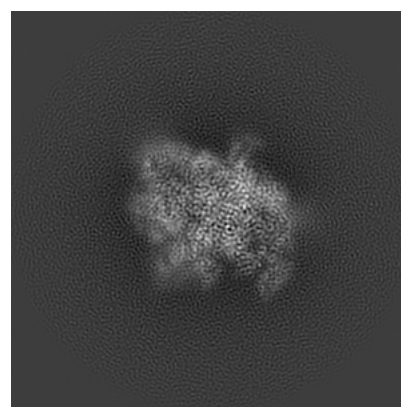
6.1.1 Primary map



X



Y

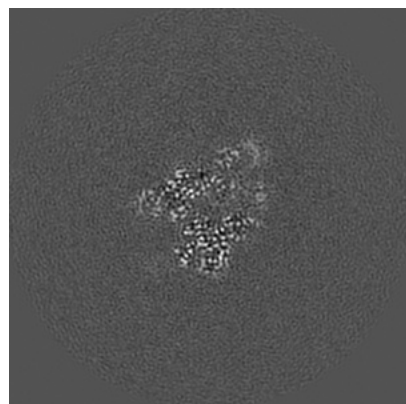


Z

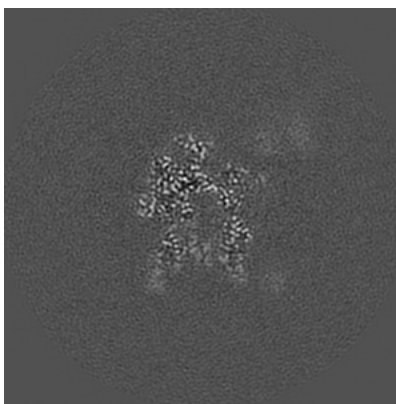
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

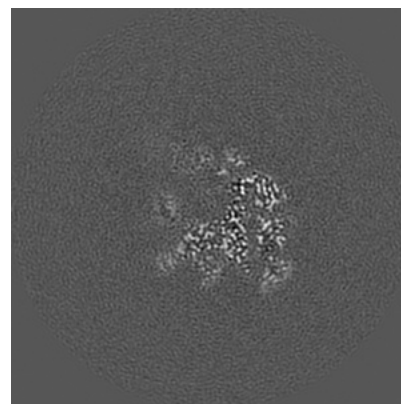
6.2.1 Primary map



X Index: 128



Y Index: 128

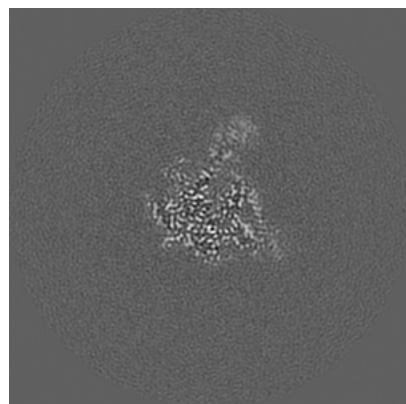


Z Index: 128

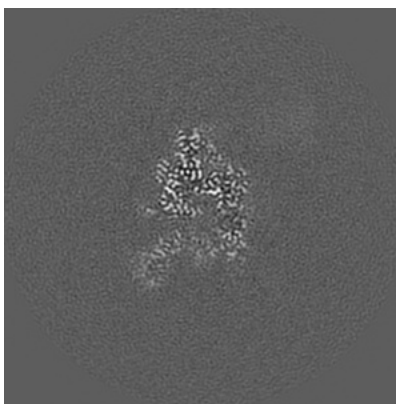
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

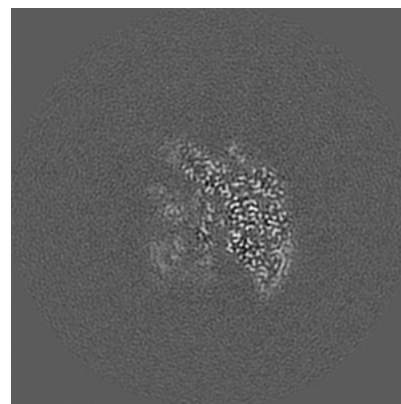
6.3.1 Primary map



X Index: 146



Y Index: 121

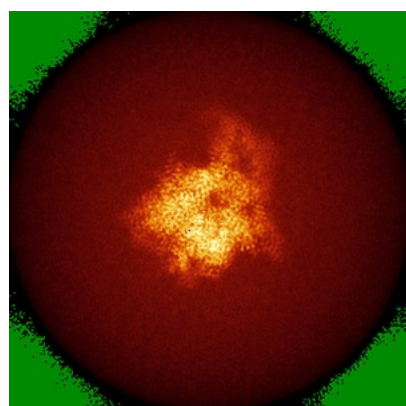


Z Index: 120

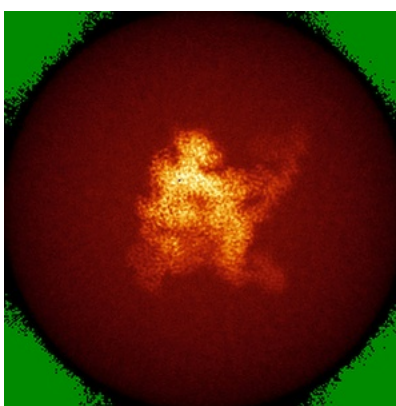
The images above show the largest variance slices of the map in three orthogonal directions.

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

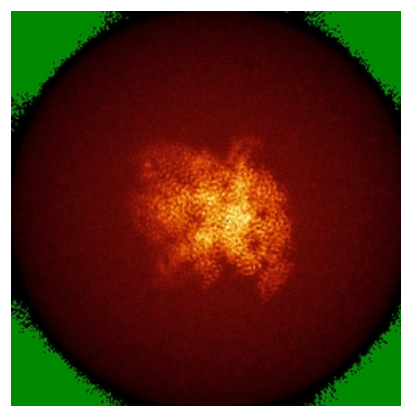
6.4.1 Primary map



X



Y

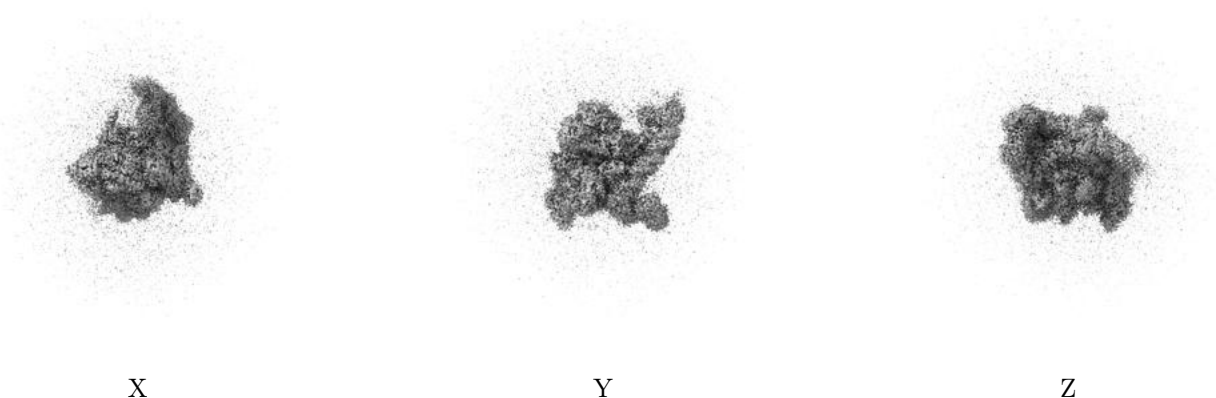


Z

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

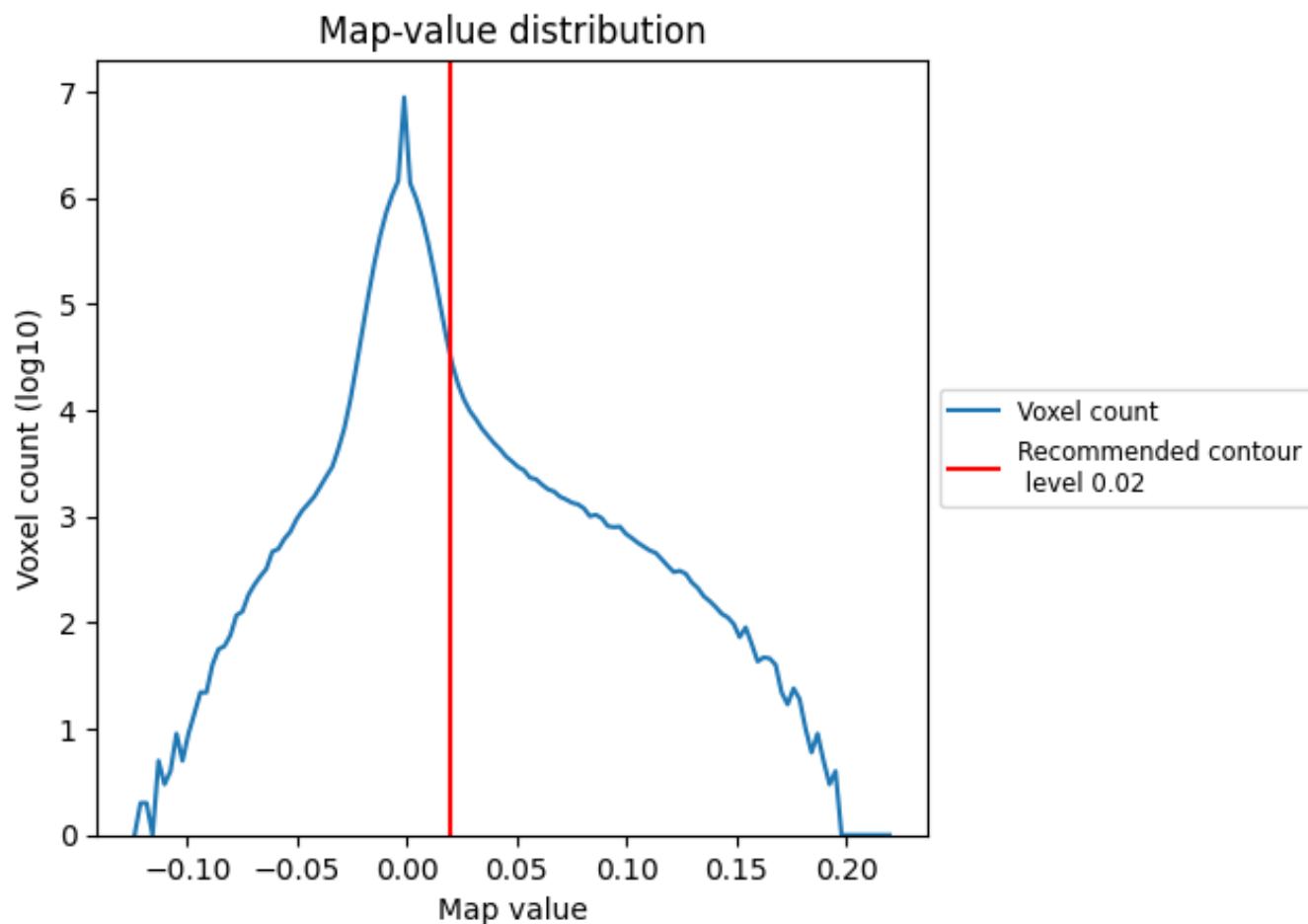
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

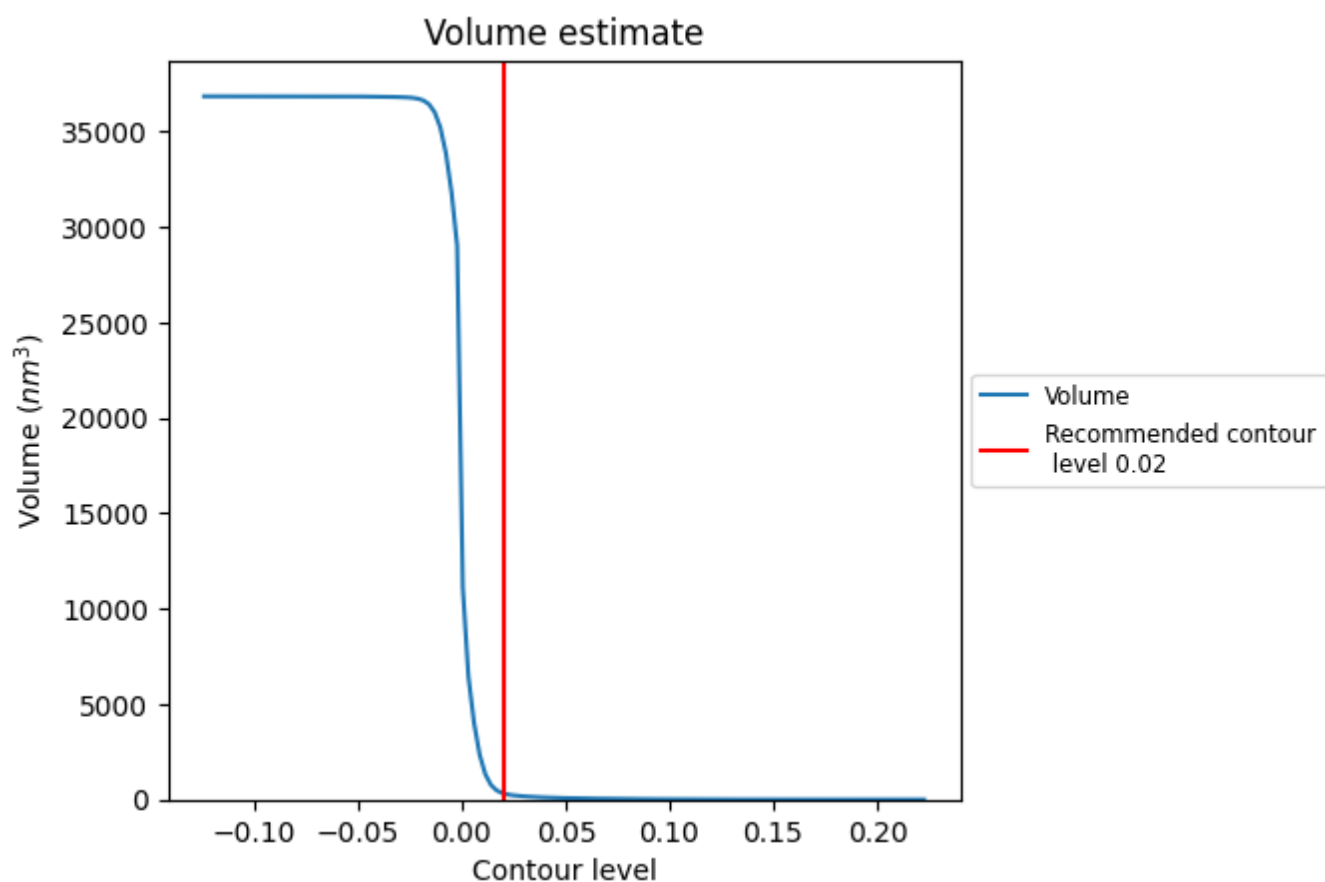
This section contains the results of statistical analysis of the map.

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.

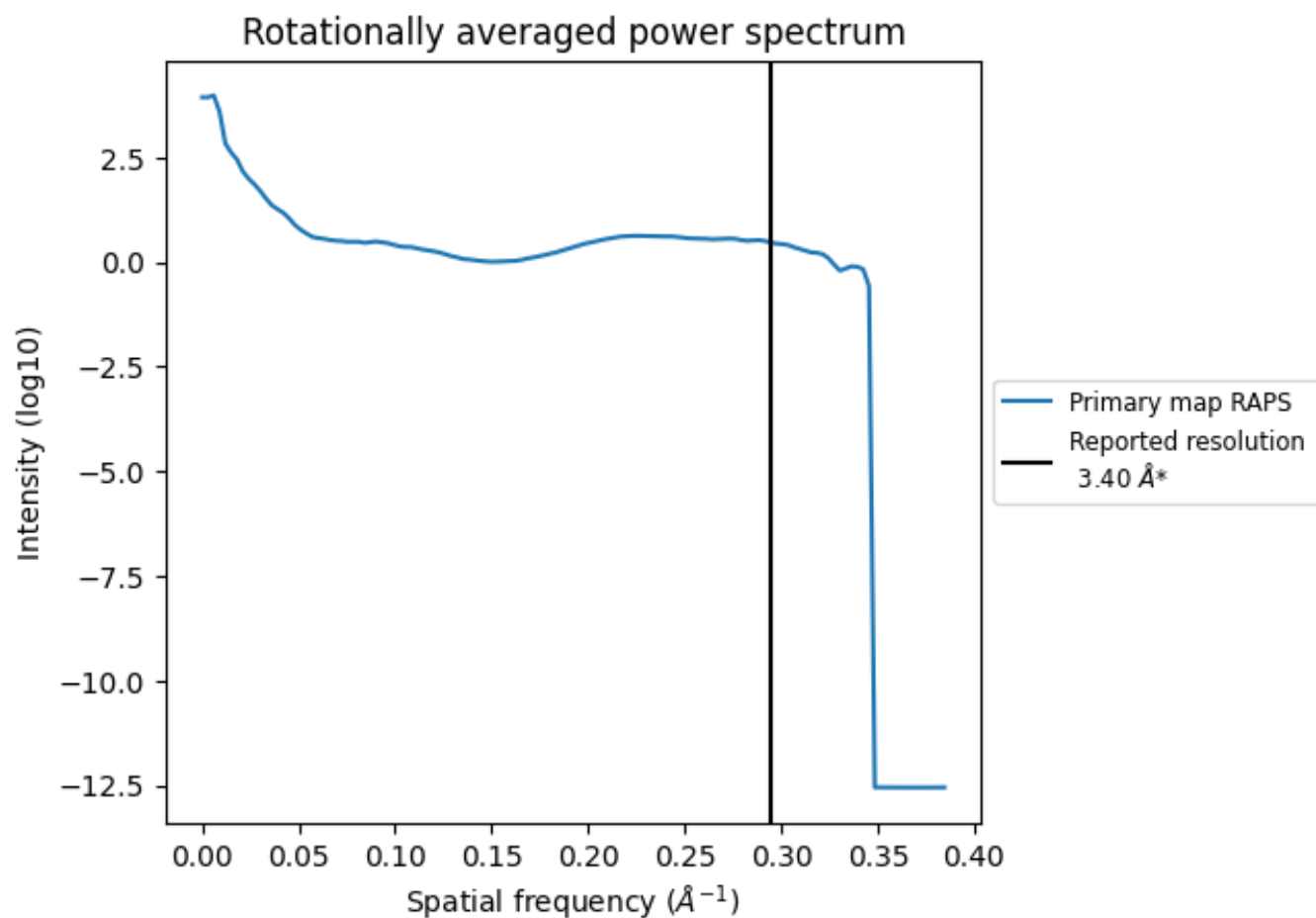
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 325 nm³; this corresponds to an approximate mass of 294 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 ⓘ

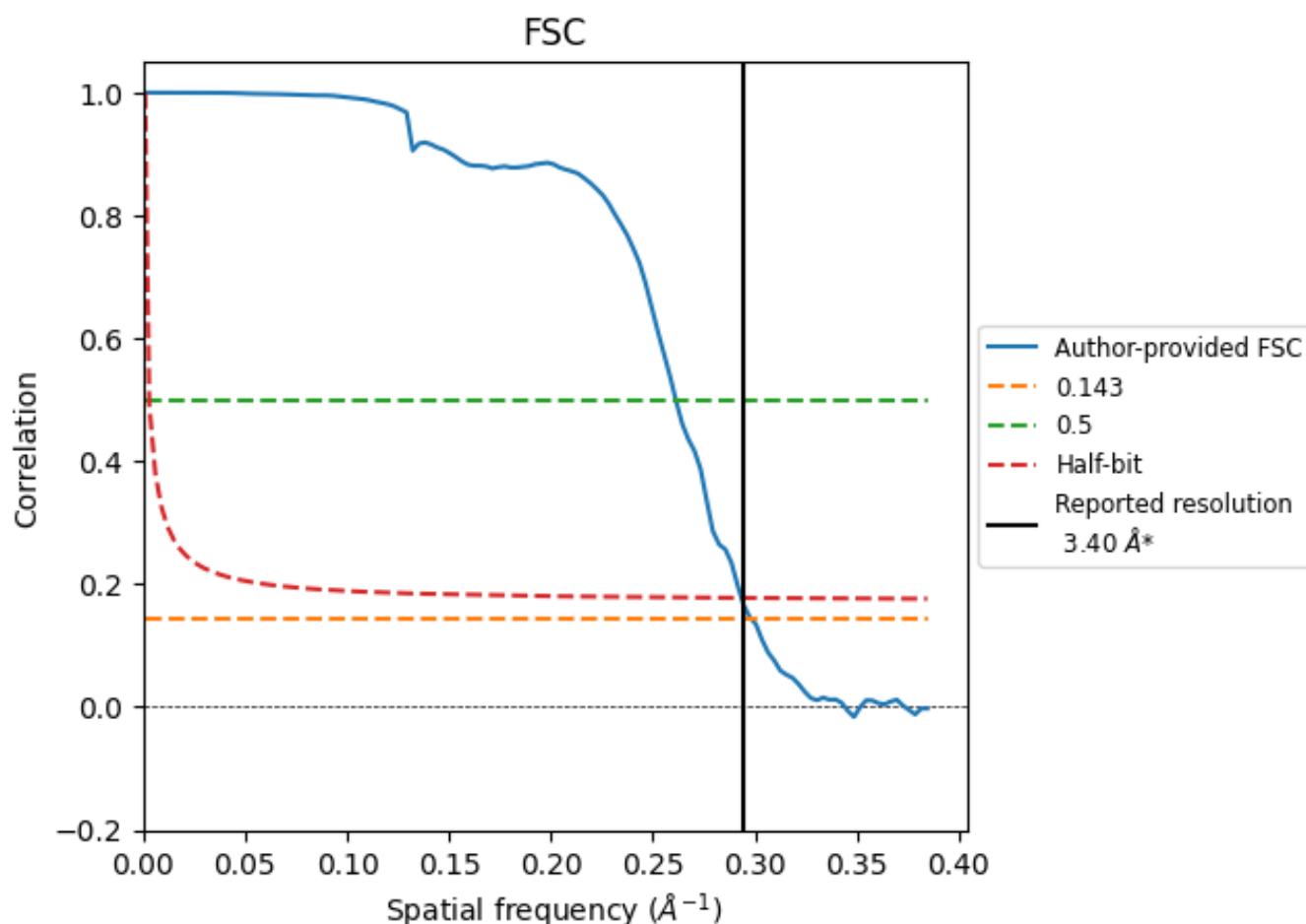


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

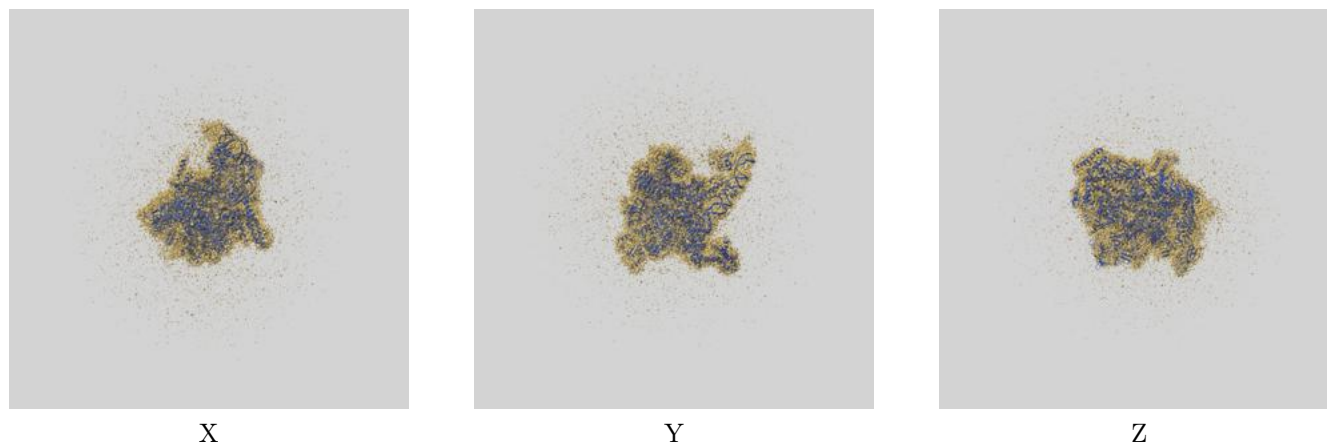
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.35	3.83	3.41
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

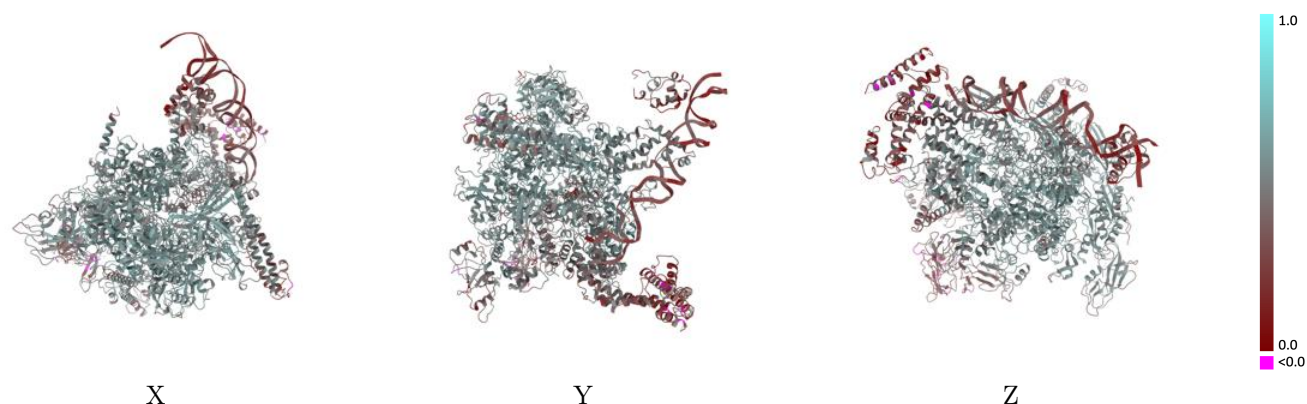
This section contains information regarding the fit between EMDB map EMD-20461 and PDB model 6PSR. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



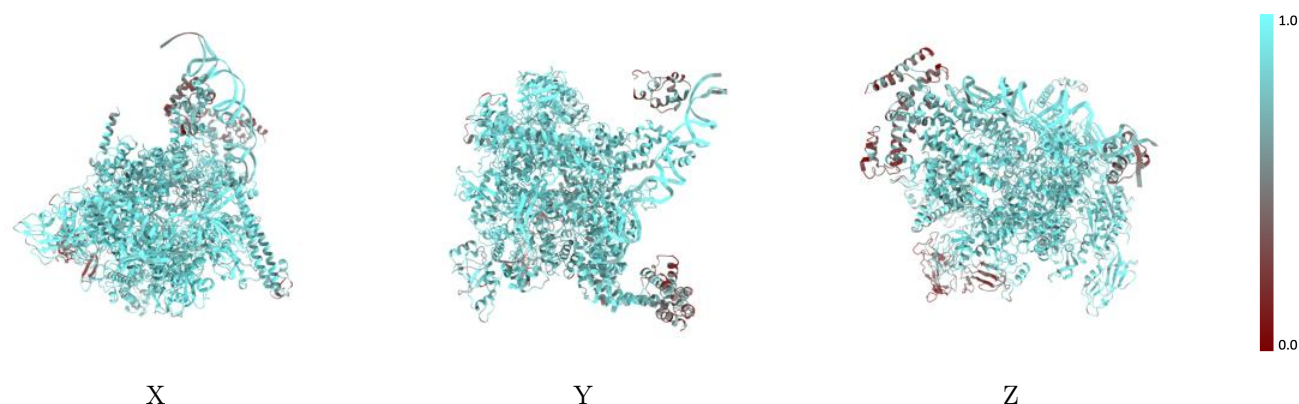
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



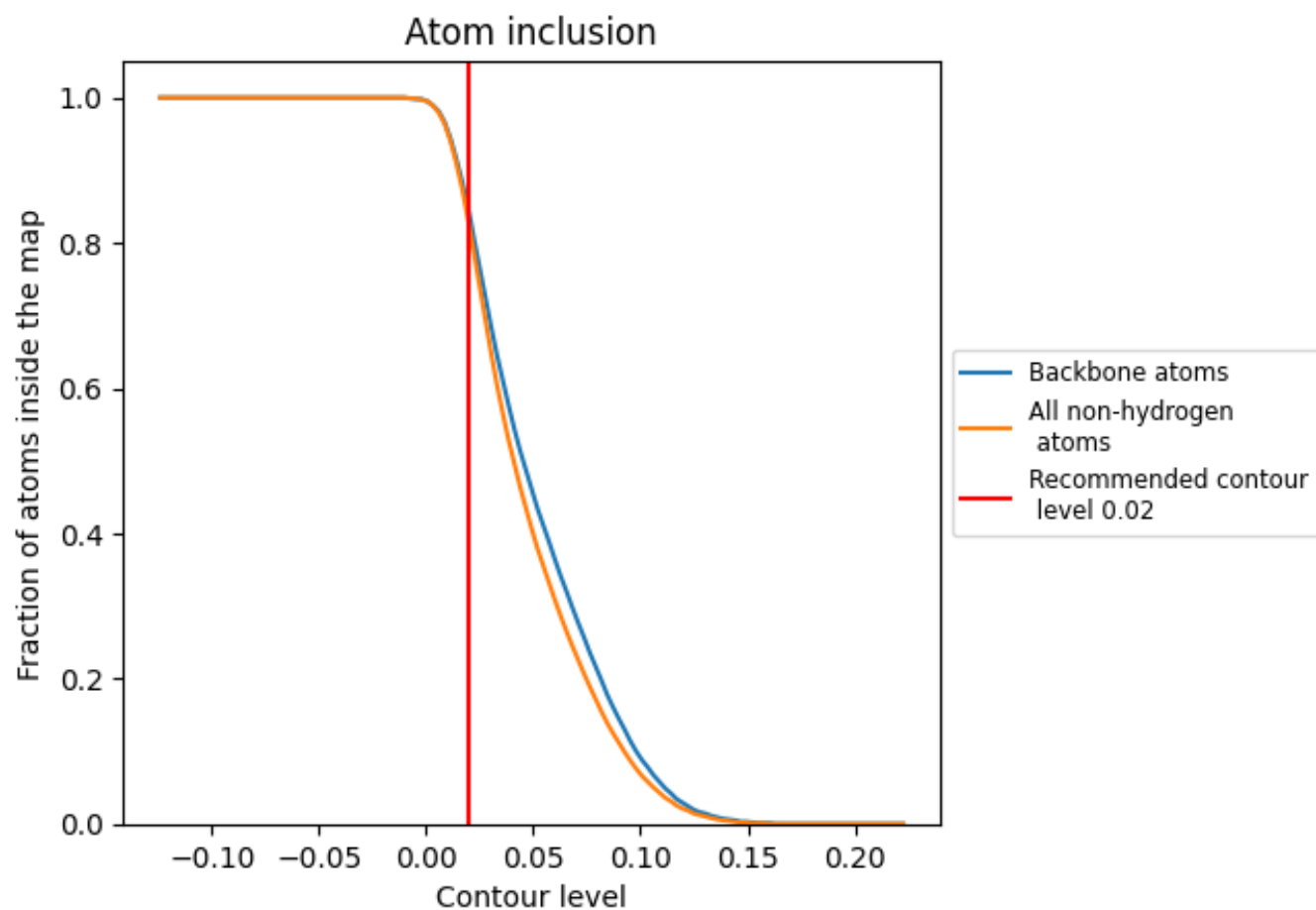
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8250	0.4800
G	0.9000	0.5390
H	0.8870	0.5150
I	0.8860	0.5260
J	0.8120	0.4940
K	0.8240	0.5280
L	0.7080	0.3850
M	0.4550	0.3030
N	0.9150	0.5220
O	0.8060	0.2790
P	0.8110	0.2510

1.0

0.0

<0.0