



Full wwPDB EM Validation Report ⓘ

Mar 22, 2026 – 10:54 PM UTC

PDB ID : 8BDA / pdb_00008bda
EMDB ID : EMD-15980
Title : IFTA complex in anterograde intraflagellar transport trains (*Chlamydomonas reinhardtii*)
Authors : Lacey, S.E.; Foster, H.E.; Pigino, G.
Deposited on : 2022-10-18
Resolution : 20.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

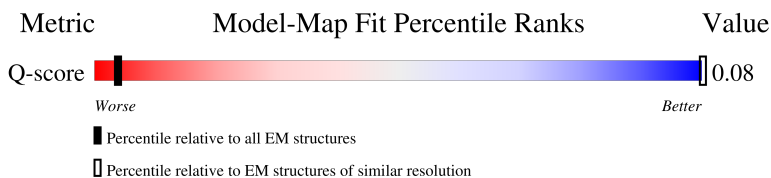
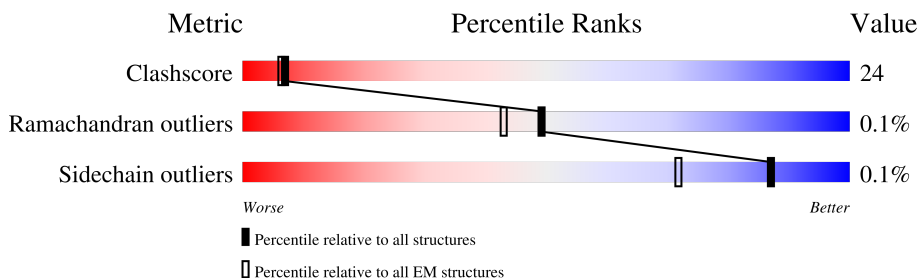
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 20.70 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	11 (20.50 - 21.00)

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	C	1224	<p>8% (red), 50% (green), 38% (yellow), 12% (grey)</p>
2	E	1355	<p>14% (red), 59% (green), 38% (yellow), . (grey)</p>
3	G	1409	<p>9% (red), 49% (green), 46% (yellow), . (grey)</p>
4	I	1367	<p>22% (red), 52% (green), 47% (yellow), . (grey)</p>

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Mol	Chain	Length	Quality of chain
5	L	1239	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a green segment on the left labeled '37%', a yellow segment in the middle labeled '43%', and a grey segment on the right labeled '20%'. A small red square is positioned at the beginning of the green segment.</p>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 48086 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Intraflagellar transport protein 121.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	C	1074	8511	5406	1464	1579	62	0	0

- Molecule 2 is a protein called Intraflagellar transport protein 139.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	1325	10464	6587	1860	1956	61	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	188	GLN	GLU	variant	UNP A9XPA6

- Molecule 3 is a protein called Intraflagellar transport particle protein 140.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	G	1354	10600	6657	1867	1998	78	0	0

- Molecule 4 is a protein called Intraflagellar transport protein 144.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	I	1367	10579	6654	1857	1998	70	0	0

- Molecule 5 is a protein called Intraflagellar transport protein 122 homolog.

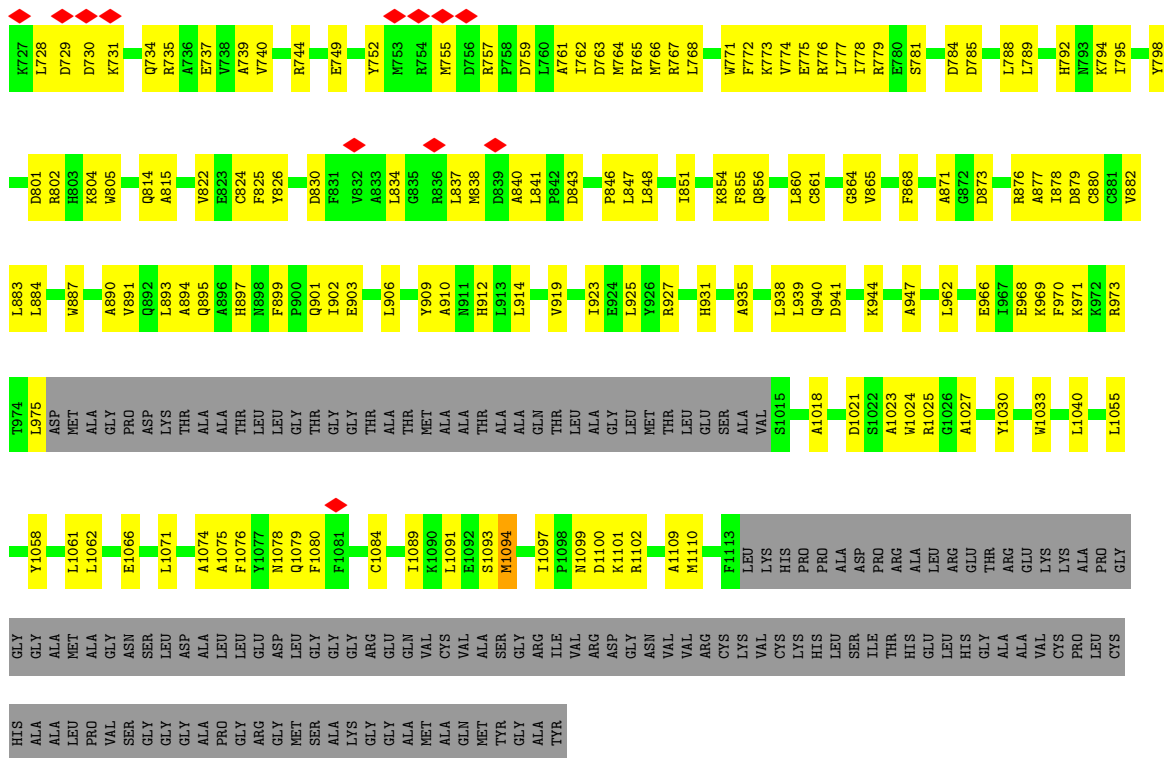
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	L	997	7932	5064	1373	1455	40	0	0

3 Residue-property plots

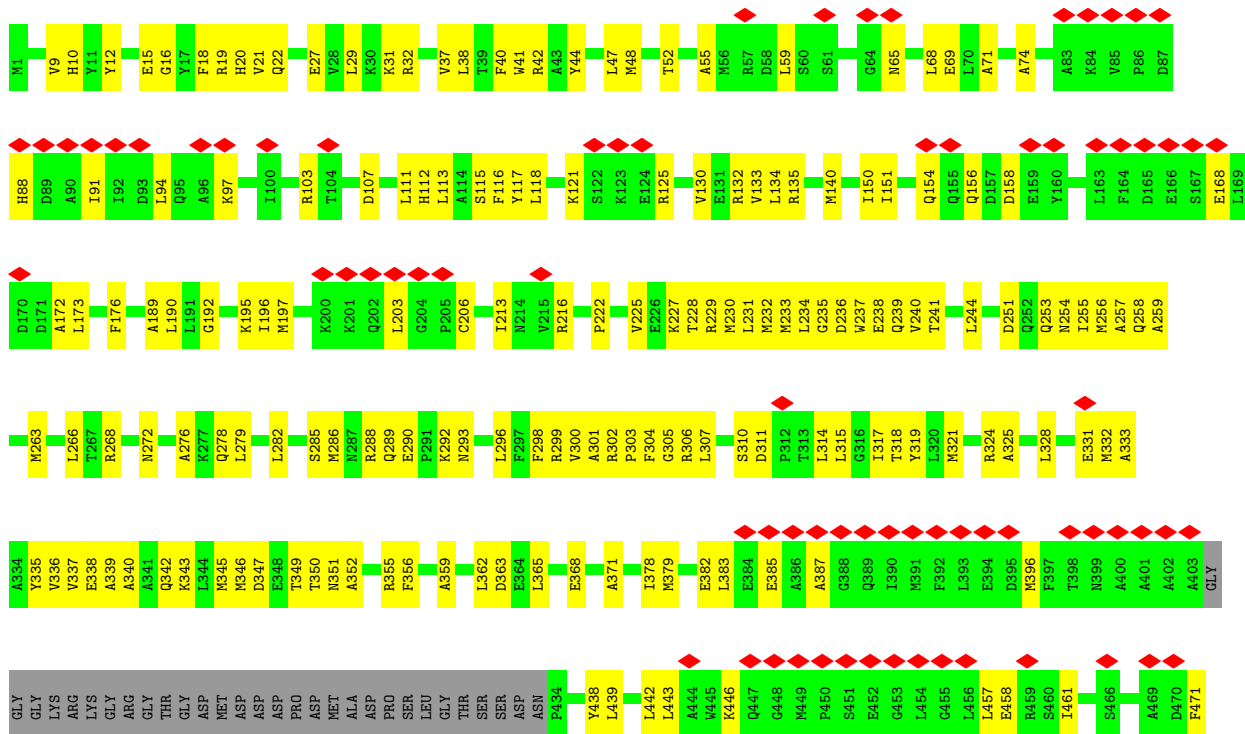
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

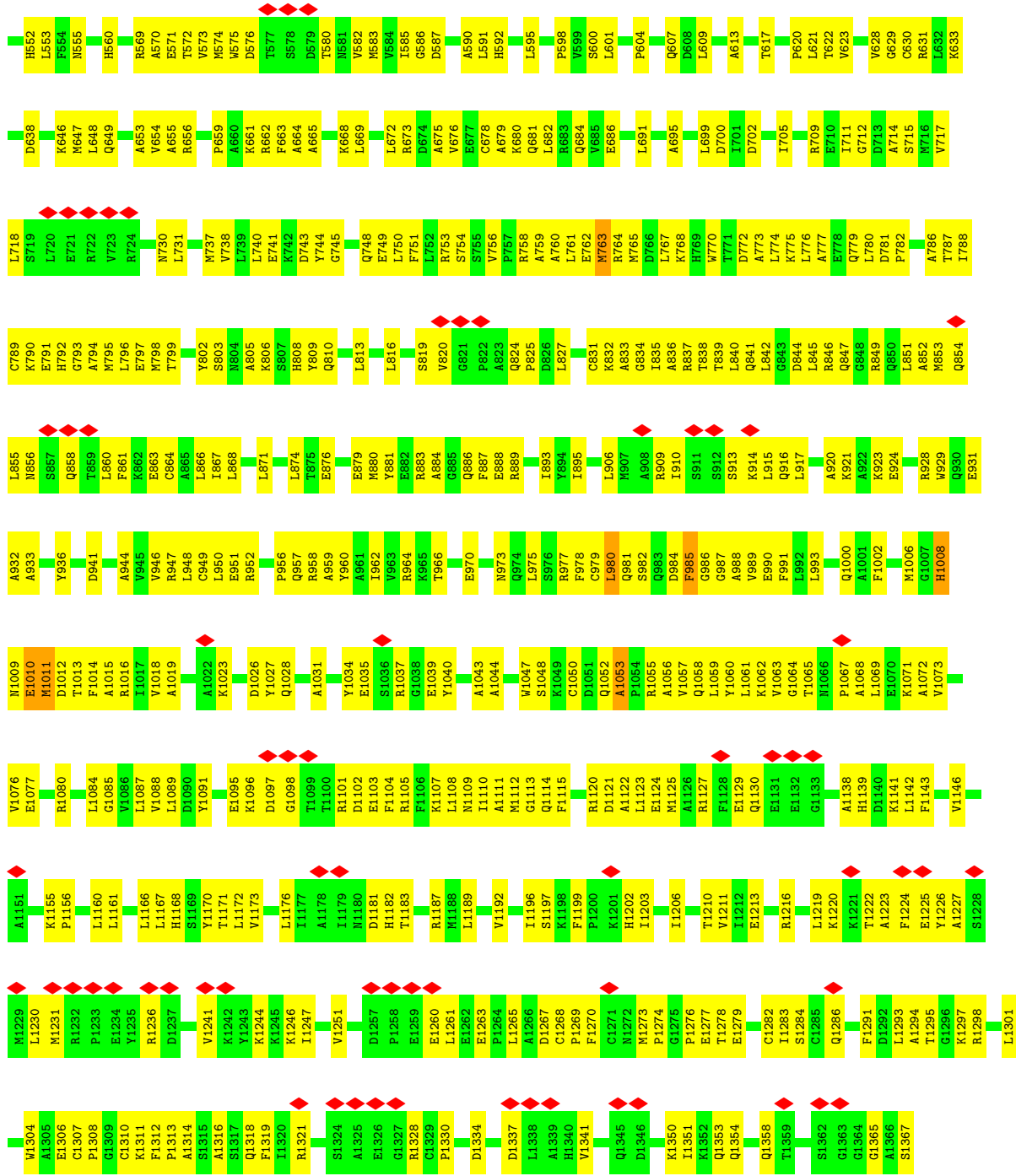
• Molecule 1: Intraflagellar transport protein 121



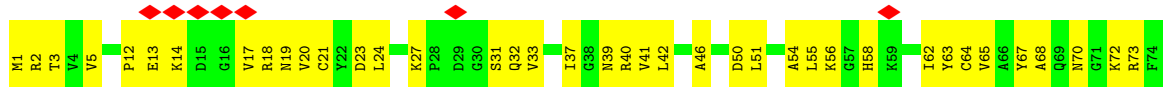


• Molecule 2: Intraflagellar transport protein 139





• Molecule 5: Intraflagellar transport protein 122 homolog



HIS
PHE
PHE
GLU
GLN
ASP
GLU
PHE
GLU
MET
ALA
ALA
LEU
GLU
ARG
GLY
THR
ALA
PRO
PHE
SER
SER
ARG
THR
THR
VAL
VAL
ARG
GLY
GLU
GLY
LEU
ALA
PRO
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ALA
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PRO
PHE
GLN
GLN
GLY
ARG
PRO
LEU
VAL

4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	3897	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Warp/Relion/M - CTF Refinement in M	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	104	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.122	Depositor
Minimum map value	-1.291	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.098	Depositor
Recommended contour level	0.5	Depositor
Map size (\AA)	727.2, 727.2, 727.2	wwPDB
Map dimensions	120, 120, 120	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	6.06, 6.06, 6.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	C	0.21	0/8701	0.47	0/11769
2	E	0.26	2/10649 (0.0%)	0.54	2/14397 (0.0%)
3	G	0.28	1/10815 (0.0%)	0.57	2/14651 (0.0%)
4	I	0.26	0/10781	0.53	3/14601 (0.0%)
5	L	0.25	0/8108	0.55	5/10978 (0.0%)
All	All	0.25	3/49054 (0.0%)	0.54	12/66396 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1147	LEU	C-N	8.04	1.43	1.33
2	E	1148	LEU	C-N	-6.05	1.25	1.33
3	G	751	ASN	C-N	5.92	1.42	1.33

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	1052	GLN	N-CA-C	-7.86	102.02	111.69
5	L	800	LEU	N-CA-C	-6.86	105.32	113.21
4	I	980	LEU	N-CA-C	-6.37	105.50	113.28
5	L	669	LEU	N-CA-C	-6.13	104.59	114.09
5	L	801	HIS	N-CA-C	-6.00	104.14	112.30
3	G	1337	ALA	CA-C-N	5.86	132.73	121.54
3	G	1337	ALA	C-N-CA	5.86	132.73	121.54
5	L	908	VAL	CA-C-N	-5.86	115.44	122.35
5	L	908	VAL	C-N-CA	-5.86	115.44	122.35
4	I	979	CYS	N-CA-C	-5.39	106.20	112.89
2	E	1011	LEU	CA-C-N	-5.16	112.58	121.66
2	E	1011	LEU	C-N-CA	-5.16	112.58	121.66

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	8511	0	8356	362	0
2	E	10464	0	10515	391	0
3	G	10600	0	10441	586	0
4	I	10579	0	10549	529	0
5	L	7932	0	7900	488	0
All	All	48086	0	47761	2305	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 24.

All (2305) 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)
5:L:796:ALA:HB1	5:L:800:LEU:HG	1.44	0.98
3:G:1028:GLU:HA	3:G:1052:LEU:HD11	1.45	0.98
2:E:1144:ALA:O	2:E:1148:LEU:HB2	1.65	0.96
5:L:907:GLU:O	5:L:911:LYS:HB2	1.70	0.91
1:C:445:GLN:HE22	1:C:524:PRO:HB3	1.38	0.89
3:G:1006:ALA:HB1	3:G:1033:LEU:HD11	1.52	0.89
5:L:315:ILE:HB	5:L:363:MET:HE1	1.57	0.87
5:L:815:ALA:O	5:L:819:SER:HB3	1.74	0.85
5:L:799:LEU:HD12	5:L:802:ALA:HB2	1.62	0.81
1:C:879:ASP:O	1:C:883:LEU:HB2	1.81	0.80
1:C:902:ILE:O	1:C:906:LEU:HB2	1.81	0.79
5:L:808:GLN:HA	5:L:834:GLY:HA2	1.65	0.79
4:I:748:GLN:HB2	4:I:760:ALA:HB1	1.63	0.79
5:L:640:MET:HG3	5:L:649:ALA:HB2	1.66	0.78
3:G:1022:PHE:HZ	3:G:1034:TYR:HE2	1.30	0.78
5:L:471:ALA:H	5:L:501:TRP:HE1	1.30	0.78
4:I:302:VAL:HB	4:I:313:LEU:HB2	1.65	0.78
3:G:638:VAL:HG12	3:G:659:ILE:HD13	1.66	0.78
3:G:1043:ALA:HA	3:G:1046:MET:HG2	1.66	0.77
2:E:1350:ARG:HH12	5:L:183:TRP:H	1.31	0.77
1:C:697:ALA:HA	1:C:700:GLN:HG2	1.67	0.76
3:G:520:ASN:HB3	3:G:541:LEU:HB3	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:663:MET:HE1	5:L:678:TRP:HB3	1.66	0.76
4:I:695:ALA:HB1	4:I:700:ASP:HB2	1.69	0.75
1:C:17:LEU:HA	1:C:33:GLY:HA2	1.67	0.75
3:G:838:GLU:HB2	3:G:845:LEU:HD12	1.68	0.75
2:E:677:ASP:HB2	2:E:712:ARG:HD2	1.68	0.75
2:E:554:ALA:HA	2:E:557:ILE:HD12	1.69	0.74
5:L:155:LEU:HD12	5:L:165:ARG:HD2	1.69	0.74
3:G:1115:GLU:O	3:G:1119:ASP:HB2	1.87	0.74
5:L:942:VAL:HG12	5:L:944:LEU:H	1.50	0.74
5:L:208:MET:HE3	5:L:214:LYS:HB2	1.68	0.74
5:L:534:PHE:HB2	5:L:546:LEU:HB3	1.70	0.74
2:E:1043:ILE:HD12	2:E:1055:VAL:HG13	1.69	0.73
2:E:1002:GLU:O	2:E:1006:ILE:HB	1.89	0.73
2:E:1280:MET:HG3	2:E:1289:ALA:HB2	1.69	0.73
5:L:587:TRP:HA	5:L:590:LEU:HD12	1.70	0.73
4:I:1048:SER:HA	4:I:1056:ALA:HB1	1.70	0.73
4:I:1073:VAL:HG11	4:I:1107:LYS:HG3	1.70	0.73
3:G:577:ARG:HD3	3:G:590:VAL:HG13	1.70	0.72
2:E:1083:ASN:HB2	2:E:1092:ALA:HB2	1.72	0.72
3:G:546:LEU:HB3	3:G:567:VAL:HG21	1.72	0.72
2:E:278:GLN:O	2:E:282:LEU:HB2	1.89	0.72
1:C:215:TYR:HB3	1:C:228:VAL:HB	1.72	0.72
3:G:979:TYR:HA	3:G:982:LEU:HB2	1.72	0.71
5:L:124:LEU:HB2	5:L:133:ALA:HB3	1.72	0.71
3:G:1127:ALA:H	3:G:1157:LYS:HZ1	1.37	0.71
4:I:856:ASN:HB3	4:I:860:LEU:HB3	1.72	0.71
3:G:786:SER:HB3	3:G:806:ASP:HB2	1.72	0.71
4:I:481:ILE:HG21	4:I:502:THR:HG21	1.72	0.71
2:E:340:ALA:HB2	2:E:355:ARG:HB2	1.71	0.71
5:L:154:ALA:HA	5:L:164:ILE:HA	1.72	0.71
2:E:1199:LEU:HD13	2:E:1221:ARG:HG3	1.72	0.70
4:I:655:ALA:HB1	4:I:662:ARG:HB2	1.72	0.70
2:E:702:THR:HB	2:E:721:LYS:HG3	1.73	0.70
3:G:473:VAL:N	3:G:484:VAL:O	2.23	0.70
4:I:647:MET:HE3	4:I:655:ALA:HB2	1.73	0.70
3:G:721:LEU:HD22	3:G:755:MET:HG2	1.73	0.70
4:I:461:VAL:HB	4:I:481:ILE:HB	1.74	0.70
3:G:718:ARG:O	3:G:722:LEU:HB2	1.90	0.70
3:G:741:LYS:HB2	4:I:798:MET:HG2	1.72	0.70
3:G:808:LYS:NZ	3:G:827:CYS:SG	2.65	0.70
5:L:787:TYR:CE2	5:L:799:LEU:HD23	2.27	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:448:THR:HG23	1:C:467:ARG:HH11	1.56	0.70
3:G:508:VAL:HA	3:G:513:LEU:HA	1.74	0.70
5:L:682:PHE:O	5:L:690:GLN:NE2	2.23	0.70
1:C:788:LEU:O	1:C:792:HIS:ND1	2.23	0.70
1:C:822:VAL:HG13	1:C:834:LEU:HG	1.74	0.69
5:L:748:LYS:NZ	5:L:777:MET:SD	2.65	0.69
1:C:234:ASP:HA	1:C:258:PRO:HD2	1.75	0.69
3:G:481:VAL:HB	3:G:494:LEU:HB2	1.75	0.69
5:L:471:ALA:HA	5:L:481:VAL:HA	1.73	0.69
4:I:764:ARG:HB3	4:I:773:ALA:HB2	1.74	0.69
4:I:1308:PRO:HG3	4:I:1341:VAL:HA	1.74	0.69
5:L:63:TYR:H	5:L:78:GLY:HA2	1.58	0.69
5:L:345:GLN:HE21	5:L:376:ASP:HA	1.56	0.69
5:L:395:LEU:HB2	5:L:408:TRP:HB2	1.75	0.69
5:L:787:TYR:HE2	5:L:799:LEU:HD23	1.57	0.69
4:I:153:ILE:HA	4:I:168:GLY:HA2	1.75	0.69
4:I:490:ILE:HA	4:I:504:SER:HA	1.75	0.69
5:L:417:ILE:HD11	5:L:429:LEU:HB3	1.74	0.69
5:L:586:ASP:O	5:L:590:LEU:HG	1.92	0.69
5:L:679:ALA:HB1	5:L:696:LEU:HB3	1.75	0.69
3:G:843:ILE:HG13	5:L:824:PHE:HD2	1.58	0.68
4:I:571:GLU:H	4:I:587:ASP:HA	1.57	0.68
2:E:22:GLN:HA	2:E:42:ARG:HH12	1.56	0.68
2:E:693:GLU:HG2	2:E:701:VAL:HG13	1.75	0.68
3:G:564:ALA:HA	3:G:580:VAL:HA	1.75	0.68
4:I:949:CYS:SG	4:I:958:ARG:NE	2.66	0.68
1:C:213:GLU:HG2	1:C:262:LYS:HA	1.73	0.68
3:G:427:LEU:HB2	3:G:434:LEU:HD11	1.76	0.68
5:L:936:LEU:HD22	5:L:955:LEU:HD13	1.76	0.68
3:G:410:PRO:HB3	3:G:696:THR:HG22	1.75	0.68
5:L:264:TRP:HB2	5:L:282:GLU:HB2	1.76	0.68
5:L:460:CYS:HB2	5:L:473:VAL:HB	1.75	0.68
2:E:964:HIS:HB3	2:E:967:HIS:HB2	1.76	0.67
4:I:1058:GLN:NE2	4:I:1087:LEU:O	2.27	0.67
5:L:571:PHE:HA	5:L:574:ALA:HB3	1.75	0.67
2:E:736:ARG:HH12	2:E:759:ASP:HB3	1.59	0.67
3:G:615:VAL:HB	3:G:641:ALA:HB3	1.77	0.67
4:I:376:TYR:HE1	4:I:386:LEU:HB3	1.59	0.67
4:I:779:GLN:HG3	4:I:780:LEU:HG	1.75	0.67
5:L:780:THR:HG1	5:L:803:HIS:HE2	1.40	0.67
1:C:384:GLN:HG3	1:C:428:ILE:HG22	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:821:ILE:HB	2:E:846:LEU:HD13	1.76	0.67
4:I:374:VAL:HG21	4:I:621:LEU:HB3	1.76	0.67
4:I:385:LEU:HB3	4:I:395:ALA:HB3	1.75	0.67
5:L:742:VAL:HA	5:L:745:GLN:HB2	1.75	0.67
4:I:852:ALA:O	4:I:856:ASN:ND2	2.26	0.67
5:L:458:VAL:HG11	5:L:461:LEU:HD23	1.76	0.67
2:E:232:MET:HE3	2:E:237:TRP:HB3	1.77	0.67
3:G:975:GLU:HA	3:G:978:ARG:HE	1.60	0.67
2:E:911:GLN:HE22	2:E:936:ILE:HG13	1.60	0.67
3:G:738:ARG:HE	4:I:866:LEU:HD22	1.60	0.67
2:E:1352:GLY:HA2	2:E:1355:PRO:HB3	1.78	0.66
3:G:1022:PHE:CZ	3:G:1034:TYR:HE2	2.12	0.66
2:E:332:MET:HE1	2:E:335:TYR:H	1.60	0.66
4:I:1196:ILE:HD11	4:I:1199:PHE:HB2	1.77	0.66
1:C:176:ALA:HA	1:C:182:CYS:HA	1.77	0.66
3:G:644:PHE:HB2	3:G:729:ALA:HB3	1.77	0.66
3:G:799:VAL:HG11	4:I:718:LEU:HD22	1.76	0.66
3:G:858:ARG:HE	4:I:705:ILE:HG21	1.59	0.66
5:L:218:ARG:HG3	5:L:252:GLY:HA3	1.78	0.66
1:C:691:ARG:NH1	1:C:713:CYS:SG	2.69	0.66
2:E:1163:VAL:HG21	2:E:1198:VAL:HG12	1.78	0.66
2:E:1259:CYS:HB3	2:E:1276:MET:HE2	1.76	0.66
3:G:555:ARG:HB3	3:G:564:ALA:HB3	1.77	0.66
3:G:616:GLN:HB2	3:G:667:CYS:HB3	1.78	0.66
2:E:604:TYR:HA	2:E:607:VAL:HG22	1.76	0.66
2:E:902:GLN:OE1	2:E:906:ARG:NH2	2.29	0.66
1:C:469:LYS:HA	1:C:485:PRO:HA	1.78	0.66
3:G:49:ASP:O	3:G:55:ASN:ND2	2.28	0.66
4:I:400:GLU:HB2	4:I:436:ARG:HH22	1.60	0.66
3:G:1106:CYS:SG	3:G:1107:VAL:N	2.69	0.66
5:L:824:PHE:HA	5:L:827:ALA:HB3	1.77	0.66
3:G:215:LEU:HB3	3:G:227:LEU:HB2	1.78	0.66
3:G:468:ILE:HA	3:G:473:VAL:HA	1.76	0.66
4:I:1098:GLY:HA2	4:I:1101:ARG:HE	1.61	0.65
1:C:762:ILE:O	1:C:766:MET:HB3	1.96	0.65
1:C:843:ASP:HA	1:C:848:LEU:HD11	1.78	0.65
5:L:753:CYS:O	5:L:757:CYS:HB2	1.96	0.65
5:L:345:GLN:HE22	5:L:350:VAL:HG22	1.61	0.65
3:G:446:LYS:HB2	3:G:456:ALA:HB2	1.79	0.65
4:I:48:ASP:OD2	4:I:92:TRP:NE1	2.29	0.65
4:I:1166:LEU:HD11	4:I:1197:SER:H	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:510:MET:HG3	1:C:518:VAL:HG11	1.79	0.65
2:E:881:VAL:HG22	2:E:910:LEU:HB3	1.76	0.65
1:C:1110:MET:SD	2:E:849:ARG:NH2	2.70	0.65
4:I:215:SER:HB2	4:I:223:LEU:HD11	1.79	0.65
5:L:697:ILE:HG23	5:L:716:MET:HE3	1.78	0.65
1:C:762:ILE:O	1:C:766:MET:CB	2.44	0.65
3:G:432:GLY:HA2	3:G:447:VAL:HB	1.78	0.65
2:E:231:LEU:O	2:E:239:GLN:NE2	2.29	0.65
2:E:1196:VAL:O	2:E:1200:LEU:HB2	1.96	0.65
3:G:721:LEU:HD11	3:G:754:HIS:H	1.61	0.65
3:G:847:SER:HA	5:L:842:ARG:HH21	1.61	0.65
3:G:275:VAL:HG12	3:G:277:MET:HE3	1.79	0.64
3:G:439:GLY:HA2	3:G:464:ARG:HA	1.79	0.64
3:G:942:ARG:NH1	3:G:975:GLU:OE1	2.30	0.64
4:I:585:ILE:HB	4:I:592:HIS:HB2	1.79	0.64
5:L:304:TYR:HD2	5:L:316:GLN:HE21	1.45	0.64
5:L:870:GLU:O	5:L:874:SER:N	2.28	0.64
4:I:1058:GLN:HG2	4:I:1087:LEU:HD12	1.79	0.64
4:I:1065:THR:H	4:I:1068:ALA:HB3	1.60	0.64
1:C:239:GLN:HB2	1:C:249:ALA:HB1	1.78	0.64
5:L:736:TRP:HB3	5:L:761:PHE:HE1	1.61	0.64
2:E:1231:GLU:HB3	2:E:1234:GLU:HB2	1.78	0.64
5:L:14:LYS:HG2	5:L:40:ARG:HH11	1.61	0.64
5:L:854:GLU:HG3	5:L:856:ARG:HB2	1.79	0.64
4:I:509:LEU:HB3	4:I:523:PHE:HB3	1.78	0.64
4:I:1009:ASN:O	4:I:1011:MET:HE3	1.96	0.64
5:L:114:LEU:HB3	5:L:125:TRP:HB3	1.78	0.64
5:L:298:GLY:HA3	5:L:336:ALA:HA	1.79	0.64
1:C:54:LYS:HB3	1:C:58:GLY:HA3	1.78	0.64
2:E:877:LEU:HD23	2:E:917:LYS:HE3	1.78	0.64
3:G:970:SER:OG	3:G:972:ARG:NH2	2.31	0.64
4:I:782:PRO:HB2	4:I:819:SER:HA	1.79	0.64
5:L:908:VAL:HG22	5:L:918:ARG:HA	1.80	0.64
3:G:1035:MET:HG2	3:G:1059:ILE:HG13	1.79	0.64
4:I:1231:MET:SD	4:I:1236:ARG:NH2	2.70	0.64
5:L:757:CYS:HA	5:L:760:HIS:HB2	1.78	0.64
1:C:518:VAL:HB	1:C:532:HIS:HB2	1.80	0.64
1:C:697:ALA:HB1	1:C:702:ASP:HB2	1.78	0.64
3:G:863:GLU:OE1	3:G:866:ARG:NH2	2.31	0.64
3:G:1032:THR:O	3:G:1035:MET:HE2	1.97	0.64
4:I:731:LEU:HB2	4:I:754:SER:HB2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:748:GLN:HG2	4:I:764:ARG:HH21	1.62	0.64
4:I:1293:LEU:HD21	4:I:1330:PRO:HD2	1.80	0.64
3:G:1128:ALA:HB2	3:G:1138:ILE:HG21	1.80	0.64
3:G:443:GLU:HA	3:G:458:GLN:HA	1.79	0.63
1:C:765:ARG:O	1:C:773:LYS:NZ	2.31	0.63
4:I:504:SER:OG	4:I:508:THR:N	2.31	0.63
5:L:588:LYS:NZ	5:L:612:ASP:OD2	2.31	0.63
1:C:112:MET:HE2	1:C:149:GLY:HA3	1.79	0.63
1:C:463:ARG:HB3	1:C:466:VAL:HB	1.80	0.63
3:G:1027:HIS:O	3:G:1046:MET:HE2	1.98	0.63
5:L:101:ALA:O	5:L:103:GLN:NE2	2.31	0.63
5:L:676:LYS:HG2	5:L:700:GLN:HG2	1.80	0.63
5:L:882:MET:HE1	5:L:890:LEU:HD22	1.79	0.63
2:E:612:LEU:HD13	2:E:620:ASP:HB3	1.80	0.63
1:C:305:VAL:HG12	1:C:307:GLY:H	1.64	0.63
1:C:366:ASP:HB2	1:C:371:ASP:HB2	1.80	0.63
3:G:496:PHE:HB2	3:G:503:PRO:HG3	1.79	0.63
3:G:1200:LEU:HD12	3:G:1215:ILE:HD11	1.81	0.63
5:L:197:ALA:HB3	5:L:205:LYS:HB2	1.81	0.63
5:L:762:ARG:NH1	5:L:789:GLU:O	2.29	0.63
1:C:725:LEU:O	1:C:734:GLN:NE2	2.31	0.63
2:E:371:ALA:HA	2:E:439:LEU:HD22	1.80	0.63
3:G:476:ALA:HA	3:G:506:MET:HE3	1.81	0.63
4:I:437:ARG:NH2	4:I:475:ASP:OD1	2.31	0.63
5:L:783:LEU:O	5:L:784:ILE:C	2.42	0.63
4:I:853:MET:SD	4:I:883:ARG:NH2	2.72	0.63
5:L:13:GLU:HB2	5:L:19:ASN:HD21	1.63	0.63
2:E:132:ARG:HA	2:E:135:ARG:HG2	1.81	0.63
2:E:1196:VAL:HG11	2:E:1234:GLU:HB3	1.81	0.63
3:G:1030:ALA:HB3	3:G:1046:MET:HE1	1.80	0.63
5:L:498:SER:OG	5:L:535:VAL:N	2.32	0.63
4:I:217:ASN:ND2	4:I:247:ILE:O	2.28	0.62
4:I:748:GLN:NE2	4:I:749:GLU:OE2	2.31	0.62
2:E:946:ARG:O	2:E:948:ARG:NH1	2.32	0.62
4:I:1265:LEU:HD22	4:I:1276:PRO:HA	1.80	0.62
5:L:334:LYS:H	5:L:345:GLN:HB2	1.64	0.62
1:C:367:THR:HB	1:C:654:MET:HG3	1.79	0.62
2:E:702:THR:HG21	2:E:724:ARG:HB3	1.79	0.62
2:E:1185:LEU:O	2:E:1189:ALA:N	2.29	0.62
5:L:41:VAL:HB	5:L:55:LEU:HB2	1.81	0.62
2:E:509:PRO:HG3	2:E:806:ARG:HH22	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:878:ILE:HD12	1:C:899:PHE:HD2	1.64	0.62
4:I:387:ASP:HB3	4:I:390:ARG:HG2	1.80	0.62
1:C:264:ASN:ND2	1:C:268:THR:OG1	2.32	0.62
1:C:541:LEU:HD22	1:C:550:MET:HE1	1.81	0.62
1:C:610:ILE:HD13	1:C:659:THR:HG22	1.81	0.62
3:G:321:VAL:HG21	3:G:369:VAL:HG11	1.82	0.62
5:L:650:ALA:HB1	5:L:659:VAL:HG13	1.80	0.62
5:L:807:ARG:HA	5:L:810:VAL:HG22	1.80	0.62
3:G:906:LEU:HD21	3:G:930:ASP:HB3	1.82	0.62
1:C:545:CYS:HB3	1:C:594:ASP:HA	1.81	0.62
1:C:865:VAL:HG13	1:C:877:ALA:HB1	1.81	0.62
2:E:19:ARG:HH21	2:E:253:GLN:HB2	1.64	0.62
2:E:538:ALA:HB2	2:E:553:LYS:HB3	1.82	0.62
2:E:1170:MET:HE3	2:E:1185:LEU:HD11	1.81	0.62
5:L:122:VAL:HG21	5:L:155:LEU:HD22	1.82	0.62
5:L:517:LEU:HG	5:L:519:ILE:HD11	1.81	0.62
1:C:207:SER:HB3	1:C:233:LEU:HD13	1.82	0.62
4:I:659:PRO:HB3	4:I:662:ARG:HH21	1.65	0.62
4:I:944:ALA:HB1	4:I:947:ARG:HH21	1.63	0.62
4:I:1060:TYR:HE2	4:I:1071:LYS:HB3	1.65	0.62
3:G:525:LEU:HA	3:G:534:PRO:HA	1.82	0.61
3:G:780:ALA:O	3:G:784:ALA:HB2	2.00	0.61
1:C:687:PRO:HB3	1:C:690:TRP:HD1	1.66	0.61
1:C:713:CYS:SG	1:C:714:ALA:N	2.70	0.61
2:E:382:GLU:HB3	2:E:385:GLU:HB2	1.82	0.61
4:I:390:ARG:HG3	4:I:392:GLN:H	1.64	0.61
4:I:1222:THR:HA	4:I:1225:GLU:HG3	1.82	0.61
5:L:314:ILE:HG12	5:L:325:ARG:HB3	1.81	0.61
1:C:89:LEU:HB3	1:C:101:TRP:HB2	1.81	0.61
5:L:787:TYR:CD2	5:L:799:LEU:HB2	2.36	0.61
1:C:764:MET:SD	1:C:767:ARG:NH2	2.69	0.61
3:G:866:ARG:NH1	3:G:884:PHE:O	2.28	0.61
3:G:1011:PRO:HA	3:G:1014:MET:HB3	1.81	0.61
4:I:672:LEU:O	4:I:676:VAL:N	2.33	0.61
4:I:679:ALA:HA	4:I:682:LEU:HG	1.83	0.61
2:E:22:GLN:OE1	2:E:42:ARG:NH2	2.34	0.61
2:E:978:HIS:HB3	2:E:983:ASP:HB2	1.82	0.61
2:E:1350:ARG:NH1	5:L:181:PRO:O	2.33	0.61
5:L:614:ARG:NH2	5:L:642:PHE:O	2.32	0.61
4:I:759:ALA:O	4:I:763:MET:HG3	2.00	0.61
1:C:463:ARG:HH11	1:C:466:VAL:HG21	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:891:VAL:O	1:C:895:GLN:NE2	2.34	0.61
2:E:301:ALA:O	2:E:305:GLY:N	2.31	0.61
3:G:793:ARG:NH1	3:G:796:THR:OG1	2.33	0.61
4:I:424:TYR:HB3	4:I:431:GLY:HA2	1.81	0.61
4:I:508:THR:OG1	4:I:524:ARG:NH2	2.34	0.61
5:L:342:LEU:HB3	5:L:353:TYR:HB2	1.83	0.61
5:L:774:LEU:HB2	5:L:786:LEU:HD22	1.81	0.61
5:L:783:LEU:O	5:L:786:LEU:N	2.34	0.61
2:E:244:LEU:HD22	2:E:257:ALA:HA	1.80	0.61
2:E:1297:TRP:HB2	2:E:1304:SER:HB3	1.83	0.61
4:I:662:ARG:NE	4:I:678:CYS:SG	2.74	0.61
5:L:459:ARG:NH1	5:L:497:ASN:O	2.33	0.61
1:C:454:LEU:HB3	1:C:456:THR:HG23	1.83	0.61
1:C:650:ASP:HB3	1:C:652:GLU:HG2	1.81	0.61
3:G:264:THR:HA	3:G:279:ASN:HA	1.83	0.61
3:G:351:VAL:O	3:G:376:ASN:ND2	2.34	0.61
1:C:340:LYS:HB2	1:C:351:ALA:HB3	1.82	0.61
1:C:422:GLU:HG2	1:C:424:LYS:HG3	1.82	0.61
2:E:1240:LEU:HD11	2:E:1262:CYS:HB2	1.82	0.61
3:G:78:ILE:HB	3:G:86:SER:HB2	1.81	0.61
5:L:173:HIS:HD2	5:L:209:MET:HE3	1.66	0.61
5:L:408:TRP:HE1	5:L:446:PRO:HA	1.64	0.61
3:G:494:LEU:HD13	3:G:525:LEU:HD22	1.83	0.60
4:I:494:ALA:HB3	4:I:501:ILE:HB	1.83	0.60
1:C:604:GLU:HG2	1:C:605:LYS:H	1.66	0.60
3:G:778:ALA:HA	3:G:781:LEU:HB3	1.82	0.60
5:L:1:MET:HE1	5:L:247:LEU:HD23	1.83	0.60
1:C:771:TRP:HA	1:C:774:VAL:HB	1.82	0.60
3:G:542:CYS:HA	3:G:579:VAL:HG11	1.82	0.60
3:G:961:PHE:HB2	3:G:985:ARG:HD2	1.83	0.60
4:I:311:ARG:HE	4:I:326:ALA:HB1	1.67	0.60
4:I:761:LEU:HG	4:I:765:MET:HE1	1.83	0.60
4:I:1076:VAL:HG21	4:I:1108:LEU:HD11	1.82	0.60
5:L:124:LEU:O	5:L:129:GLN:NE2	2.33	0.60
1:C:80:VAL:HA	1:C:91:THR:HG22	1.82	0.60
1:C:530:ALA:HB1	1:C:576:MET:HG2	1.83	0.60
2:E:15:GLU:OE2	2:E:299:ARG:NH1	2.34	0.60
2:E:584:ALA:HB1	2:E:611:VAL:HG22	1.82	0.60
4:I:810:GLN:HA	4:I:813:LEU:HD12	1.81	0.60
5:L:394:LYS:HG2	5:L:409:VAL:HG22	1.84	0.60
5:L:991:ALA:HA	5:L:994:VAL:HB	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:73:HIS:NE2	1:C:91:THR:OG1	2.30	0.60
3:G:275:VAL:HB	3:G:288:LEU:HB2	1.83	0.60
3:G:794:VAL:O	3:G:798:ALA:HB2	2.00	0.60
4:I:813:LEU:HD22	4:I:832:LYS:HG3	1.84	0.60
1:C:512:GLY:HA2	1:C:518:VAL:HG22	1.82	0.60
1:C:854:LYS:NZ	5:L:466:SER:OG	2.34	0.60
2:E:693:GLU:HA	2:E:701:VAL:HG22	1.82	0.60
2:E:828:ILE:HD12	2:E:839:LEU:HD21	1.83	0.60
5:L:682:PHE:HA	5:L:686:GLY:HA2	1.84	0.60
2:E:703:VAL:HG13	2:E:735:ALA:HB2	1.84	0.60
2:E:1148:LEU:HB3	2:E:1149:LYS:HZ2	1.66	0.60
3:G:640:CYS:N	3:G:657:GLN:O	2.29	0.60
4:I:630:CYS:N	4:I:638:ASP:O	2.34	0.60
1:C:927:ARG:HH11	1:C:938:LEU:HD22	1.67	0.60
2:E:235:GLY:HA2	2:E:474:PRO:HD2	1.84	0.60
2:E:1341:ILE:HG23	2:E:1342:ARG:HD2	1.83	0.60
5:L:33:VAL:HB	5:L:46:ALA:HB2	1.83	0.60
5:L:415:ARG:HH12	5:L:475:GLU:HB3	1.67	0.60
5:L:679:ALA:HA	5:L:696:LEU:HD13	1.83	0.60
2:E:886:MET:HA	2:E:889:LYS:HB2	1.84	0.60
2:E:1048:ARG:NH1	2:E:1230:ASP:O	2.35	0.60
3:G:621:PHE:HE2	3:G:629:ARG:HB3	1.66	0.60
4:I:67:ALA:HA	4:I:83:PRO:HA	1.84	0.60
4:I:536:GLN:NE2	4:I:580:THR:OG1	2.35	0.60
5:L:818:LEU:HG	5:L:823:ARG:HD2	1.82	0.60
2:E:1036:TYR:HB3	2:E:1074:GLY:HA3	1.83	0.60
3:G:39:GLY:HA2	3:G:55:ASN:HB3	1.82	0.60
3:G:883:LEU:HD21	3:G:886:ALA:HB2	1.84	0.60
5:L:659:VAL:HB	5:L:682:PHE:HZ	1.67	0.60
1:C:855:PHE:HB3	1:C:860:LEU:HB2	1.83	0.59
2:E:804:ILE:HD11	2:E:826:LYS:HB3	1.83	0.59
2:E:874:THR:OG1	2:E:917:LYS:NZ	2.26	0.59
2:E:1158:THR:H	2:E:1161:TYR:HB3	1.66	0.59
2:E:478:LEU:O	2:E:482:LEU:N	2.31	0.59
2:E:878:GLN:OE1	2:E:917:LYS:NZ	2.35	0.59
4:I:159:ASN:HD21	4:I:163:ILE:HB	1.67	0.59
4:I:423:PHE:HD2	4:I:435:GLN:HB2	1.68	0.59
4:I:738:VAL:HG21	4:I:763:MET:HG2	1.84	0.59
2:E:21:VAL:HG21	2:E:48:MET:HE1	1.83	0.59
2:E:268:ARG:HG3	2:E:560:MET:HE2	1.84	0.59
2:E:1170:MET:CE	2:E:1185:LEU:HD11	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:1:MET:HG3	4:I:325:ASP:HA	1.83	0.59
4:I:1105:ARG:NH2	4:I:1124:GLU:OE2	2.35	0.59
5:L:842:ARG:NH1	5:L:846:GLN:OE1	2.36	0.59
1:C:151:ARG:HE	1:C:154:GLY:HA3	1.66	0.59
2:E:307:LEU:HA	2:E:485:ALA:HB2	1.83	0.59
5:L:108:ASN:HB2	5:L:113:GLN:HB3	1.84	0.59
5:L:730:LEU:HD22	5:L:738:LYS:HB3	1.83	0.59
5:L:773:THR:HA	5:L:776:LYS:HD2	1.84	0.59
3:G:74:PRO:HB2	3:G:90:ALA:HB3	1.84	0.59
3:G:215:LEU:HD23	3:G:227:LEU:HD12	1.83	0.59
3:G:769:LEU:O	3:G:773:GLU:N	2.35	0.59
3:G:1133:GLU:HG2	3:G:1138:ILE:HG12	1.84	0.59
2:E:1100:ARG:NH2	2:E:1113:MET:SD	2.76	0.59
3:G:738:ARG:HH12	4:I:863:GLU:HA	1.67	0.59
3:G:1155:ALA:HA	3:G:1158:TYR:HB2	1.84	0.59
4:I:1105:ARG:O	4:I:1109:ASN:ND2	2.36	0.59
5:L:578:ALA:HA	5:L:582:VAL:HG22	1.84	0.59
5:L:723:TYR:HE2	5:L:745:GLN:HB3	1.68	0.59
5:L:723:TYR:O	5:L:727:ILE:HB	2.03	0.59
3:G:945:LYS:HZ3	3:G:982:LEU:HG	1.67	0.59
3:G:1044:VAL:HG11	3:G:1069:ASP:HB2	1.85	0.59
4:I:758:ARG:HH12	4:I:781:ASP:HB2	1.68	0.59
4:I:916:GLN:NE2	4:I:931:GLU:OE2	2.36	0.59
5:L:761:PHE:HA	5:L:764:ALA:HB3	1.84	0.59
3:G:1090:VAL:HG21	3:G:1117:MET:HE1	1.84	0.59
4:I:802:TYR:HA	4:I:805:ALA:HB3	1.85	0.59
5:L:109:PRO:HD2	5:L:150:GLY:HA2	1.85	0.59
1:C:1099:ASN:HA	1:C:1102:ARG:HB3	1.84	0.59
3:G:1183:PHE:HA	3:G:1186:VAL:HG12	1.85	0.59
3:G:82:ASP:N	3:G:82:ASP:OD1	2.33	0.59
4:I:86:ASN:ND2	4:I:88:HIS:O	2.36	0.59
4:I:1354:GLN:OE1	4:I:1358:GLN:NE2	2.35	0.59
5:L:14:LYS:HD2	5:L:56:LYS:HD2	1.85	0.59
1:C:83:ASN:ND2	1:C:130:GLY:O	2.36	0.58
2:E:238:GLU:OE2	2:E:268:ARG:NH2	2.36	0.58
3:G:387:PHE:HA	3:G:392:ALA:HA	1.84	0.58
4:I:837:ARG:NH1	4:I:863:GLU:OE2	2.36	0.58
1:C:21:SER:HG	1:C:82:TRP:CD1	2.21	0.58
1:C:300:LEU:O	1:C:301:ARG:NE	2.32	0.58
3:G:643:ILE:HG21	3:G:651:ILE:HG23	1.85	0.58
3:G:705:THR:O	3:G:708:GLN:NE2	2.28	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:804:ILE:HB	4:I:715:SER:HB3	1.84	0.58
4:I:220:ARG:NH1	4:I:248:MET:O	2.37	0.58
4:I:1009:ASN:O	4:I:1011:MET:N	2.37	0.58
5:L:261:ARG:NH1	5:L:279:VAL:O	2.36	0.58
1:C:660:ARG:HA	1:C:663:ARG:HB2	1.85	0.58
2:E:658:ARG:NH2	2:E:691:GLU:OE1	2.36	0.58
3:G:120:THR:OG1	3:G:128:SER:O	2.21	0.58
3:G:481:VAL:HG22	3:G:506:MET:HE1	1.85	0.58
3:G:613:LEU:N	3:G:643:ILE:O	2.36	0.58
3:G:752:MET:HE1	4:I:799:THR:HG23	1.85	0.58
3:G:900:ASP:HA	5:L:914:HIS:HA	1.85	0.58
4:I:946:VAL:HG13	4:I:959:ALA:HB1	1.84	0.58
4:I:947:ARG:O	4:I:951:GLU:HB2	2.03	0.58
5:L:351:VAL:HA	5:L:370:LYS:HG2	1.85	0.58
5:L:980:LEU:H	5:L:988:VAL:HG11	1.69	0.58
2:E:255:ILE:HG23	2:E:282:LEU:HD11	1.86	0.58
3:G:1026:GLN:HB3	3:G:1029:LYS:HB2	1.84	0.58
4:I:1139:HIS:CD2	4:I:1167:LEU:HD22	2.38	0.58
5:L:156:GLY:HA2	5:L:162:ILE:HA	1.85	0.58
2:E:1029:LEU:HD11	2:E:1039:LEU:HA	1.84	0.58
4:I:866:LEU:HD21	4:I:889:ARG:HH12	1.68	0.58
5:L:854:GLU:HB2	5:L:856:ARG:HH11	1.68	0.58
5:L:867:LEU:HB3	5:L:896:LEU:HD13	1.86	0.58
1:C:310:ILE:HG12	1:C:326:VAL:HG22	1.84	0.58
2:E:303:PRO:HB2	2:E:476:LEU:HG	1.85	0.58
3:G:1134:ARG:HB3	3:G:1161:ALA:HB3	1.85	0.58
4:I:1129:GLU:HG3	4:I:1138:ALA:HB2	1.85	0.58
5:L:600:LEU:HD12	5:L:626:ARG:HD2	1.84	0.58
5:L:928:ALA:HB1	5:L:932:LEU:HD22	1.86	0.58
3:G:707:PHE:HD2	3:G:710:MET:HE3	1.69	0.58
4:I:1199:PHE:HB3	4:I:1202:HIS:HB2	1.86	0.58
5:L:303:ARG:HB2	5:L:337:VAL:HG11	1.84	0.58
5:L:775:LEU:HG	5:L:783:LEU:HD11	1.85	0.58
1:C:79:CYS:HB3	1:C:124:MET:HB3	1.86	0.58
2:E:1104:ARG:NH1	2:E:1104:ARG:O	2.36	0.58
3:G:175:VAL:HA	3:G:184:VAL:HA	1.85	0.58
3:G:734:ASP:HA	3:G:738:ARG:HB3	1.86	0.58
5:L:20:VAL:HG13	5:L:282:GLU:HA	1.85	0.58
5:L:27:LYS:HE2	5:L:32:GLN:HB2	1.85	0.58
5:L:737:ASP:OD1	5:L:738:LYS:N	2.37	0.58
5:L:960:VAL:HA	5:L:968:ALA:HA	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:446:PHE:O	1:C:467:ARG:NH2	2.37	0.58
1:C:695:GLU:HA	1:C:698:LEU:HB3	1.85	0.58
3:G:385:TYR:HB3	3:G:668:ILE:HG22	1.86	0.58
3:G:420:GLN:O	3:G:441:ARG:NH2	2.37	0.58
3:G:422:MET:HE2	3:G:436:VAL:HG23	1.85	0.58
3:G:1339:ASN:ND2	3:G:1342:GLU:OE1	2.37	0.58
4:I:412:HIS:HD2	4:I:434:VAL:HG21	1.68	0.58
5:L:780:THR:OG1	5:L:803:HIS:NE2	2.26	0.58
1:C:801:ASP:O	1:C:802:ARG:NH1	2.37	0.58
1:C:878:ILE:HD11	1:C:897:HIS:HB2	1.86	0.58
2:E:736:ARG:NH2	2:E:759:ASP:OD1	2.36	0.58
5:L:73:ARG:HD3	5:L:112:GLN:HG2	1.86	0.58
1:C:730:ASP:O	1:C:734:GLN:N	2.37	0.57
2:E:74:ALA:HB1	2:E:117:TYR:HE2	1.69	0.57
3:G:397:ALA:HB3	3:G:400:ARG:HB3	1.85	0.57
3:G:435:LEU:HD11	3:G:442:ALA:HB1	1.86	0.57
3:G:563:VAL:O	3:G:581:TRP:N	2.35	0.57
3:G:752:MET:CG	3:G:768:CYS:HB2	2.34	0.57
3:G:1241:ASP:O	3:G:1244:ARG:NH1	2.37	0.57
1:C:902:ILE:HG13	1:C:903:GLU:HG2	1.86	0.57
1:C:1080:PHE:O	1:C:1084:CYS:N	2.30	0.57
2:E:1174:ASP:O	2:E:1178:ILE:N	2.31	0.57
1:C:594:ASP:HB2	1:C:630:HIS:HB2	1.85	0.57
2:E:88:HIS:HA	2:E:91:ILE:HD12	1.87	0.57
2:E:272:ASN:O	2:E:276:ALA:N	2.35	0.57
2:E:1167:TYR:HE1	2:E:1201:ALA:HB2	1.68	0.57
4:I:300:GLY:O	4:I:315:ALA:N	2.36	0.57
1:C:275:PHE:HA	1:C:288:TRP:HA	1.87	0.57
1:C:365:TRP:NE1	1:C:370:ASN:OD1	2.38	0.57
1:C:1033:TRP:HB2	1:C:1055:LEU:HD21	1.86	0.57
2:E:864:LEU:HB3	2:E:883:ALA:HB3	1.87	0.57
4:I:1211:VAL:HG11	4:I:1230:LEU:HD11	1.86	0.57
3:G:215:LEU:N	3:G:227:LEU:O	2.32	0.57
3:G:467:ALA:O	3:G:474:TYR:N	2.38	0.57
3:G:555:ARG:NE	3:G:604:MET:HA	2.19	0.57
4:I:19:PHE:H	4:I:337:LYS:HD3	1.69	0.57
4:I:802:TYR:HD2	4:I:838:THR:HA	1.68	0.57
5:L:949:VAL:HG12	5:L:996:ARG:HD2	1.85	0.57
1:C:772:PHE:HB3	1:C:776:ARG:HH12	1.69	0.57
1:C:789:LEU:HD22	1:C:815:ALA:HA	1.87	0.57
2:E:94:LEU:HD13	2:E:97:LYS:HD3	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:17:ALA:HB1	3:G:29:LEU:HD11	1.86	0.57
4:I:111:PHE:HA	4:I:127:THR:HA	1.85	0.57
4:I:888:GLU:OE2	4:I:909:ARG:NH1	2.38	0.57
1:C:136:VAL:HG21	1:C:164:VAL:HG11	1.85	0.57
2:E:801:VAL:HG13	2:E:827:ALA:HB1	1.86	0.57
2:E:1342:ARG:HA	2:E:1346:LEU:HD23	1.85	0.57
3:G:67:ILE:HB	3:G:76:LEU:HD11	1.85	0.57
3:G:297:VAL:O	3:G:317:THR:OG1	2.22	0.57
4:I:204:ASP:H	4:I:275:ARG:HH12	1.51	0.57
4:I:543:VAL:HG21	4:I:583:MET:HG3	1.86	0.57
3:G:442:ALA:N	3:G:459:PHE:O	2.37	0.57
3:G:979:TYR:O	3:G:983:ALA:N	2.37	0.57
3:G:1044:VAL:HG22	3:G:1056:LEU:HD11	1.86	0.57
5:L:565:TYR:HB3	5:L:574:ALA:HB2	1.87	0.57
3:G:445:TYR:HA	3:G:455:PRO:HA	1.87	0.57
3:G:981:THR:HA	3:G:1005:LEU:HD11	1.87	0.57
4:I:365:MET:HE1	4:I:631:ARG:HD3	1.85	0.57
4:I:793:GLY:HA2	4:I:805:ALA:HA	1.87	0.57
4:I:816:LEU:HD22	4:I:824:GLN:HB3	1.86	0.57
4:I:1108:LEU:O	4:I:1112:MET:N	2.33	0.57
5:L:474:ASP:OD2	5:L:478:LYS:NZ	2.35	0.57
5:L:730:LEU:HD23	5:L:735:TRP:HE3	1.70	0.57
1:C:861:CYS:HA	1:C:884:LEU:HD12	1.86	0.57
3:G:70:HIS:HB2	3:G:75:LEU:HB3	1.86	0.57
3:G:1301:ARG:NH1	3:G:1304:ASP:OD2	2.38	0.57
4:I:738:VAL:CG2	4:I:763:MET:HG2	2.35	0.57
4:I:884:ALA:O	4:I:886:GLN:NE2	2.37	0.57
4:I:1011:MET:SD	4:I:1012:ASP:N	2.78	0.57
5:L:985:GLN:NE2	5:L:989:ASP:OD1	2.38	0.57
1:C:367:THR:HG21	1:C:654:MET:HE2	1.86	0.56
5:L:663:MET:O	5:L:699:ARG:NH1	2.38	0.56
1:C:701:LEU:HD21	1:C:735:ARG:HH12	1.69	0.56
2:E:286:MET:SD	2:E:289:GLN:NE2	2.78	0.56
2:E:1308:GLY:HA2	2:E:1311:LEU:HD12	1.87	0.56
3:G:1014:MET:HG3	3:G:1033:LEU:O	2.04	0.56
4:I:429:LYS:HB3	4:I:432:LYS:HB3	1.87	0.56
4:I:538:THR:HG23	4:I:540:ALA:H	1.70	0.56
4:I:1105:ARG:HA	4:I:1108:LEU:HB3	1.87	0.56
5:L:909:VAL:HB	5:L:951:VAL:HG22	1.88	0.56
1:C:234:ASP:HB2	1:C:257:LYS:HD2	1.88	0.56
2:E:10:HIS:HA	2:E:118:LEU:HD21	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:29:LEU:HA	2:E:38:LEU:HD13	1.87	0.56
3:G:123:GLU:HA	3:G:150:VAL:HG13	1.87	0.56
4:I:844:ASP:HB3	4:I:847:GLN:HB3	1.87	0.56
4:I:1170:TYR:HB2	4:I:1192:VAL:HG21	1.87	0.56
5:L:96:TYR:HD2	5:L:132:VAL:HG22	1.70	0.56
5:L:134:LYS:HD2	5:L:136:LYS:HZ2	1.70	0.56
5:L:692:SER:HB2	5:L:695:GLU:HB3	1.88	0.56
5:L:739:LEU:HD21	5:L:760:HIS:HB3	1.87	0.56
5:L:774:LEU:HD22	5:L:786:LEU:HB2	1.88	0.56
1:C:64:LEU:HD11	1:C:67:ASN:HB2	1.88	0.56
2:E:333:ALA:O	2:E:337:VAL:HB	2.05	0.56
2:E:687:ASP:OD1	2:E:690:ARG:NH2	2.39	0.56
3:G:639:ASP:HA	3:G:658:PRO:HA	1.86	0.56
3:G:906:LEU:HG	3:G:928:ALA:HB1	1.87	0.56
4:I:1053:ALA:HB1	4:I:1084:LEU:HD22	1.87	0.56
1:C:632:LEU:HB2	1:C:662:LEU:HD13	1.88	0.56
2:E:522:LEU:HD22	2:E:832:ARG:HH21	1.70	0.56
3:G:185:LYS:HA	3:G:196:VAL:H	1.71	0.56
3:G:404:GLU:OE2	3:G:698:ASN:ND2	2.38	0.56
3:G:1235:CYS:O	3:G:1239:GLU:HB2	2.05	0.56
4:I:895:ILE:HG21	4:I:915:LEU:HD22	1.87	0.56
4:I:1196:ILE:HG12	4:I:1203:ILE:HD13	1.86	0.56
5:L:68:ALA:HB3	5:L:72:LYS:H	1.70	0.56
5:L:966:LYS:HA	5:L:969:ARG:HE	1.69	0.56
2:E:554:ALA:HB2	2:E:570:LEU:HD23	1.87	0.56
3:G:440:GLU:OE2	3:G:441:ARG:NH1	2.39	0.56
3:G:670:SER:HA	3:G:675:LEU:HA	1.87	0.56
3:G:944:TRP:HB3	3:G:982:LEU:HD23	1.88	0.56
4:I:509:LEU:HD11	4:I:533:LEU:HD21	1.88	0.56
4:I:1294:ALA:HB1	4:I:1318:GLN:HB2	1.88	0.56
5:L:771:LYS:NZ	5:L:772:GLU:OE2	2.39	0.56
1:C:612:ARG:NH2	1:C:661:SER:OG	2.28	0.56
2:E:1029:LEU:HD12	2:E:1042:LEU:HD23	1.88	0.56
3:G:591:HIS:HB2	3:G:651:ILE:HB	1.86	0.56
1:C:1024:TRP:HD1	1:C:1027:ALA:HB3	1.70	0.56
2:E:677:ASP:OD2	2:E:712:ARG:NH1	2.39	0.56
3:G:88:TRP:HB2	3:G:95:LEU:HD12	1.87	0.56
3:G:576:VAL:N	3:G:594:THR:OG1	2.36	0.56
3:G:1018:ALA:HB2	3:G:1033:LEU:HB3	1.88	0.56
3:G:1043:ALA:HB1	3:G:1059:ILE:HD13	1.87	0.56
3:G:1306:LEU:HD13	3:G:1326:VAL:HG22	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:435:GLN:NE2	4:I:466:ILE:O	2.38	0.56
4:I:758:ARG:O	4:I:762:GLU:HG3	2.06	0.56
4:I:1269:PRO:HA	4:I:1301:LEU:HD21	1.87	0.56
5:L:673:ASP:OD1	5:L:674:GLU:N	2.39	0.56
1:C:146:SER:OG	1:C:148:ASP:OD1	2.23	0.56
1:C:711:VAL:HG22	5:L:668:ASP:HB2	1.87	0.56
2:E:736:ARG:HG3	2:E:760:LEU:HD13	1.87	0.56
3:G:446:LYS:N	3:G:454:MET:O	2.39	0.56
3:G:749:TRP:HE3	3:G:752:MET:HA	1.71	0.56
3:G:804:ILE:HG22	4:I:714:ALA:HB1	1.87	0.56
3:G:811:TYR:HE2	3:G:823:LEU:HD12	1.70	0.56
4:I:760:ALA:HA	4:I:763:MET:SD	2.46	0.56
4:I:1008:HIS:CE1	4:I:1010:GLU:HG3	2.40	0.56
1:C:262:LYS:HG2	1:C:314:SER:HA	1.88	0.56
3:G:1114:THR:H	3:G:1117:MET:HB3	1.70	0.56
4:I:225:ILE:HD12	4:I:277:ILE:HD11	1.88	0.56
4:I:1202:HIS:O	4:I:1206:ILE:N	2.36	0.56
1:C:891:VAL:HG22	1:C:902:ILE:HD12	1.87	0.55
2:E:292:LYS:HB3	2:E:328:LEU:HD22	1.87	0.55
2:E:1148:LEU:HB3	2:E:1149:LYS:NZ	2.20	0.55
4:I:407:GLY:HA3	4:I:448:LEU:HD13	1.88	0.55
4:I:950:LEU:HD13	4:I:978:PHE:HB2	1.89	0.55
4:I:1307:CYS:O	4:I:1311:LYS:N	2.36	0.55
1:C:66:LEU:HD11	1:C:107:MET:HE1	1.86	0.55
3:G:293:ASP:OD2	3:G:320:ARG:NH2	2.40	0.55
4:I:1091:TYR:O	4:I:1095:GLU:HB2	2.06	0.55
5:L:255:LEU:HD22	5:L:310:MET:HG3	1.87	0.55
2:E:331:GLU:HG3	2:E:362:LEU:HD11	1.88	0.55
3:G:399:ASP:HB3	3:G:419:LEU:H	1.71	0.55
3:G:800:HIS:ND1	4:I:741:GLU:OE2	2.38	0.55
3:G:1151:PHE:HD2	3:G:1179:LYS:HG2	1.69	0.55
4:I:189:LEU:HD11	4:I:216:LEU:HD22	1.89	0.55
4:I:532:ARG:NE	4:I:545:GLU:OE1	2.34	0.55
4:I:591:LEU:HD22	4:I:628:VAL:HG21	1.87	0.55
4:I:813:LEU:HD23	4:I:831:CYS:HB2	1.87	0.55
5:L:573:SER:OG	5:L:576:ARG:NH2	2.39	0.55
5:L:675:ALA:O	5:L:679:ALA:CB	2.53	0.55
1:C:638:PHE:HB2	1:C:653:PHE:HB3	1.88	0.55
2:E:289:GLN:NE2	2:E:290:GLU:O	2.39	0.55
4:I:532:ARG:NH1	4:I:570:ALA:O	2.40	0.55
4:I:1283:ILE:HG12	4:I:1298:ARG:HH22	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:608:MET:H	1:C:621:THR:HA	1.71	0.55
2:E:337:VAL:HG11	2:E:368:GLU:HB3	1.88	0.55
2:E:1077:TYR:HB2	2:E:1109:ALA:HB2	1.89	0.55
2:E:1311:LEU:HB3	2:E:1327:VAL:HG21	1.89	0.55
3:G:327:ASN:ND2	3:G:342:CYS:O	2.39	0.55
3:G:1226:GLU:HG3	3:G:1263:SER:HB3	1.87	0.55
4:I:1035:GLU:HG2	4:I:1040:TYR:HD1	1.72	0.55
5:L:95:LYS:O	5:L:130:LYS:NZ	2.35	0.55
5:L:225:LEU:H	5:L:240:GLY:HA2	1.72	0.55
1:C:98:ILE:HB	1:C:114:ASN:HB3	1.88	0.55
1:C:229:LEU:HG	1:C:241:MET:HE2	1.88	0.55
1:C:878:ILE:HG21	1:C:899:PHE:HB2	1.88	0.55
3:G:819:LEU:HA	3:G:822:GLN:HG3	1.88	0.55
3:G:935:VAL:HA	3:G:939:CYS:HB2	1.88	0.55
4:I:439:TYR:OH	4:I:464:HIS:NE2	2.40	0.55
4:I:678:CYS:HA	4:I:681:GLN:HG3	1.88	0.55
4:I:749:GLU:OE1	4:I:753:ARG:NH1	2.33	0.55
4:I:1096:LYS:HB2	4:I:1101:ARG:HB3	1.89	0.55
4:I:1328:ARG:HH12	4:I:1330:PRO:HB3	1.71	0.55
1:C:533:VAL:O	1:C:535:ARG:NH1	2.40	0.55
2:E:944:SER:HB2	2:E:949:GLN:HG3	1.89	0.55
4:I:977:ARG:O	4:I:981:GLN:HG3	2.07	0.55
5:L:13:GLU:OE1	5:L:19:ASN:ND2	2.39	0.55
5:L:230:PHE:HB3	5:L:235:TYR:HB2	1.89	0.55
5:L:303:ARG:HA	5:L:317:HIS:HA	1.89	0.55
1:C:445:GLN:HG2	1:C:467:ARG:HD2	1.88	0.55
1:C:910:ALA:HB2	1:C:925:LEU:HD11	1.89	0.55
2:E:71:ALA:HA	2:E:113:LEU:HD13	1.89	0.55
2:E:349:THR:HA	2:E:352:ALA:HB3	1.89	0.55
2:E:771:CYS:SG	2:E:806:ARG:NH1	2.80	0.55
2:E:860:ILE:HD13	2:E:886:MET:HE1	1.88	0.55
3:G:308:ARG:NH2	3:G:361:GLY:O	2.37	0.55
3:G:707:PHE:O	3:G:711:GLN:NE2	2.40	0.55
4:I:849:ARG:HG3	4:I:876:GLU:HB3	1.88	0.55
4:I:864:CYS:HA	4:I:867:ILE:HB	1.88	0.55
4:I:1084:LEU:O	4:I:1088:VAL:N	2.39	0.55
4:I:1102:ASP:OD1	4:I:1105:ARG:NH1	2.40	0.55
5:L:731:ALA:O	5:L:763:ARG:NH2	2.40	0.55
1:C:378:ARG:HG3	1:C:379:LYS:HG3	1.89	0.55
1:C:752:TYR:HB2	1:C:761:ALA:HB2	1.89	0.55
2:E:190:LEU:HB3	2:E:213:ILE:HG21	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:845:LEU:HG	3:G:849:HIS:CE1	2.42	0.55
4:I:15:GLY:HA2	4:I:63:ARG:HA	1.87	0.55
1:C:1055:LEU:HA	1:C:1058:TYR:HB2	1.89	0.55
3:G:513:LEU:N	3:G:525:LEU:O	2.37	0.55
4:I:1044:ALA:HB1	4:I:1059:LEU:HB3	1.89	0.55
5:L:412:SER:HB3	5:L:433:LEU:HD13	1.88	0.55
1:C:59:ALA:HA	1:C:606:THR:HG21	1.88	0.54
3:G:175:VAL:HG22	3:G:184:VAL:HG22	1.88	0.54
3:G:311:LEU:HD12	3:G:364:PRO:HB2	1.90	0.54
5:L:659:VAL:H	5:L:691:ARG:HH12	1.55	0.54
1:C:100:VAL:HG23	1:C:112:MET:HE3	1.89	0.54
1:C:270:LEU:HD23	1:C:293:TYR:HB2	1.90	0.54
3:G:507:ASP:O	3:G:514:ALA:N	2.40	0.54
3:G:566:LEU:HG	3:G:603:LEU:HD11	1.87	0.54
3:G:755:MET:HA	3:G:780:ALA:HB1	1.89	0.54
3:G:1035:MET:SD	3:G:1058:HIS:HB2	2.47	0.54
4:I:796:LEU:CB	4:I:805:ALA:HB2	2.37	0.54
5:L:379:LEU:HB2	5:L:390:CYS:HB3	1.88	0.54
1:C:20:ILE:HB	1:C:325:SER:HB2	1.89	0.54
2:E:173:LEU:HG	2:E:196:ILE:HD13	1.89	0.54
2:E:1005:SER:HB3	2:E:1024:HIS:CD2	2.42	0.54
3:G:752:MET:HG2	3:G:768:CYS:SG	2.47	0.54
4:I:309:CYS:SG	4:I:311:ARG:NH1	2.80	0.54
4:I:420:GLN:HA	4:I:438:GLU:HA	1.89	0.54
4:I:957:GLN:OE1	4:I:964:ARG:NH2	2.40	0.54
1:C:669:LEU:HD22	1:C:693:LEU:HB2	1.88	0.54
3:G:718:ARG:HH21	3:G:722:LEU:HD11	1.72	0.54
3:G:741:LYS:O	4:I:802:TYR:OH	2.21	0.54
4:I:335:ILE:HA	4:I:351:THR:HA	1.89	0.54
4:I:600:SER:OG	4:I:601:LEU:N	2.40	0.54
4:I:653:ALA:HA	4:I:656:ARG:HB2	1.89	0.54
5:L:481:VAL:HB	5:L:491:PHE:HB3	1.89	0.54
5:L:847:LEU:HB2	5:L:863:TYR:HE2	1.72	0.54
1:C:568:ALA:HA	1:C:575:THR:HB	1.90	0.54
1:C:771:TRP:HB3	1:C:792:HIS:CE1	2.43	0.54
1:C:1074:ALA:O	1:C:1078:ASN:ND2	2.41	0.54
2:E:59:LEU:HD11	2:E:68:LEU:HD22	1.89	0.54
3:G:402:VAL:HG12	3:G:404:GLU:HG3	1.88	0.54
3:G:473:VAL:O	3:G:484:VAL:N	2.40	0.54
4:I:1059:LEU:HD23	4:I:1062:LYS:HD2	1.90	0.54
5:L:351:VAL:HG22	5:L:370:LYS:HE3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:502:ASN:HB2	5:L:508:MET:HB3	1.90	0.54
5:L:651:ARG:HA	5:L:654:THR:HG23	1.89	0.54
5:L:957:LYS:HZ3	5:L:975:LEU:HD11	1.71	0.54
2:E:538:ALA:HB1	2:E:570:LEU:HD21	1.88	0.54
3:G:968:GLU:OE1	3:G:980:TYR:OH	2.24	0.54
4:I:153:ILE:HD13	4:I:166:LEU:HD22	1.90	0.54
4:I:399:LEU:HD22	4:I:415:VAL:HG21	1.88	0.54
5:L:112:GLN:H	5:L:127:PRO:HG3	1.71	0.54
5:L:857:TYR:HB3	5:L:903:TYR:HD1	1.72	0.54
2:E:9:VAL:HA	2:E:20:HIS:HE1	1.72	0.54
2:E:349:THR:O	2:E:350:THR:C	2.51	0.54
2:E:707:GLU:HA	2:E:710:ILE:HD12	1.89	0.54
4:I:663:PHE:HA	4:I:675:ALA:HA	1.88	0.54
1:C:533:VAL:HB	1:C:575:THR:HG23	1.90	0.54
3:G:594:THR:HG21	3:G:622:THR:HG23	1.90	0.54
4:I:304:MET:HB2	4:I:311:ARG:H	1.72	0.54
4:I:813:LEU:CD2	4:I:832:LYS:HG3	2.38	0.54
4:I:1011:MET:HE2	4:I:1039:GLU:OE2	2.08	0.54
2:E:293:ASN:HB3	2:E:296:LEU:HB3	1.90	0.54
2:E:736:ARG:NH1	2:E:756:CYS:O	2.41	0.54
3:G:543:PRO:O	3:G:547:LYS:N	2.41	0.54
3:G:834:LEU:HD23	3:G:848:THR:HG22	1.89	0.54
4:I:840:LEU:HD21	4:I:868:LEU:HG	1.89	0.54
1:C:222:ALA:HB2	1:C:268:THR:HG22	1.90	0.54
1:C:275:PHE:HB3	1:C:288:TRP:CE2	2.42	0.54
2:E:65:ASN:O	2:E:69:GLU:N	2.31	0.54
3:G:616:GLN:OE1	3:G:667:CYS:N	2.41	0.54
3:G:804:ILE:HD11	3:G:823:LEU:HB3	1.90	0.54
3:G:834:LEU:HB3	3:G:849:HIS:NE2	2.23	0.54
3:G:1296:PRO:HG3	3:G:1337:ALA:HB1	1.90	0.54
4:I:512:TYR:HA	4:I:519:PRO:HA	1.89	0.54
4:I:959:ALA:HA	4:I:962:ILE:HG22	1.90	0.54
4:I:1105:ARG:HA	4:I:1108:LEU:CB	2.38	0.54
4:I:1124:GLU:HA	4:I:1127:ARG:HG2	1.90	0.54
5:L:318:LEU:HD11	5:L:551:MET:HG3	1.89	0.54
1:C:518:VAL:N	1:C:532:HIS:O	2.41	0.53
2:E:1010:GLU:HA	2:E:1013:PHE:HB3	1.90	0.53
3:G:160:GLU:OE2	3:G:229:ARG:NH2	2.41	0.53
3:G:555:ARG:HE	3:G:604:MET:HA	1.72	0.53
1:C:464:LYS:O	1:C:467:ARG:NE	2.41	0.53
1:C:591:ARG:NH1	1:C:592:TRP:O	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1093:SER:C	1:C:1094:MET:HG3	2.33	0.53
2:E:629:MET:HE2	2:E:661:VAL:HG12	1.90	0.53
2:E:1189:ALA:HA	2:E:1198:VAL:HB	1.91	0.53
3:G:841:ASP:HB2	3:G:844:HIS:H	1.73	0.53
3:G:1109:HIS:HB3	3:G:1111:VAL:HG22	1.90	0.53
5:L:350:VAL:HB	5:L:371:ILE:HB	1.89	0.53
1:C:137:TYR:HB2	1:C:141:ALA:HB3	1.90	0.53
1:C:763:ASP:HA	1:C:766:MET:HB3	1.90	0.53
2:E:347:ASP:HB3	2:E:643:ARG:HB3	1.90	0.53
3:G:447:VAL:HG13	3:G:453:ILE:HG13	1.90	0.53
4:I:21:TRP:NE1	4:I:348:THR:OG1	2.32	0.53
4:I:768:LYS:HE2	4:I:791:GLU:HG3	1.91	0.53
4:I:1034:TYR:HB2	4:I:1043:ALA:HB2	1.88	0.53
4:I:1080:ARG:NH1	4:I:1110:ILE:O	2.40	0.53
4:I:1183:THR:OG1	4:I:1261:LEU:O	2.24	0.53
4:I:1263:GLU:HG3	4:I:1277:GLU:HB2	1.90	0.53
5:L:247:LEU:HD13	5:L:258:ILE:HD11	1.88	0.53
5:L:577:VAL:HA	5:L:580:LEU:HD12	1.90	0.53
1:C:51:VAL:HA	1:C:54:LYS:HB2	1.91	0.53
1:C:902:ILE:O	1:C:906:LEU:CB	2.54	0.53
3:G:794:VAL:O	3:G:798:ALA:CB	2.56	0.53
3:G:821:ASN:O	3:G:825:ARG:NH1	2.42	0.53
3:G:886:ALA:O	3:G:890:THR:N	2.30	0.53
4:I:1073:VAL:HG13	4:I:1108:LEU:HD13	1.91	0.53
5:L:230:PHE:HB2	5:L:237:THR:HG23	1.90	0.53
5:L:350:VAL:HG21	5:L:371:ILE:HD12	1.91	0.53
5:L:793:TRP:HB2	5:L:814:TYR:HE1	1.74	0.53
1:C:966:GLU:HA	1:C:969:LYS:HE2	1.91	0.53
2:E:743:TYR:HA	2:E:747:ARG:HB2	1.91	0.53
2:E:811:LEU:HD13	2:E:819:ARG:HB3	1.90	0.53
3:G:465:CYS:SG	3:G:466:MET:N	2.81	0.53
4:I:1161:LEU:HD13	4:I:1291:PHE:HE2	1.73	0.53
4:I:1316:ALA:HA	4:I:1319:PHE:HB3	1.91	0.53
5:L:73:ARG:HG3	5:L:87:THR:HA	1.90	0.53
5:L:295:THR:O	5:L:297:HIS:ND1	2.37	0.53
5:L:342:LEU:N	5:L:353:TYR:O	2.41	0.53
5:L:787:TYR:CE2	5:L:798:LEU:HB3	2.42	0.53
5:L:832:GLN:HA	5:L:837:PRO:HD3	1.91	0.53
1:C:568:ALA:HB2	1:C:575:THR:H	1.73	0.53
1:C:774:VAL:HA	1:C:777:LEU:HD12	1.90	0.53
1:C:856:GLN:OE1	1:C:876:ARG:NH2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:808:LYS:HG2	3:G:820:LEU:HA	1.88	0.53
3:G:1281:VAL:HG11	3:G:1306:LEU:HD11	1.90	0.53
4:I:238:LEU:HD21	4:I:277:ILE:HG13	1.89	0.53
4:I:1182:HIS:ND1	4:I:1213:GLU:OE1	2.42	0.53
5:L:394:LYS:HA	5:L:409:VAL:HA	1.89	0.53
3:G:19:TRP:HE1	3:G:368:VAL:N	2.07	0.53
3:G:568:VAL:HA	3:G:576:VAL:HA	1.89	0.53
3:G:598:ARG:NH2	3:G:639:ASP:OD2	2.42	0.53
3:G:667:CYS:HA	3:G:677:THR:HA	1.90	0.53
4:I:294:THR:HG21	4:I:339:GLY:HA2	1.89	0.53
4:I:684:GLN:HG3	4:I:686:GLU:HG3	1.90	0.53
4:I:796:LEU:HB3	4:I:805:ALA:HB2	1.91	0.53
5:L:40:ARG:HG3	5:L:56:LYS:HG3	1.90	0.53
5:L:779:ASP:O	5:L:783:LEU:N	2.42	0.53
1:C:17:LEU:O	1:C:311:SER:OG	2.26	0.53
1:C:83:ASN:HB3	1:C:88:LYS:H	1.74	0.53
3:G:286:TYR:CZ	3:G:339:PHE:HB2	2.44	0.53
3:G:799:VAL:HG22	3:G:804:ILE:HG13	1.89	0.53
3:G:820:LEU:O	3:G:824:TYR:HB2	2.08	0.53
4:I:794:ALA:C	4:I:796:LEU:H	2.17	0.53
4:I:840:LEU:HD12	4:I:845:LEU:HA	1.91	0.53
2:E:1076:HIS:ND1	2:E:1095:GLU:OE1	2.41	0.53
3:G:394:MET:O	3:G:402:VAL:N	2.40	0.53
4:I:816:LEU:HD21	4:I:827:LEU:HD23	1.91	0.53
1:C:262:LYS:HB3	1:C:313:ILE:HG13	1.91	0.53
2:E:883:ALA:O	2:E:887:LEU:HB2	2.08	0.53
3:G:182:ALA:HB2	3:G:202:GLY:HA2	1.91	0.53
3:G:265:LEU:HB3	3:G:278:TYR:HB3	1.91	0.53
3:G:669:GLY:N	3:G:676:LEU:O	2.41	0.53
3:G:927:LYS:NZ	5:L:915:SER:O	2.42	0.53
1:C:352:PHE:HE2	1:C:354:ARG:HG2	1.74	0.52
1:C:784:ASP:HB3	1:C:788:LEU:HD23	1.90	0.52
2:E:918:LEU:HB3	2:E:929:GLN:HG3	1.89	0.52
3:G:756:CYS:HB3	3:G:761:ARG:HG3	1.92	0.52
4:I:299:LEU:O	4:I:316:ASN:ND2	2.42	0.52
1:C:382:ALA:H	1:C:393:ALA:HB3	1.74	0.52
1:C:822:VAL:O	1:C:826:TYR:HB2	2.09	0.52
2:E:303:PRO:HA	2:E:480:ALA:HB2	1.91	0.52
2:E:1239:TRP:HB3	2:E:1258:LEU:HD22	1.91	0.52
3:G:654:GLN:HB2	3:G:729:ALA:HB2	1.90	0.52
3:G:789:GLU:HB3	3:G:810:LEU:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:913:GLU:HG3	3:G:934:MET:HE3	1.90	0.52
4:I:1097:ASP:OD1	4:I:1097:ASP:N	2.42	0.52
4:I:1108:LEU:HD12	4:I:1111:ALA:HB3	1.91	0.52
5:L:345:GLN:HG2	5:L:380:LEU:HD22	1.90	0.52
5:L:505:PHE:HB3	5:L:508:MET:HB2	1.91	0.52
1:C:116:ARG:NH2	1:C:156:GLU:OE2	2.43	0.52
2:E:619:ASP:OD1	2:E:619:ASP:N	2.42	0.52
2:E:1096:LEU:HB3	2:E:1113:MET:HE2	1.91	0.52
3:G:496:PHE:CE2	3:G:523:ARG:HB3	2.44	0.52
3:G:580:VAL:HG11	3:G:645:VAL:HG11	1.91	0.52
3:G:1017:THR:HB	3:G:1033:LEU:HG	1.92	0.52
3:G:1176:ASP:HA	3:G:1203:LEU:HD22	1.91	0.52
5:L:55:LEU:HD11	5:L:90:ALA:HB1	1.90	0.52
5:L:171:GLU:OE2	5:L:174:ARG:NH1	2.42	0.52
5:L:177:THR:O	5:L:205:LYS:NZ	2.37	0.52
5:L:483:ASN:O	5:L:487:LYS:N	2.41	0.52
1:C:42:ARG:HH21	1:C:65:SER:HB2	1.75	0.52
2:E:896:GLU:O	2:E:900:TYR:N	2.35	0.52
2:E:1026:GLN:NE2	2:E:1027:GLN:OE1	2.43	0.52
3:G:612:LEU:HD11	3:G:642:ILE:HG23	1.91	0.52
4:I:1130:GLN:HE21	4:I:1167:LEU:HD12	1.74	0.52
5:L:110:VAL:HG12	5:L:111:THR:HG23	1.91	0.52
2:E:551:LEU:HG	2:E:574:VAL:HG11	1.90	0.52
2:E:1167:TYR:HA	2:E:1170:MET:SD	2.49	0.52
3:G:182:ALA:HB3	3:G:199:MET:HG3	1.91	0.52
3:G:569:GLY:N	3:G:575:ALA:O	2.43	0.52
3:G:825:ARG:HD3	3:G:833:ALA:HA	1.91	0.52
5:L:302:ASP:O	5:L:318:LEU:N	2.37	0.52
5:L:618:LEU:HD13	5:L:642:PHE:HB2	1.91	0.52
5:L:721:LYS:HD3	5:L:723:TYR:HE1	1.73	0.52
1:C:697:ALA:O	1:C:702:ASP:N	2.42	0.52
1:C:728:LEU:HD23	1:C:734:GLN:HA	1.91	0.52
1:C:1030:TYR:HD1	1:C:1062:LEU:HD11	1.74	0.52
2:E:285:SER:O	2:E:288:ARG:NH1	2.42	0.52
3:G:821:ASN:O	3:G:825:ARG:HG2	2.08	0.52
5:L:801:HIS:HB2	5:L:811:TYR:OH	2.10	0.52
2:E:959:GLU:HG2	2:E:963:HIS:CE1	2.44	0.52
3:G:599:GLN:HB2	3:G:620:VAL:HB	1.90	0.52
3:G:604:MET:HE1	3:G:670:SER:HB3	1.92	0.52
3:G:898:ALA:HB2	5:L:855:THR:HG21	1.91	0.52
3:G:1237:GLN:NE2	3:G:1322:ARG:O	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:1002:PHE:HZ	4:I:1037:ARG:HH22	1.58	0.52
5:L:18:ARG:NH2	5:L:282:GLU:OE2	2.41	0.52
5:L:906:TYR:O	5:L:910:HIS:HB3	2.10	0.52
1:C:212:VAL:HG13	1:C:231:ILE:HG12	1.92	0.52
3:G:642:ILE:HD11	3:G:675:LEU:HD11	1.92	0.52
5:L:388:ILE:HD11	5:L:443:VAL:HG22	1.92	0.52
5:L:775:LEU:CG	5:L:783:LEU:HD11	2.40	0.52
1:C:1089:ILE:HD12	2:E:783:PRO:HG3	1.92	0.52
3:G:58:ASN:HD22	3:G:62:THR:H	1.57	0.52
3:G:405:ASN:HB3	3:G:408:VAL:HG23	1.92	0.52
3:G:842:ARG:NH1	5:L:822:ASP:OD2	2.42	0.52
4:I:1268:CYS:SG	4:I:1284:SER:OG	2.62	0.52
5:L:317:HIS:O	5:L:321:GLU:N	2.33	0.52
5:L:980:LEU:HD21	5:L:996:ARG:HH22	1.75	0.52
1:C:762:ILE:HG13	1:C:765:ARG:HH21	1.74	0.52
2:E:850:LEU:HB3	2:E:852:GLN:HE22	1.74	0.52
2:E:985:ASP:N	2:E:985:ASP:OD1	2.43	0.52
3:G:720:ALA:CB	3:G:752:MET:O	2.58	0.52
4:I:1146:VAL:HA	4:I:1156:PRO:HD2	1.91	0.52
5:L:96:TYR:CZ	5:L:125:TRP:HB2	2.45	0.52
5:L:343:ALA:HA	5:L:352:ILE:HA	1.92	0.52
5:L:793:TRP:HB3	5:L:817:TRP:HB3	1.91	0.52
1:C:610:ILE:HB	1:C:617:GLU:HB2	1.91	0.51
2:E:1294:GLU:HB3	2:E:1311:LEU:HD21	1.92	0.51
3:G:526:LYS:N	3:G:533:LYS:O	2.42	0.51
4:I:1143:PHE:HE2	4:I:1310:CYS:HB2	1.74	0.51
2:E:927:ALA:HA	2:E:930:ARG:HE	1.74	0.51
2:E:1221:ARG:HA	2:E:1224:LYS:HB2	1.92	0.51
3:G:707:PHE:HA	3:G:755:MET:SD	2.51	0.51
4:I:437:ARG:NH1	4:I:439:TYR:OH	2.43	0.51
4:I:590:ALA:HA	4:I:613:ALA:HA	1.92	0.51
4:I:803:SER:HA	4:I:842:LEU:HD11	1.93	0.51
4:I:854:GLN:HG3	4:I:855:LEU:HG	1.91	0.51
5:L:228:SER:OG	5:L:237:THR:OG1	2.27	0.51
5:L:637:ALA:HB2	5:L:652:LEU:HB2	1.92	0.51
3:G:913:GLU:HA	3:G:921:ALA:HB2	1.92	0.51
3:G:1028:GLU:HA	3:G:1052:LEU:CD1	2.29	0.51
4:I:138:ARG:HG3	4:I:139:GLU:HG3	1.92	0.51
4:I:920:ALA:HB1	4:I:932:ALA:HA	1.92	0.51
4:I:1227:ALA:HB1	4:I:1247:ILE:HG23	1.91	0.51
5:L:24:LEU:HD22	5:L:278:ALA:HB1	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:188:ASN:HB3	5:L:191:GLU:HB2	1.91	0.51
5:L:412:SER:OG	5:L:413:VAL:N	2.42	0.51
2:E:134:LEU:HD13	2:E:140:MET:HB3	1.92	0.51
3:G:469:ASN:HB2	3:G:474:TYR:CE2	2.45	0.51
3:G:1237:GLN:HE22	3:G:1325:ASP:H	1.59	0.51
4:I:1139:HIS:HD2	4:I:1167:LEU:HD22	1.74	0.51
5:L:512:SER:HB2	5:L:531:LEU:HB3	1.92	0.51
5:L:525:PRO:HG2	5:L:564:ARG:HG3	1.92	0.51
5:L:780:THR:HB	5:L:799:LEU:CD1	2.40	0.51
2:E:319:TYR:HE1	2:E:355:ARG:HD2	1.75	0.51
2:E:337:VAL:HG13	2:E:356:PHE:HE1	1.75	0.51
3:G:874:CYS:HB3	5:L:842:ARG:NH1	2.26	0.51
3:G:1296:PRO:HG2	3:G:1338:ARG:HE	1.76	0.51
4:I:400:GLU:OE1	4:I:436:ARG:NH2	2.44	0.51
4:I:622:THR:O	4:I:629:GLY:N	2.44	0.51
4:I:795:MET:SD	4:I:796:LEU:HG	2.50	0.51
4:I:1112:MET:O	4:I:1114:GLN:NE2	2.43	0.51
4:I:1123:LEU:HB2	4:I:1160:LEU:HD12	1.92	0.51
5:L:964:ALA:O	5:L:967:LEU:N	2.42	0.51
1:C:288:TRP:CD1	1:C:309:GLY:HA2	2.45	0.51
1:C:608:MET:HB3	1:C:620:VAL:O	2.11	0.51
1:C:971:LYS:O	1:C:975:LEU:N	2.37	0.51
2:E:1173:LYS:HD3	2:E:1178:ILE:HD11	1.93	0.51
3:G:106:ILE:HG21	3:G:109:MET:HE3	1.93	0.51
4:I:248:MET:SD	4:I:249:LYS:N	2.84	0.51
4:I:452:GLN:HB2	4:I:495:LEU:HD21	1.92	0.51
5:L:535:VAL:HG13	5:L:543:ILE:HG23	1.93	0.51
5:L:663:MET:HE3	5:L:682:PHE:HE2	1.75	0.51
2:E:844:GLY:HA2	2:E:847:LEU:HD12	1.92	0.51
4:I:15:GLY:HA3	4:I:33:SER:HB3	1.91	0.51
4:I:576:ASP:HA	4:I:623:VAL:HG13	1.93	0.51
4:I:1108:LEU:O	4:I:1111:ALA:HB3	2.10	0.51
5:L:309:GLN:OE1	5:L:325:ARG:NH1	2.42	0.51
5:L:454:HIS:CE1	5:L:474:ASP:HB3	2.45	0.51
1:C:70:LEU:HD11	1:C:108:TRP:HB2	1.91	0.51
1:C:841:LEU:HD22	1:C:847:LEU:HD13	1.92	0.51
2:E:1252:TYR:HB3	2:E:1279:ILE:HG23	1.92	0.51
3:G:621:PHE:HB3	3:G:625:ASN:HB2	1.93	0.51
3:G:1274:VAL:HG22	3:G:1317:LEU:HB3	1.92	0.51
4:I:415:VAL:O	4:I:422:ALA:N	2.33	0.51
5:L:516:MET:HE1	5:L:528:GLN:HG3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:682:PHE:CD1	5:L:691:ARG:HB2	2.45	0.51
5:L:799:LEU:HD12	5:L:802:ALA:CB	2.38	0.51
1:C:88:LYS:HG2	1:C:102:MET:HE1	1.93	0.51
1:C:198:TYR:HA	1:C:201:GLU:HB2	1.93	0.51
2:E:904:GLN:HG3	2:E:936:ILE:HG23	1.93	0.51
3:G:216:LEU:HB3	3:G:224:LEU:HD11	1.93	0.51
3:G:265:LEU:O	3:G:278:TYR:N	2.42	0.51
3:G:724:PHE:HZ	3:G:758:ARG:HB2	1.76	0.51
3:G:925:TYR:O	3:G:929:GLY:N	2.44	0.51
3:G:1237:GLN:HG2	3:G:1322:ARG:HB2	1.93	0.51
4:I:1044:ALA:HA	4:I:1047:TRP:HB2	1.93	0.51
4:I:1337:ASP:OD1	4:I:1337:ASP:N	2.44	0.51
5:L:247:LEU:HG	5:L:255:LEU:HD12	1.93	0.51
1:C:825:PHE:HB3	1:C:830:ASP:HB2	1.92	0.51
1:C:1100:ASP:OD1	1:C:1100:ASP:N	2.44	0.51
2:E:192:GLY:HA2	2:E:195:LYS:HE3	1.93	0.51
2:E:709:ALA:O	2:E:714:ASP:N	2.44	0.51
3:G:751:ASN:HD21	3:G:774:HIS:CE1	2.29	0.51
3:G:1281:VAL:O	3:G:1285:PHE:N	2.41	0.51
4:I:573:VAL:HG22	4:I:585:ILE:HG12	1.93	0.51
4:I:773:ALA:O	4:I:777:ALA:HB2	2.11	0.51
4:I:833:ALA:HB1	4:I:860:LEU:HD13	1.93	0.51
4:I:962:ILE:O	4:I:966:THR:OG1	2.25	0.51
5:L:675:ALA:O	5:L:679:ALA:HB2	2.11	0.51
1:C:395:LYS:HA	1:C:402:HIS:HA	1.92	0.50
1:C:507:SER:HA	1:C:523:LEU:HB2	1.93	0.50
2:E:458:GLU:HA	2:E:461:ILE:HG12	1.92	0.50
2:E:1035:HIS:O	2:E:1039:LEU:N	2.36	0.50
3:G:104:ASN:HB3	3:G:122:ASP:HB2	1.92	0.50
3:G:484:VAL:HA	3:G:490:VAL:HA	1.93	0.50
3:G:887:GLU:CD	3:G:887:GLU:H	2.19	0.50
3:G:1052:LEU:HB3	3:G:1055:VAL:HB	1.94	0.50
4:I:265:GLY:HA2	4:I:290:LEU:HB2	1.92	0.50
4:I:374:VAL:HG11	4:I:621:LEU:HD13	1.93	0.50
4:I:455:VAL:N	4:I:462:VAL:O	2.43	0.50
5:L:665:MET:SD	5:L:669:LEU:HD12	2.51	0.50
5:L:933:LEU:HA	5:L:955:LEU:HD21	1.94	0.50
1:C:596:ASN:HB3	1:C:599:LEU:HD12	1.93	0.50
2:E:596:PHE:HZ	2:E:623:ARG:HH12	1.59	0.50
3:G:577:ARG:HA	3:G:592:ASP:HA	1.93	0.50
3:G:659:ILE:O	3:G:661:THR:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:87:THR:HG21	4:I:108:THR:HA	1.93	0.50
4:I:164:MET:N	4:I:176:THR:O	2.44	0.50
4:I:259:LEU:HD21	4:I:302:VAL:HG13	1.93	0.50
5:L:871:ALA:HA	5:L:892:ARG:HH21	1.75	0.50
1:C:115:ASN:OD1	1:C:117:ASN:ND2	2.39	0.50
1:C:801:ASP:HB3	5:L:580:LEU:HD23	1.93	0.50
1:C:906:LEU:HG	1:C:925:LEU:HD13	1.93	0.50
2:E:113:LEU:O	2:E:117:TYR:N	2.33	0.50
2:E:655:LEU:HB3	2:E:692:PHE:HD1	1.75	0.50
2:E:874:THR:HG23	2:E:878:GLN:HE22	1.76	0.50
2:E:1009:ALA:HB1	2:E:1021:ALA:HA	1.94	0.50
3:G:176:ALA:HB3	3:G:183:VAL:HB	1.93	0.50
3:G:643:ILE:HG12	3:G:653:LEU:HA	1.93	0.50
3:G:805:GLU:HA	3:G:808:LYS:HE3	1.92	0.50
3:G:1039:LYS:HG3	3:G:1042:LYS:HB2	1.94	0.50
3:G:1200:LEU:HA	3:G:1203:LEU:HG	1.91	0.50
3:G:1296:PRO:HB2	3:G:1338:ARG:HH21	1.77	0.50
4:I:338:VAL:HG23	4:I:349:VAL:HG22	1.93	0.50
4:I:623:VAL:HA	4:I:628:VAL:HA	1.91	0.50
4:I:663:PHE:HE1	4:I:691:LEU:HD23	1.76	0.50
1:C:207:SER:OG	1:C:234:ASP:OD1	2.29	0.50
3:G:710:MET:HA	3:G:717:THR:HG21	1.93	0.50
3:G:1330:MET:HA	3:G:1333:TYR:CZ	2.46	0.50
4:I:510:SER:HA	4:I:522:GLU:HG2	1.93	0.50
5:L:558:GLN:O	5:L:562:MET:N	2.43	0.50
5:L:772:GLU:O	5:L:776:LYS:N	2.44	0.50
3:G:286:TYR:OH	3:G:343:TRP:NE1	2.45	0.50
3:G:306:ASP:O	3:G:310:ASN:N	2.42	0.50
3:G:434:LEU:O	3:G:445:TYR:N	2.38	0.50
4:I:198:VAL:HG12	4:I:211:GLU:HB3	1.93	0.50
4:I:978:PHE:O	4:I:982:SER:N	2.43	0.50
5:L:632:GLU:HG2	5:L:635:LEU:HD12	1.93	0.50
5:L:637:ALA:O	5:L:641:ALA:HB2	2.12	0.50
5:L:748:LYS:HG2	5:L:754:LEU:HD11	1.93	0.50
5:L:828:ARG:HE	5:L:840:ALA:HB1	1.75	0.50
1:C:347:THR:HA	1:C:366:ASP:HA	1.94	0.50
1:C:543:LEU:HB3	1:C:547:LEU:HG	1.93	0.50
1:C:774:VAL:HG12	1:C:792:HIS:HE1	1.76	0.50
2:E:40:PHE:CE2	2:E:71:ALA:HB1	2.47	0.50
2:E:339:ALA:HA	2:E:342:GLN:HG3	1.94	0.50
2:E:580:LYS:HD2	2:E:583:LEU:HD12	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:965:ASP:OD1	2:E:965:ASP:N	2.42	0.50
3:G:88:TRP:HZ2	3:G:93:ARG:HD3	1.76	0.50
3:G:184:VAL:HB	3:G:197:VAL:HG12	1.93	0.50
3:G:1168:MET:HE3	3:G:1183:PHE:CG	2.47	0.50
1:C:598:GLU:HB3	1:C:613:GLY:HA2	1.92	0.50
2:E:310:SER:HA	2:E:532:GLU:HB3	1.94	0.50
3:G:206:LEU:HD12	3:G:217:VAL:HG22	1.94	0.50
3:G:834:LEU:HB3	3:G:849:HIS:CE1	2.46	0.50
3:G:1234:ALA:HA	3:G:1278:ARG:HH12	1.75	0.50
4:I:295:TYR:HD1	4:I:302:VAL:HG22	1.77	0.50
5:L:784:ILE:HG12	5:L:810:VAL:HA	1.94	0.50
5:L:883:ALA:O	5:L:887:ARG:N	2.27	0.50
5:L:949:VAL:HG22	5:L:978:LEU:HB3	1.94	0.50
1:C:258:PRO:HA	1:C:274:GLY:HA3	1.92	0.50
1:C:687:PRO:HB3	1:C:690:TRP:CD1	2.47	0.50
2:E:266:LEU:HD13	2:E:314:LEU:HA	1.93	0.50
4:I:936:TYR:O	4:I:941:ASP:N	2.43	0.50
5:L:480:LEU:HG	5:L:492:GLU:HG3	1.92	0.50
1:C:739:ALA:HA	1:C:744:ARG:HE	1.77	0.50
1:C:837:LEU:HD23	1:C:840:ALA:HB3	1.93	0.50
3:G:589:HIS:HB3	3:G:651:ILE:HD12	1.94	0.50
4:I:375:LEU:HD13	4:I:408:LEU:HD13	1.93	0.50
1:C:685:SER:OG	1:C:686:HIS:N	2.44	0.49
2:E:925:ALA:HA	2:E:928:LEU:HB3	1.94	0.49
3:G:379:ARG:HH22	3:G:423:GLN:HG3	1.77	0.49
3:G:842:ARG:HD3	5:L:822:ASP:HB2	1.93	0.49
3:G:980:TYR:HB3	3:G:985:ARG:HB2	1.93	0.49
3:G:1011:PRO:HA	3:G:1014:MET:CB	2.41	0.49
3:G:1017:THR:HB	3:G:1033:LEU:CD1	2.42	0.49
4:I:525:HIS:CE1	4:I:527:ASP:HB2	2.47	0.49
4:I:790:LYS:HD3	4:I:831:CYS:SG	2.52	0.49
5:L:436:GLY:HA2	5:L:458:VAL:HG23	1.93	0.49
5:L:507:ASP:HB3	5:L:522:GLY:HA2	1.94	0.49
1:C:231:ILE:H	1:C:241:MET:HE1	1.76	0.49
1:C:432:HIS:HB3	1:C:443:VAL:HG13	1.93	0.49
1:C:795:ILE:HA	1:C:798:TYR:HB3	1.93	0.49
2:E:387:ALA:HB2	2:E:443:LEU:HD11	1.93	0.49
2:E:938:PHE:HZ	2:E:970:SER:HA	1.77	0.49
2:E:1295:ASN:HA	2:E:1298:LYS:HD2	1.94	0.49
5:L:3:THR:HG21	5:L:258:ILE:HA	1.94	0.49
1:C:313:ILE:HB	1:C:322:LEU:HD11	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:592:TRP:CE3	1:C:600:PHE:HB3	2.47	0.49
2:E:19:ARG:HH12	2:E:289:GLN:HB3	1.77	0.49
2:E:703:VAL:HA	2:E:706:CYS:HB2	1.93	0.49
2:E:1086:ILE:HG22	2:E:1086:ILE:O	2.12	0.49
3:G:935:VAL:O	3:G:940:PHE:N	2.46	0.49
3:G:1053:PHE:HA	3:G:1056:LEU:HB3	1.94	0.49
4:I:772:ASP:HA	4:I:775:LYS:HB2	1.94	0.49
4:I:845:LEU:O	4:I:849:ARG:HB2	2.12	0.49
4:I:1125:MET:SD	4:I:1141:LYS:NZ	2.77	0.49
1:C:421:VAL:HA	1:C:437:ASN:HD21	1.78	0.49
1:C:882:VAL:HG11	1:C:901:GLN:HG2	1.94	0.49
2:E:557:ILE:HA	2:E:560:MET:HG3	1.94	0.49
2:E:564:GLU:HG3	2:E:567:ALA:H	1.78	0.49
3:G:543:PRO:HD2	3:G:546:LEU:HB2	1.94	0.49
3:G:712:ASP:O	3:G:776:ARG:NE	2.38	0.49
3:G:808:LYS:HZ2	3:G:824:TYR:HA	1.77	0.49
3:G:811:TYR:CE2	3:G:823:LEU:HD12	2.47	0.49
3:G:927:LYS:HE2	5:L:856:ARG:HG2	1.94	0.49
3:G:1225:TRP:HD1	3:G:1263:SER:HA	1.77	0.49
4:I:413:ALA:O	4:I:424:TYR:N	2.42	0.49
4:I:879:GLU:OE1	4:I:883:ARG:NH1	2.45	0.49
5:L:23:ASP:HB3	5:L:65:VAL:HG22	1.93	0.49
1:C:182:CYS:HB3	1:C:195:VAL:HB	1.94	0.49
1:C:402:HIS:N	1:C:419:ILE:O	2.41	0.49
1:C:441:VAL:HG21	1:C:511:ILE:HD13	1.93	0.49
1:C:724:HIS:O	1:C:728:LEU:N	2.46	0.49
2:E:1012:MET:O	2:E:1017:HIS:ND1	2.45	0.49
3:G:270:GLU:HG2	3:G:301:VAL:HA	1.93	0.49
3:G:483:VAL:O	3:G:491:LYS:N	2.45	0.49
3:G:842:ARG:HB3	5:L:822:ASP:HB2	1.94	0.49
4:I:7:VAL:H	4:I:356:MET:HB3	1.76	0.49
4:I:170:ASP:OD1	4:I:170:ASP:N	2.43	0.49
5:L:114:LEU:O	5:L:125:TRP:N	2.38	0.49
5:L:270:PRO:HA	5:L:277:VAL:HA	1.93	0.49
5:L:725:ARG:HH22	5:L:732:LYS:HZ2	1.59	0.49
1:C:417:LYS:NZ	1:C:465:ASP:OD2	2.46	0.49
1:C:604:GLU:HG2	1:C:605:LYS:HD3	1.95	0.49
1:C:843:ASP:N	1:C:843:ASP:OD1	2.42	0.49
2:E:735:ALA:HB1	2:E:739:MET:HE1	1.93	0.49
3:G:429:LEU:HA	3:G:434:LEU:HA	1.94	0.49
3:G:675:LEU:O	3:G:702:ALA:N	2.36	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:1056:LEU:HD12	3:G:1059:ILE:HB	1.93	0.49
4:I:880:MET:HA	4:I:883:ARG:HG2	1.93	0.49
5:L:126:SER:H	5:L:129:GLN:NE2	2.11	0.49
5:L:389:LEU:HB2	5:L:396:GLN:HB2	1.94	0.49
1:C:352:PHE:HE1	1:C:363:MET:HB2	1.77	0.49
1:C:518:VAL:O	1:C:532:HIS:N	2.46	0.49
1:C:668:LEU:HD11	1:C:680:PHE:HB3	1.95	0.49
2:E:47:LEU:HG	2:E:52:THR:HA	1.95	0.49
2:E:1087:ASN:O	2:E:1301:ASN:ND2	2.42	0.49
3:G:117:ARG:HA	3:G:131:LYS:HA	1.95	0.49
3:G:277:MET:HB2	3:G:286:TYR:CZ	2.48	0.49
3:G:279:ASN:HB3	3:G:284:ASP:HB2	1.94	0.49
3:G:403:LEU:HD13	3:G:453:ILE:HG12	1.94	0.49
3:G:516:VAL:HG13	3:G:520:ASN:HA	1.94	0.49
4:I:754:SER:OG	4:I:756:VAL:O	2.31	0.49
5:L:845:GLU:HA	5:L:848:CYS:HB2	1.94	0.49
1:C:292:PHE:HE2	1:C:303:LEU:HB2	1.78	0.49
1:C:510:MET:SD	1:C:550:MET:HE3	2.53	0.49
1:C:654:MET:N	1:C:654:MET:SD	2.85	0.49
1:C:1033:TRP:HZ2	1:C:1066:GLU:HG3	1.77	0.49
2:E:491:VAL:HG22	2:E:516:VAL:HG13	1.95	0.49
2:E:538:ALA:CB	2:E:570:LEU:HD21	2.43	0.49
3:G:119:ILE:HG13	3:G:129:MET:HG3	1.95	0.49
3:G:425:LEU:HD12	3:G:464:ARG:HB3	1.94	0.49
3:G:513:LEU:HB3	3:G:525:LEU:HB2	1.93	0.49
3:G:523:ARG:HE	3:G:525:LEU:HD11	1.76	0.49
3:G:1191:ASP:N	3:G:1191:ASP:OD1	2.45	0.49
4:I:676:VAL:HG22	4:I:691:LEU:HD13	1.95	0.49
4:I:874:LEU:HD11	4:I:893:ILE:HG21	1.93	0.49
4:I:933:ALA:HB2	4:I:948:LEU:HD12	1.94	0.49
5:L:37:ILE:HB	5:L:42:LEU:HD12	1.95	0.49
5:L:50:ASP:OD1	5:L:50:ASP:N	2.46	0.49
5:L:980:LEU:HG	5:L:996:ARG:HH12	1.77	0.49
2:E:19:ARG:HE	2:E:253:GLN:HB2	1.77	0.49
2:E:65:ASN:HB3	2:E:68:LEU:HG	1.95	0.49
2:E:961:LEU:HG	2:E:971:MET:HE1	1.95	0.49
2:E:1202:MET:HB3	2:E:1218:GLN:HG3	1.93	0.49
5:L:663:MET:HE3	5:L:682:PHE:CE2	2.48	0.49
5:L:800:LEU:HB3	5:L:814:TYR:HB2	1.95	0.49
1:C:2:PHE:HA	1:C:301:ARG:HD2	1.94	0.49
3:G:318:ASP:OD2	3:G:320:ARG:NH2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:678:CYS:O	4:I:681:GLN:NE2	2.45	0.49
5:L:328:CYS:HB3	5:L:346:LEU:HD11	1.93	0.49
5:L:375:LEU:HD11	5:L:389:LEU:HD11	1.95	0.49
5:L:796:ALA:O	5:L:800:LEU:HD23	2.13	0.49
2:E:233:MET:HE1	2:E:471:PHE:HD1	1.78	0.48
2:E:538:ALA:HA	2:E:541:LEU:HD12	1.94	0.48
2:E:599:ARG:HA	2:E:604:TYR:HD2	1.78	0.48
2:E:810:ALA:HA	2:E:813:THR:HG22	1.95	0.48
2:E:878:GLN:HG2	2:E:918:LEU:HD22	1.96	0.48
3:G:1142:ALA:HB2	3:G:1157:LYS:HB2	1.95	0.48
4:I:229:THR:OG1	4:I:230:ALA:N	2.46	0.48
4:I:452:GLN:HA	4:I:465:PRO:HA	1.95	0.48
4:I:546:ASP:HB3	4:I:552:HIS:CD2	2.48	0.48
4:I:986:GLY:HA2	4:I:989:VAL:HG12	1.95	0.48
4:I:1279:GLU:OE2	4:I:1298:ARG:NH2	2.43	0.48
5:L:987:GLU:HG2	5:L:988:VAL:HG23	1.94	0.48
1:C:759:ASP:OD1	1:C:781:SER:OG	2.29	0.48
2:E:943:GLN:O	2:E:947:ALA:N	2.45	0.48
3:G:20:SER:HB2	3:G:27:SER:HA	1.93	0.48
3:G:37:ALA:HB2	3:G:57:LYS:HG3	1.94	0.48
3:G:324:TYR:HB3	3:G:343:TRP:CE3	2.49	0.48
3:G:704:MET:HE1	3:G:718:ARG:HH22	1.77	0.48
3:G:1289:ARG:NH2	3:G:1332:GLU:OE2	2.36	0.48
4:I:924:GLU:HG3	4:I:929:TRP:CD2	2.48	0.48
4:I:1023:LYS:HG3	4:I:1026:ASP:H	1.78	0.48
4:I:1268:CYS:HB3	4:I:1273:MET:H	1.78	0.48
5:L:473:VAL:HG23	5:L:499:VAL:HG12	1.95	0.48
5:L:980:LEU:HB2	5:L:988:VAL:HG21	1.95	0.48
2:E:1290:ALA:HB2	2:E:1314:ASN:HB2	1.95	0.48
3:G:217:VAL:O	3:G:225:ASN:N	2.46	0.48
3:G:1068:SER:OG	3:G:1069:ASP:N	2.46	0.48
4:I:393:THR:OG1	4:I:396:ARG:NH2	2.46	0.48
4:I:646:LYS:HA	4:I:649:GLN:HG2	1.95	0.48
1:C:432:HIS:CE1	1:C:523:LEU:HD13	2.48	0.48
1:C:538:PRO:HB3	1:C:552:ILE:HG23	1.95	0.48
2:E:1219:LEU:HD21	2:E:1241:LEU:HD23	1.96	0.48
3:G:33:LEU:HD12	3:G:37:ALA:HB3	1.96	0.48
3:G:415:GLY:HA2	3:G:451:ASN:HB3	1.96	0.48
3:G:752:MET:HG3	3:G:768:CYS:HB2	1.95	0.48
4:I:730:ASN:ND2	4:I:750:LEU:O	2.40	0.48
4:I:764:ARG:NE	4:I:772:ASP:HB2	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:813:LEU:CD2	4:I:831:CYS:HB2	2.43	0.48
5:L:744:ARG:HE	5:L:776:LYS:NZ	2.11	0.48
5:L:910:HIS:HA	5:L:950:ASN:HB2	1.95	0.48
1:C:391:VAL:HG21	1:C:433:VAL:HG11	1.95	0.48
2:E:736:ARG:NH1	2:E:759:ASP:HB3	2.27	0.48
2:E:737:MET:HB3	2:E:772:MET:SD	2.53	0.48
3:G:896:ILE:HG13	3:G:904:LEU:HB2	1.95	0.48
4:I:159:ASN:HB3	4:I:198:VAL:HG11	1.95	0.48
4:I:292:ASP:OD2	4:I:337:LYS:HG3	2.14	0.48
4:I:364:PRO:HG2	4:I:377:LEU:HD22	1.96	0.48
5:L:662:ALA:HB1	5:L:666:PHE:CE2	2.49	0.48
5:L:725:ARG:NH1	5:L:729:ILE:HG13	2.29	0.48
1:C:544:ASN:ND2	1:C:597:PRO:O	2.38	0.48
1:C:939:LEU:HD13	1:C:962:LEU:HB3	1.95	0.48
1:C:947:ALA:HB1	1:C:1062:LEU:HD23	1.94	0.48
2:E:823:TYR:O	2:E:827:ALA:N	2.42	0.48
3:G:908:TRP:O	3:G:920:LYS:HE2	2.13	0.48
3:G:990:VAL:HG21	3:G:1013:VAL:HB	1.96	0.48
3:G:1125:LYS:O	3:G:1157:LYS:NZ	2.46	0.48
4:I:267:VAL:HG21	4:I:313:LEU:HD11	1.95	0.48
4:I:923:LYS:O	4:I:928:ARG:N	2.46	0.48
5:L:173:HIS:CD2	5:L:209:MET:HE3	2.46	0.48
5:L:518:SER:HB3	5:L:526:LEU:HD21	1.95	0.48
5:L:908:VAL:HG22	5:L:919:THR:H	1.78	0.48
1:C:442:TYR:HB2	1:C:470:MET:HG2	1.95	0.48
2:E:236:ASP:N	2:E:236:ASP:OD1	2.46	0.48
3:G:31:VAL:O	3:G:39:GLY:N	2.33	0.48
3:G:70:HIS:N	3:G:75:LEU:O	2.45	0.48
3:G:324:TYR:HB3	3:G:343:TRP:HE3	1.77	0.48
3:G:336:VAL:HG22	3:G:338:ASP:H	1.78	0.48
3:G:591:HIS:NE2	3:G:596:GLU:OE1	2.47	0.48
3:G:604:MET:HE3	3:G:669:GLY:HA2	1.96	0.48
3:G:769:LEU:HD22	3:G:774:HIS:HB3	1.95	0.48
3:G:939:CYS:HB3	3:G:963:LEU:HD13	1.95	0.48
5:L:388:ILE:HG21	5:L:429:LEU:HD11	1.96	0.48
1:C:104:HIS:N	1:C:107:MET:O	2.47	0.48
3:G:80:TRP:HB2	3:G:84:ALA:HB3	1.95	0.48
3:G:598:ARG:HH21	3:G:637:VAL:HG13	1.79	0.48
3:G:942:ARG:NH2	3:G:967:TYR:OH	2.46	0.48
4:I:582:VAL:HA	4:I:595:LEU:HA	1.96	0.48
4:I:860:LEU:HA	4:I:863:GLU:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:110:VAL:HG23	5:L:150:GLY:HA3	1.96	0.48
5:L:672:PHE:HA	5:L:675:ALA:HB3	1.95	0.48
1:C:310:ILE:HD13	1:C:324:LEU:HD23	1.95	0.48
2:E:12:TYR:OH	2:E:254:ASN:ND2	2.46	0.48
2:E:884:TRP:HD1	2:E:907:ALA:HB2	1.78	0.48
3:G:828:GLY:HA3	4:I:711:ILE:HD12	1.94	0.48
4:I:1109:ASN:ND2	4:I:1121:ASP:OD2	2.47	0.48
5:L:304:TYR:HB2	5:L:318:LEU:HD11	1.96	0.48
5:L:910:HIS:NE2	5:L:947:SER:OG	2.46	0.48
1:C:731:LYS:HD3	1:C:731:LYS:HA	1.72	0.48
1:C:778:ILE:HG12	1:C:785:ASP:HA	1.96	0.48
2:E:251:ASP:OD1	2:E:251:ASP:N	2.46	0.48
2:E:1004:ALA:O	2:E:1008:LEU:HB2	2.14	0.48
3:G:31:VAL:HG22	3:G:375:ILE:HG21	1.96	0.48
3:G:60:ARG:HD3	3:G:84:ALA:HB2	1.96	0.48
3:G:545:GLU:HG2	3:G:546:LEU:HG	1.95	0.48
3:G:721:LEU:HD13	3:G:755:MET:HE3	1.95	0.48
3:G:1138:ILE:HG22	3:G:1157:LYS:HB3	1.96	0.48
4:I:157:ALA:H	4:I:196:LEU:HD23	1.79	0.48
4:I:373:ARG:HB3	4:I:385:LEU:HD11	1.96	0.48
4:I:412:HIS:CD2	4:I:434:VAL:HG21	2.48	0.48
4:I:764:ARG:HE	4:I:772:ASP:HB2	1.78	0.48
4:I:1142:LEU:HD22	4:I:1160:LEU:HG	1.95	0.48
5:L:600:LEU:HB3	5:L:619:VAL:HG13	1.96	0.48
1:C:639:LEU:O	1:C:643:MET:N	2.45	0.47
1:C:1071:LEU:O	1:C:1075:ALA:HB3	2.14	0.47
2:E:547:LEU:HB3	2:E:574:VAL:HG13	1.96	0.47
2:E:635:ARG:O	2:E:658:ARG:NH2	2.46	0.47
2:E:919:ARG:HH21	2:E:929:GLN:HB2	1.79	0.47
2:E:1006:ILE:HD13	2:E:1024:HIS:HB3	1.96	0.47
3:G:578:LEU:HD23	3:G:651:ILE:HG12	1.96	0.47
3:G:790:ALA:H	3:G:794:VAL:HG23	1.78	0.47
3:G:1053:PHE:O	3:G:1057:GLN:N	2.46	0.47
3:G:1072:LEU:HA	3:G:1075:LYS:HE3	1.96	0.47
4:I:437:ARG:NH1	4:I:478:ASP:OD1	2.35	0.47
4:I:450:GLU:HG2	4:I:451:THR:HG23	1.95	0.47
4:I:846:ARG:NH1	4:I:876:GLU:OE2	2.47	0.47
5:L:85:ILE:HG21	5:L:125:TRP:CH2	2.49	0.47
5:L:236:ILE:N	5:L:248:TYR:O	2.45	0.47
5:L:724:ASP:N	5:L:724:ASP:OD1	2.45	0.47
5:L:796:ALA:C	5:L:800:LEU:HB2	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:143:ILE:HG23	1:C:151:ARG:HG3	1.96	0.47
1:C:805:TRP:CE3	1:C:824:CYS:HA	2.49	0.47
1:C:1021:ASP:N	1:C:1021:ASP:OD1	2.47	0.47
2:E:842:GLU:O	2:E:846:LEU:HG	2.14	0.47
3:G:431:LYS:HA	3:G:431:LYS:HD2	1.66	0.47
3:G:621:PHE:HB2	3:G:629:ARG:HH21	1.78	0.47
3:G:704:MET:HE3	3:G:707:PHE:CG	2.50	0.47
3:G:751:ASN:HD22	3:G:769:LEU:HD21	1.79	0.47
4:I:175:LEU:HD12	4:I:185:LYS:HB2	1.95	0.47
5:L:523:ASP:N	5:L:523:ASP:OD1	2.46	0.47
1:C:30:ALA:HA	1:C:40:VAL:HA	1.96	0.47
2:E:968:VAL:HG22	2:E:994:LEU:HD11	1.94	0.47
3:G:403:LEU:HD22	3:G:447:VAL:HG11	1.96	0.47
4:I:494:ALA:HB2	4:I:533:LEU:HB3	1.97	0.47
4:I:648:LEU:HD21	4:I:665:ALA:HB3	1.96	0.47
4:I:676:VAL:O	4:I:680:LYS:HG2	2.13	0.47
5:L:587:TRP:HA	5:L:590:LEU:CD1	2.40	0.47
1:C:254:THR:HB	1:C:291:GLN:HE22	1.80	0.47
1:C:548:SER:OG	1:C:549:LYS:N	2.45	0.47
2:E:44:TYR:HB2	2:E:116:PHE:HD1	1.79	0.47
4:I:208:ARG:H	4:I:229:THR:HB	1.79	0.47
4:I:290:LEU:HD21	4:I:293:VAL:HB	1.95	0.47
4:I:1189:LEU:HD13	4:I:1210:THR:HA	1.97	0.47
5:L:328:CYS:SG	5:L:353:TYR:OH	2.66	0.47
5:L:383:THR:OG1	5:L:386:HIS:N	2.44	0.47
5:L:429:LEU:N	5:L:441:ILE:O	2.42	0.47
1:C:148:ASP:OD1	1:C:148:ASP:N	2.45	0.47
1:C:532:HIS:HA	1:C:576:MET:H	1.80	0.47
1:C:651:LEU:HA	1:C:654:MET:HG2	1.94	0.47
1:C:691:ARG:HH21	1:C:710:PHE:HA	1.79	0.47
1:C:691:ARG:HH12	1:C:714:ALA:N	2.12	0.47
3:G:275:VAL:H	3:G:288:LEU:H	1.61	0.47
3:G:484:VAL:HG12	3:G:490:VAL:HG22	1.96	0.47
3:G:949:ASP:HB2	3:G:957:ASN:HA	1.97	0.47
3:G:1232:TYR:HD2	3:G:1256:ALA:HA	1.79	0.47
4:I:913:SER:O	4:I:917:LEU:HB3	2.15	0.47
5:L:647:GLN:HE22	5:L:678:TRP:HD1	1.60	0.47
1:C:432:HIS:CD2	1:C:523:LEU:HD22	2.49	0.47
1:C:681:VAL:HG11	1:C:690:TRP:CG	2.50	0.47
1:C:804:LYS:HD3	1:C:804:LYS:HA	1.71	0.47
2:E:263:MET:HB3	2:E:476:LEU:HD11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:638:LEU:HG	2:E:653:PRO:HD3	1.95	0.47
2:E:685:ILE:HG13	2:E:708:LEU:HD22	1.96	0.47
2:E:994:LEU:HD21	2:E:1001:ASN:HD22	1.79	0.47
3:G:1128:ALA:HB1	3:G:1134:ARG:HG2	1.96	0.47
3:G:1200:LEU:HD22	3:G:1203:LEU:HD11	1.97	0.47
4:I:203:GLU:OE2	4:I:227:GLN:NE2	2.48	0.47
4:I:792:HIS:HA	4:I:795:MET:HG3	1.96	0.47
4:I:881:TYR:O	4:I:886:GLN:N	2.44	0.47
5:L:106:SER:HG	5:L:146:TRP:CD1	2.32	0.47
5:L:807:ARG:HH22	5:L:876:LYS:HE2	1.80	0.47
1:C:37:LEU:HD21	1:C:39:LYS:HE2	1.96	0.47
1:C:56:GLU:HA	1:C:621:THR:H	1.79	0.47
1:C:716:TYR:HE2	5:L:665:MET:HG3	1.80	0.47
1:C:1097:ILE:HG23	1:C:1101:LYS:HE2	1.96	0.47
2:E:495:LEU:HG	2:E:543:LEU:HD12	1.96	0.47
2:E:974:VAL:O	2:E:978:HIS:ND1	2.48	0.47
2:E:1110:ILE:O	2:E:1114:VAL:HG22	2.14	0.47
2:E:1128:GLU:HB2	2:E:1247:ILE:HG22	1.97	0.47
2:E:1247:ILE:HD13	2:E:1252:TYR:HA	1.96	0.47
2:E:1322:VAL:HG22	2:E:1353:LEU:H	1.79	0.47
3:G:19:TRP:CZ3	3:G:29:LEU:HB2	2.50	0.47
3:G:526:LYS:HB2	3:G:535:HIS:HB2	1.96	0.47
3:G:902:ARG:HH11	5:L:916:PRO:HD3	1.78	0.47
3:G:974:PRO:HA	3:G:977:ILE:HG12	1.97	0.47
3:G:1164:LYS:O	3:G:1166:LYS:N	2.48	0.47
4:I:513:LEU:HB2	4:I:520:VAL:HG22	1.96	0.47
4:I:851:LEU:HA	4:I:854:GLN:HG2	1.96	0.47
4:I:1127:ARG:HA	4:I:1130:GLN:HB2	1.95	0.47
4:I:1306:GLU:OE2	4:I:1311:LYS:NZ	2.44	0.47
5:L:21:CYS:HA	5:L:37:ILE:HG12	1.97	0.47
5:L:230:PHE:N	5:L:235:TYR:O	2.47	0.47
5:L:793:TRP:HB2	5:L:814:TYR:CE1	2.50	0.47
5:L:933:LEU:HB3	5:L:967:LEU:HD11	1.96	0.47
1:C:688:ARG:NH1	1:C:692:ASN:OD1	2.47	0.47
3:G:218:VAL:HG21	3:G:257:VAL:HG21	1.97	0.47
3:G:315:GLY:HA2	3:G:321:VAL:HG22	1.97	0.47
3:G:720:ALA:HB1	3:G:752:MET:O	2.14	0.47
3:G:977:ILE:HA	3:G:980:TYR:CD2	2.49	0.47
3:G:988:HIS:O	3:G:993:ALA:N	2.48	0.47
4:I:28:LEU:O	4:I:40:PHE:N	2.43	0.47
4:I:500:VAL:HB	4:I:512:TYR:HD2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:761:LEU:HB2	4:I:776:LEU:HD22	1.97	0.47
4:I:786:ALA:HB1	4:I:816:LEU:HG	1.96	0.47
4:I:1282:CYS:O	4:I:1286:GLN:N	2.48	0.47
5:L:350:VAL:HG11	5:L:387:VAL:HG11	1.97	0.47
5:L:622:THR:HG21	5:L:639:ILE:HG13	1.97	0.47
5:L:659:VAL:HG21	5:L:687:ARG:HG3	1.96	0.47
5:L:862:PHE:HA	5:L:865:TYR:HB3	1.97	0.47
5:L:934:MET:O	5:L:940:ARG:NH1	2.48	0.47
1:C:240:LEU:HD21	1:C:270:LEU:HD22	1.97	0.47
1:C:384:GLN:HG2	1:C:427:ALA:HA	1.97	0.47
1:C:941:ASP:HA	1:C:944:LYS:HE2	1.97	0.47
2:E:484:PRO:O	2:E:488:THR:OG1	2.27	0.47
2:E:588:LEU:HD21	2:E:608:GLN:HG3	1.97	0.47
2:E:1023:TYR:O	2:E:1026:GLN:HG3	2.14	0.47
3:G:520:ASN:O	3:G:541:LEU:N	2.40	0.47
3:G:808:LYS:HA	3:G:811:TYR:CD2	2.50	0.47
4:I:731:LEU:HD12	4:I:751:PHE:CE1	2.50	0.47
4:I:797:GLU:OE2	4:I:834:GLY:HA2	2.15	0.47
4:I:924:GLU:OE1	4:I:936:TYR:OH	2.31	0.47
5:L:1:MET:HE2	5:L:310:MET:HE3	1.96	0.47
5:L:773:THR:HG22	5:L:776:LYS:HZ2	1.80	0.47
1:C:18:ARG:N	1:C:32:GLY:O	2.48	0.47
1:C:263:TRP:HZ3	1:C:295:HIS:HA	1.79	0.47
3:G:968:GLU:HG3	3:G:973:ILE:HG12	1.97	0.47
3:G:1146:LYS:HG3	3:G:1171:LEU:HG	1.96	0.47
3:G:1158:TYR:HA	3:G:1162:GLY:HA3	1.97	0.47
3:G:1289:ARG:NH2	3:G:1292:ILE:HG21	2.30	0.47
4:I:437:ARG:HH11	4:I:464:HIS:CE1	2.32	0.47
4:I:759:ALA:HA	4:I:762:GLU:CD	2.40	0.47
5:L:875:ILE:HD12	5:L:889:ALA:HB1	1.96	0.47
2:E:18:PHE:O	2:E:22:GLN:NE2	2.48	0.46
2:E:500:GLY:O	2:E:542:TYR:OH	2.31	0.46
2:E:588:LEU:HD11	2:E:608:GLN:HG3	1.97	0.46
2:E:1123:ASP:H	2:E:1237:ARG:HD2	1.80	0.46
3:G:267:SER:OG	3:G:276:ARG:O	2.28	0.46
3:G:275:VAL:HG22	3:G:300:VAL:HG21	1.97	0.46
3:G:520:ASN:OD1	3:G:547:LYS:NZ	2.48	0.46
3:G:863:GLU:HA	3:G:866:ARG:HE	1.80	0.46
3:G:1272:VAL:HA	3:G:1275:ILE:HB	1.96	0.46
4:I:23:PRO:HG3	4:I:74:PRO:HA	1.97	0.46
4:I:413:ALA:N	4:I:424:TYR:O	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:465:PRO:HD2	4:I:477:LEU:HG	1.96	0.46
4:I:802:TYR:O	4:I:806:LYS:HB2	2.15	0.46
5:L:349:LYS:HD2	5:L:370:LYS:HE2	1.96	0.46
5:L:654:THR:HG22	5:L:687:ARG:HB2	1.97	0.46
1:C:234:ASP:OD1	1:C:234:ASP:N	2.42	0.46
1:C:591:ARG:HA	1:C:591:ARG:HD2	1.71	0.46
1:C:762:ILE:O	1:C:766:MET:HB2	2.14	0.46
1:C:968:GLU:HB2	1:C:1024:TRP:HB3	1.98	0.46
2:E:1034:ASN:HD21	2:E:1075:TYR:HB2	1.79	0.46
3:G:6:THR:O	3:G:8:LYS:NZ	2.42	0.46
3:G:738:ARG:HH22	4:I:863:GLU:HA	1.79	0.46
3:G:819:LEU:HD22	3:G:822:GLN:HE21	1.80	0.46
3:G:1310:ILE:HD13	3:G:1323:ILE:HD11	1.97	0.46
4:I:436:ARG:HD3	4:I:436:ARG:HA	1.72	0.46
4:I:482:PRO:HG3	4:I:490:ILE:HD12	1.97	0.46
4:I:595:LEU:N	4:I:607:GLN:O	2.47	0.46
4:I:760:ALA:O	4:I:764:ARG:HG2	2.14	0.46
4:I:840:LEU:HD23	4:I:867:ILE:HG22	1.97	0.46
4:I:868:LEU:HD13	4:I:876:GLU:HB2	1.98	0.46
4:I:1173:VAL:HG21	4:I:1189:LEU:HG	1.95	0.46
4:I:1211:VAL:HG12	4:I:1226:TYR:HB3	1.98	0.46
4:I:1273:MET:HG3	4:I:1284:SER:HB3	1.96	0.46
5:L:307:ARG:HD3	5:L:332:VAL:HB	1.96	0.46
1:C:32:GLY:HA3	1:C:80:VAL:HG21	1.97	0.46
1:C:364:PHE:N	1:C:373:TYR:O	2.48	0.46
2:E:111:LEU:HD12	2:E:130:VAL:HG12	1.97	0.46
2:E:229:ARG:HD3	2:E:229:ARG:H	1.80	0.46
2:E:346:MET:HB2	2:E:648:ARG:HB2	1.97	0.46
3:G:209:TYR:HB3	3:G:214:GLN:HB2	1.95	0.46
3:G:503:PRO:HA	3:G:517:THR:HA	1.97	0.46
3:G:1034:TYR:CG	3:G:1039:LYS:HB3	2.50	0.46
4:I:224:TYR:HB3	4:I:235:PRO:HB3	1.98	0.46
5:L:501:TRP:HZ3	5:L:507:ASP:HA	1.80	0.46
5:L:844:LEU:HG	5:L:863:TYR:HB3	1.97	0.46
1:C:56:GLU:HG3	1:C:620:VAL:HA	1.96	0.46
1:C:123:ASP:HB3	1:C:164:VAL:H	1.80	0.46
1:C:442:TYR:OH	1:C:468:GLU:OE1	2.28	0.46
1:C:878:ILE:HG12	1:C:893:LEU:HD23	1.97	0.46
1:C:914:LEU:HD23	1:C:919:VAL:HG22	1.96	0.46
2:E:203:LEU:HD21	2:E:234:LEU:HA	1.98	0.46
3:G:229:ARG:HG3	3:G:236:TRP:CE2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:712:ASP:OD1	3:G:779:ARG:NH2	2.49	0.46
3:G:738:ARG:HH21	4:I:866:LEU:HD13	1.79	0.46
3:G:749:TRP:CE3	3:G:752:MET:SD	3.09	0.46
4:I:203:GLU:HG2	4:I:273:HIS:HA	1.97	0.46
5:L:104:CYS:SG	5:L:144:ILE:HG12	2.56	0.46
5:L:378:ASN:ND2	5:L:392:GLU:OE2	2.48	0.46
5:L:410:LEU:HD12	5:L:414:ILE:HD11	1.98	0.46
1:C:20:ILE:HG13	1:C:31:CYS:HA	1.96	0.46
1:C:586:ASP:HB2	1:C:605:LYS:HD2	1.97	0.46
2:E:238:GLU:O	2:E:241:THR:OG1	2.25	0.46
2:E:492:ARG:HD3	2:E:648:ARG:HH22	1.81	0.46
2:E:1198:VAL:HG23	2:E:1199:LEU:HG	1.98	0.46
3:G:274:VAL:HB	3:G:287:VAL:HB	1.98	0.46
3:G:516:VAL:HG21	3:G:541:LEU:HD22	1.96	0.46
3:G:1134:ARG:HH21	3:G:1160:GLN:HG2	1.81	0.46
4:I:12:LEU:HB3	4:I:32:GLY:HA3	1.97	0.46
4:I:31:ALA:HB2	4:I:37:VAL:HG22	1.97	0.46
4:I:114:MET:HB3	4:I:125:VAL:HG13	1.97	0.46
4:I:449:ASN:ND2	4:I:450:GLU:OE1	2.48	0.46
4:I:460:HIS:HB3	4:I:480:VAL:HG13	1.98	0.46
4:I:836:ALA:O	4:I:840:LEU:HB2	2.16	0.46
4:I:1080:ARG:HA	4:I:1080:ARG:HD3	1.82	0.46
5:L:235:TYR:HB3	5:L:247:LEU:HD11	1.97	0.46
5:L:241:THR:HA	5:L:264:TRP:CD1	2.51	0.46
5:L:414:ILE:HG23	5:L:431:VAL:HG13	1.97	0.46
5:L:799:LEU:C	5:L:801:HIS:H	2.23	0.46
5:L:930:ARG:HG3	5:L:964:ALA:HB2	1.98	0.46
1:C:420:GLU:HB2	1:C:489:ARG:HH21	1.79	0.46
1:C:749:GLU:HG3	1:C:761:ALA:HB1	1.97	0.46
2:E:904:GLN:HB3	2:E:940:LEU:HD21	1.97	0.46
2:E:937:CYS:HB2	2:E:956:LEU:HD23	1.98	0.46
3:G:757:ILE:HG21	3:G:784:ALA:HA	1.97	0.46
3:G:951:VAL:HA	3:G:955:ALA:HA	1.98	0.46
3:G:1093:LEU:O	3:G:1098:GLN:N	2.39	0.46
3:G:1235:CYS:O	3:G:1239:GLU:CB	2.63	0.46
4:I:1101:ARG:HA	4:I:1104:PHE:HB2	1.96	0.46
4:I:1120:ARG:NH1	4:I:1124:GLU:OE1	2.48	0.46
4:I:1270:PHE:HE1	4:I:1351:ILE:HA	1.79	0.46
5:L:121:ASP:HB2	5:L:134:LYS:HB3	1.97	0.46
5:L:342:LEU:O	5:L:353:TYR:N	2.40	0.46
5:L:566:LEU:HD22	5:L:589:GLN:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:752:ARG:O	5:L:756:MET:HG3	2.16	0.46
3:G:468:ILE:HG12	3:G:470:ASN:H	1.80	0.46
3:G:612:LEU:HB2	3:G:644:PHE:CE1	2.51	0.46
3:G:613:LEU:HG	3:G:615:VAL:HG22	1.96	0.46
3:G:710:MET:HE1	3:G:721:LEU:HB2	1.98	0.46
3:G:717:THR:HG23	3:G:721:LEU:HD12	1.97	0.46
3:G:763:ASP:O	3:G:767:HIS:ND1	2.47	0.46
3:G:801:LEU:H	3:G:803:MET:HG3	1.81	0.46
4:I:72:TRP:CE2	4:I:79:LEU:HD13	2.51	0.46
4:I:398:GLU:OE2	4:I:429:LYS:NZ	2.48	0.46
4:I:547:ASP:OD1	4:I:547:ASP:N	2.45	0.46
5:L:799:LEU:CD1	5:L:802:ALA:HB2	2.41	0.46
1:C:124:MET:HE2	1:C:133:ILE:HD11	1.98	0.46
2:E:345:MET:HG3	2:E:485:ALA:HB1	1.97	0.46
3:G:735:GLU:O	3:G:739:SER:OG	2.31	0.46
3:G:883:LEU:HG	3:G:885:GLU:H	1.80	0.46
5:L:27:LYS:HG3	5:L:67:TYR:CZ	2.50	0.46
5:L:94:LEU:HG	5:L:125:TRP:HE1	1.81	0.46
5:L:143:SER:HB2	5:L:185:ILE:HG12	1.97	0.46
5:L:294:SER:O	5:L:307:ARG:NH2	2.48	0.46
5:L:724:ASP:H	5:L:752:ARG:HH21	1.62	0.46
5:L:787:TYR:CD2	5:L:798:LEU:HB3	2.50	0.46
1:C:425:TYR:HB2	1:C:436:ALA:HB3	1.98	0.46
2:E:1047:ARG:HH11	2:E:1052:LEU:HD21	1.81	0.46
2:E:1167:TYR:HD1	2:E:1170:MET:HE1	1.80	0.46
3:G:152:ARG:NH2	3:G:177:ASP:O	2.49	0.46
3:G:212:ARG:HH21	3:G:280:PHE:HB3	1.81	0.46
3:G:279:ASN:HD21	3:G:281:ASP:HB3	1.80	0.46
3:G:555:ARG:CZ	3:G:605:PHE:H	2.29	0.46
3:G:605:PHE:HA	3:G:613:LEU:HA	1.97	0.46
3:G:724:PHE:CD2	3:G:755:MET:HG3	2.51	0.46
3:G:1113:ILE:HB	3:G:1118:ALA:HB2	1.96	0.46
4:I:1077:GLU:O	4:I:1080:ARG:NE	2.48	0.46
5:L:387:VAL:HG23	5:L:400:PHE:HD1	1.80	0.46
1:C:534:LEU:HB3	1:C:552:ILE:HD13	1.98	0.46
2:E:1086:ILE:HD12	2:E:1086:ILE:N	2.30	0.46
3:G:704:MET:HG3	3:G:707:PHE:CD1	2.51	0.46
3:G:1043:ALA:HA	3:G:1046:MET:CG	2.41	0.46
4:I:105:GLU:HB2	4:I:144:PRO:HB3	1.98	0.46
4:I:654:VAL:HG12	4:I:661:LYS:HD2	1.98	0.46
4:I:1122:ALA:HA	4:I:1125:MET:HE3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:250:ARG:NH1	5:L:251:ASP:OD1	2.49	0.46
5:L:428:GLY:HA2	5:L:442:PHE:HA	1.98	0.46
5:L:430:LEU:HD12	5:L:430:LEU:HA	1.81	0.46
5:L:902:VAL:HG11	5:L:942:VAL:HG22	1.98	0.46
1:C:197:LEU:HB3	1:C:200:ASN:HB2	1.99	0.45
1:C:214:TRP:HE1	1:C:228:VAL:HG23	1.81	0.45
1:C:891:VAL:HA	1:C:902:ILE:HG21	1.98	0.45
2:E:1231:GLU:O	2:E:1235:PHE:N	2.40	0.45
3:G:412:ARG:NH1	3:G:449:GLU:O	2.49	0.45
4:I:745:GLY:O	4:I:748:GLN:HG3	2.16	0.45
4:I:1113:GLY:HA3	4:I:1367:SER:HB3	1.98	0.45
5:L:229:TYR:HB3	5:L:233:GLY:HA2	1.97	0.45
5:L:633:GLN:HB2	5:L:652:LEU:HD22	1.97	0.45
5:L:669:LEU:HD23	5:L:669:LEU:HA	1.82	0.45
5:L:856:ARG:O	5:L:858:ALA:N	2.47	0.45
5:L:909:VAL:HG12	5:L:950:ASN:HB3	1.98	0.45
1:C:509:LEU:HB3	1:C:521:TYR:HB2	1.97	0.45
1:C:1076:PHE:O	1:C:1079:GLN:NE2	2.49	0.45
2:E:10:HIS:HE1	2:E:150:ILE:HD11	1.81	0.45
2:E:461:ILE:HG22	2:E:487:ILE:HA	1.98	0.45
2:E:653:PRO:HB2	2:E:658:ARG:HD2	1.98	0.45
2:E:767:TYR:HD2	2:E:803:LEU:HD22	1.81	0.45
3:G:627:ASP:OD1	3:G:627:ASP:N	2.48	0.45
3:G:1030:ALA:CB	3:G:1046:MET:HE1	2.47	0.45
3:G:1071:ASN:OD1	3:G:1072:LEU:N	2.50	0.45
3:G:1345:LYS:O	3:G:1349:ALA:N	2.41	0.45
4:I:291:THR:OG1	4:I:336:GLU:HA	2.16	0.45
4:I:738:VAL:HA	4:I:744:TYR:CE1	2.52	0.45
4:I:924:GLU:HB2	4:I:932:ALA:HB2	1.98	0.45
1:C:136:VAL:HG22	1:C:142:VAL:HA	1.98	0.45
2:E:151:ILE:HG13	2:E:172:ALA:HB2	1.98	0.45
2:E:689:ILE:HG13	2:E:704:ALA:HB3	1.97	0.45
3:G:58:ASN:ND2	3:G:62:THR:H	2.13	0.45
3:G:527:VAL:HG12	3:G:532:ALA:HA	1.98	0.45
3:G:609:GLU:OE1	3:G:722:LEU:HB3	2.16	0.45
3:G:989:GLY:O	3:G:1002:LEU:HA	2.16	0.45
3:G:1259:TYR:HA	3:G:1262:LYS:HB2	1.99	0.45
5:L:390:CYS:HA	5:L:395:LEU:HD23	1.98	0.45
5:L:393:LYS:NZ	5:L:411:ASP:O	2.48	0.45
5:L:397:LEU:HD23	5:L:405:GLU:HB2	1.97	0.45
5:L:418:LYS:HZ2	5:L:420:VAL:HA	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:445:GLN:NE2	1:C:524:PRO:HB3	2.19	0.45
2:E:336:VAL:HA	2:E:355:ARG:HH21	1.79	0.45
2:E:709:ALA:HB1	2:E:714:ASP:HB3	1.98	0.45
2:E:1110:ILE:HA	2:E:1113:MET:HE3	1.98	0.45
2:E:1207:MET:HE1	2:E:1241:LEU:HD11	1.98	0.45
3:G:463:SER:H	3:G:475:ARG:HD3	1.81	0.45
3:G:894:ASN:HB3	5:L:854:GLU:HA	1.98	0.45
4:I:296:CYS:SG	4:I:298:SER:OG	2.74	0.45
4:I:329:LEU:HD21	4:I:359:PHE:HZ	1.82	0.45
4:I:489:ASN:O	4:I:505:ARG:N	2.42	0.45
4:I:1103:GLU:O	4:I:1107:LYS:HG2	2.17	0.45
4:I:1189:LEU:HA	4:I:1192:VAL:HG12	1.98	0.45
5:L:135:HIS:CD2	5:L:155:LEU:HD11	2.50	0.45
5:L:155:LEU:O	5:L:163:SER:OG	2.35	0.45
1:C:968:GLU:HA	1:C:1023:ALA:HB1	1.99	0.45
4:I:921:LYS:HA	4:I:921:LYS:HD2	1.78	0.45
4:I:944:ALA:HA	4:I:947:ARG:HB3	1.98	0.45
4:I:1241:VAL:HG23	4:I:1244:LYS:HD3	1.98	0.45
5:L:929:SER:HA	5:L:958:GLN:HG3	1.97	0.45
1:C:270:LEU:N	1:C:293:TYR:O	2.49	0.45
1:C:362:VAL:HG22	1:C:380:LEU:HD22	1.99	0.45
3:G:750:GLU:OE2	3:G:774:HIS:NE2	2.49	0.45
3:G:802:GLY:HA2	4:I:714:ALA:HB3	1.98	0.45
3:G:825:ARG:NH1	3:G:836:VAL:HG11	2.32	0.45
3:G:872:ALA:O	3:G:876:LEU:N	2.47	0.45
3:G:874:CYS:HB3	5:L:842:ARG:HH12	1.82	0.45
4:I:909:ARG:HG3	4:I:910:ILE:HD12	1.97	0.45
4:I:956:PRO:HG3	4:I:978:PHE:CZ	2.51	0.45
4:I:1168:HIS:CE1	4:I:1172:LEU:HD22	2.51	0.45
4:I:1220:LYS:HA	4:I:1223:ALA:HB3	1.98	0.45
1:C:445:GLN:NE2	1:C:448:THR:HA	2.32	0.45
1:C:775:GLU:OE2	1:C:779:ARG:NE	2.50	0.45
2:E:27:GLU:O	2:E:31:LYS:HG2	2.16	0.45
2:E:279:LEU:HD11	2:E:317:ILE:HB	1.99	0.45
2:E:1107:SER:OG	2:E:1155:ASP:OD2	2.29	0.45
3:G:967:TYR:O	3:G:972:ARG:N	2.50	0.45
3:G:1192:ILE:HA	3:G:1195:MET:HG3	1.99	0.45
4:I:114:MET:HA	4:I:125:VAL:HA	1.99	0.45
4:I:468:VAL:HG13	4:I:472:HIS:HB2	1.98	0.45
4:I:601:LEU:HD22	4:I:699:LEU:HG	1.99	0.45
4:I:809:TYR:O	4:I:813:LEU:HG	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:842:LEU:HA	4:I:842:LEU:HD23	1.76	0.45
4:I:858:GLN:NE2	4:I:884:ALA:O	2.44	0.45
5:L:783:LEU:HD12	5:L:799:LEU:HG	1.99	0.45
5:L:912:SER:HB3	5:L:918:ARG:HH21	1.80	0.45
1:C:17:LEU:O	1:C:325:SER:OG	2.35	0.45
2:E:37:VAL:HG23	2:E:112:HIS:ND1	2.32	0.45
2:E:359:ALA:O	2:E:363:ASP:N	2.48	0.45
2:E:1107:SER:OG	2:E:1152:ARG:O	2.35	0.45
3:G:273:ASN:HB2	3:G:290:LEU:HB2	1.98	0.45
3:G:611:LYS:HB2	3:G:611:LYS:HE3	1.67	0.45
3:G:810:LEU:HA	3:G:813:ALA:HB3	1.98	0.45
4:I:421:ALA:HB3	4:I:437:ARG:HB2	1.99	0.45
4:I:709:ARG:NE	4:I:717:VAL:HG12	2.31	0.45
5:L:501:TRP:CE3	5:L:509:PHE:HB3	2.52	0.45
5:L:749:THR:OG1	5:L:750:ASP:N	2.50	0.45
1:C:595:ASP:OD2	1:C:632:LEU:N	2.47	0.45
1:C:739:ALA:HB1	1:C:744:ARG:HB2	1.99	0.45
2:E:378:ILE:HB	2:E:446:LYS:HG3	1.99	0.45
2:E:929:GLN:O	2:E:933:THR:HG22	2.17	0.45
2:E:1322:VAL:HG22	2:E:1353:LEU:N	2.32	0.45
3:G:182:ALA:HB1	3:G:203:VAL:HG23	1.98	0.45
3:G:186:TRP:N	3:G:194:GLY:O	2.39	0.45
3:G:578:LEU:HB2	3:G:593:PHE:HE2	1.82	0.45
3:G:652:LEU:HD22	3:G:730:THR:HA	1.98	0.45
3:G:973:ILE:O	3:G:977:ILE:HG12	2.17	0.45
4:I:373:ARG:HH11	4:I:385:LEU:HD21	1.82	0.45
4:I:541:ARG:HG3	4:I:555:ASN:HA	1.97	0.45
5:L:345:GLN:NE2	5:L:350:VAL:HG22	2.30	0.45
5:L:458:VAL:HG13	5:L:472:VAL:HG13	1.99	0.45
5:L:772:GLU:HA	5:L:775:LEU:HB2	1.99	0.45
1:C:199:CYS:HB3	1:C:239:GLN:HG2	1.98	0.45
2:E:282:LEU:O	2:E:286:MET:HG2	2.17	0.45
2:E:913:GLN:O	2:E:917:LYS:N	2.37	0.45
3:G:513:LEU:O	3:G:525:LEU:N	2.37	0.45
3:G:797:VAL:HA	3:G:800:HIS:CE1	2.51	0.45
4:I:412:HIS:HA	4:I:425:SER:HA	1.98	0.45
5:L:243:LYS:HD3	5:L:263:SER:HA	1.99	0.45
5:L:271:ARG:HB3	5:L:274:HIS:HB2	1.99	0.45
1:C:665:THR:HG21	1:C:689:LEU:HD13	1.98	0.44
2:E:491:VAL:O	2:E:495:LEU:HD13	2.17	0.44
2:E:705:ASP:OD1	2:E:705:ASP:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:737:MET:HE2	2:E:772:MET:SD	2.57	0.44
2:E:1350:ARG:HH21	2:E:1353:LEU:HD13	1.82	0.44
3:G:86:SER:OG	3:G:97:GLU:OE1	2.35	0.44
3:G:571:GLU:OE2	3:G:574:ARG:NH2	2.48	0.44
4:I:1027:TYR:O	4:I:1031:ALA:CB	2.65	0.44
4:I:1267:ASP:HA	4:I:1274:PRO:HA	1.99	0.44
5:L:184:SER:OG	5:L:198:GLY:O	2.35	0.44
5:L:725:ARG:NH1	5:L:725:ARG:O	2.50	0.44
5:L:783:LEU:O	5:L:787:TYR:N	2.48	0.44
1:C:6:SER:OG	1:C:332:PHE:O	2.29	0.44
1:C:589:ASP:H	1:C:603:MET:HB2	1.83	0.44
1:C:594:ASP:N	1:C:629:PHE:O	2.36	0.44
1:C:728:LEU:HB3	1:C:734:GLN:HG2	1.99	0.44
1:C:838:MET:HE1	1:C:851:ILE:HB	1.99	0.44
2:E:103:ARG:HH22	2:E:125:ARG:HH12	1.65	0.44
2:E:234:LEU:HD22	2:E:239:GLN:HE22	1.83	0.44
2:E:1043:ILE:HG23	2:E:1055:VAL:HG13	1.98	0.44
3:G:817:TYR:O	3:G:820:LEU:HB3	2.18	0.44
3:G:901:SER:HB2	3:G:903:GLU:OE1	2.17	0.44
4:I:39:ILE:HG22	4:I:47:TYR:HB3	1.98	0.44
5:L:175:ILE:HG23	5:L:211:GLY:HA2	1.99	0.44
1:C:104:HIS:HB3	1:C:109:PHE:HD2	1.82	0.44
1:C:181:GLU:HG2	1:C:197:LEU:HD11	1.99	0.44
1:C:437:ASN:HB2	1:C:440:VAL:HB	1.99	0.44
1:C:589:ASP:HB3	1:C:603:MET:HG3	1.98	0.44
3:G:618:THR:HB	3:G:636:HIS:HD2	1.82	0.44
3:G:679:LYS:HE2	3:G:700:SER:HB3	1.99	0.44
4:I:495:LEU:HD13	4:I:500:VAL:HG13	2.00	0.44
4:I:572:THR:HG23	4:I:574:MET:HE3	1.99	0.44
4:I:861:PHE:HB3	4:I:884:ALA:HB2	1.98	0.44
4:I:960:TYR:HD1	4:I:991:PHE:HE2	1.63	0.44
4:I:1224:PHE:HE1	4:I:1251:VAL:HA	1.82	0.44
5:L:23:ASP:HB2	5:L:64:CYS:HA	1.98	0.44
5:L:77:GLY:HA2	5:L:83:VAL:HG22	2.00	0.44
5:L:117:ALA:HA	5:L:122:VAL:HA	2.00	0.44
5:L:638:GLU:HA	5:L:641:ALA:HB3	1.99	0.44
5:L:988:VAL:HA	5:L:991:ALA:HB3	1.99	0.44
1:C:293:TYR:HB3	1:C:297:GLY:HA2	2.00	0.44
1:C:931:HIS:O	1:C:935:ALA:N	2.43	0.44
2:E:256:MET:HE3	2:E:296:LEU:HD12	2.00	0.44
2:E:258:GLN:HB2	2:E:282:LEU:HD22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:1192:ASP:OD1	2:E:1192:ASP:N	2.51	0.44
2:E:1199:LEU:HD22	2:E:1218:GLN:HE21	1.81	0.44
3:G:721:LEU:HA	3:G:724:PHE:HB3	1.98	0.44
3:G:874:CYS:O	3:G:877:VAL:HG22	2.17	0.44
3:G:1015:ILE:HA	3:G:1018:ALA:HB3	1.99	0.44
4:I:383:MET:HB3	4:I:399:LEU:HD11	2.00	0.44
4:I:1183:THR:HB	4:I:1261:LEU:HD23	2.00	0.44
5:L:653:PHE:CD1	5:L:657:GLY:HA3	2.52	0.44
1:C:349:VAL:HG12	1:C:383:ILE:HD13	1.98	0.44
2:E:343:LYS:HE2	2:E:351:ASN:HB2	1.99	0.44
2:E:457:LEU:HD13	2:E:490:VAL:HG22	1.99	0.44
2:E:1007:MET:HA	2:E:1010:GLU:HG3	1.99	0.44
2:E:1009:ALA:HA	2:E:1012:MET:SD	2.57	0.44
2:E:1216:ARG:HH21	2:E:1246:HIS:HA	1.82	0.44
3:G:13:ALA:HB1	3:G:375:ILE:HG12	1.98	0.44
3:G:843:ILE:HG12	5:L:822:ASP:HA	2.00	0.44
3:G:1026:GLN:CD	3:G:1029:LYS:HG3	2.42	0.44
3:G:1188:ARG:NH1	3:G:1193:TYR:OH	2.51	0.44
4:I:73:ASP:HB3	4:I:116:TRP:CD2	2.52	0.44
4:I:269:VAL:HG21	4:I:319:TYR:CZ	2.53	0.44
4:I:574:MET:HE1	4:I:586:GLY:H	1.81	0.44
4:I:1307:CYS:N	4:I:1312:PHE:O	2.49	0.44
5:L:107:TYR:CZ	5:L:114:LEU:HB2	2.53	0.44
5:L:511:TYR:CE2	5:L:518:SER:HB2	2.53	0.44
5:L:559:SER:HA	5:L:562:MET:HB2	1.98	0.44
5:L:995:ILE:HG23	5:L:996:ARG:HG3	1.99	0.44
1:C:177:THR:N	1:C:181:GLU:O	2.49	0.44
1:C:1071:LEU:O	1:C:1075:ALA:CB	2.66	0.44
2:E:700:ARG:HG2	2:E:704:ALA:N	2.32	0.44
2:E:877:LEU:O	2:E:881:VAL:HG23	2.17	0.44
3:G:164:ASP:OD1	3:G:164:ASP:N	2.49	0.44
3:G:708:GLN:O	3:G:755:MET:HE2	2.18	0.44
3:G:883:LEU:HD12	3:G:912:LEU:HD12	1.99	0.44
3:G:1093:LEU:HB3	3:G:1098:GLN:HB2	2.00	0.44
3:G:1267:ASP:OD2	3:G:1271:ARG:NH2	2.50	0.44
4:I:648:LEU:O	4:I:656:ARG:NH2	2.37	0.44
4:I:980:LEU:HD21	4:I:1000:GLN:CG	2.48	0.44
1:C:729:ASP:OD1	1:C:729:ASP:N	2.51	0.44
1:C:775:GLU:HG2	1:C:814:GLN:HG2	2.00	0.44
2:E:197:MET:HG3	2:E:206:CYS:HB2	2.00	0.44
3:G:413:PRO:HA	3:G:414:PRO:HD3	1.92	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:653:LEU:HD11	3:G:656:TYR:CE1	2.53	0.44
3:G:725:SER:HA	3:G:728:LEU:HB2	2.00	0.44
3:G:952:THR:OG1	3:G:956:ASP:OD2	2.29	0.44
4:I:816:LEU:HD11	4:I:827:LEU:HG	1.99	0.44
4:I:1213:GLU:OE2	4:I:1216:ARG:NH2	2.50	0.44
5:L:143:SER:O	5:L:156:GLY:N	2.50	0.44
5:L:304:TYR:CZ	5:L:306:TYR:HB3	2.52	0.44
5:L:386:HIS:CD2	5:L:425:ARG:HD3	2.52	0.44
5:L:717:TYR:HA	5:L:720:ALA:HB3	1.99	0.44
1:C:445:GLN:HE21	1:C:448:THR:HA	1.83	0.44
3:G:589:HIS:CG	3:G:650:GLY:HA2	2.53	0.44
3:G:716:LYS:HD2	3:G:719:ARG:HH21	1.83	0.44
4:I:793:GLY:O	4:I:797:GLU:N	2.51	0.44
4:I:871:LEU:HD23	4:I:871:LEU:HA	1.81	0.44
4:I:1076:VAL:HG22	4:I:1084:LEU:HG	1.99	0.44
4:I:1156:PRO:HB3	4:I:1160:LEU:HD13	2.00	0.44
5:L:334:LYS:HD2	5:L:334:LYS:HA	1.81	0.44
5:L:468:ASN:HA	5:L:484:LEU:HD12	2.00	0.44
5:L:518:SER:HB3	5:L:526:LEU:HD11	1.99	0.44
5:L:966:LYS:HA	5:L:969:ARG:HH21	1.82	0.44
1:C:944:LYS:HG2	1:C:1061:LEU:HA	1.99	0.44
2:E:896:GLU:HB3	2:E:899:GLY:HA3	2.00	0.44
3:G:403:LEU:HD11	3:G:429:LEU:HD13	2.00	0.44
3:G:1080:PHE:HB3	3:G:1089:ALA:HB2	2.00	0.44
4:I:787:THR:O	4:I:790:LYS:N	2.50	0.44
4:I:835:ILE:O	4:I:839:THR:OG1	2.36	0.44
4:I:950:LEU:HD22	4:I:978:PHE:CG	2.53	0.44
5:L:632:GLU:HA	5:L:635:LEU:HD12	2.00	0.44
1:C:240:LEU:HD11	1:C:270:LEU:HD22	2.00	0.43
1:C:599:LEU:HA	1:C:611:PHE:O	2.18	0.43
1:C:822:VAL:HG11	1:C:851:ILE:HG12	2.00	0.43
2:E:121:LYS:HA	2:E:121:LYS:HD2	1.73	0.43
2:E:811:LEU:HB3	2:E:816:ASP:O	2.18	0.43
3:G:417:LEU:HB2	3:G:453:ILE:HB	1.99	0.43
3:G:603:LEU:HD23	3:G:615:VAL:HG13	2.00	0.43
3:G:723:ASP:HB3	3:G:735:GLU:HB3	2.00	0.43
3:G:1205:TRP:CZ3	3:G:1238:ILE:HG13	2.53	0.43
3:G:1267:ASP:O	3:G:1271:ARG:HG2	2.17	0.43
3:G:1297:GLN:HG2	3:G:1338:ARG:HH22	1.83	0.43
4:I:853:MET:HG3	4:I:861:PHE:HE1	1.81	0.43
4:I:1072:ALA:O	4:I:1076:VAL:HG23	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:162:ILE:HG21	5:L:195:LEU:HD21	2.00	0.43
5:L:370:LYS:O	5:L:372:GLN:NE2	2.50	0.43
5:L:386:HIS:HA	5:L:399:ASN:HA	2.00	0.43
5:L:452:ILE:HD13	5:L:452:ILE:HA	1.91	0.43
5:L:600:LEU:HD22	5:L:619:VAL:HA	1.99	0.43
5:L:847:LEU:HA	5:L:850:ASN:HB2	2.00	0.43
5:L:888:SER:HA	5:L:891:GLU:HB2	1.99	0.43
1:C:40:VAL:HG11	1:C:108:TRP:NE1	2.33	0.43
1:C:88:LYS:HE3	1:C:147:VAL:HG22	1.99	0.43
1:C:116:ARG:HD2	1:C:143:ILE:HD11	2.00	0.43
1:C:522:SER:HB3	1:C:529:ASP:CG	2.43	0.43
1:C:768:LEU:HB2	5:L:611:ARG:NE	2.33	0.43
2:E:1026:GLN:HB2	2:E:1058:TYR:CZ	2.54	0.43
3:G:1013:VAL:HA	3:G:1016:ASP:HB3	1.99	0.43
4:I:176:THR:HA	4:I:183:THR:HA	2.00	0.43
4:I:259:LEU:HD22	4:I:295:TYR:HB2	2.00	0.43
4:I:730:ASN:HB2	4:I:750:LEU:HB3	2.00	0.43
5:L:793:TRP:HE3	5:L:817:TRP:HB3	1.83	0.43
5:L:814:TYR:HE2	5:L:830:ALA:HB2	1.83	0.43
1:C:737:GLU:HA	1:C:740:VAL:HG12	2.00	0.43
2:E:213:ILE:HA	2:E:216:ARG:HD2	1.99	0.43
2:E:379:MET:HE1	2:E:442:LEU:HD21	2.00	0.43
2:E:881:VAL:HG22	2:E:910:LEU:HD23	2.00	0.43
2:E:892:LYS:HB2	2:E:900:TYR:CD1	2.52	0.43
3:G:505:SER:HB3	3:G:516:VAL:HB	2.01	0.43
3:G:987:SER:HA	3:G:1013:VAL:HG11	1.99	0.43
3:G:1144:VAL:O	3:G:1148:GLN:N	2.51	0.43
4:I:42:ARG:HH21	4:I:402:GLU:HG2	1.83	0.43
4:I:923:LYS:HE3	4:I:928:ARG:HH21	1.83	0.43
4:I:1109:ASN:HB3	4:I:1114:GLN:O	2.18	0.43
4:I:1318:GLN:HA	4:I:1321:ARG:HG3	1.99	0.43
5:L:5:VAL:HG22	5:L:289:PHE:CE1	2.53	0.43
5:L:112:GLN:N	5:L:127:PRO:HG3	2.33	0.43
5:L:224:PRO:HA	5:L:240:GLY:HA3	2.00	0.43
5:L:247:LEU:HD22	5:L:291:LEU:HD23	2.00	0.43
5:L:454:HIS:ND1	5:L:456:ALA:O	2.52	0.43
5:L:646:TYR:HB3	5:L:661:ARG:HH12	1.83	0.43
5:L:743:VAL:HG22	5:L:753:CYS:HB3	2.00	0.43
5:L:783:LEU:C	5:L:786:LEU:H	2.24	0.43
1:C:606:THR:HG23	1:C:623:SER:HB2	1.99	0.43
2:E:343:LYS:HA	2:E:343:LYS:HD2	1.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:884:TRP:NE1	2:E:903:ALA:O	2.52	0.43
3:G:497:ASP:O	3:G:501:GLY:N	2.45	0.43
3:G:1033:LEU:HD13	3:G:1033:LEU:HA	1.81	0.43
3:G:1237:GLN:NE2	3:G:1325:ASP:H	2.17	0.43
4:I:454:ALA:HB2	4:I:495:LEU:HB2	1.99	0.43
4:I:837:ARG:HB3	4:I:867:ILE:HD13	2.01	0.43
4:I:923:LYS:HD3	4:I:923:LYS:HA	1.83	0.43
3:G:387:PHE:N	3:G:668:ILE:O	2.51	0.43
3:G:474:TYR:HD1	3:G:483:VAL:HG22	1.83	0.43
3:G:685:PRO:HA	3:G:692:PHE:HA	1.99	0.43
3:G:1064:THR:HA	3:G:1065:PRO:HD3	1.86	0.43
3:G:1292:ILE:HG12	3:G:1329:LEU:HD11	2.00	0.43
4:I:946:VAL:HA	4:I:949:CYS:HB2	2.01	0.43
4:I:970:GLU:HA	4:I:973:ASN:HB3	2.00	0.43
4:I:985:PHE:O	4:I:988:ALA:N	2.52	0.43
5:L:122:VAL:H	5:L:135:HIS:H	1.65	0.43
5:L:421:GLY:O	5:L:467:ARG:NH1	2.52	0.43
5:L:729:ILE:HA	5:L:732:LYS:NZ	2.34	0.43
1:C:389:PHE:HB2	1:C:428:ILE:HD11	2.00	0.43
1:C:444:TRP:CE2	1:C:446:PHE:HB3	2.53	0.43
1:C:971:LYS:HZ3	1:C:1018:ALA:HA	1.82	0.43
2:E:576:VAL:HG13	2:E:610:LYS:HE2	2.00	0.43
2:E:1148:LEU:HG	2:E:1161:TYR:CZ	2.53	0.43
3:G:441:ARG:HA	3:G:460:GLU:HA	2.00	0.43
3:G:561:ASN:ND2	3:G:584:GLU:HG3	2.33	0.43
4:I:269:VAL:HB	4:I:282:HIS:HB3	2.00	0.43
4:I:717:VAL:HG23	4:I:718:LEU:HD12	2.01	0.43
4:I:1048:SER:HB3	4:I:1057:VAL:HG12	2.00	0.43
4:I:1246:LYS:HA	4:I:1246:LYS:HD3	1.65	0.43
5:L:334:LYS:NZ	5:L:335:ILE:O	2.51	0.43
5:L:625:GLY:HA3	5:L:635:LEU:HD22	2.00	0.43
1:C:146:SER:HB3	1:C:152:LEU:HD11	2.00	0.43
1:C:423:PRO:HB2	1:C:426:LEU:HD22	2.01	0.43
1:C:447:ARG:HE	1:C:452:LYS:HD3	1.84	0.43
1:C:500:ALA:H	1:C:513:ARG:HA	1.83	0.43
2:E:40:PHE:HE1	2:E:55:ALA:HB1	1.84	0.43
2:E:321:MET:HA	2:E:324:ARG:HB2	2.00	0.43
2:E:1039:LEU:O	2:E:1043:ILE:HG12	2.18	0.43
3:G:621:PHE:CE2	3:G:629:ARG:HB3	2.51	0.43
3:G:808:LYS:HB3	3:G:820:LEU:HD12	2.00	0.43
3:G:842:ARG:HB3	5:L:822:ASP:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:1259:TYR:O	3:G:1263:SER:N	2.52	0.43
4:I:1047:TRP:HZ3	4:I:1055:ARG:HH12	1.65	0.43
4:I:1314:ALA:HB1	4:I:1319:PHE:CG	2.53	0.43
5:L:258:ILE:HG23	5:L:291:LEU:HD11	2.01	0.43
5:L:676:LYS:NZ	5:L:700:GLN:HB3	2.33	0.43
1:C:522:SER:HB3	1:C:529:ASP:OD2	2.18	0.43
2:E:227:LYS:HD2	2:E:230:MET:HE3	2.01	0.43
2:E:228:THR:HA	2:E:240:VAL:HG13	2.01	0.43
2:E:457:LEU:HD22	2:E:490:VAL:HG22	2.01	0.43
3:G:446:LYS:NZ	3:G:447:VAL:O	2.50	0.43
3:G:715:ASP:HA	3:G:718:ARG:HG2	2.01	0.43
3:G:721:LEU:HB3	3:G:755:MET:SD	2.59	0.43
3:G:1345:LYS:HD2	3:G:1345:LYS:HA	1.82	0.43
4:I:311:ARG:HB3	4:I:321:GLU:HG2	2.00	0.43
4:I:802:TYR:CD2	4:I:838:THR:HA	2.51	0.43
4:I:1350:LYS:HD2	4:I:1353:GLN:HB3	2.00	0.43
5:L:347:GLN:HA	5:L:374:LYS:HE2	2.01	0.43
5:L:679:ALA:HB2	5:L:699:ARG:HH21	1.83	0.43
5:L:746:LEU:HD12	5:L:746:LEU:HA	1.89	0.43
1:C:771:TRP:CD1	1:C:792:HIS:HA	2.54	0.43
1:C:794:LYS:HE2	5:L:609:ARG:HD2	2.01	0.43
2:E:957:TYR:HB3	2:E:974:VAL:HG12	1.99	0.43
3:G:386:LYS:HA	3:G:386:LYS:HD2	1.79	0.43
3:G:447:VAL:HG22	3:G:453:ILE:HG23	2.00	0.43
3:G:981:THR:OG1	3:G:1001:ASP:OD1	2.31	0.43
3:G:1214:HIS:O	3:G:1217:SER:OG	2.23	0.43
3:G:1281:VAL:HG21	3:G:1306:LEU:HD21	2.00	0.43
4:I:133:MET:HE1	4:I:135:TYR:HB2	2.01	0.43
4:I:914:LYS:HG3	4:I:915:LEU:HD23	2.00	0.43
4:I:1048:SER:OG	4:I:1060:TYR:HB2	2.19	0.43
4:I:1063:VAL:HG23	4:I:1064:GLY:H	1.84	0.43
1:C:120:VAL:HB	1:C:138:GLU:HB2	2.01	0.43
1:C:771:TRP:O	1:C:792:HIS:NE2	2.51	0.43
1:C:878:ILE:HD13	1:C:894:ALA:HA	2.01	0.43
2:E:9:VAL:HA	2:E:20:HIS:CE1	2.52	0.43
2:E:158:ASP:HB3	2:E:302:ARG:HE	1.84	0.43
2:E:301:ALA:HB1	2:E:318:THR:HG22	2.01	0.43
2:E:1043:ILE:HG22	2:E:1085:TYR:HE2	1.84	0.43
3:G:43:GLU:HB2	3:G:366:LEU:HD11	1.99	0.43
3:G:462:THR:H	3:G:475:ARG:NH1	2.16	0.43
4:I:960:TYR:HD1	4:I:991:PHE:CE2	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:1065:THR:HB	4:I:1067:PRO:HD2	1.99	0.43
5:L:682:PHE:CE1	5:L:687:ARG:HD2	2.54	0.43
1:C:522:SER:HB3	1:C:529:ASP:OD1	2.19	0.42
1:C:665:THR:O	1:C:669:LEU:HG	2.19	0.42
2:E:263:MET:SD	2:E:301:ALA:HA	2.59	0.42
2:E:365:LEU:HB3	2:E:396:MET:SD	2.59	0.42
2:E:703:VAL:HG21	2:E:731:HIS:HB2	2.00	0.42
2:E:1304:SER:H	2:E:1334:ALA:HB1	1.83	0.42
3:G:809:LYS:HA	3:G:812:ILE:HD12	1.99	0.42
3:G:867:LYS:O	3:G:871:ALA:N	2.49	0.42
3:G:1106:CYS:SG	3:G:1122:THR:OG1	2.52	0.42
4:I:173:VAL:HB	4:I:187:PHE:HB2	1.99	0.42
4:I:673:ARG:HA	4:I:673:ARG:HD3	1.68	0.42
4:I:841:GLN:NE2	4:I:867:ILE:O	2.52	0.42
5:L:27:LYS:NZ	5:L:67:TYR:OH	2.33	0.42
5:L:117:ALA:HA	5:L:122:VAL:HG22	2.00	0.42
5:L:705:GLU:HG3	5:L:717:TYR:OH	2.19	0.42
5:L:793:TRP:HB3	5:L:817:TRP:CB	2.49	0.42
1:C:513:ARG:HD2	1:C:515:SER:HG	1.83	0.42
2:E:863:ALA:HB1	2:E:866:ARG:NH2	2.33	0.42
2:E:933:THR:HG23	2:E:963:HIS:CG	2.54	0.42
2:E:1205:GLY:HA2	2:E:1208:MET:HE2	2.01	0.42
3:G:279:ASN:HB2	3:G:286:TYR:HE2	1.84	0.42
3:G:927:LYS:HZ3	5:L:917:PHE:HB2	1.84	0.42
3:G:975:GLU:HA	3:G:978:ARG:NE	2.30	0.42
3:G:1330:MET:HA	3:G:1333:TYR:CE2	2.54	0.42
5:L:70:ASN:ND2	5:L:112:GLN:OE1	2.52	0.42
5:L:350:VAL:HG11	5:L:387:VAL:HG21	2.01	0.42
5:L:619:VAL:O	5:L:623:GLU:HB2	2.19	0.42
5:L:659:VAL:HB	5:L:682:PHE:CZ	2.52	0.42
5:L:724:ASP:N	5:L:752:ARG:HH21	2.17	0.42
1:C:288:TRP:CG	1:C:309:GLY:HA2	2.54	0.42
2:E:41:TRP:CH2	2:E:115:SER:HB2	2.53	0.42
2:E:237:TRP:HZ2	2:E:268:ARG:HB3	1.83	0.42
3:G:912:LEU:HD22	3:G:915:LEU:HD22	1.99	0.42
3:G:1014:MET:O	3:G:1033:LEU:HD12	2.20	0.42
4:I:160:LYS:HD2	4:I:211:GLU:HG3	2.01	0.42
4:I:339:GLY:N	4:I:348:THR:O	2.41	0.42
4:I:574:MET:HE2	4:I:620:PRO:HB2	2.02	0.42
4:I:774:LEU:HG	4:I:788:ILE:HD13	2.01	0.42
4:I:906:LEU:HD23	4:I:906:LEU:HA	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:921:LYS:NZ	4:I:936:TYR:OH	2.33	0.42
4:I:1028:GLN:HG3	4:I:1050:CYS:SG	2.59	0.42
4:I:1076:VAL:HA	4:I:1084:LEU:HD23	2.00	0.42
4:I:1155:LYS:NZ	4:I:1156:PRO:O	2.49	0.42
5:L:51:LEU:HD21	5:L:54:ALA:HB2	2.02	0.42
1:C:174:LEU:HD11	1:C:214:TRP:CE3	2.54	0.42
1:C:429:THR:HB	1:C:506:ASP:HA	2.01	0.42
1:C:887:TRP:HZ2	1:C:909:TYR:HB2	1.83	0.42
2:E:742:ILE:O	2:E:746:HIS:HB3	2.20	0.42
2:E:1015:LYS:HB2	2:E:1017:HIS:CE1	2.55	0.42
2:E:1026:GLN:HB2	2:E:1058:TYR:CE2	2.55	0.42
3:G:207:VAL:O	3:G:216:LEU:N	2.52	0.42
3:G:485:ASN:N	3:G:489:THR:O	2.51	0.42
3:G:1039:LYS:HE3	3:G:1039:LYS:HB2	1.73	0.42
4:I:401:ASN:OD1	4:I:436:ARG:NH1	2.51	0.42
4:I:920:ALA:HA	4:I:931:GLU:HG3	2.01	0.42
5:L:255:LEU:HD21	5:L:311:THR:HG23	2.01	0.42
5:L:472:VAL:O	5:L:480:LEU:N	2.45	0.42
1:C:29:ILE:HG23	1:C:41:LEU:HB2	2.00	0.42
1:C:126:TRP:CE2	1:C:133:ILE:HD12	2.54	0.42
1:C:856:GLN:HE21	1:C:880:CYS:HB2	1.84	0.42
1:C:887:TRP:HA	1:C:890:ALA:HB3	2.02	0.42
2:E:689:ILE:O	2:E:693:GLU:HG3	2.19	0.42
2:E:1100:ARG:HH22	2:E:1147:LEU:HD11	1.84	0.42
2:E:1353:LEU:HG	5:L:225:LEU:HA	2.01	0.42
3:G:47:PRO:HG2	3:G:50:PRO:HG3	2.02	0.42
3:G:238:THR:HG21	3:G:241:LYS:HE3	2.02	0.42
3:G:401:VAL:HB	3:G:417:LEU:HD23	2.02	0.42
3:G:403:LEU:HD12	3:G:434:LEU:HD22	2.01	0.42
3:G:752:MET:HG2	3:G:768:CYS:HB2	2.02	0.42
3:G:843:ILE:HG13	5:L:824:PHE:CD2	2.47	0.42
3:G:1230:SER:HB3	3:G:1271:ARG:NE	2.33	0.42
4:I:225:ILE:HD11	4:I:258:ILE:HD11	2.01	0.42
4:I:226:MET:SD	4:I:226:MET:N	2.87	0.42
4:I:790:LYS:HD2	4:I:809:TYR:HE1	1.83	0.42
4:I:824:GLN:HA	4:I:825:PRO:HD3	1.88	0.42
4:I:1176:LEU:HB3	4:I:1181:ASP:HB3	2.02	0.42
5:L:202:GLY:HA2	5:L:224:PRO:HD3	2.00	0.42
5:L:517:LEU:HB3	5:L:529:GLN:HB3	2.00	0.42
1:C:502:VAL:HG22	1:C:511:ILE:HA	2.01	0.42
2:E:12:TYR:HB2	2:E:20:HIS:CE1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:176:PHE:CD1	2:E:189:ALA:HA	2.55	0.42
2:E:342:GLN:HA	2:E:345:MET:HG2	2.02	0.42
2:E:509:PRO:HG2	2:E:767:TYR:HE2	1.85	0.42
2:E:722:LEU:HD12	2:E:722:LEU:HA	1.84	0.42
2:E:1110:ILE:HA	2:E:1113:MET:HG2	2.02	0.42
3:G:383:LEU:HB3	3:G:395:GLN:HB3	2.00	0.42
3:G:519:ALA:C	3:G:547:LYS:HZ3	2.26	0.42
3:G:716:LYS:HG2	3:G:749:TRP:HB3	2.01	0.42
3:G:1146:LYS:HA	3:G:1171:LEU:HD21	2.00	0.42
5:L:218:ARG:NH1	5:L:252:GLY:O	2.53	0.42
5:L:276:PHE:HA	5:L:289:PHE:O	2.19	0.42
5:L:426:ARG:HH11	5:L:444:ASP:HB2	1.85	0.42
5:L:683:ALA:HA	5:L:693:VAL:HA	2.02	0.42
5:L:804:PRO:C	5:L:806:CYS:H	2.28	0.42
1:C:341:TRP:HZ3	1:C:343:TYR:HB2	1.84	0.42
1:C:468:GLU:HG3	1:C:485:PRO:HB3	2.02	0.42
1:C:912:HIS:CE1	5:L:448:PRO:HD2	2.55	0.42
1:C:940:GLN:HG2	1:C:1025:ARG:HH22	1.84	0.42
3:G:122:ASP:OD1	3:G:122:ASP:N	2.52	0.42
3:G:268:ALA:HB2	3:G:275:VAL:HG13	2.02	0.42
3:G:333:LEU:HB3	3:G:626:VAL:HG11	2.00	0.42
3:G:423:GLN:HB2	3:G:438:ASP:HB2	2.01	0.42
3:G:429:LEU:HB2	3:G:434:LEU:HD13	2.01	0.42
3:G:468:ILE:HG12	3:G:470:ASN:N	2.34	0.42
3:G:786:SER:HB2	3:G:803:MET:HE2	2.02	0.42
3:G:786:SER:OG	3:G:807:ALA:N	2.53	0.42
3:G:801:LEU:HD13	4:I:740:LEU:HD23	2.02	0.42
3:G:1153:LEU:HD11	3:G:1157:LYS:HE2	2.01	0.42
4:I:86:ASN:HD22	4:I:88:HIS:CE1	2.37	0.42
4:I:543:VAL:HA	4:I:553:LEU:HA	2.02	0.42
4:I:574:MET:HG2	4:I:623:VAL:HG12	2.01	0.42
5:L:58:HIS:NE2	5:L:76:SER:O	2.34	0.42
5:L:578:ALA:HB1	5:L:587:TRP:NE1	2.35	0.42
1:C:499:ILE:HA	1:C:513:ARG:HA	2.01	0.42
1:C:755:MET:HE3	1:C:757:ARG:HD2	2.01	0.42
1:C:1091:LEU:O	1:C:1102:ARG:HG2	2.19	0.42
2:E:222:PRO:HA	2:E:225:VAL:HG12	2.01	0.42
2:E:282:LEU:HA	2:E:282:LEU:HD12	1.74	0.42
3:G:19:TRP:CD2	3:G:29:LEU:HD13	2.54	0.42
4:I:363:LEU:HB2	4:I:631:ARG:NH2	2.35	0.42
4:I:424:TYR:OH	4:I:436:ARG:NH2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:534:PHE:CG	4:I:573:VAL:HB	2.54	0.42
4:I:832:LYS:O	4:I:835:ILE:HG22	2.19	0.42
5:L:31:SER:OG	5:L:32:GLN:N	2.51	0.42
5:L:62:ILE:HD13	5:L:76:SER:HB2	2.00	0.42
5:L:261:ARG:HH22	5:L:285:GLY:C	2.27	0.42
5:L:647:GLN:HE22	5:L:678:TRP:CD1	2.36	0.42
5:L:819:SER:HA	5:L:827:ALA:HB2	2.02	0.42
1:C:281:VAL:HG23	1:C:284:GLY:H	1.84	0.42
1:C:350:TYR:CZ	1:C:363:MET:HG2	2.54	0.42
1:C:895:GLN:HE22	1:C:902:ILE:HD13	1.85	0.42
2:E:758:MET:HE2	2:E:773:LEU:HD22	2.01	0.42
2:E:977:LEU:O	2:E:981:ASN:ND2	2.53	0.42
3:G:883:LEU:HB2	3:G:917:GLU:OE1	2.20	0.42
3:G:961:PHE:CZ	3:G:965:ARG:HB3	2.55	0.42
4:I:705:ILE:HA	4:I:709:ARG:HD3	2.02	0.42
4:I:803:SER:HB3	4:I:842:LEU:HD21	2.02	0.42
4:I:960:TYR:CE1	4:I:984:ASP:HB2	2.55	0.42
5:L:39:ASN:HA	5:L:62:ILE:H	1.85	0.42
5:L:277:VAL:O	5:L:288:MET:HA	2.20	0.42
5:L:760:HIS:ND1	5:L:763:ARG:HD3	2.35	0.42
5:L:787:TYR:HD2	5:L:799:LEU:H	1.68	0.42
5:L:837:PRO:HD2	5:L:874:SER:HB2	2.01	0.42
1:C:271:ALA:HB2	1:C:315:TRP:HZ2	1.84	0.42
2:E:345:MET:HA	2:E:492:ARG:HH22	1.85	0.42
2:E:438:TYR:O	2:E:442:LEU:HB2	2.20	0.42
2:E:911:GLN:NE2	2:E:936:ILE:HG13	2.32	0.42
3:G:112:THR:HG21	3:G:117:ARG:HB2	2.02	0.42
4:I:204:ASP:H	4:I:275:ARG:NH1	2.16	0.42
4:I:375:LEU:HB2	4:I:408:LEU:HD22	2.02	0.42
4:I:1085:GLY:O	4:I:1089:LEU:HB3	2.20	0.42
4:I:1167:LEU:HD23	4:I:1171:THR:OG1	2.19	0.42
5:L:12:PRO:HG2	5:L:51:LEU:HD22	2.01	0.42
5:L:157:CYS:SG	5:L:163:SER:OG	2.60	0.42
5:L:330:ASP:OD1	5:L:331:TYR:N	2.53	0.42
5:L:598:LEU:O	5:L:626:ARG:NE	2.53	0.42
5:L:831:TYR:HA	5:L:834:GLY:O	2.20	0.42
5:L:906:TYR:HA	5:L:951:VAL:HG21	2.01	0.42
5:L:931:PHE:HA	5:L:967:LEU:HD22	2.02	0.42
2:E:539:ARG:HA	2:E:539:ARG:HD2	1.82	0.41
2:E:910:LEU:HA	2:E:913:GLN:CD	2.45	0.41
3:G:185:LYS:HE2	3:G:185:LYS:HB3	1.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:417:LEU:HD22	3:G:453:ILE:HG21	2.02	0.41
3:G:476:ALA:HB1	3:G:504:THR:HA	2.02	0.41
3:G:481:VAL:HG13	3:G:506:MET:HE1	2.02	0.41
3:G:576:VAL:HG11	3:G:600:PRO:HD2	2.02	0.41
3:G:1301:ARG:HA	3:G:1301:ARG:HD3	1.71	0.41
4:I:248:MET:HE3	4:I:291:THR:O	2.20	0.41
4:I:292:ASP:HB2	4:I:336:GLU:O	2.20	0.41
4:I:664:ALA:O	4:I:668:LYS:HG2	2.19	0.41
4:I:794:ALA:C	4:I:796:LEU:N	2.78	0.41
4:I:797:GLU:OE2	4:I:837:ARG:HB2	2.20	0.41
5:L:79:ALA:HA	5:L:101:ALA:HB1	2.01	0.41
5:L:587:TRP:HB3	5:L:610:ILE:HD11	2.02	0.41
5:L:637:ALA:O	5:L:641:ALA:CB	2.68	0.41
5:L:723:TYR:CE2	5:L:745:GLN:HB3	2.52	0.41
1:C:719:ILE:HD12	1:C:722:VAL:HB	2.02	0.41
1:C:766:MET:HG3	1:C:788:LEU:HG	2.01	0.41
1:C:855:PHE:HD2	1:C:864:GLY:HA2	1.85	0.41
2:E:40:PHE:CD1	2:E:59:LEU:HB2	2.55	0.41
2:E:1054:ASP:OD1	2:E:1054:ASP:N	2.44	0.41
3:G:724:PHE:CE1	3:G:756:CYS:HA	2.55	0.41
3:G:805:GLU:OE1	3:G:808:LYS:NZ	2.40	0.41
4:I:266:TYR:HD1	4:I:285:LYS:HD2	1.84	0.41
4:I:535:PRO:HA	4:I:542:LEU:HB3	2.01	0.41
5:L:158:PHE:HA	5:L:181:PRO:HB3	2.01	0.41
5:L:495:ASN:HB3	5:L:516:MET:HB3	2.02	0.41
5:L:508:MET:SD	5:L:521:THR:HG23	2.60	0.41
5:L:725:ARG:HH22	5:L:732:LYS:NZ	2.18	0.41
5:L:857:TYR:N	5:L:907:GLU:OE1	2.52	0.41
1:C:199:CYS:HB2	1:C:233:LEU:HG	2.02	0.41
1:C:1109:ALA:HB1	2:E:815:HIS:CD2	2.54	0.41
2:E:154:GLN:NE2	2:E:168:GLU:OE1	2.53	0.41
2:E:1273:TRP:O	2:E:1276:MET:HG2	2.21	0.41
3:G:387:PHE:HD1	3:G:392:ALA:HB2	1.85	0.41
3:G:828:GLY:HA3	4:I:712:GLY:H	1.85	0.41
3:G:980:TYR:HA	3:G:985:ARG:HG3	2.02	0.41
4:I:79:LEU:HB3	4:I:92:TRP:HE3	1.86	0.41
4:I:609:LEU:HD22	4:I:669:LEU:HA	2.02	0.41
4:I:949:CYS:SG	4:I:958:ARG:NH2	2.89	0.41
5:L:627:LYS:HB2	5:L:627:LYS:HE2	1.86	0.41
1:C:30:ALA:HB1	1:C:38:LEU:HG	2.02	0.41
1:C:33:GLY:HA3	1:C:37:LEU:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:107:ASP:HB3	2:E:133:VAL:HG13	2.01	0.41
2:E:314:LEU:O	2:E:318:THR:OG1	2.26	0.41
2:E:944:SER:HA	2:E:947:ALA:HB3	2.02	0.41
2:E:1036:TYR:HB2	2:E:1105:TRP:CE2	2.55	0.41
2:E:1104:ARG:HD2	2:E:1104:ARG:HA	1.82	0.41
2:E:1321:TYR:HA	2:E:1348:LYS:HD2	2.01	0.41
3:G:266:ALA:HB1	3:G:303:LEU:HD13	2.02	0.41
3:G:389:ASP:HB3	3:G:431:LYS:HG2	2.02	0.41
3:G:494:LEU:HB3	3:G:523:ARG:HH22	1.85	0.41
4:I:266:TYR:HE2	4:I:268:ALA:HB2	1.86	0.41
4:I:375:LEU:HG	4:I:383:MET:HE3	2.02	0.41
4:I:376:TYR:CE1	4:I:386:LEU:HB3	2.48	0.41
4:I:960:TYR:HA	4:I:991:PHE:CE2	2.55	0.41
4:I:1018:VAL:HG13	4:I:1019:ALA:H	1.85	0.41
4:I:1115:PHE:CD2	4:I:1365:GLY:HA3	2.54	0.41
5:L:89:LYS:HB2	5:L:89:LYS:HE2	1.84	0.41
5:L:324:VAL:HG11	5:L:364:HIS:CD2	2.54	0.41
5:L:484:LEU:HD22	5:L:487:LYS:HZ2	1.85	0.41
5:L:724:ASP:O	5:L:727:ILE:HG22	2.19	0.41
5:L:800:LEU:C	5:L:810:VAL:HB	2.44	0.41
1:C:517:VAL:HG22	1:C:533:VAL:HG22	2.02	0.41
1:C:707:ASP:O	1:C:711:VAL:HG23	2.20	0.41
1:C:923:ILE:HD13	1:C:923:ILE:HA	1.93	0.41
2:E:304:PHE:HB2	2:E:476:LEU:HD11	2.02	0.41
2:E:306:ARG:NH1	2:E:338:GLU:HG2	2.35	0.41
2:E:1351:MET:HE1	5:L:140:ARG:NH2	2.36	0.41
3:G:717:THR:OG1	3:G:751:ASN:OD1	2.37	0.41
3:G:1081:MET:HG3	3:G:1101:ARG:HH21	1.85	0.41
4:I:481:ILE:HD12	4:I:512:TYR:CE2	2.55	0.41
4:I:509:LEU:HD12	4:I:509:LEU:HA	1.97	0.41
4:I:617:THR:HG22	4:I:633:LYS:HE3	2.03	0.41
4:I:656:ARG:CZ	4:I:662:ARG:HD3	2.50	0.41
4:I:950:LEU:HD22	4:I:978:PHE:CD1	2.54	0.41
5:L:245:VAL:H	5:L:259:ALA:HB3	1.85	0.41
5:L:872:LEU:HB2	5:L:893:PHE:CG	2.54	0.41
1:C:970:PHE:O	1:C:973:ARG:HG2	2.21	0.41
1:C:1040:LEU:HD12	1:C:1040:LEU:HA	1.92	0.41
2:E:195:LYS:HB3	2:E:230:MET:SD	2.60	0.41
2:E:259:ALA:O	2:E:263:MET:HG2	2.20	0.41
3:G:5:TYR:CZ	3:G:398:VAL:HG13	2.56	0.41
3:G:385:TYR:HE2	3:G:678:ASN:HD22	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:1056:LEU:HD12	3:G:1056:LEU:HA	1.77	0.41
3:G:1310:ILE:HG13	3:G:1319:ALA:HB3	2.02	0.41
4:I:782:PRO:HD2	4:I:820:VAL:HG22	2.03	0.41
4:I:789:CYS:O	4:I:808:HIS:HB3	2.19	0.41
4:I:868:LEU:HA	4:I:868:LEU:HD23	1.75	0.41
4:I:1069:LEU:HD21	4:I:1091:TYR:HD1	1.85	0.41
4:I:1143:PHE:CE2	4:I:1310:CYS:HB2	2.56	0.41
4:I:1219:LEU:HA	4:I:1260:GLU:HA	2.02	0.41
5:L:75:ALA:HA	5:L:85:ILE:HA	2.02	0.41
1:C:171:ARG:HH21	1:C:186:ASP:HB2	1.84	0.41
1:C:600:PHE:CZ	1:C:611:PHE:HB2	2.55	0.41
1:C:868:PHE:HB3	1:C:873:ASP:HB3	2.03	0.41
2:E:552:ARG:HA	2:E:552:ARG:HD2	1.87	0.41
2:E:611:VAL:O	2:E:615:ASN:N	2.39	0.41
2:E:678:ALA:H	2:E:681:ALA:HB3	1.85	0.41
2:E:1258:LEU:HD23	2:E:1258:LEU:HA	1.93	0.41
3:G:9:ILE:HB	3:G:375:ILE:HB	2.03	0.41
3:G:841:ASP:O	3:G:845:LEU:N	2.47	0.41
3:G:1337:ALA:O	3:G:1338:ARG:HG2	2.20	0.41
4:I:673:ARG:HH22	4:I:702:ASP:HB3	1.86	0.41
4:I:737:MET:SD	4:I:743:ASP:HB3	2.61	0.41
4:I:987:GLY:O	4:I:990:GLU:HB2	2.20	0.41
4:I:1057:VAL:O	4:I:1061:LEU:HG	2.21	0.41
4:I:1167:LEU:HA	4:I:1199:PHE:CE2	2.56	0.41
5:L:2:ARG:NH1	5:L:294:SER:HB3	2.36	0.41
5:L:65:VAL:HG12	5:L:76:SER:HA	2.03	0.41
5:L:72:LYS:HB3	5:L:73:ARG:HD2	2.02	0.41
5:L:125:TRP:HA	5:L:129:GLN:HE21	1.85	0.41
5:L:618:LEU:HD11	5:L:639:ILE:HA	2.03	0.41
5:L:705:GLU:HG2	5:L:713:ALA:HB1	2.02	0.41
1:C:242:ARG:HH22	1:C:248:ASN:HB3	1.86	0.41
1:C:347:THR:OG1	1:C:366:ASP:OD1	2.22	0.41
2:E:173:LEU:HG	2:E:196:ILE:HG21	2.03	0.41
2:E:383:LEU:HD11	2:E:640:VAL:HG21	2.02	0.41
2:E:618:LEU:O	2:E:622:LYS:HB2	2.21	0.41
2:E:979:LEU:HD12	2:E:979:LEU:HA	1.95	0.41
3:G:9:ILE:HD12	3:G:29:LEU:HD23	2.03	0.41
3:G:780:ALA:O	3:G:784:ALA:CB	2.68	0.41
4:I:770:TRP:HH2	4:I:795:MET:HG2	1.85	0.41
4:I:924:GLU:O	4:I:929:TRP:NE1	2.53	0.41
4:I:1060:TYR:CE2	4:I:1068:ALA:HA	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:295:THR:HB	5:L:306:TYR:HB2	2.02	0.41
5:L:723:TYR:CG	5:L:746:LEU:HD13	2.55	0.41
1:C:214:TRP:CE2	1:C:229:LEU:HB2	2.55	0.41
1:C:272:VAL:O	1:C:291:GLN:N	2.46	0.41
1:C:535:ARG:HB2	1:C:579:HIS:CE1	2.56	0.41
1:C:868:PHE:HB3	1:C:873:ASP:O	2.21	0.41
1:C:882:VAL:HG22	1:C:890:ALA:HB1	2.03	0.41
1:C:940:GLN:O	1:C:944:LYS:HG3	2.21	0.41
1:C:1110:MET:HG2	2:E:817:TYR:CE1	2.55	0.41
2:E:12:TYR:O	2:E:16:GLY:N	2.54	0.41
2:E:156:GLN:HG3	2:E:229:ARG:HG2	2.02	0.41
2:E:298:PHE:CE1	2:E:325:ALA:HB1	2.56	0.41
2:E:310:SER:OG	2:E:311:ASP:N	2.54	0.41
2:E:811:LEU:HA	2:E:811:LEU:HD23	1.93	0.41
2:E:1165:GLU:O	2:E:1169:ILE:HG13	2.20	0.41
3:G:130:TRP:CE2	3:G:140:HIS:HB2	2.56	0.41
3:G:315:GLY:HA3	3:G:355:ALA:HB3	2.03	0.41
3:G:392:ALA:HB3	3:G:699:VAL:HG21	2.02	0.41
3:G:668:ILE:HD11	3:G:699:VAL:HG13	2.03	0.41
3:G:676:LEU:HD23	3:G:701:LYS:HG2	2.03	0.41
3:G:677:THR:OG1	3:G:700:SER:OG	2.30	0.41
3:G:959:ALA:HB1	3:G:983:ALA:HB1	2.03	0.41
3:G:1035:MET:HG2	3:G:1059:ILE:CG1	2.47	0.41
3:G:1325:ASP:HA	3:G:1328:ALA:HB3	2.02	0.41
4:I:12:LEU:HD11	4:I:356:MET:HB2	2.03	0.41
4:I:252:TRP:NE1	4:I:258:ILE:HG12	2.35	0.41
4:I:531:VAL:HG23	4:I:547:ASP:HA	2.03	0.41
4:I:543:VAL:HG21	4:I:583:MET:HE2	2.01	0.41
4:I:598:PRO:HA	4:I:604:PRO:HA	2.02	0.41
4:I:744:TYR:CE2	4:I:767:LEU:HD12	2.56	0.41
4:I:993:LEU:HD11	4:I:1014:PHE:HA	2.03	0.41
4:I:1015:ALA:HA	4:I:1018:VAL:HG12	2.02	0.41
4:I:1155:LYS:HE2	4:I:1155:LYS:HB2	1.92	0.41
4:I:1187:ARG:NH1	4:I:1278:THR:OG1	2.54	0.41
5:L:247:LEU:HD12	5:L:247:LEU:HA	1.89	0.41
5:L:303:ARG:HH21	5:L:360:ASP:HA	1.85	0.41
5:L:371:ILE:HD13	5:L:375:LEU:HD23	2.02	0.41
5:L:469:LYS:O	5:L:501:TRP:NE1	2.53	0.41
5:L:739:LEU:O	5:L:743:VAL:HG23	2.20	0.41
2:E:300:VAL:HG21	2:E:321:MET:HE2	2.03	0.41
2:E:874:THR:O	2:E:878:GLN:NE2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:967:HIS:CE1	2:E:969:PRO:HG2	2.56	0.41
2:E:1029:LEU:HD13	2:E:1039:LEU:HD12	2.02	0.41
2:E:1272:ALA:C	2:E:1276:MET:HE3	2.46	0.41
2:E:1304:SER:HA	2:E:1307:VAL:HB	2.03	0.41
2:E:1333:LYS:HD3	2:E:1333:LYS:HA	1.77	0.41
3:G:85:ILE:HD13	3:G:120:THR:HG21	2.02	0.41
3:G:479:ASN:OD1	3:G:479:ASN:N	2.53	0.41
3:G:721:LEU:HA	3:G:721:LEU:HD23	1.81	0.41
3:G:1127:ALA:H	3:G:1157:LYS:NZ	2.13	0.41
5:L:812:LEU:HB3	5:L:816:LYS:NZ	2.36	0.41
1:C:5:LEU:HD11	1:C:305:VAL:HG22	2.03	0.40
1:C:82:TRP:CZ3	1:C:89:LEU:HB2	2.55	0.40
1:C:522:SER:O	1:C:526:LEU:HA	2.20	0.40
2:E:263:MET:SD	2:E:304:PHE:HB3	2.61	0.40
2:E:496:GLN:HB2	2:E:654:THR:HB	2.03	0.40
3:G:394:MET:HE2	3:G:668:ILE:HD13	2.04	0.40
3:G:577:ARG:HG3	3:G:591:HIS:C	2.46	0.40
3:G:846:LYS:HE3	5:L:842:ARG:HD2	2.02	0.40
3:G:967:TYR:CE2	3:G:979:TYR:HE2	2.39	0.40
3:G:986:TYR:O	3:G:1013:VAL:HG21	2.21	0.40
3:G:999:ASP:HA	3:G:1002:LEU:HB3	2.03	0.40
3:G:1329:LEU:HA	3:G:1329:LEU:HD12	1.83	0.40
4:I:543:VAL:HG23	4:I:575:TRP:CH2	2.56	0.40
4:I:545:GLU:OE1	4:I:569:ARG:NH1	2.54	0.40
4:I:764:ARG:HA	4:I:764:ARG:HD3	1.91	0.40
4:I:975:LEU:HD13	4:I:991:PHE:CD2	2.55	0.40
4:I:1013:THR:HA	4:I:1016:ARG:HB3	2.03	0.40
5:L:197:ALA:N	5:L:205:LYS:O	2.49	0.40
5:L:305:ALA:HA	5:L:315:ILE:HA	2.03	0.40
5:L:474:ASP:OD1	5:L:474:ASP:N	2.51	0.40
5:L:847:LEU:HB2	5:L:863:TYR:CE2	2.55	0.40
5:L:911:LYS:HB3	5:L:915:SER:O	2.20	0.40
1:C:30:ALA:HB2	1:C:40:VAL:HG22	2.03	0.40
1:C:551:SER:CB	1:C:590:MET:HG3	2.51	0.40
1:C:711:VAL:HG13	5:L:668:ASP:HA	2.03	0.40
1:C:846:PRO:HA	1:C:871:ALA:HB1	2.04	0.40
2:E:539:ARG:NH1	2:E:570:LEU:HA	2.36	0.40
2:E:602:PRO:HA	2:E:605:HIS:HB2	2.03	0.40
2:E:900:TYR:OH	2:E:939:ASP:OD2	2.37	0.40
2:E:1141:VAL:HG23	2:E:1168:ALA:HB1	2.02	0.40
2:E:1323:GLU:HA	5:L:264:TRP:CZ3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:70:HIS:CD2	3:G:75:LEU:HD23	2.56	0.40
3:G:435:LEU:HD21	3:G:466:MET:SD	2.62	0.40
3:G:696:THR:OG1	3:G:697:SER:N	2.54	0.40
4:I:201:LYS:HB2	4:I:213:THR:HG21	2.04	0.40
4:I:357:HIS:HB3	4:I:359:PHE:CE2	2.56	0.40
4:I:560:HIS:CG	4:I:604:PRO:HG2	2.56	0.40
4:I:856:ASN:HD22	4:I:861:PHE:N	2.19	0.40
4:I:1304:TRP:CZ3	4:I:1313:PRO:HA	2.56	0.40
5:L:39:ASN:HA	5:L:62:ILE:HG13	2.02	0.40
5:L:276:PHE:HB3	5:L:288:MET:HB3	2.04	0.40
5:L:762:ARG:NH2	5:L:767:PHE:HA	2.36	0.40
5:L:907:GLU:CD	5:L:911:LYS:HG3	2.45	0.40
5:L:926:PHE:O	5:L:929:SER:OG	2.31	0.40
1:C:20:ILE:HG12	1:C:29:ILE:HD11	2.03	0.40
1:C:346:ASN:O	1:C:367:THR:N	2.42	0.40
2:E:32:ARG:HD3	2:E:32:ARG:HA	1.90	0.40
2:E:290:GLU:OE2	2:E:293:ASN:ND2	2.54	0.40
2:E:617:LYS:HB3	2:E:620:ASP:HB2	2.02	0.40
2:E:770:TYR:HA	2:E:773:LEU:HG	2.02	0.40
3:G:64:CYS:SG	3:G:67:ILE:HG23	2.62	0.40
3:G:229:ARG:HG2	3:G:235:THR:HA	2.04	0.40
3:G:753:ALA:HB3	3:G:764:VAL:HG21	2.03	0.40
3:G:849:HIS:HB3	3:G:868:HIS:O	2.21	0.40
3:G:910:LYS:NZ	3:G:913:GLU:OE1	2.42	0.40
3:G:1090:VAL:HG13	3:G:1121:MET:HE1	2.03	0.40
3:G:1090:VAL:HG22	3:G:1102:ALA:HB1	2.04	0.40
4:I:461:VAL:HG12	4:I:463:VAL:HG23	2.04	0.40
4:I:776:LEU:O	4:I:780:LEU:HB2	2.21	0.40
4:I:887:PHE:HD2	4:I:906:LEU:HD21	1.86	0.40
4:I:929:TRP:CE3	4:I:952:ARG:HG2	2.57	0.40
4:I:949:CYS:SG	4:I:959:ALA:HB2	2.61	0.40
4:I:1002:PHE:O	4:I:1006:MET:HG2	2.21	0.40
4:I:1098:GLY:HA2	4:I:1101:ARG:NE	2.34	0.40
4:I:1293:LEU:HD23	4:I:1319:PHE:HE1	1.86	0.40
5:L:17:VAL:HG11	5:L:39:ASN:H	1.86	0.40
5:L:565:TYR:CE2	5:L:577:VAL:HG21	2.57	0.40
5:L:855:THR:HA	5:L:857:TYR:CE1	2.57	0.40
5:L:951:VAL:O	5:L:955:LEU:HB3	2.21	0.40
1:C:435:ALA:N	1:C:442:TYR:O	2.55	0.40
2:E:919:ARG:NH1	2:E:926:VAL:O	2.55	0.40
2:E:979:LEU:HA	2:E:983:ASP:H	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:1081:ILE:HG22	2:E:1112:HIS:CE1	2.56	0.40
2:E:1137:SER:HB2	2:E:1140:ALA:HB3	2.02	0.40
3:G:1047:CYS:SG	3:G:1056:LEU:HD13	2.62	0.40
4:I:481:ILE:HD13	4:I:481:ILE:HA	1.94	0.40
4:I:1084:LEU:HA	4:I:1084:LEU:HD12	1.79	0.40
4:I:1295:THR:HG22	4:I:1297:LYS:HD2	2.02	0.40
4:I:1334:ASP:OD1	4:I:1334:ASP:N	2.47	0.40
5:L:386:HIS:HD2	5:L:425:ARG:HD3	1.86	0.40
5:L:454:HIS:CD2	5:L:480:LEU:HD22	2.56	0.40
5:L:960:VAL:HG23	5:L:971:ALA:HB3	2.04	0.40
1:C:633:GLU:HG3	1:C:658:GLU:HG2	2.04	0.40
1:C:759:ASP:HA	1:C:762:ILE:HB	2.03	0.40
2:E:315:LEU:HD21	2:E:343:LYS:NZ	2.37	0.40
2:E:574:VAL:O	2:E:578:GLN:N	2.46	0.40
2:E:815:HIS:HA	2:E:817:TYR:CZ	2.57	0.40
3:G:3:ILE:HB	3:G:383:LEU:HD11	2.04	0.40
3:G:443:GLU:HG3	3:G:445:TYR:CZ	2.57	0.40
3:G:444:VAL:N	3:G:457:SER:O	2.44	0.40
3:G:593:PHE:CZ	3:G:615:VAL:HG11	2.56	0.40
3:G:774:HIS:CE1	3:G:776:ARG:HB2	2.56	0.40
3:G:852:TYR:HA	3:G:855:PHE:HB3	2.03	0.40
3:G:1289:ARG:HH21	3:G:1292:ILE:HG21	1.87	0.40
3:G:1331:VAL:HG12	3:G:1335:TYR:HE2	1.86	0.40
4:I:201:LYS:NZ	4:I:227:GLN:HE21	2.19	0.40
4:I:329:LEU:HD11	4:I:349:VAL:HG11	2.04	0.40
4:I:501:ILE:HG21	4:I:542:LEU:HD21	2.02	0.40
4:I:1350:LYS:HD2	4:I:1350:LYS:HA	1.83	0.40
5:L:723:TYR:HB2	5:L:746:LEU:HD22	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [\(i\)](#)

5.3.1 Protein backbone [\(i\)](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	1070/1224 (87%)	974 (91%)	96 (9%)	0	100	100
2	E	1321/1355 (98%)	1229 (93%)	91 (7%)	1 (0%)	48	83
3	G	1352/1409 (96%)	1191 (88%)	160 (12%)	1 (0%)	48	83
4	I	1365/1367 (100%)	1245 (91%)	116 (8%)	4 (0%)	36	72
5	L	995/1239 (80%)	872 (88%)	121 (12%)	2 (0%)	43	78
All	All	6103/6594 (93%)	5511 (90%)	584 (10%)	8 (0%)	49	83

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	730	PRO
3	G	1165	VAL
4	I	1053	ALA
5	L	778	ASP
4	I	1008	HIS
4	I	1010	GLU
5	L	784	ILE
4	I	985	PHE

5.3.2 Protein sidechains [i](#)

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	C	904/1005 (90%)	903 (100%)	1 (0%)	88	89
2	E	1092/1114 (98%)	1092 (100%)	0	100	100
3	G	1117/1162 (96%)	1115 (100%)	2 (0%)	87	87
4	I	1119/1119 (100%)	1117 (100%)	2 (0%)	87	87
5	L	840/1035 (81%)	839 (100%)	1 (0%)	88	89
All	All	5072/5435 (93%)	5066 (100%)	6 (0%)	87	89

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1094	MET
3	G	554	MET
3	G	1033	LEU
4	I	763	MET
4	I	1011	MET
5	L	799	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (87) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	264	ASN
1	C	384	GLN
1	C	398	ASN
1	C	445	GLN
1	C	556	ASN
1	C	686	HIS
1	C	717	GLN
1	C	720	GLN
1	C	814	GLN
1	C	895	GLN
1	C	898	ASN
1	C	901	GLN
1	C	1083	GLN
2	E	20	HIS
2	E	239	GLN
2	E	287	ASN
2	E	289	GLN
2	E	327	GLN
2	E	351	ASN
2	E	358	GLN
2	E	370	ASN
2	E	389	GLN
2	E	524	ASN
2	E	630	ASN
2	E	779	GLN
2	E	837	HIS
2	E	967	HIS
2	E	990	GLN
2	E	1034	ASN
2	E	1083	ASN
2	E	1097	ASN
2	E	1150	GLN
2	E	1159	GLN

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Mol	Chain	Res	Type
2	E	1302	GLN
3	G	36	ASN
3	G	55	ASN
3	G	58	ASN
3	G	179	GLN
3	G	376	ASN
3	G	470	ASN
3	G	636	HIS
3	G	698	ASN
3	G	751	ASN
3	G	822	GLN
3	G	1085	HIS
3	G	1097	GLN
3	G	1136	ASN
3	G	1204	ASN
3	G	1206	HIS
3	G	1284	GLN
4	I	51	HIS
4	I	69	GLN
4	I	88	HIS
4	I	227	GLN
4	I	345	GLN
4	I	353	ASN
4	I	357	HIS
4	I	418	ASN
4	I	452	GLN
4	I	536	GLN
4	I	555	ASN
4	I	811	GLN
4	I	824	GLN
4	I	847	GLN
4	I	974	GLN
4	I	983	GLN
4	I	997	GLN
4	I	1028	GLN
4	I	1032	GLN
4	I	1052	GLN
4	I	1074	GLN
4	I	1130	GLN
4	I	1168	HIS
4	I	1286	GLN
4	I	1287	ASN

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Mol	Chain	Res	Type
4	I	1333	ASN
5	L	19	ASN
5	L	129	GLN
5	L	290	GLN
5	L	345	GLN
5	L	357	ASN
5	L	589	GLN
5	L	647	GLN
5	L	698	ASN
5	L	733	HIS
5	L	881	ASN
5	L	973	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15980. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

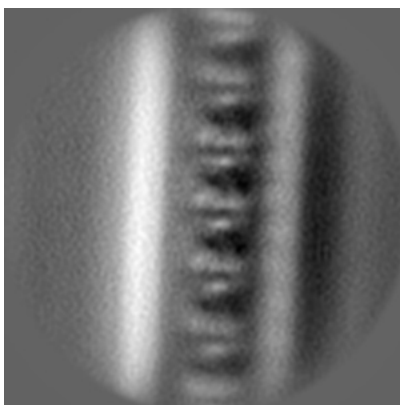


Y

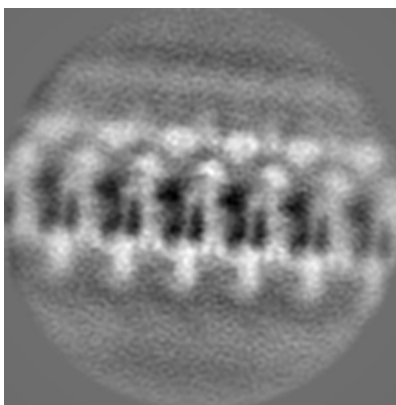


Z

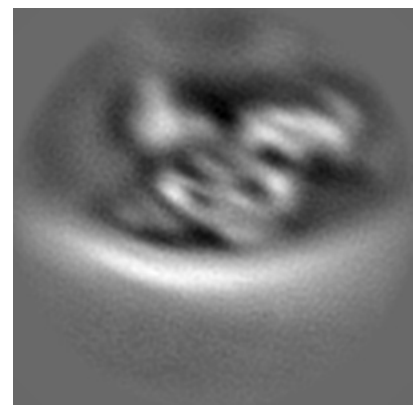
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 60

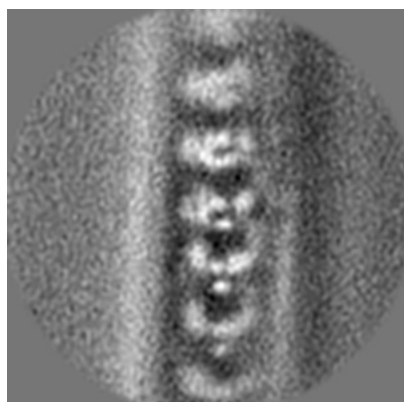


Y Index: 60

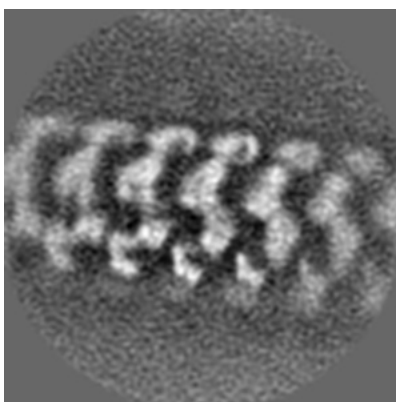


Z Index: 60

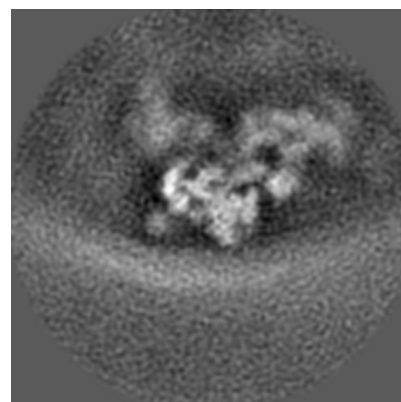
6.2.2 Raw map



X Index: 60



Y Index: 60



Z Index: 60

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: 48



Y Index: 63

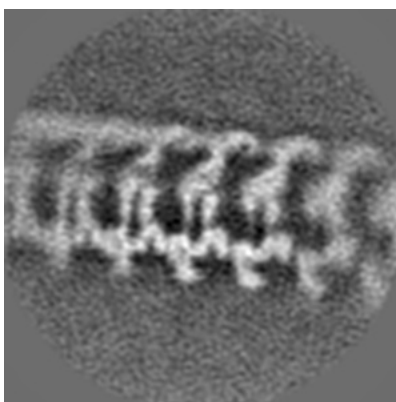


Z Index: 61

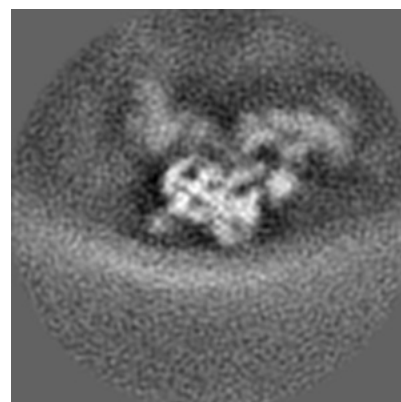
6.3.2 Raw map



X Index: 49



Y Index: 63



Z Index: 61

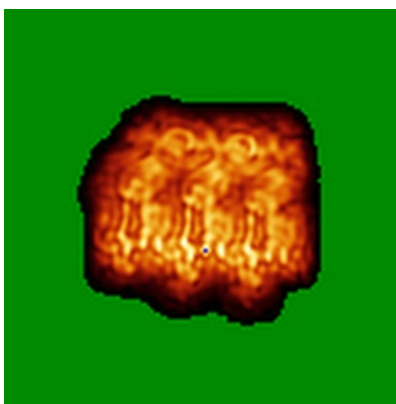
The images above show the largest variance slices of the map in three orthogonal directions.

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

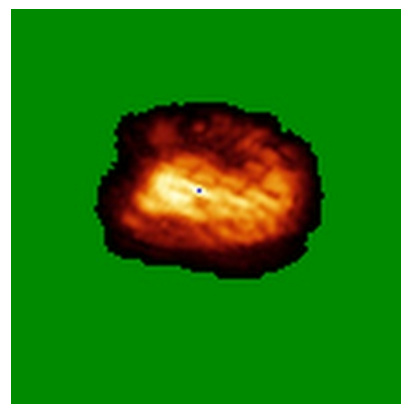
6.4.1 Primary map



X

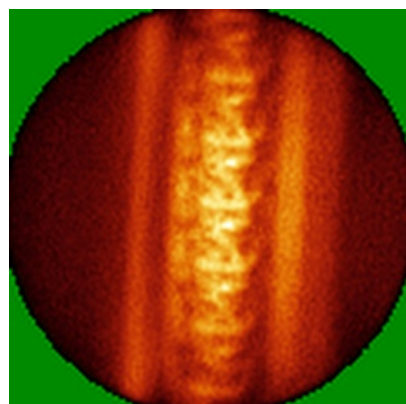


Y

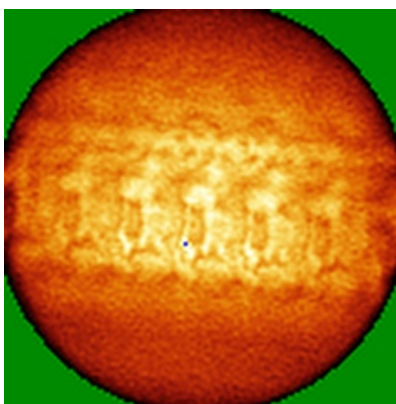


Z

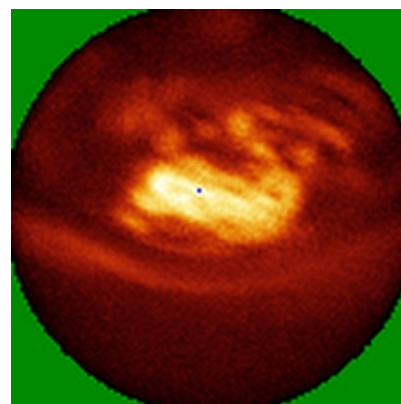
6.4.2 Raw map



X



Y

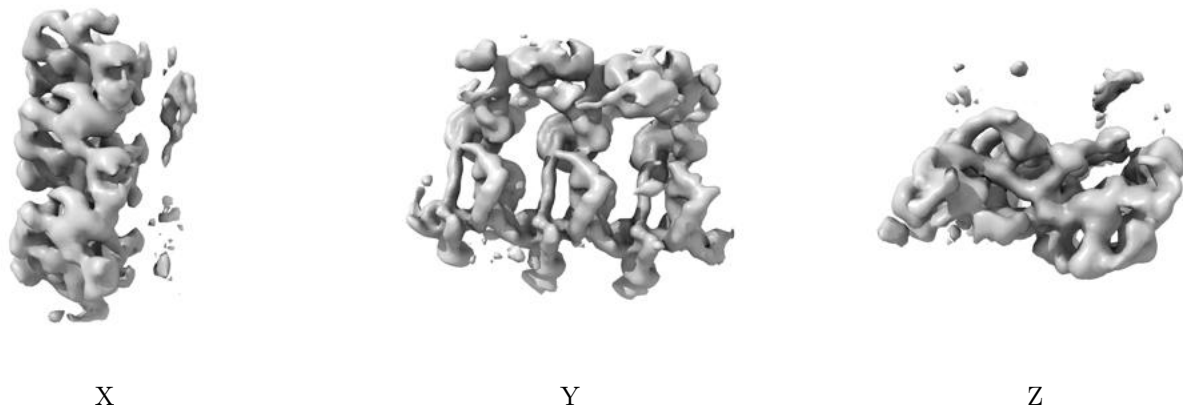


Z

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

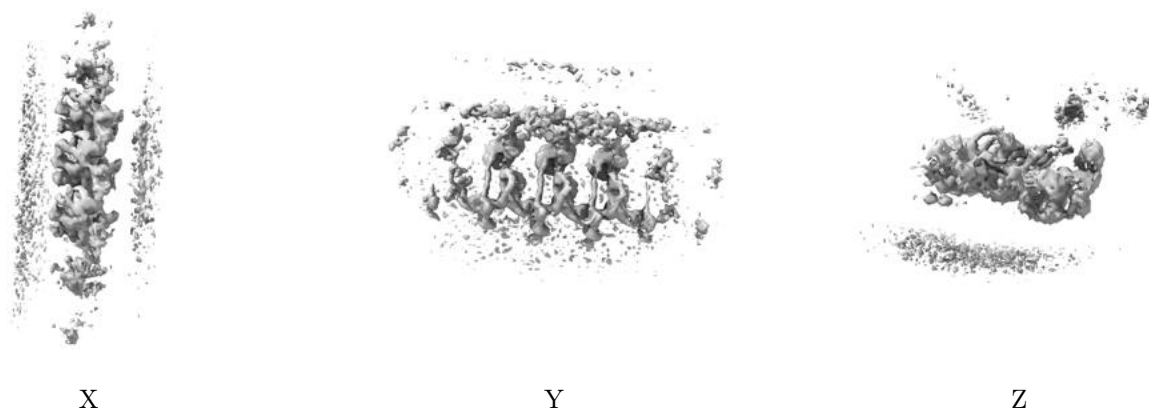
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

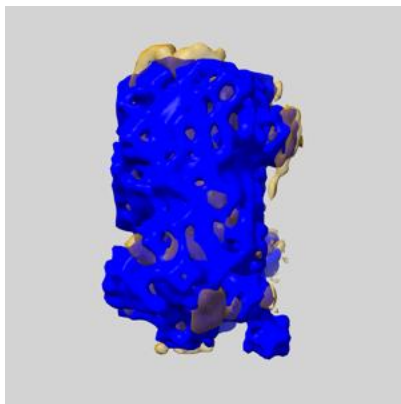
6.6 Mask visualisation [i](#)

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

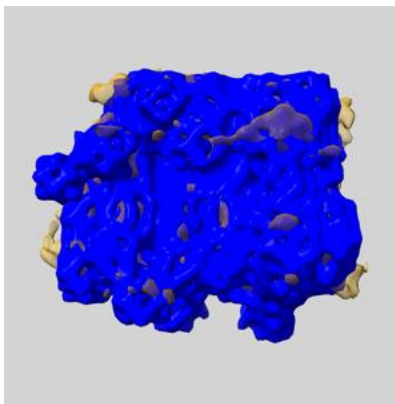
A mask typically either:

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

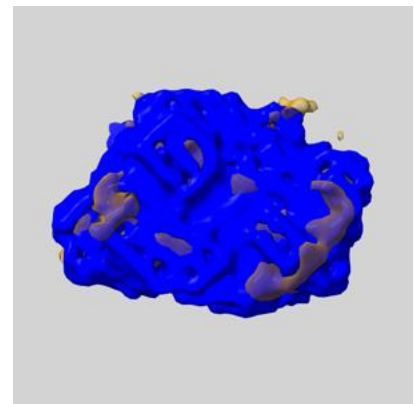
6.6.1 emd_15980_msk_1.map [i](#)



X



Y

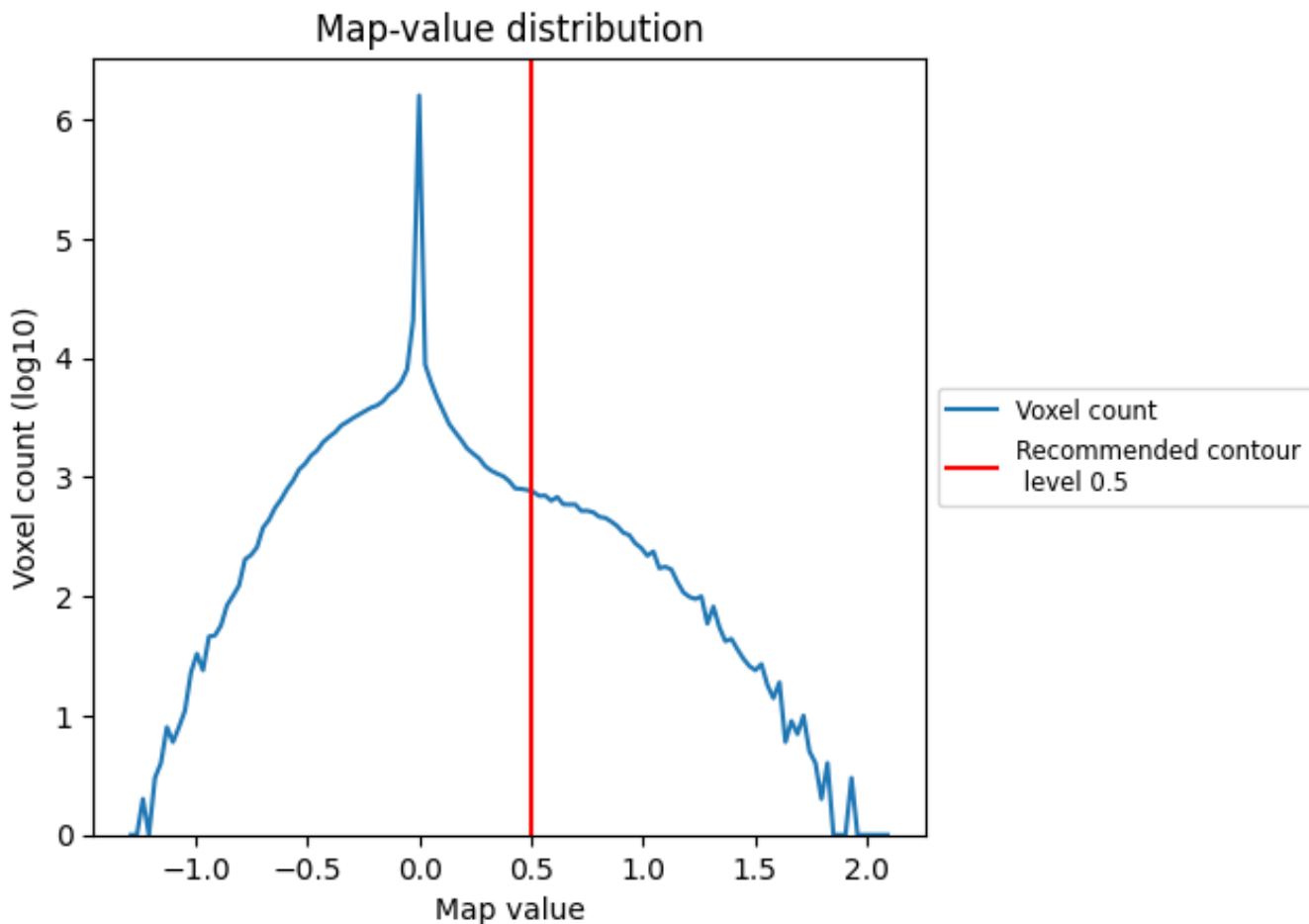


Z

7 Map analysis [i](#)

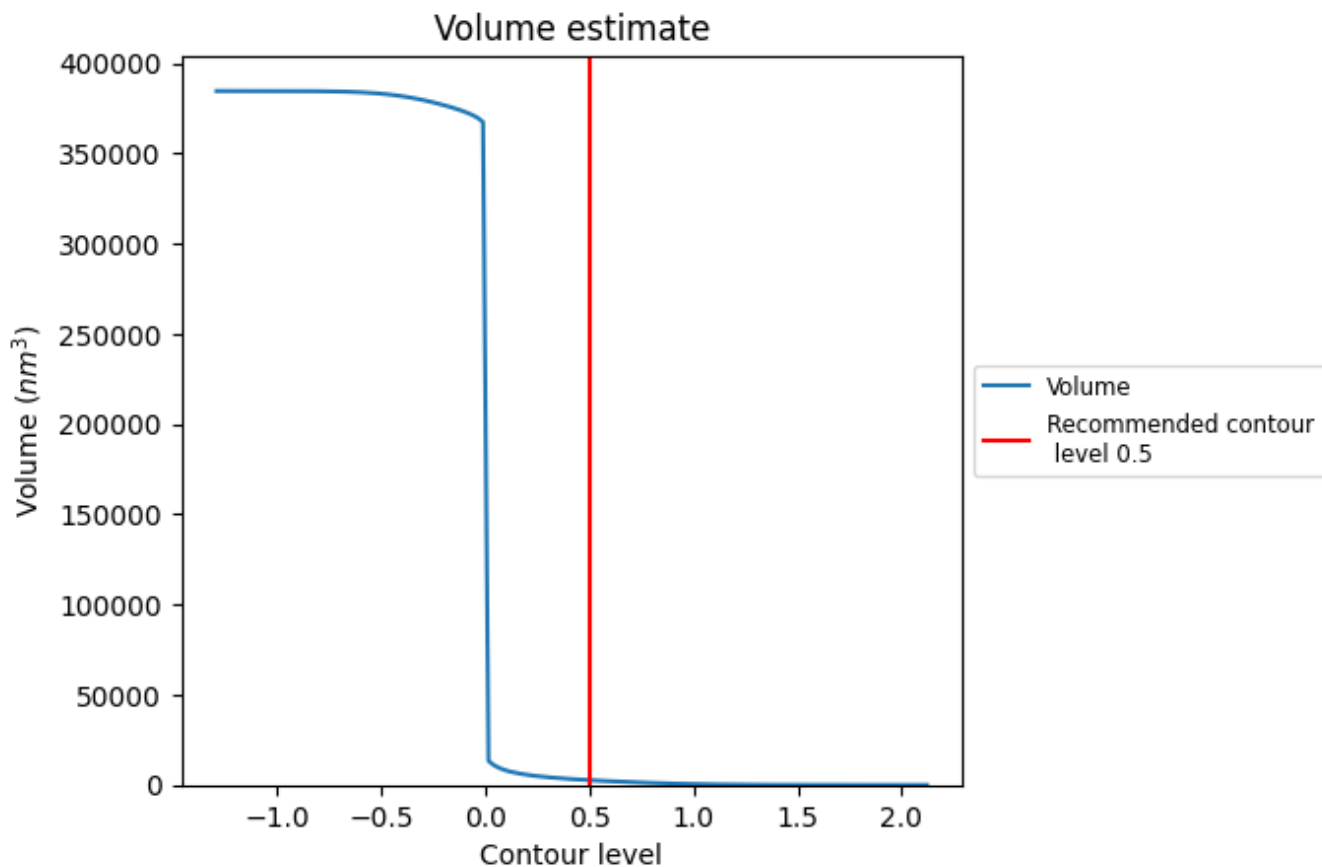
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

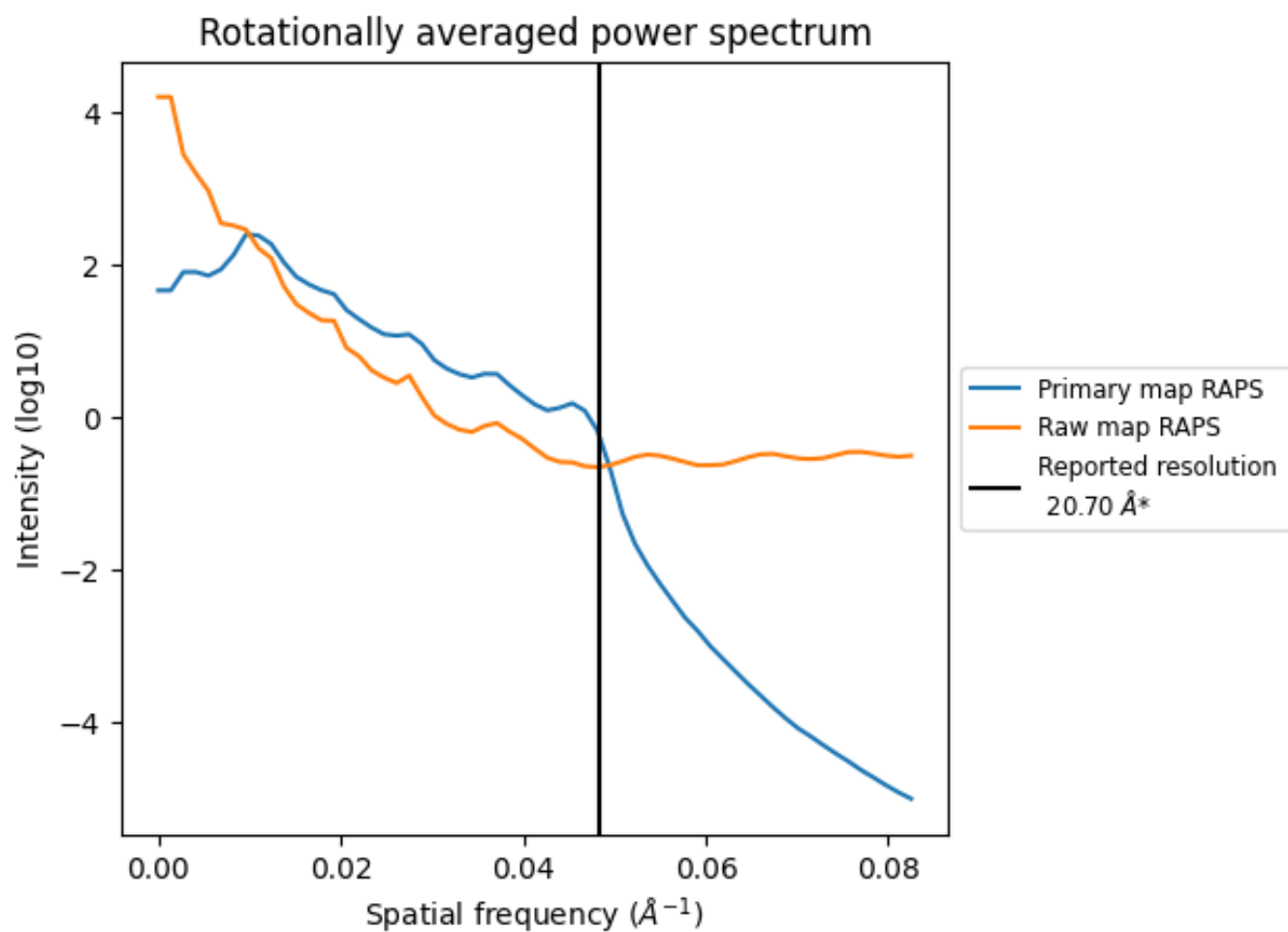
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2681 nm³; this corresponds to an approximate mass of 2422 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 [i](#)

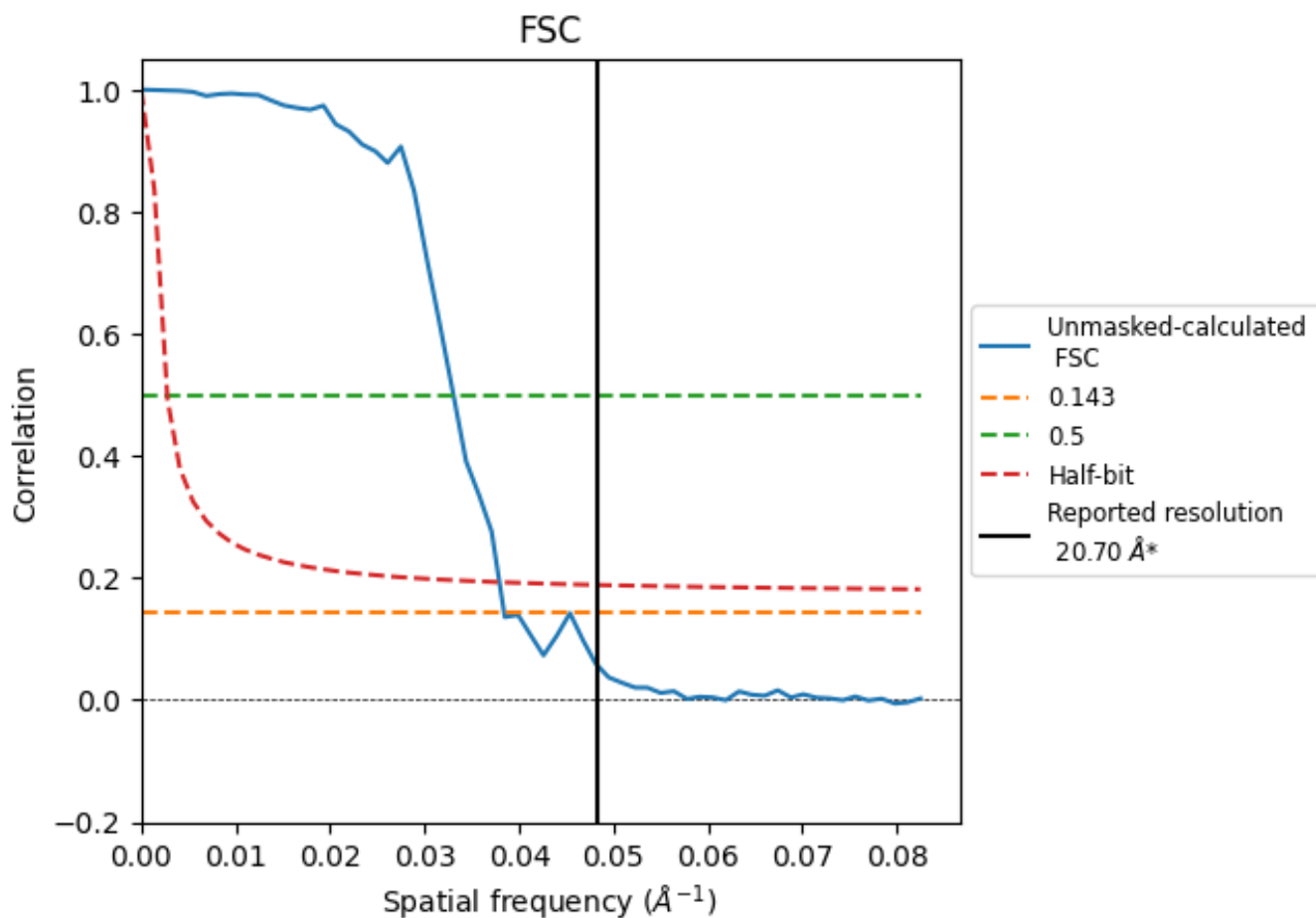


*Reported resolution corresponds to spatial frequency of 0.048 Å⁻¹

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 0.048 Å⁻¹

8.2 Resolution estimates

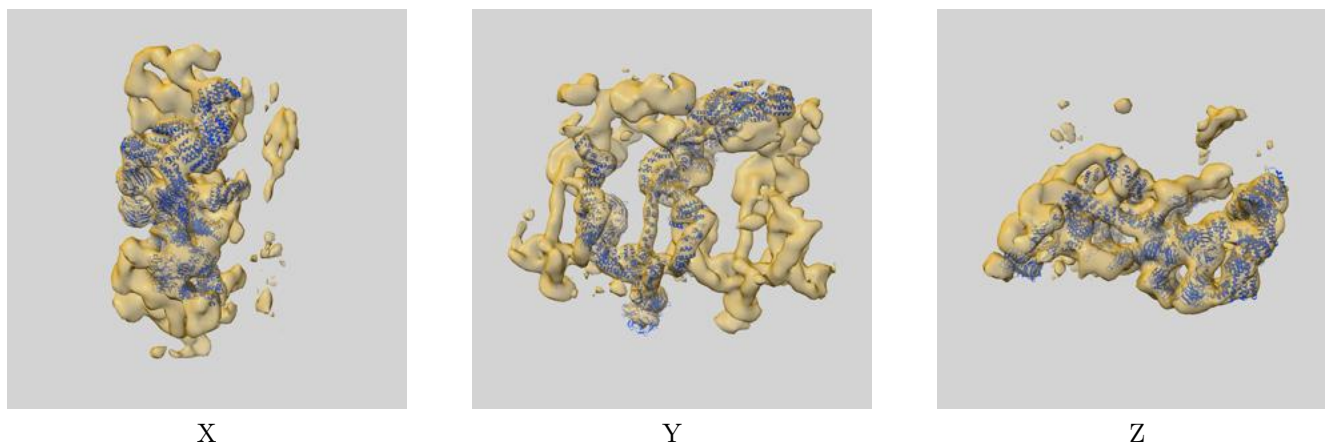
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	20.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	26.04	30.21	26.39

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 26.04 differs from the reported value 20.7 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-15980 and PDB model 8BDA. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



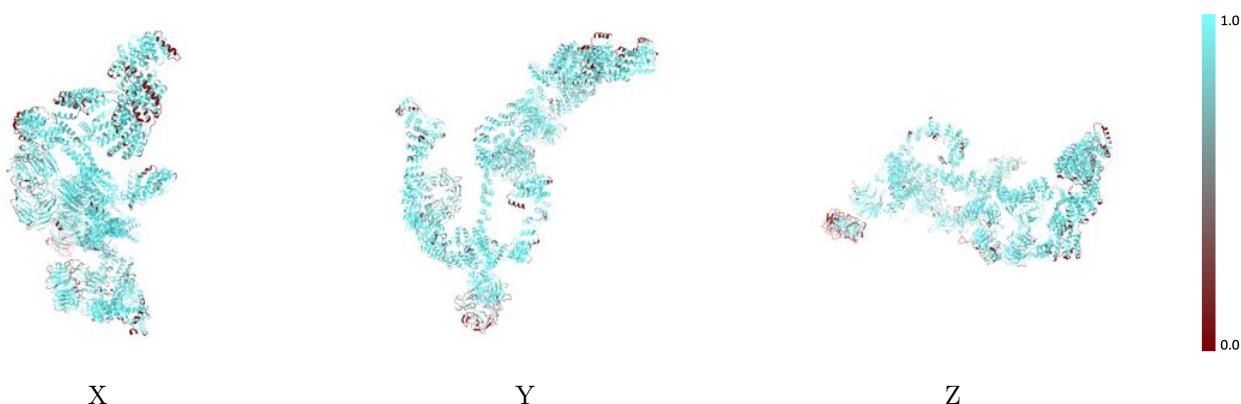
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



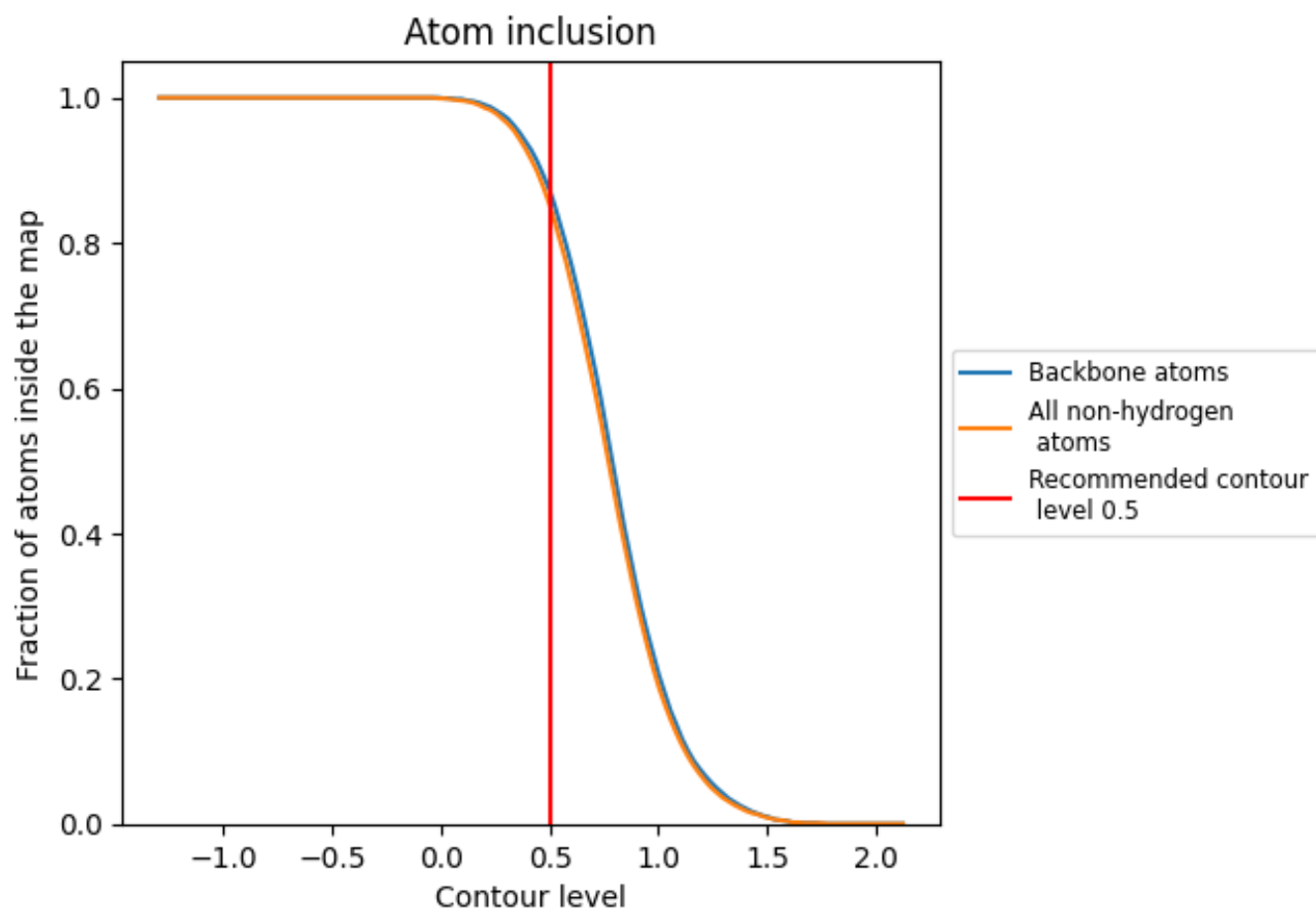
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).













9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 85% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8530	 0.0800
C	 0.8840	 0.0780
E	 0.8250	 0.0740
G	 0.8790	 0.0840
I	 0.7550	 0.0810
L	 0.9510	 0.0840

