



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 01:50 AM UTC

PDB ID : 9NGY / pdb_00009ngy
EMDB ID : EMD-49396
Title : In situ cryo-EM structure of protochannel (DotA-IcmX) of the Legionella Dot/Icm T4SS machine
Authors : Yue, J.; Liu, J.
Deposited on : 2025-02-22
Resolution : 3.63 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:

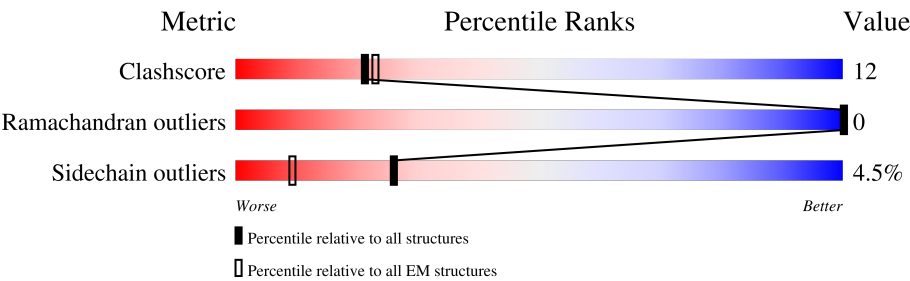
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.63 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



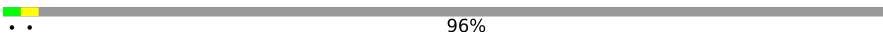
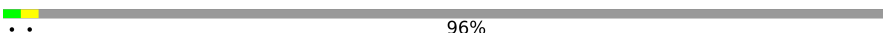
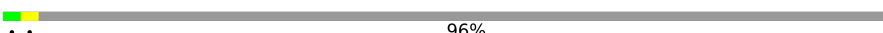
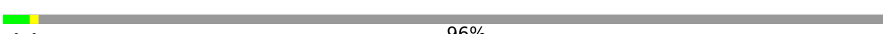
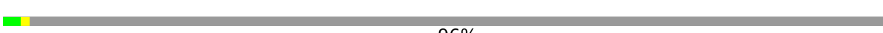
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	AP1	466	69% 19% • 11%
1	BP1	466	67% 22% • 11%
1	CP1	466	70% 19% • 11%
1	DP1	466	69% 20% • 11%
1	EP1	466	70% 19% • 11%
2	FP1	1048	60% 20% • 18%
2	GP1	1048	57% 23% • 18%
2	HP1	1048	57% 23% • 18%
2	IP1	1048	58% 23% • 18%

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Mol	Chain	Length	Quality of chain
2	JP1	1048	 57%23%18%
3	KP1	1048	 96%
3	LP1	1048	 96%
3	MP1	1048	 96%
3	NP1	1048	 96%
3	OP1	1048	 96%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 50535 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 IcmX (IcmY).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AP1	417	Total	C	N	O	S	0	0
			3213	2013	542	646	12		
1	BP1	417	Total	C	N	O	S	0	0
			3213	2013	542	646	12		
1	CP1	417	Total	C	N	O	S	0	0
			3213	2013	542	646	12		
1	DP1	417	Total	C	N	O	S	0	0
			3213	2013	542	646	12		
1	EP1	417	Total	C	N	O	S	0	0
			3213	2013	542	646	12		

- Molecule 2 is a protein called DotA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	FP1	857	Total	C	N	O	S	0	0
			6560	4256	1051	1202	51		
2	GP1	857	Total	C	N	O	S	0	0
			6560	4256	1051	1202	51		
2	HP1	857	Total	C	N	O	S	0	0
			6560	4256	1051	1202	51		
2	IP1	857	Total	C	N	O	S	0	0
			6560	4256	1051	1202	51		
2	JP1	857	Total	C	N	O	S	0	0
			6560	4256	1051	1202	51		

- Molecule 3 is a protein called IcmE (DotG).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	KP1	43	Total	C	N	O	S	0	0
			334	221	58	54	1		
3	LP1	43	Total	C	N	O	S	0	0
			334	221	58	54	1		
3	MP1	43	Total	C	N	O	S	0	0
			334	221	58	54	1		

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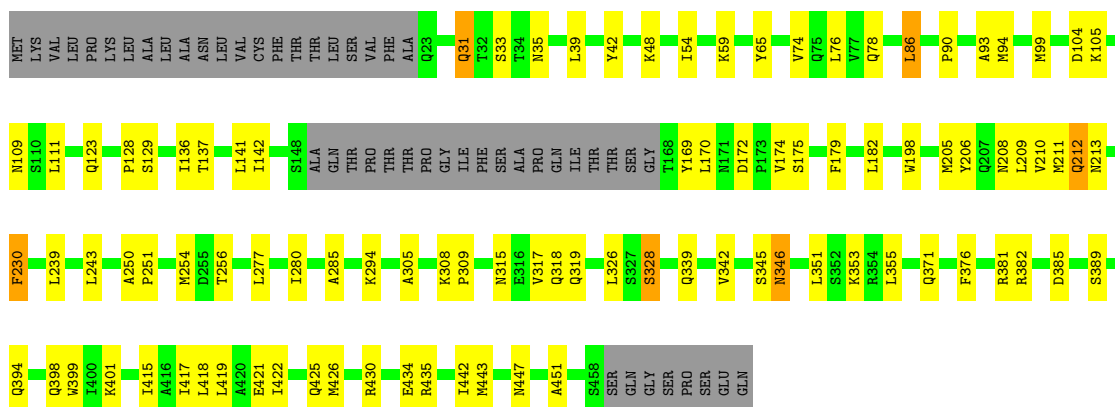
Mol	Chain	Residues	Atoms					AltConf	Trace
3	NP1	43	Total	C	N	O	S	0	0
			334	221	58	54	1		
3	OP1	43	Total	C	N	O	S	0	0
			334	221	58	54	1		

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. 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. 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.

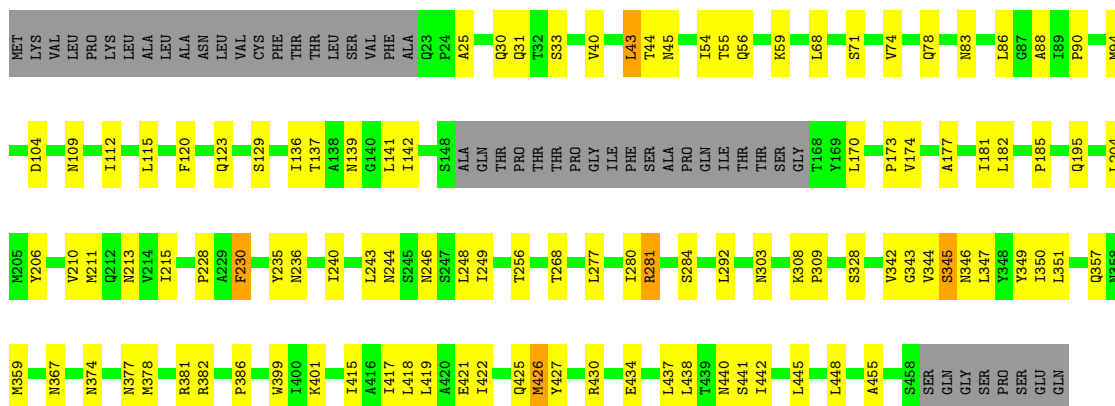
- Molecule 1: IcmX (IcmY)

Chain AP1: 



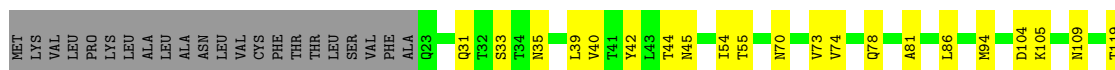
- Molecule 1: IcmX (IcmY)

Chain BP1: 

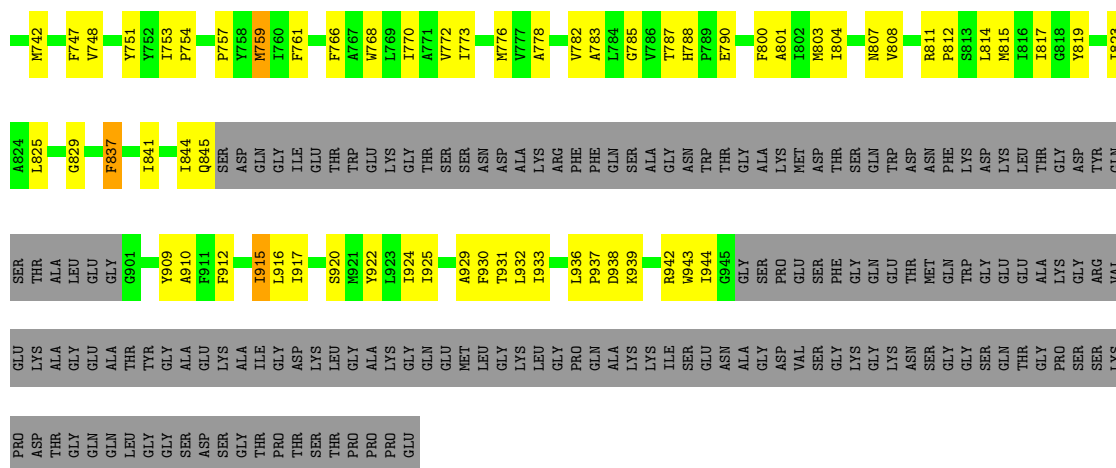


- Molecule 1: IcmX (IcmY)

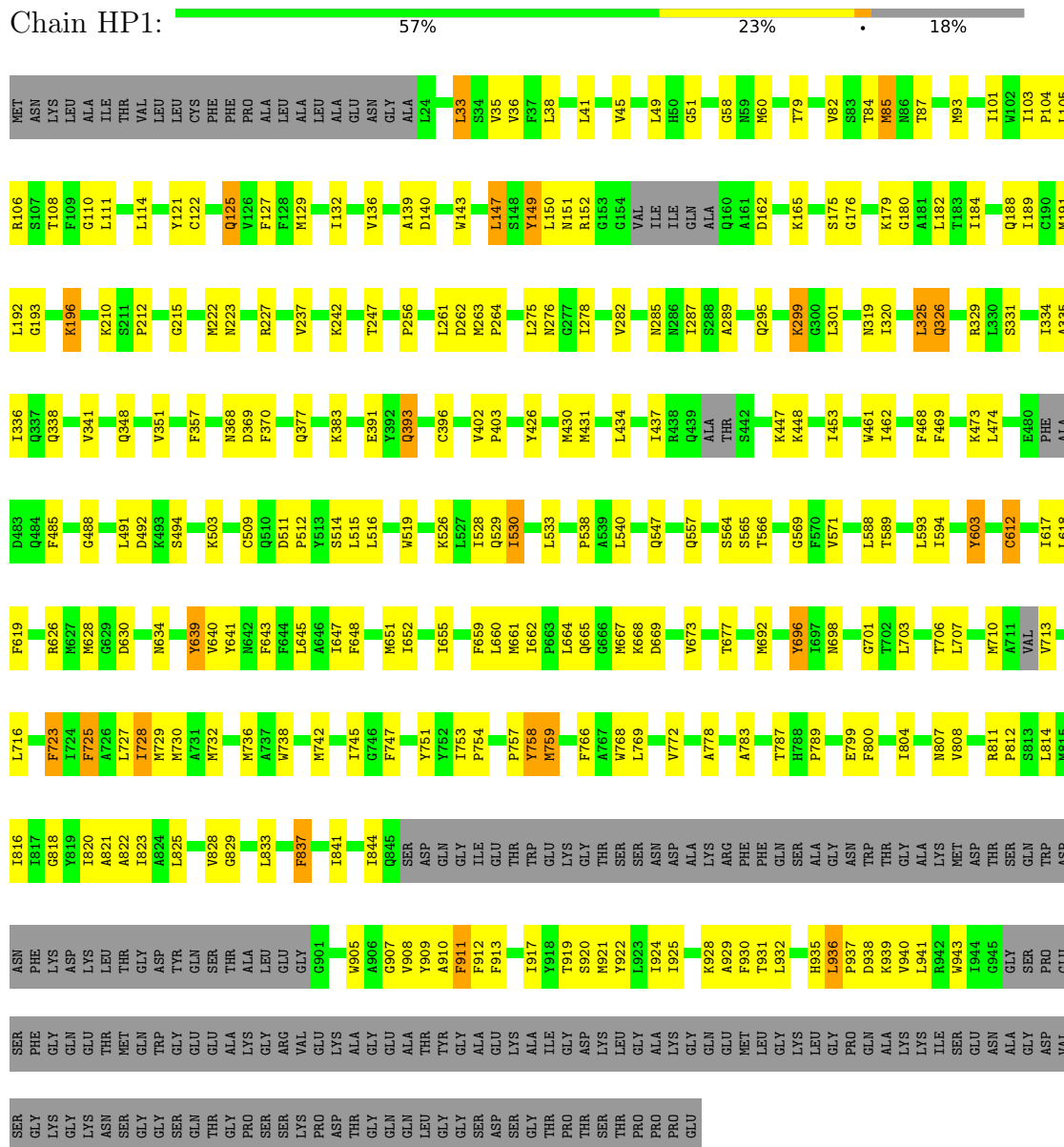
Chain CP1: 





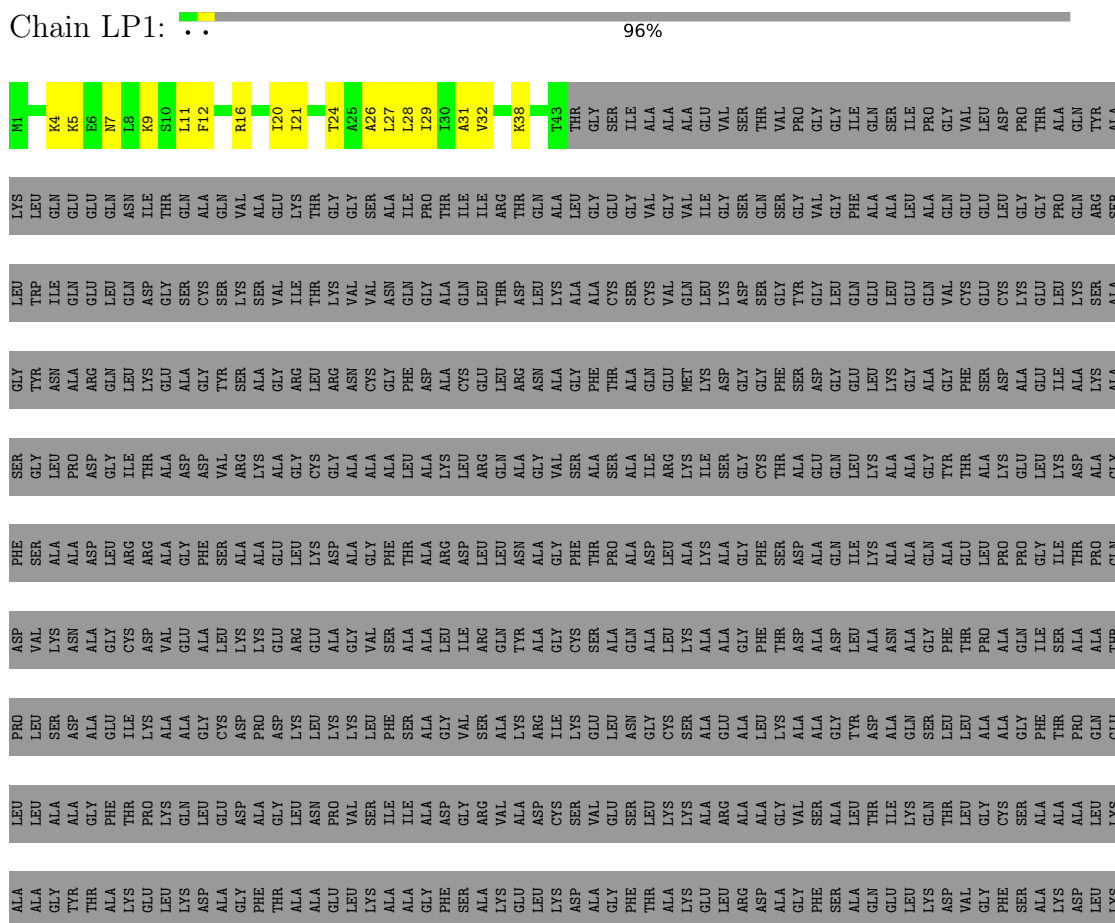


• Molecule 2: DotA



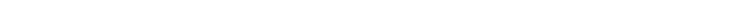
[illegible]

- Molecule 3: IcmE (DotG)



[illegible]

- Molecule 3: IcmE (DotG)

Chain NP1:  96%

[illegible]

- Molecule 3: IcmE (DotG)

[illegible]

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	37503	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TECNAI 12	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	73	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	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	AP1	0.17	0/3277	0.35	0/4473
1	BP1	0.17	0/3277	0.35	0/4473
1	CP1	0.16	0/3277	0.32	0/4473
1	DP1	0.16	0/3277	0.32	0/4473
1	EP1	0.17	0/3277	0.32	0/4473
2	FP1	0.16	0/6715	0.36	0/9115
2	GP1	0.16	0/6715	0.39	0/9115
2	HP1	0.16	0/6715	0.39	0/9115
2	IP1	0.16	0/6715	0.39	0/9115
2	JP1	0.16	0/6715	0.36	0/9115
3	KP1	0.16	0/337	0.52	0/451
3	LP1	0.09	0/337	0.27	0/451
3	MP1	0.12	0/337	0.38	0/451
3	NP1	0.14	0/337	0.41	0/451
3	OP1	0.18	0/337	0.54	0/451
All	All	0.16	0/51645	0.37	0/70195

There are no bond length outliers.

There are no bond angle outliers.

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	AP1	3213	0	3131	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BP1	3213	0	3131	91	0
1	CP1	3213	0	3131	74	0
1	DP1	3213	0	3131	75	0
1	EP1	3213	0	3131	78	0
2	FP1	6560	0	6545	165	0
2	GP1	6560	0	6545	208	0
2	HP1	6560	0	6545	198	0
2	IP1	6560	0	6545	185	0
2	JP1	6560	0	6545	174	0
3	KP1	334	0	378	15	0
3	LP1	334	0	378	14	0
3	MP1	334	0	378	12	0
3	NP1	334	0	378	11	0
3	OP1	334	0	378	13	0
All	All	50535	0	50270	1188	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 12.

All (1188) 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)
2:FP1:671:PHE:HE1	2:FP1:915:ILE:HD13	1.29	0.97
2:HP1:193:GLY:HA3	2:HP1:530:ILE:HD11	1.51	0.92
1:DP1:443:MET:HE2	1:EP1:443:MET:HE1	1.53	0.91
2:GP1:929:ALA:O	2:GP1:932:LEU:HB3	1.73	0.88
2:GP1:193:GLY:HA3	2:GP1:530:ILE:HD11	1.55	0.87
3:MP1:16:ARG:HE	3:MP1:20:ILE:HD11	1.37	0.87
2:HP1:326:GLN:HA	2:HP1:329:ARG:HE	1.39	0.86
2:JP1:193:GLY:HA3	2:JP1:530:ILE:HD11	1.57	0.85
2:FP1:594:ILE:HG23	2:JP1:705:LEU:HD11	1.59	0.84
2:FP1:671:PHE:CE1	2:FP1:915:ILE:HD13	2.13	0.84
2:FP1:78:TYR:HA	2:FP1:81:MET:HE2	1.59	0.84
1:BP1:94:MET:HE1	1:BP1:170:LEU:HD23	1.56	0.83
2:GP1:768:TRP:HB2	2:GP1:815:MET:HE1	1.59	0.83
2:IP1:662:ILE:HG23	2:IP1:663:PRO:HD3	1.59	0.83
2:FP1:828:VAL:HG21	2:JP1:41:LEU:HB2	1.62	0.82
1:CP1:426:MET:HE1	1:DP1:422:ILE:HG23	1.64	0.80
2:FP1:766:PHE:HZ	2:GP1:829:GLY:HA2	1.46	0.79
2:FP1:60:MET:HE1	2:GP1:817:ILE:HG12	1.65	0.78
2:IP1:193:GLY:HA3	2:IP1:530:ILE:HD11	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:FP1:660:LEU:HD21	2:FP1:661:MET:HE2	1.64	0.78
2:FP1:73:GLY:HA2	2:FP1:76:ILE:HD12	1.64	0.78
2:HP1:909:TYR:O	2:HP1:912:PHE:HB2	1.85	0.76
2:HP1:41:LEU:HB2	2:IP1:828:VAL:HG11	1.66	0.76
2:HP1:917:ILE:HA	2:HP1:920:SER:HB3	1.67	0.75
2:HP1:60:MET:HE3	2:IP1:817:ILE:HD13	1.69	0.75
1:DP1:444:LEU:HD23	1:EP1:443:MET:HB2	1.69	0.74
1:AP1:422:ILE:HG23	1:EP1:426:MET:HE1	1.68	0.74
2:IP1:540:LEU:HD23	2:IP1:562:PRO:HB2	1.69	0.74
1:DP1:94:MET:HE1	1:DP1:170:LEU:HD23	1.67	0.74
2:JP1:302:VAL:HG11	2:JP1:325:LEU:HD13	1.70	0.73
2:IP1:612:CYS:HB2	2:IP1:626:ARG:HE	1.52	0.73
2:HP1:101:ILE:HD13	3:OP1:16:ARG:HH21	1.54	0.73
2:GP1:697:ILE:HD12	2:GP1:751:TYR:HE2	1.53	0.72
2:JP1:612:CYS:HB2	2:JP1:626:ARG:HE	1.53	0.72
2:FP1:72:GLY:HA3	2:FP1:784:LEU:HD21	1.71	0.72
2:IP1:41:LEU:HB2	2:JP1:828:VAL:HG11	1.72	0.72
1:DP1:123:GLN:HE22	1:DP1:256:THR:HG21	1.54	0.72
2:IP1:756:LEU:HA	2:IP1:759:MET:HG3	1.73	0.71
1:DP1:426:MET:HE1	1:EP1:422:ILE:HG23	1.72	0.71
2:IP1:266:PHE:H	2:IP1:276:ASN:HD21	1.36	0.71
2:GP1:759:MET:HE3	2:HP1:917:ILE:HG12	1.71	0.71
2:HP1:103:ILE:HG13	2:HP1:104:PRO:HD3	1.73	0.71
1:BP1:139:ASN:HB2	1:BP1:281:ARG:HH12	1.56	0.70
2:IP1:377:GLN:HE22	2:IP1:402:VAL:HG12	1.56	0.70
2:JP1:627:MET:HG2	2:JP1:628:MET:HE2	1.73	0.70
1:EP1:371:GLN:O	1:EP1:375:GLU:HB2	1.91	0.70
2:GP1:180:GLY:O	2:GP1:184:ILE:HD12	1.90	0.70
1:DP1:328:SER:HA	1:EP1:211:MET:HE2	1.74	0.70
2:FP1:732:MET:HA	2:FP1:732:MET:HE2	1.74	0.69
2:JP1:662:ILE:HG12	2:JP1:703:LEU:HD12	1.74	0.69
2:JP1:920:SER:O	2:JP1:924:ILE:HD12	1.92	0.69
2:GP1:648:PHE:O	2:GP1:652:ILE:HG13	1.93	0.69
1:BP1:94:MET:HG3	1:CP1:241:SER:HB2	1.73	0.69
1:DP1:426:MET:HE3	1:EP1:425:GLN:HB2	1.75	0.69
2:FP1:566:THR:HG23	2:FP1:569:GLY:H	1.56	0.69
2:HP1:377:GLN:HE22	2:HP1:402:VAL:H	1.40	0.69
2:GP1:788:HIS:HB3	2:GP1:790:GLU:HG3	1.75	0.68
2:HP1:320:ILE:HD11	2:HP1:325:LEU:HD12	1.75	0.68
2:IP1:932:LEU:HA	2:IP1:935:HIS:HB3	1.75	0.68
2:FP1:74:ILE:HA	2:FP1:77:MET:HE2	1.73	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP1:104:ASP:HA	1:BP1:109:ASN:HD22	1.58	0.68
2:IP1:920:SER:O	2:IP1:924:ILE:HD12	1.94	0.68
2:GP1:716:LEU:HA	2:HP1:723:PHE:CD1	2.29	0.68
1:CP1:342:VAL:HG21	1:CP1:442:ILE:HG13	1.75	0.68
2:IP1:391:GLU:HG3	2:IP1:393:GLN:H	1.59	0.68
2:IP1:741:THR:HG23	2:IP1:916:LEU:HD21	1.75	0.68
1:BP1:342:VAL:HG21	1:BP1:442:ILE:HG13	1.75	0.68
2:IP1:566:THR:HG23	2:IP1:569:GLY:H	1.58	0.68
2:HP1:929:ALA:O	2:HP1:932:LEU:HD12	1.94	0.68
2:FP1:266:PHE:H	2:FP1:276:ASN:HD21	1.42	0.68
1:AP1:104:ASP:HA	1:AP1:109:ASN:HD22	1.59	0.67
2:HP1:757:PRO:HG3	2:HP1:930:PHE:HE1	1.60	0.67
1:EP1:185:PRO:HG3	1:EP1:204:LEU:HD12	1.76	0.67
1:BP1:123:GLN:HE22	1:BP1:256:THR:HG21	1.59	0.67
1:EP1:74:VAL:O	1:EP1:78:GLN:HG2	1.95	0.67
2:GP1:920:SER:O	2:GP1:924:ILE:HD12	1.95	0.67
2:GP1:656:VAL:HG12	2:GP1:660:LEU:HD23	1.76	0.67
2:JP1:723:PHE:CD2	2:JP1:724:ILE:HD13	2.29	0.67
1:AP1:342:VAL:HG21	1:AP1:442:ILE:HG13	1.75	0.67
1:BP1:248:LEU:HD22	1:BP1:249:ILE:HG22	1.75	0.67
2:HP1:192:LEU:HB2	2:HP1:351:VAL:HG21	1.75	0.67
2:HP1:594:ILE:HB	2:HP1:660:LEU:HD12	1.75	0.67
2:FP1:242:LYS:HG2	2:FP1:261:LEU:HD23	1.76	0.67
2:HP1:651:MET:O	2:HP1:655:ILE:HG13	1.95	0.67
3:MP1:25:ALA:O	3:MP1:29:ILE:HG12	1.95	0.67
2:FP1:78:TYR:O	2:FP1:82:VAL:HG23	1.95	0.66
1:BP1:54:ILE:HG22	1:CP1:42:TYR:HD2	1.60	0.66
2:FP1:745:ILE:HG23	2:FP1:919:THR:HG21	1.78	0.66
2:IP1:709:ASN:HD21	2:JP1:597:LYS:H	1.44	0.66
1:CP1:136:ILE:HG23	1:CP1:277:LEU:HD22	1.77	0.66
1:CP1:328:SER:HA	1:DP1:211:MET:HE2	1.78	0.66
2:IP1:72:GLY:O	2:IP1:76:ILE:HG13	1.95	0.66
1:BP1:40:VAL:O	1:BP1:44:THR:HG23	1.96	0.66
2:IP1:759:MET:HA	2:JP1:921:MET:HE1	1.76	0.66
2:GP1:450:ARG:O	2:GP1:453:ILE:HG13	1.96	0.65
2:GP1:651:MET:O	2:GP1:655:ILE:HG12	1.96	0.65
2:HP1:242:LYS:HG2	2:HP1:261:LEU:HD23	1.76	0.65
2:IP1:72:GLY:HA3	2:IP1:784:LEU:HD11	1.76	0.65
2:JP1:566:THR:HG23	2:JP1:569:GLY:H	1.60	0.65
1:BP1:430:ARG:HH21	1:CP1:425:GLN:HB3	1.59	0.65
1:DP1:74:VAL:O	1:DP1:78:GLN:HG2	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:IP1:627:MET:HG2	2:IP1:628:MET:HE2	1.78	0.65
3:LP1:24:THR:HA	3:LP1:27:LEU:HD12	1.77	0.65
1:AP1:33:SER:HB2	1:BP1:31:GLN:OE1	1.96	0.65
2:GP1:732:MET:HE2	2:GP1:732:MET:HA	1.79	0.65
2:IP1:757:PRO:HG3	2:IP1:930:PHE:CE1	2.32	0.64
2:IP1:841:ILE:HD12	2:IP1:844:ILE:HB	1.79	0.64
2:GP1:702:THR:HG23	2:HP1:905:TRP:HE1	1.61	0.64
2:HP1:180:GLY:O	2:HP1:184:ILE:HD12	1.96	0.64
1:CP1:74:VAL:O	1:CP1:78:GLN:HG2	1.96	0.64
2:GP1:706:THR:HG22	2:GP1:710:MET:HE2	1.80	0.64
2:HP1:662:ILE:HG12	2:HP1:703:LEU:HD11	1.80	0.64
2:JP1:72:GLY:HA3	2:JP1:784:LEU:HD11	1.79	0.64
3:MP1:16:ARG:O	3:MP1:20:ILE:HG13	1.97	0.64
1:AP1:74:VAL:O	1:AP1:78:GLN:HG2	1.98	0.64
2:HP1:738:TRP:CD1	2:HP1:912:PHE:HZ	2.15	0.64
2:HP1:648:PHE:O	2:HP1:652:ILE:HG22	1.98	0.64
2:IP1:639:TYR:HE2	2:JP1:605:MET:HE1	1.61	0.64
2:HP1:932:LEU:HA	2:HP1:935:HIS:CD2	2.33	0.64
2:GP1:132:ILE:HG13	2:GP1:772:VAL:HG13	1.80	0.63
2:GP1:759:MET:HG3	2:HP1:921:MET:HE2	1.78	0.63
2:FP1:667:MET:HE1	2:FP1:915:ILE:HG21	1.80	0.63
2:HP1:182:LEU:HD23	2:HP1:571:VAL:HG21	1.80	0.63
2:IP1:332:ARG:HH21	2:IP1:489:THR:HA	1.63	0.63
2:FP1:741:THR:O	2:FP1:745:ILE:HG13	1.99	0.63
2:GP1:766:PHE:HZ	2:HP1:829:GLY:HA3	1.63	0.63
2:JP1:807:ASN:HD22	2:JP1:941:LEU:HG	1.64	0.63
1:AP1:254:MET:HG3	1:AP1:355:LEU:HD12	1.81	0.63
1:EP1:136:ILE:HG23	1:EP1:277:LEU:HD22	1.81	0.63
2:HP1:728:ILE:HD11	2:IP1:729:MET:HE3	1.80	0.63
1:EP1:141:LEU:HB3	1:EP1:213:ASN:HB3	1.81	0.63
1:AP1:111:LEU:HD23	1:BP1:386:PRO:HB3	1.81	0.62
2:HP1:804:ILE:HD12	2:HP1:807:ASN:HD22	1.64	0.62
2:IP1:45:VAL:HG11	2:IP1:129:MET:HG2	1.81	0.62
1:DP1:129:SER:HB2	1:DP1:137:THR:HG21	1.81	0.62
2:HP1:932:LEU:HB3	2:HP1:936:LEU:HD12	1.82	0.62
2:IP1:100:SER:HA	2:IP1:103:ILE:HD12	1.81	0.62
1:BP1:83:ASN:HB2	1:BP1:359:MET:HE1	1.82	0.62
2:GP1:110:GLY:HA3	2:GP1:787:THR:HG23	1.82	0.62
2:JP1:905:TRP:HA	2:JP1:908:VAL:HB	1.80	0.62
3:MP1:16:ARG:NE	3:MP1:20:ILE:HD11	2.13	0.62
1:AP1:211:MET:HE2	1:EP1:328:SER:HA	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:HP1:804:ILE:O	2:HP1:808:VAL:HG22	2.00	0.62
2:IP1:744:SER:O	2:IP1:748:VAL:HG23	2.00	0.62
1:DP1:427:TYR:HA	1:DP1:430:ARG:NH1	2.15	0.62
2:IP1:704:TRP:HA	2:IP1:707:LEU:HD12	1.81	0.62
1:CP1:104:ASP:HA	1:CP1:109:ASN:HD22	1.65	0.61
3:KP1:16:ARG:O	3:KP1:20:ILE:HG12	2.00	0.61
1:AP1:31:GLN:HE21	1:EP1:33:SER:HB2	1.63	0.61
2:JP1:402:VAL:HG12	2:JP1:404:SER:H	1.65	0.61
2:HP1:732:MET:HA	2:HP1:732:MET:HE2	1.80	0.61
2:JP1:616:LYS:HA	2:JP1:620:PHE:O	2.00	0.61
3:MP1:24:THR:HA	3:MP1:27:LEU:HD12	1.82	0.61
1:BP1:142:ILE:HA	1:BP1:210:VAL:HG23	1.83	0.61
2:IP1:131:VAL:HG21	2:IP1:805:LEU:HD11	1.82	0.61
2:JP1:101:ILE:HG12	3:MP1:16:ARG:HH22	1.65	0.61
1:DP1:427:TYR:HA	1:DP1:430:ARG:HH11	1.65	0.61
2:GP1:708:LEU:HD13	2:HP1:730:MET:HB3	1.81	0.61
2:GP1:768:TRP:O	2:GP1:772:VAL:HG23	2.00	0.61
2:IP1:528:ILE:HD11	2:IP1:538:PRO:HD3	1.81	0.61
2:JP1:590:PHE:CE2	2:JP1:664:LEU:HD13	2.35	0.61
2:JP1:630:ASP:HA	2:JP1:634:ASN:HB2	1.82	0.61
1:DP1:427:TYR:HD1	1:DP1:430:ARG:HH12	1.49	0.61
1:EP1:104:ASP:HA	1:EP1:109:ASN:HD22	1.65	0.61
2:FP1:330:LEU:O	2:FP1:334:ILE:HG13	2.00	0.61
2:GP1:721:GLY:HA3	2:HP1:723:PHE:HE1	1.66	0.61
2:IP1:183:THR:HG23	2:IP1:496:PHE:HB2	1.83	0.61
1:DP1:136:ILE:HG23	1:DP1:277:LEU:HD22	1.82	0.61
2:GP1:103:ILE:HG13	2:GP1:104:PRO:HD3	1.82	0.61
3:NP1:16:ARG:HE	3:NP1:17:THR:HG22	1.65	0.61
2:JP1:932:LEU:HA	2:JP1:935:HIS:HB3	1.82	0.61
2:FP1:804:ILE:O	2:FP1:808:VAL:HG22	2.00	0.60
2:GP1:747:PHE:HA	2:GP1:751:TYR:HD2	1.65	0.60
2:IP1:106:ARG:HE	2:IP1:794:ALA:HA	1.67	0.60
1:BP1:129:SER:HB2	1:BP1:137:THR:HG21	1.83	0.60
2:FP1:113:LEU:HD13	2:FP1:123:MET:HG3	1.82	0.60
2:FP1:593:LEU:H	2:FP1:593:LEU:HD23	1.67	0.60
2:GP1:804:ILE:O	2:GP1:808:VAL:HG22	2.00	0.60
2:HP1:816:ILE:O	2:HP1:820:ILE:HG13	2.02	0.60
1:BP1:55:THR:HA	1:CP1:42:TYR:HE2	1.67	0.60
2:HP1:928:LYS:O	2:HP1:931:THR:HG22	2.01	0.60
1:AP1:339:GLN:HB3	1:EP1:448:LEU:HD11	1.84	0.60
1:CP1:81:ALA:HB2	1:CP1:378:MET:HE1	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GP1:470:ASP:HA	2:GP1:473:LYS:HD2	1.84	0.59
1:CP1:40:VAL:O	1:CP1:44:THR:HG23	2.02	0.59
2:GP1:757:PRO:HG3	2:GP1:930:PHE:CE2	2.38	0.59
2:IP1:732:MET:HE2	2:IP1:732:MET:HA	1.84	0.59
1:AP1:174:VAL:HG13	1:BP1:244:ASN:HD21	1.67	0.59
1:CP1:141:LEU:HD22	1:CP1:213:ASN:HB3	1.83	0.59
2:HP1:907:GLY:O	2:HP1:910:ALA:HB3	2.02	0.59
1:DP1:182:LEU:HD11	1:EP1:243:LEU:HD12	1.84	0.59
2:GP1:612:CYS:HB3	2:GP1:626:ARG:HB2	1.85	0.59
2:HP1:391:GLU:HG3	2:HP1:393:GLN:H	1.67	0.59
1:DP1:352:SER:HA	1:DP1:355:LEU:HD23	1.84	0.59
2:FP1:504:PRO:HG3	2:FP1:513:TYR:HB2	1.85	0.59
2:GP1:785:GLY:HA2	2:GP1:788:HIS:CD2	2.37	0.59
1:CP1:352:SER:HA	1:CP1:355:LEU:HD12	1.85	0.59
2:JP1:188:GLN:O	2:JP1:192:LEU:HD13	2.03	0.59
2:FP1:287:ILE:HD12	2:FP1:287:ILE:H	1.68	0.59
2:JP1:287:ILE:HD12	2:JP1:287:ILE:H	1.67	0.59
2:FP1:675:VAL:O	2:FP1:679:THR:HG23	2.03	0.59
2:HP1:566:THR:HG23	2:HP1:569:GLY:H	1.67	0.59
2:JP1:289:ALA:HA	2:JP1:312:SER:HB2	1.84	0.59
2:HP1:150:LEU:HD12	2:HP1:474:LEU:HG	1.85	0.59
2:JP1:136:VAL:HG22	2:JP1:461:TRP:HE1	1.68	0.59
1:BP1:430:ARG:NH2	1:CP1:425:GLN:HB3	2.18	0.58
2:GP1:182:LEU:HD23	2:GP1:571:VAL:HG21	1.85	0.58
2:IP1:38:LEU:HD21	2:IP1:129:MET:HE1	1.85	0.58
2:IP1:77:MET:O	2:IP1:81:MET:HG3	2.02	0.58
2:FP1:722:ILE:O	2:FP1:725:PHE:HB3	2.04	0.58
2:JP1:556:ARG:HD2	2:JP1:576:MET:HG2	1.85	0.58
2:HP1:938:ASP:O	2:HP1:941:LEU:HB2	2.04	0.58
1:DP1:191:MET:HG2	1:DP1:198:TRP:HA	1.86	0.58
2:FP1:403:PRO:HB3	2:JP1:268:LYS:HB3	1.84	0.58
2:FP1:588:LEU:HD13	2:FP1:661:MET:HG3	1.86	0.58
2:FP1:627:MET:HG2	2:FP1:628:MET:HE2	1.84	0.58
2:GP1:147:LEU:HB2	2:GP1:453:ILE:HG23	1.84	0.58
2:JP1:296:SER:HA	2:JP1:302:VAL:HG13	1.86	0.58
3:KP1:38:LYS:HE2	3:KP1:38:LYS:HA	1.86	0.58
2:IP1:367:LYS:HD3	2:IP1:367:LYS:N	2.19	0.58
1:EP1:142:ILE:HA	1:EP1:210:VAL:HG23	1.86	0.58
2:JP1:824:ALA:O	2:JP1:827:TYR:HB2	2.03	0.58
2:GP1:814:LEU:HD23	2:GP1:937:PRO:HA	1.87	0.57
3:OP1:30:ILE:O	3:OP1:34:ILE:HG22	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GP1:242:LYS:HG2	2:GP1:261:LEU:HD23	1.86	0.57
1:CP1:105:LYS:HZ3	1:DP1:367:ASN:HA	1.67	0.57
1:AP1:141:LEU:HD23	1:AP1:213:ASN:HB3	1.86	0.57
1:AP1:94:MET:HE3	1:BP1:240:ILE:HB	1.85	0.57
1:BP1:427:TYR:HD1	1:BP1:430:ARG:HH12	1.51	0.57
2:GP1:528:ILE:HD11	2:GP1:538:PRO:HD3	1.86	0.57
2:IP1:77:MET:HE1	3:NP1:32:VAL:HG11	1.86	0.57
1:BP1:136:ILE:HG23	1:BP1:277:LEU:HD22	1.87	0.57
2:GP1:489:THR:HG23	2:GP1:491:LEU:H	1.70	0.57
2:JP1:512:PRO:HG2	2:JP1:513:TYR:CE1	2.39	0.57
2:JP1:702:THR:O	2:JP1:706:THR:HG23	2.05	0.57
2:GP1:785:GLY:HA2	2:GP1:788:HIS:NE2	2.19	0.57
2:HP1:757:PRO:HG3	2:HP1:930:PHE:CE1	2.40	0.57
2:IP1:402:VAL:HG13	2:IP1:405:SER:HB3	1.86	0.57
1:AP1:353:LYS:HG2	1:AP1:371:GLN:HE21	1.69	0.57
2:FP1:247:THR:HG22	2:FP1:256:PRO:HD2	1.87	0.57
2:HP1:151:ASN:HB3	2:HP1:152:ARG:HH11	1.69	0.56
2:JP1:668:LYS:HA	2:JP1:911:PHE:HE2	1.70	0.56
2:JP1:793:GLU:HG3	2:JP1:795:PHE:H	1.68	0.56
2:GP1:122:CYS:H	2:GP1:125:GLN:HG3	1.71	0.56
2:IP1:766:PHE:CZ	2:JP1:829:GLY:HA2	2.40	0.56
1:DP1:385:ASP:H	1:DP1:398:GLN:HE22	1.52	0.56
2:GP1:770:ILE:HA	2:GP1:773:ILE:HD12	1.87	0.56
2:IP1:766:PHE:CD1	2:JP1:925:ILE:HD11	2.40	0.56
2:IP1:940:VAL:O	2:IP1:944:ILE:HD12	2.05	0.56
2:FP1:807:ASN:HB2	2:FP1:941:LEU:HD11	1.87	0.56
2:HP1:287:ILE:HG22	2:HP1:289:ALA:H	1.71	0.56
2:HP1:766:PHE:HZ	2:IP1:829:GLY:HA2	1.71	0.56
1:BP1:236:ASN:O	1:BP1:240:ILE:HG13	2.05	0.56
2:FP1:33:LEU:HA	2:FP1:36:VAL:HB	1.86	0.56
2:FP1:148:SER:O	2:FP1:152:ARG:HD3	2.05	0.56
2:FP1:660:LEU:HD23	2:FP1:661:MET:H	1.70	0.56
2:HP1:528:ILE:HD11	2:HP1:538:PRO:HD3	1.87	0.56
2:GP1:690:ALA:O	2:GP1:694:THR:HG23	2.06	0.56
2:IP1:837:PHE:O	2:IP1:841:ILE:HG22	2.06	0.56
1:EP1:94:MET:HB2	1:EP1:98:LEU:HD23	1.88	0.56
2:HP1:383:LYS:HA	2:HP1:396:CYS:HA	1.88	0.56
2:JP1:222:MET:HE1	2:JP1:519:TRP:HA	1.87	0.56
2:FP1:685:PRO:HB2	2:FP1:830:VAL:HG11	1.88	0.56
2:IP1:136:VAL:HG13	2:IP1:461:TRP:HE1	1.71	0.56
2:FP1:555:GLN:HE22	2:FP1:588:LEU:HD12	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:FP1:684:ASN:HD22	2:FP1:687:VAL:HG23	1.71	0.56
2:GP1:600:THR:HB	2:GP1:645:LEU:HD22	1.87	0.56
1:AP1:426:MET:HE1	1:BP1:422:ILE:HG23	1.88	0.56
2:FP1:640:VAL:HG22	2:GP1:605:MET:HE1	1.88	0.56
2:IP1:434:LEU:HD13	2:IP1:437:ILE:HD12	1.88	0.56
1:AP1:123:GLN:HE22	1:AP1:256:THR:HG21	1.70	0.55
1:DP1:263:GLN:H	1:DP1:268:THR:HG21	1.71	0.55
1:EP1:208:ASN:O	1:EP1:212:GLN:HG2	2.06	0.55
2:HP1:593:LEU:HD21	2:HP1:905:TRP:HB3	1.87	0.55
2:IP1:690:ALA:O	2:IP1:694:THR:HG23	2.05	0.55
2:JP1:590:PHE:HE2	2:JP1:664:LEU:HD13	1.70	0.55
1:CP1:208:ASN:O	1:CP1:212:GLN:HG2	2.06	0.55
2:HP1:630:ASP:HA	2:HP1:634:ASN:HB2	1.87	0.55
3:NP1:14:ASN:HB3	3:NP1:17:THR:HG23	1.88	0.55
1:AP1:285:ALA:HB1	1:EP1:449:LYS:HE3	1.89	0.55
2:GP1:724:ILE:O	2:GP1:728:ILE:HG22	2.06	0.55
2:HP1:35:VAL:HA	2:HP1:38:LEU:HB2	1.87	0.55
2:HP1:331:SER:HA	2:HP1:334:ILE:HD12	1.87	0.55
2:FP1:548:PRO:HD3	2:FP1:568:TYR:CD1	2.41	0.55
2:JP1:844:ILE:HA	2:JP1:902:TYR:HE2	1.72	0.55
1:CP1:142:ILE:HD11	1:CP1:267:LEU:HD22	1.88	0.55
1:BP1:426:MET:HE1	1:CP1:422:ILE:HG23	1.88	0.55
1:EP1:342:VAL:HG21	1:EP1:442:ILE:HG13	1.89	0.55
2:JP1:667:MET:HE2	2:JP1:912:PHE:CD1	2.41	0.55
1:DP1:193:ASN:HD21	2:JP1:216:GLY:HA3	1.71	0.55
2:FP1:821:ALA:HA	2:JP1:57:MET:HE1	1.88	0.55
2:GP1:773:ILE:HD11	2:HP1:825:LEU:HD21	1.88	0.55
2:IP1:618:LEU:HD23	2:JP1:618:LEU:HB2	1.89	0.55
2:GP1:179:LYS:HA	2:GP1:550:LEU:HD23	1.89	0.55
2:JP1:807:ASN:ND2	2:JP1:941:LEU:HG	2.22	0.55
2:GP1:671:PHE:CG	2:GP1:915:ILE:HD11	2.42	0.55
2:IP1:788:HIS:HB3	2:IP1:790:GLU:HG3	1.89	0.54
2:IP1:911:PHE:O	2:IP1:915:ILE:HG22	2.07	0.54
2:JP1:392:TYR:HE2	2:JP1:585:ILE:HG21	1.71	0.54
1:BP1:139:ASN:HB2	1:BP1:281:ARG:NH1	2.22	0.54
2:HP1:180:GLY:HA3	2:HP1:491:LEU:HD23	1.88	0.54
2:HP1:931:THR:HG23	2:HP1:935:HIS:NE2	2.22	0.54
1:EP1:123:GLN:HE22	1:EP1:256:THR:HG21	1.71	0.54
2:IP1:768:TRP:HB2	2:IP1:815:MET:HE1	1.89	0.54
2:FP1:648:PHE:CZ	2:FP1:652:ILE:HD11	2.42	0.54
2:HP1:814:LEU:HD13	2:HP1:937:PRO:HA	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:HP1:822:ALA:HB1	2:HP1:930:PHE:HD2	1.72	0.54
1:AP1:93:ALA:HB3	1:AP1:172:ASP:HB2	1.90	0.54
1:CP1:129:SER:H	1:CP1:137:THR:HG21	1.72	0.54
2:HP1:738:TRP:CD1	2:HP1:912:PHE:CZ	2.96	0.54
2:IP1:162:ASP:HB3	2:IP1:165:LYS:HB2	1.90	0.54
2:IP1:932:LEU:HB3	2:IP1:936:LEU:HD23	1.90	0.54
2:GP1:532:SER:HA	2:GP1:537:VAL:H	1.71	0.54
2:HP1:212:PRO:HA	2:HP1:215:GLY:H	1.73	0.54
3:KP1:23:PHE:O	3:KP1:27:LEU:HG	2.07	0.54
2:HP1:745:ILE:HG12	2:HP1:919:THR:HG21	1.89	0.54
2:IP1:287:ILE:HG13	2:IP1:332:ARG:HH12	1.73	0.54
1:AP1:206:TYR:O	1:AP1:210:VAL:HG12	2.08	0.54
1:BP1:185:PRO:HG3	1:BP1:204:LEU:HD22	1.88	0.54
2:IP1:837:PHE:HZ	2:IP1:917:ILE:HG23	1.72	0.54
2:JP1:147:LEU:HD22	2:JP1:453:ILE:HG23	1.90	0.54
2:FP1:60:MET:CE	2:GP1:817:ILE:HG12	2.36	0.54
2:FP1:182:LEU:HD23	2:FP1:571:VAL:HG21	1.89	0.54
2:FP1:556:ARG:HD2	2:FP1:576:MET:HG2	1.90	0.54
2:JP1:554:PRO:HB3	2:JP1:587:PRO:HA	1.89	0.54
1:BP1:280:ILE:HG23	1:BP1:347:LEU:HD23	1.90	0.53
2:GP1:594:ILE:HG21	2:GP1:660:LEU:HD22	1.89	0.53
2:IP1:73:GLY:C	2:IP1:77:MET:HE2	2.32	0.53
2:JP1:187:GLY:HA2	2:JP1:279:CYS:HB3	1.90	0.53
3:OP1:16:ARG:O	3:OP1:20:ILE:HG22	2.08	0.53
3:OP1:38:LYS:HE2	3:OP1:38:LYS:HA	1.89	0.53
2:HP1:822:ALA:HB1	2:HP1:930:PHE:CD2	2.43	0.53
2:JP1:450:ARG:HG2	2:JP1:453:ILE:HD11	1.90	0.53
1:BP1:177:ALA:O	1:BP1:181:ILE:HG12	2.08	0.53
1:DP1:298:TYR:HD1	1:DP1:298:TYR:O	1.91	0.53
2:GP1:648:PHE:HA	2:GP1:651:MET:HB2	1.90	0.53
2:IP1:669:ASP:HA	2:IP1:672:ILE:HG12	1.90	0.53
2:JP1:532:SER:HA	2:JP1:537:VAL:H	1.74	0.53
1:BP1:182:LEU:HD11	1:CP1:243:LEU:HD12	1.89	0.53
2:FP1:45:VAL:HG21	2:FP1:129:MET:HG2	1.90	0.53
2:FP1:548:PRO:HD3	2:FP1:568:TYR:HD1	1.74	0.53
2:GP1:667:MET:HE2	2:GP1:912:PHE:CD2	2.44	0.53
2:HP1:725:PHE:CD1	2:IP1:729:MET:HE1	2.43	0.53
2:HP1:725:PHE:CE1	2:IP1:729:MET:HE1	2.43	0.53
3:OP1:9:LYS:HD3	3:OP1:9:LYS:N	2.23	0.53
2:GP1:261:LEU:HB2	2:GP1:284:TRP:HZ3	1.71	0.53
2:GP1:841:ILE:HD12	2:GP1:844:ILE:HB	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:IP1:721:GLY:O	2:IP1:724:ILE:HG22	2.09	0.53
2:FP1:617:ILE:HG22	2:FP1:618:LEU:H	1.73	0.53
2:HP1:725:PHE:CD1	2:HP1:725:PHE:C	2.87	0.53
3:KP1:16:ARG:NH1	3:KP1:20:ILE:HD13	2.24	0.53
1:BP1:141:LEU:HB3	1:BP1:213:ASN:HB3	1.91	0.53
2:HP1:732:MET:O	2:HP1:736:MET:HB2	2.09	0.53
2:IP1:151:ASN:HB2	2:IP1:453:ILE:HD13	1.89	0.53
2:IP1:668:LYS:O	2:IP1:672:ILE:HG23	2.09	0.53
2:FP1:618:LEU:HD23	2:GP1:618:LEU:HB2	1.91	0.53
2:FP1:756:LEU:HA	2:FP1:759:MET:HG3	1.91	0.53
2:IP1:929:ALA:O	2:IP1:932:LEU:HD12	2.09	0.53
1:AP1:90:PRO:HG2	1:BP1:246:ASN:HD21	1.73	0.53
1:CP1:421:GLU:O	1:CP1:425:GLN:HG3	2.09	0.53
2:FP1:630:ASP:HA	2:FP1:634:ASN:HB2	1.89	0.53
2:IP1:164:THR:HG21	2:IP1:583:PRO:HA	1.90	0.53
2:IP1:588:LEU:HD13	2:IP1:660:LEU:HD11	1.90	0.53
2:JP1:94:LEU:HD13	2:JP1:98:TRP:HD1	1.74	0.53
2:JP1:347:ALA:O	2:JP1:351:VAL:HG12	2.08	0.53
2:GP1:221:GLU:CD	2:GP1:221:GLU:H	2.17	0.52
2:GP1:652:ILE:O	2:GP1:656:VAL:HG23	2.09	0.52
2:HP1:920:SER:O	2:HP1:924:ILE:HD12	2.09	0.52
2:HP1:640:VAL:HG22	2:IP1:605:MET:HE1	1.91	0.52
2:IP1:148:SER:O	2:IP1:152:ARG:HD3	2.09	0.52
2:IP1:685:PRO:HB2	2:IP1:830:VAL:HG11	1.92	0.52
2:JP1:33:LEU:HD12	2:JP1:37:PHE:CZ	2.43	0.52
3:OP1:23:PHE:O	3:OP1:27:LEU:HD22	2.09	0.52
2:FP1:722:ILE:HG23	2:FP1:723:PHE:HD1	1.74	0.52
2:GP1:176:GLY:HA3	2:GP1:492:ASP:HB2	1.90	0.52
2:HP1:673:VAL:O	2:HP1:677:THR:HG22	2.10	0.52
2:IP1:213:PRO:O	2:IP1:218:PRO:HB3	2.09	0.52
2:IP1:804:ILE:O	2:IP1:808:VAL:HG22	2.09	0.52
2:JP1:757:PRO:HB3	2:JP1:930:PHE:HE2	1.74	0.52
3:NP1:18:ARG:O	3:NP1:22:ILE:HD13	2.10	0.52
2:FP1:663:PRO:HG3	2:FP1:703:LEU:HD11	1.91	0.52
2:IP1:706:THR:O	2:IP1:710:MET:HG2	2.09	0.52
2:IP1:713:VAL:HG13	2:JP1:723:PHE:CD1	2.44	0.52
1:AP1:305:ALA:HA	1:AP1:319:GLN:HG2	1.91	0.52
1:BP1:328:SER:HA	1:CP1:211:MET:HE2	1.92	0.52
1:CP1:42:TYR:HA	1:CP1:45:ASN:ND2	2.23	0.52
2:FP1:723:PHE:CZ	2:JP1:724:ILE:HG13	2.44	0.52
1:AP1:48:LYS:HG2	1:EP1:64:PRO:HG3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:FP1:819:TYR:O	2:FP1:823:ILE:HG22	2.10	0.52
1:AP1:280:ILE:HD11	1:AP1:351:LEU:HB2	1.90	0.52
2:FP1:124:MET:HG3	2:FP1:779:ALA:HB1	1.91	0.52
2:FP1:732:MET:O	2:FP1:736:MET:HB2	2.10	0.52
2:GP1:757:PRO:HG3	2:GP1:930:PHE:CZ	2.45	0.52
2:FP1:725:PHE:CD2	2:GP1:729:MET:HE1	2.44	0.52
2:HP1:122:CYS:H	2:HP1:125:GLN:HG3	1.74	0.52
2:HP1:766:PHE:CZ	2:IP1:829:GLY:HA2	2.45	0.52
2:JP1:304:VAL:HB	2:JP1:318:LEU:H	1.74	0.52
2:JP1:237:VAL:HG13	2:JP1:261:LEU:HD21	1.90	0.52
3:KP1:15:THR:HG22	3:KP1:18:ARG:HH22	1.75	0.52
2:HP1:747:PHE:HA	2:HP1:751:TYR:HD2	1.74	0.52
1:DP1:254:MET:HB3	1:DP1:273:ALA:HB2	1.93	0.51
2:HP1:275:LEU:O	2:HP1:278:ILE:HG22	2.10	0.51
2:HP1:905:TRP:HA	2:HP1:908:VAL:HG13	1.92	0.51
2:JP1:175:SER:HB2	2:JP1:488:GLY:H	1.74	0.51
1:CP1:55:THR:HA	1:DP1:42:TYR:CE1	2.46	0.51
2:GP1:468:PHE:CD1	2:GP1:757:PRO:HG2	2.44	0.51
2:GP1:605:MET:HE2	2:GP1:637:PHE:HE2	1.74	0.51
2:HP1:841:ILE:HD12	2:HP1:844:ILE:HB	1.92	0.51
2:IP1:73:GLY:O	2:IP1:77:MET:HE2	2.11	0.51
2:JP1:183:THR:HG23	2:JP1:496:PHE:HB2	1.92	0.51
2:FP1:77:MET:HG2	3:LP1:28:LEU:HD11	1.91	0.51
2:HP1:33:LEU:HD23	2:HP1:462:ILE:HD11	1.91	0.51
1:AP1:346:ASN:OD1	1:EP1:437:LEU:HD11	2.09	0.51
2:GP1:41:LEU:HD22	2:GP1:42:PHE:CD2	2.45	0.51
2:IP1:182:LEU:HD23	2:IP1:571:VAL:HG21	1.91	0.51
2:IP1:468:PHE:CE1	2:IP1:930:PHE:HZ	2.28	0.51
2:IP1:74:ILE:HA	2:IP1:77:MET:HG2	1.91	0.51
2:JP1:318:LEU:HD11	2:JP1:439:GLN:HB2	1.91	0.51
1:CP1:430:ARG:HH21	1:DP1:425:GLN:HB3	1.76	0.51
2:FP1:718:PRO:HB3	2:GP1:719:LEU:HD11	1.92	0.51
2:GP1:107:SER:HA	2:GP1:787:THR:HG22	1.91	0.51
2:GP1:290:LEU:HB2	2:GP1:329:ARG:NH1	2.26	0.51
2:IP1:673:VAL:O	2:IP1:677:THR:HG22	2.11	0.51
1:AP1:182:LEU:HD11	1:BP1:243:LEU:HD12	1.92	0.51
2:FP1:745:ILE:HD13	2:FP1:915:ILE:HG13	1.93	0.51
2:GP1:656:VAL:HG12	2:GP1:660:LEU:CD2	2.41	0.51
2:GP1:909:TYR:O	2:GP1:912:PHE:HB2	2.11	0.51
2:IP1:944:ILE:HD12	2:IP1:944:ILE:H	1.76	0.51
1:AP1:451:ALA:HB1	2:HP1:619:PHE:HE2	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GP1:78:TYR:HA	2:GP1:81:MET:SD	2.51	0.51
2:GP1:179:LYS:HE2	2:GP1:547:GLN:HE22	1.75	0.51
2:GP1:192:LEU:HB2	2:GP1:351:VAL:HG21	1.93	0.51
2:GP1:373:ILE:HG13	2:GP1:533:LEU:HD23	1.92	0.51
2:HP1:713:VAL:O	2:HP1:716:LEU:HD23	2.11	0.51
2:IP1:728:ILE:HD11	2:JP1:730:MET:SD	2.51	0.51
3:OP1:15:THR:HG22	3:OP1:18:ARG:HH22	1.76	0.51
1:AP1:136:ILE:HG23	1:AP1:277:LEU:HD22	1.93	0.51
2:GP1:566:THR:HG23	2:GP1:569:GLY:H	1.76	0.51
2:GP1:670:ILE:HD13	2:GP1:695:MET:HB3	1.93	0.51
2:HP1:222:MET:HE1	2:HP1:519:TRP:HA	1.91	0.51
2:HP1:669:ASP:O	2:HP1:673:VAL:HG13	2.10	0.51
2:IP1:501:LEU:HB3	2:IP1:527:LEU:HD23	1.93	0.51
1:BP1:230:PHE:CD1	1:BP1:230:PHE:C	2.89	0.50
1:DP1:142:ILE:HG22	1:DP1:210:VAL:HG23	1.94	0.50
2:FP1:69:LEU:HD21	3:LP1:31:ALA:HB1	1.94	0.50
2:FP1:150:LEU:HD12	2:FP1:474:LEU:HD23	1.93	0.50
2:FP1:648:PHE:HB2	2:FP1:717:ILE:HD12	1.92	0.50
2:IP1:60:MET:SD	2:JP1:817:ILE:HD13	2.51	0.50
2:IP1:338:GLN:HA	2:IP1:341:VAL:HG22	1.91	0.50
2:JP1:182:LEU:HD23	2:JP1:571:VAL:HG21	1.92	0.50
3:OP1:15:THR:HA	3:OP1:18:ARG:CZ	2.41	0.50
2:FP1:132:ILE:HG12	2:FP1:772:VAL:HG23	1.93	0.50
2:FP1:450:ARG:O	2:FP1:453:ILE:HD12	2.11	0.50
2:JP1:470:ASP:O	2:JP1:473:LYS:HG2	2.11	0.50
1:BP1:206:TYR:O	1:BP1:210:VAL:HG12	2.11	0.50
2:GP1:634:ASN:O	2:GP1:638:ARG:HB3	2.12	0.50
2:HP1:706:THR:O	2:HP1:710:MET:HG2	2.11	0.50
2:HP1:922:TYR:O	2:HP1:925:ILE:HB	2.12	0.50
1:AP1:208:ASN:O	1:AP1:212:GLN:HG2	2.11	0.50
1:CP1:182:LEU:HD11	1:DP1:243:LEU:HD12	1.92	0.50
2:FP1:643:PHE:O	2:FP1:647:ILE:HG22	2.12	0.50
2:IP1:330:LEU:HB3	2:IP1:333:ALA:HB3	1.93	0.50
2:IP1:814:LEU:HD13	2:IP1:937:PRO:HA	1.93	0.50
1:AP1:54:ILE:HG23	1:BP1:45:ASN:OD1	2.12	0.50
1:BP1:174:VAL:HG11	1:BP1:345:SER:HB2	1.94	0.50
2:GP1:630:ASP:HA	2:GP1:634:ASN:HB2	1.93	0.50
2:IP1:468:PHE:HE1	2:IP1:930:PHE:HZ	1.59	0.50
2:GP1:722:ILE:O	2:GP1:725:PHE:HB3	2.11	0.50
2:IP1:370:PHE:CD1	2:IP1:377:GLN:HB3	2.46	0.50
2:IP1:662:ILE:HD13	2:IP1:703:LEU:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:JP1:113:LEU:HA	2:JP1:123:MET:HB2	1.93	0.50
2:JP1:392:TYR:CE2	2:JP1:585:ILE:HG21	2.46	0.50
2:JP1:661:MET:O	2:JP1:665:GLN:HB2	2.12	0.50
1:AP1:42:TYR:CE1	1:EP1:55:THR:HA	2.47	0.50
2:FP1:841:ILE:HD12	2:FP1:844:ILE:HB	1.93	0.50
2:GP1:77:MET:HG3	2:GP1:81:MET:HE3	1.93	0.50
2:IP1:167:LEU:HD12	2:IP1:585:ILE:HD11	1.94	0.50
2:IP1:347:ALA:O	2:IP1:351:VAL:HG22	2.11	0.50
2:IP1:655:ILE:HD11	2:IP1:710:MET:HB2	1.92	0.50
3:LP1:7:ASN:O	3:LP1:11:LEU:HG	2.12	0.50
1:AP1:142:ILE:HA	1:AP1:210:VAL:HG23	1.93	0.50
1:BP1:55:THR:HA	1:CP1:42:TYR:CE2	2.47	0.50
1:BP1:347:LEU:HA	1:BP1:350:ILE:HG22	1.91	0.50
2:GP1:370:PHE:HB2	2:GP1:410:THR:HG21	1.93	0.50
1:AP1:179:PHE:HB2	1:BP1:240:ILE:HD13	1.93	0.49
1:DP1:104:ASP:HA	1:DP1:109:ASN:HD22	1.75	0.49
2:HP1:49:LEU:HG	2:HP1:51:GLY:H	1.77	0.49
2:HP1:468:PHE:CD1	2:HP1:757:PRO:HG2	2.47	0.49
2:HP1:939:LYS:HE3	2:HP1:939:LYS:HA	1.94	0.49
1:EP1:280:ILE:HD11	1:EP1:351:LEU:HB2	1.94	0.49
2:GP1:103:ILE:HG22	2:GP1:106:ARG:HH21	1.76	0.49
2:HP1:147:LEU:HB2	2:HP1:453:ILE:HG23	1.94	0.49
1:AP1:35:ASN:O	1:AP1:39:LEU:HD23	2.12	0.49
2:FP1:594:ILE:HB	2:FP1:660:LEU:HD12	1.95	0.49
2:HP1:738:TRP:HD1	2:HP1:912:PHE:CZ	2.29	0.49
2:IP1:268:LYS:HB3	2:JP1:403:PRO:HB3	1.95	0.49
2:JP1:338:GLN:HA	2:JP1:341:VAL:HG12	1.94	0.49
1:AP1:434:GLU:OE2	1:BP1:350:ILE:HD11	2.12	0.49
1:CP1:94:MET:HG3	1:DP1:241:SER:HB3	1.94	0.49
1:DP1:206:TYR:O	1:DP1:210:VAL:HG12	2.12	0.49
2:FP1:183:THR:HG23	2:FP1:496:PHE:HB2	1.94	0.49
2:GP1:381:PRO:HD2	2:GP1:573:ASN:ND2	2.27	0.49
2:HP1:593:LEU:HD11	2:HP1:905:TRP:HB3	1.93	0.49
2:IP1:692:MET:HA	2:IP1:695:MET:HE3	1.94	0.49
2:IP1:718:PRO:O	2:IP1:719:LEU:HB2	2.11	0.49
3:KP1:18:ARG:O	3:KP1:22:ILE:HD13	2.12	0.49
1:CP1:172:ASP:HB3	1:CP1:175:SER:OG	2.12	0.49
1:DP1:342:VAL:HG21	1:DP1:442:ILE:HG13	1.94	0.49
1:EP1:269:ALA:HB1	1:EP1:274:GLN:HB3	1.93	0.49
2:FP1:124:MET:HG2	2:FP1:783:ALA:HB2	1.94	0.49
2:GP1:666:GLY:O	2:GP1:670:ILE:HG13	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:IP1:110:GLY:HA3	2:IP1:787:THR:HG22	1.94	0.49
3:MP1:36:PHE:HA	3:MP1:39:ILE:HD11	1.95	0.49
2:GP1:713:VAL:HG22	2:HP1:727:LEU:HB2	1.94	0.49
2:JP1:103:ILE:HG22	2:JP1:104:PRO:HD3	1.93	0.49
3:KP1:28:LEU:O	3:KP1:32:VAL:HG13	2.11	0.49
2:GP1:223:ASN:O	2:GP1:227:ARG:HG2	2.13	0.49
2:GP1:766:PHE:CZ	2:HP1:925:ILE:HG23	2.48	0.49
2:HP1:84:THR:HA	2:HP1:87:THR:HG22	1.94	0.49
2:IP1:663:PRO:HG3	2:IP1:738:TRP:CH2	2.48	0.49
1:BP1:280:ILE:HD11	1:BP1:351:LEU:HB2	1.93	0.49
1:CP1:444:LEU:HD13	1:DP1:443:MET:HB2	1.95	0.49
2:GP1:136:VAL:HG22	2:GP1:461:TRP:HE1	1.78	0.49
2:JP1:259:PHE:HE2	2:JP1:286:ASN:HB2	1.77	0.49
1:AP1:230:PHE:C	1:AP1:230:PHE:CD1	2.91	0.49
2:FP1:605:MET:HE1	2:JP1:640:VAL:HG22	1.95	0.49
2:HP1:664:LEU:O	2:HP1:668:LYS:HB2	2.13	0.49
1:CP1:86:LEU:HD21	1:DP1:376:PHE:CZ	2.48	0.48
1:DP1:455:ALA:HB1	1:EP1:293:PRO:HA	1.95	0.48
1:EP1:382:ARG:HB3	1:EP1:399:TRP:CD2	2.48	0.48
2:GP1:61:PHE:CE1	2:GP1:776:MET:HG3	2.48	0.48
2:JP1:247:THR:HG22	2:JP1:256:PRO:HD2	1.94	0.48
2:JP1:540:LEU:HD23	2:JP1:562:PRO:HB2	1.94	0.48
1:AP1:415:ILE:HG23	1:EP1:419:LEU:HD12	1.96	0.48
2:FP1:78:TYR:HA	2:FP1:81:MET:CE	2.36	0.48
2:FP1:111:LEU:HD13	3:LP1:31:ALA:HB2	1.96	0.48
2:GP1:57:MET:HE1	2:HP1:821:ALA:HA	1.93	0.48
2:IP1:662:ILE:HB	2:IP1:703:LEU:HD11	1.93	0.48
2:FP1:920:SER:O	2:FP1:924:ILE:HD12	2.13	0.48
2:HP1:111:LEU:HD13	3:OP1:31:ALA:HB2	1.95	0.48
2:HP1:176:GLY:HA3	2:HP1:492:ASP:HB2	1.95	0.48
1:CP1:119:THR:HG21	1:CP1:352:SER:HB2	1.96	0.48
2:JP1:184:ILE:HG13	2:JP1:263:MET:HE1	1.96	0.48
1:DP1:141:LEU:HD23	1:DP1:213:ASN:HB3	1.94	0.48
1:EP1:68:LEU:HD11	1:EP1:417:ILE:HD11	1.96	0.48
2:FP1:113:LEU:HD12	2:FP1:124:MET:HE2	1.96	0.48
2:FP1:769:LEU:HA	2:FP1:772:VAL:HG12	1.95	0.48
2:GP1:837:PHE:O	2:GP1:841:ILE:HG22	2.13	0.48
2:JP1:391:GLU:HG3	2:JP1:393:GLN:H	1.79	0.48
1:AP1:308:LYS:HG2	1:AP1:309:PRO:HD2	1.95	0.48
1:AP1:419:LEU:HD12	1:BP1:415:ILE:HG23	1.96	0.48
1:BP1:86:LEU:HD21	1:BP1:112:ILE:HG12	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP1:292:LEU:HD13	1:CP1:230:PHE:HE2	1.78	0.48
1:BP1:382:ARG:HB3	1:BP1:399:TRP:CE3	2.49	0.48
2:GP1:147:LEU:HB2	2:GP1:453:ILE:CG2	2.43	0.48
2:HP1:132:ILE:HG13	2:HP1:772:VAL:HG23	1.95	0.48
1:AP1:205:MET:HG3	1:AP1:209:LEU:HG	1.94	0.48
2:HP1:589:THR:HG22	2:HP1:664:LEU:HD21	1.96	0.48
2:JP1:461:TRP:CZ2	2:JP1:812:PRO:HB3	2.48	0.48
2:JP1:647:ILE:HG22	2:JP1:717:ILE:HG12	1.95	0.48
1:BP1:419:LEU:HD12	1:CP1:415:ILE:HG23	1.96	0.48
1:CP1:142:ILE:HD12	1:CP1:281:ARG:HD2	1.96	0.48
2:FP1:766:PHE:CE2	2:GP1:925:ILE:HD12	2.49	0.48
2:GP1:468:PHE:CG	2:GP1:757:PRO:HG2	2.49	0.48
2:GP1:612:CYS:HB2	2:GP1:623:CYS:HB2	1.61	0.48
2:HP1:936:LEU:O	2:HP1:940:VAL:HG23	2.14	0.48
2:IP1:450:ARG:HD3	2:IP1:474:LEU:HD11	1.95	0.48
2:FP1:723:PHE:HZ	2:JP1:724:ILE:HG13	1.79	0.48
2:GP1:663:PRO:HG3	2:GP1:703:LEU:HD11	1.96	0.48
2:HP1:338:GLN:HA	2:HP1:341:VAL:HG12	1.95	0.48
2:IP1:129:MET:O	2:IP1:132:ILE:HG13	2.13	0.48
2:JP1:799:GLU:HA	2:JP1:802:ILE:HD12	1.96	0.48
1:AP1:376:PHE:CZ	1:EP1:86:LEU:HD21	2.49	0.48
1:EP1:207:GLN:O	1:EP1:211:MET:HB2	2.13	0.48
2:FP1:434:LEU:HA	2:FP1:437:ILE:HG22	1.95	0.48
2:FP1:707:LEU:HD13	2:FP1:735:LEU:HD21	1.95	0.48
2:GP1:738:TRP:O	2:GP1:742:MET:HG3	2.14	0.48
2:HP1:165:LYS:HB3	2:HP1:485:PHE:HE2	1.78	0.48
2:IP1:136:VAL:HG13	2:IP1:461:TRP:NE1	2.28	0.48
2:IP1:354:ASP:HB3	2:IP1:357:PHE:HD1	1.78	0.48
2:IP1:732:MET:O	2:IP1:736:MET:HB2	2.13	0.48
1:BP1:90:PRO:HG3	1:BP1:349:TYR:HB2	1.95	0.47
1:BP1:421:GLU:O	1:BP1:425:GLN:HG3	2.14	0.47
1:EP1:206:TYR:O	1:EP1:210:VAL:HG12	2.14	0.47
2:GP1:114:LEU:HD21	2:GP1:783:ALA:HB3	1.96	0.47
2:GP1:179:LYS:HG2	2:GP1:492:ASP:HA	1.95	0.47
2:GP1:288:SER:HA	2:GP1:291:ASN:HB3	1.95	0.47
2:HP1:223:ASN:O	2:HP1:227:ARG:HG2	2.14	0.47
1:AP1:418:LEU:HD12	1:AP1:418:LEU:HA	1.77	0.47
1:EP1:126:SER:HB2	1:EP1:171:ASN:HA	1.96	0.47
2:HP1:526:LYS:HA	2:HP1:529:GLN:HE21	1.79	0.47
1:BP1:25:ALA:HB1	1:BP1:30:GLN:HE22	1.80	0.47
2:HP1:60:MET:HE3	2:IP1:817:ILE:CD1	2.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:HP1:732:MET:O	2:HP1:736:MET:CB	2.62	0.47
2:JP1:768:TRP:HB2	2:JP1:815:MET:HE1	1.96	0.47
2:FP1:829:GLY:HA2	2:JP1:766:PHE:CZ	2.50	0.47
2:FP1:940:VAL:O	2:FP1:944:ILE:HG13	2.14	0.47
2:HP1:188:GLN:O	2:HP1:191:MET:HB2	2.14	0.47
2:IP1:406:THR:O	2:IP1:406:THR:HG22	2.14	0.47
1:EP1:191:MET:HE3	1:EP1:195:GLN:HA	1.96	0.47
2:IP1:41:LEU:HD12	2:JP1:825:LEU:HA	1.96	0.47
3:LP1:5:LYS:O	3:LP1:9:LYS:HG3	2.15	0.47
1:CP1:443:MET:SD	1:DP1:443:MET:HE1	2.55	0.47
1:DP1:389:SER:HB3	1:DP1:394:GLN:OE1	2.15	0.47
2:IP1:189:ILE:HD11	2:IP1:350:MET:HB3	1.95	0.47
2:IP1:524:SER:O	2:IP1:528:ILE:HG22	2.14	0.47
2:JP1:58:GLY:HA2	2:JP1:121:TYR:CE1	2.50	0.47
2:JP1:77:MET:HE3	2:JP1:77:MET:HB2	1.77	0.47
2:JP1:103:ILE:HD11	2:JP1:789:PRO:HA	1.97	0.47
2:JP1:558:SER:HB3	2:JP1:576:MET:HE1	1.97	0.47
2:JP1:732:MET:HE2	2:JP1:732:MET:HA	1.95	0.47
1:BP1:437:LEU:HD11	1:CP1:346:ASN:HB3	1.96	0.47
2:FP1:94:LEU:HD21	3:LP1:21:ILE:HD11	1.96	0.47
2:GP1:608:GLN:HG2	2:GP1:633:TYR:CE2	2.50	0.47
2:HP1:79:THR:HA	2:HP1:82:VAL:HG22	1.97	0.47
2:HP1:713:VAL:HG22	2:IP1:727:LEU:HB2	1.96	0.47
2:JP1:462:ILE:HG13	2:JP1:463:MET:SD	2.55	0.47
2:JP1:833:LEU:HD21	2:JP1:921:MET:HB3	1.97	0.47
3:KP1:35:GLY:O	3:KP1:39:ILE:HG12	2.15	0.47
3:OP1:24:THR:HA	3:OP1:27:LEU:HD23	1.95	0.47
1:BP1:88:ALA:HB2	1:BP1:357:GLN:HE22	1.80	0.47
2:GP1:338:GLN:HA	2:GP1:341:VAL:HG12	1.97	0.47
2:HP1:82:VAL:HA	2:HP1:85:MET:HG3	1.96	0.47
2:HP1:106:ARG:HH11	2:HP1:789:PRO:HA	1.80	0.47
1:BP1:68:LEU:HD11	1:BP1:417:ILE:HD11	1.96	0.47
2:FP1:716:LEU:HD13	2:GP1:648:PHE:HE2	1.80	0.47
2:FP1:826:SER:O	2:FP1:830:VAL:HG23	2.15	0.47
2:GP1:213:PRO:HB2	2:GP1:222:MET:HE2	1.96	0.47
2:HP1:759:MET:HE3	2:IP1:917:ILE:HD11	1.96	0.47
1:AP1:243:LEU:HD12	1:EP1:182:LEU:HD11	1.97	0.46
2:GP1:117:LYS:HA	2:GP1:117:LYS:HD3	1.66	0.46
2:IP1:111:LEU:HD13	3:NP1:31:ALA:HB2	1.96	0.46
2:IP1:287:ILE:HG13	2:IP1:332:ARG:NH1	2.29	0.46
2:IP1:559:VAL:HG22	2:IP1:573:ASN:OD1	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:JP1:72:GLY:O	2:JP1:76:ILE:HG12	2.14	0.46
2:JP1:189:ILE:HD11	2:JP1:533:LEU:HD21	1.96	0.46
2:JP1:747:PHE:HA	2:JP1:751:TYR:HD2	1.81	0.46
1:AP1:35:ASN:HB3	1:EP1:36:THR:HB	1.96	0.46
2:HP1:189:ILE:HD11	2:HP1:533:LEU:HD21	1.96	0.46
1:BP1:228:PRO:HB2	1:BP1:235:TYR:HB2	1.97	0.46
2:FP1:829:GLY:HA2	2:JP1:766:PHE:HZ	1.79	0.46
2:GP1:55:GLN:HB3	2:HP1:149:TYR:OH	2.15	0.46
2:HP1:778:ALA:HB2	2:IP1:943:TRP:CH2	2.50	0.46
2:IP1:336:ILE:HD11	2:IP1:491:LEU:HD21	1.97	0.46
2:IP1:826:SER:O	2:IP1:830:VAL:HG23	2.14	0.46
3:LP1:28:LEU:O	3:LP1:32:VAL:HG13	2.15	0.46
1:CP1:445:LEU:HD11	1:DP1:340:THR:HG23	1.97	0.46
2:JP1:69:LEU:HD21	2:JP1:114:LEU:HB3	1.97	0.46
1:AP1:430:ARG:NH2	1:BP1:425:GLN:HE21	2.14	0.46
2:FP1:338:GLN:HA	2:FP1:341:VAL:HG12	1.97	0.46
2:GP1:150:LEU:HD12	2:GP1:474:LEU:HG	1.97	0.46
2:HP1:196:LYS:NZ	2:HP1:357:PHE:HB3	2.31	0.46
3:LP1:4:LYS:H	3:LP1:4:LYS:HD3	1.79	0.46
1:BP1:30:GLN:CD	1:BP1:30:GLN:H	2.24	0.46
1:EP1:254:MET:HG3	1:EP1:355:LEU:HD23	1.97	0.46
2:FP1:55:GLN:HB3	2:GP1:149:TYR:OH	2.16	0.46
2:FP1:925:ILE:HG12	2:JP1:766:PHE:CE2	2.51	0.46
2:GP1:41:LEU:HB2	2:HP1:828:VAL:HG21	1.97	0.46
2:GP1:111:LEU:HD13	3:KP1:31:ALA:HB2	1.98	0.46
2:GP1:475:ASN:HB3	2:GP1:684:ASN:HD21	1.80	0.46
2:HP1:698:ASN:HA	2:IP1:905:TRP:CZ3	2.50	0.46
2:HP1:751:TYR:HB3	2:IP1:913:PHE:CD2	2.50	0.46
2:JP1:757:PRO:HB3	2:JP1:930:PHE:CE2	2.51	0.46
2:JP1:811:ARG:O	2:JP1:815:MET:HE3	2.14	0.46
1:BP1:94:MET:HE2	1:BP1:94:MET:HA	1.97	0.46
1:BP1:438:LEU:HD12	1:CP1:350:ILE:HD13	1.98	0.46
2:FP1:464:ALA:HB3	2:FP1:761:PHE:HE2	1.80	0.46
2:IP1:663:PRO:HB3	2:IP1:738:TRP:CD2	2.50	0.46
2:JP1:434:LEU:HA	2:JP1:437:ILE:HG22	1.97	0.46
2:JP1:608:GLN:HG3	2:JP1:633:TYR:HE2	1.80	0.46
2:JP1:659:PHE:CZ	2:JP1:707:LEU:HD11	2.51	0.46
3:KP1:23:PHE:CZ	3:KP1:27:LEU:HD21	2.51	0.46
1:CP1:419:LEU:HD12	1:DP1:415:ILE:HG23	1.98	0.46
1:DP1:419:LEU:HD12	1:EP1:415:ILE:HG23	1.98	0.46
2:FP1:189:ILE:HD11	2:FP1:350:MET:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:HP1:659:PHE:HA	2:HP1:662:ILE:HD11	1.97	0.46
2:IP1:667:MET:HE2	2:IP1:915:ILE:HD13	1.98	0.46
1:DP1:89:ILE:HD11	1:EP1:250:ALA:HA	1.98	0.46
2:FP1:357:PHE:HZ	2:FP1:530:ILE:HD13	1.80	0.46
2:IP1:77:MET:SD	3:NP1:28:LEU:HD21	2.56	0.46
1:DP1:421:GLU:O	1:DP1:425:GLN:HG3	2.16	0.46
2:FP1:741:THR:HG23	2:FP1:916:LEU:HD21	1.97	0.46
2:FP1:757:PRO:HG3	2:FP1:930:PHE:CE2	2.51	0.46
2:GP1:589:THR:H	2:GP1:665:GLN:HE22	1.64	0.46
2:GP1:944:ILE:HD12	2:GP1:944:ILE:H	1.81	0.46
2:HP1:212:PRO:HB3	2:HP1:215:GLY:O	2.16	0.46
2:IP1:708:LEU:HA	2:JP1:730:MET:HG2	1.97	0.46
2:IP1:713:VAL:HG13	2:JP1:723:PHE:HD1	1.81	0.46
2:IP1:819:TYR:CZ	2:IP1:823:ILE:HD11	2.51	0.46
2:JP1:28:PRO:HB2	2:JP1:32:ASP:OD2	2.16	0.46
2:JP1:184:ILE:O	2:JP1:188:GLN:HG3	2.16	0.46
1:CP1:242:GLN:O	1:CP1:279:PHE:HB2	2.16	0.45
1:DP1:382:ARG:HD3	1:DP1:399:TRP:CE2	2.51	0.45
1:DP1:401:LYS:HA	1:DP1:401:LYS:HD2	1.79	0.45
2:GP1:330:LEU:O	2:GP1:334:ILE:HG13	2.16	0.45
2:GP1:399:TRP:CE3	2:GP1:416:GLY:HA3	2.51	0.45
2:IP1:132:ILE:HG22	2:IP1:808:VAL:HB	1.98	0.45
2:JP1:49:LEU:HD23	2:JP1:129:MET:HE3	1.98	0.45
2:JP1:822:ALA:HB1	2:JP1:930:PHE:CD1	2.51	0.45
1:BP1:78:GLN:HB3	1:CP1:383:LEU:HD13	1.98	0.45
1:BP1:377:ASN:O	1:BP1:381:ARG:HB2	2.15	0.45
2:FP1:94:LEU:HD23	2:FP1:94:LEU:HA	1.81	0.45
2:IP1:132:ILE:HG21	2:IP1:772:VAL:HG23	1.97	0.45
2:JP1:377:GLN:OE1	2:JP1:402:VAL:HB	2.16	0.45
2:JP1:643:PHE:O	2:JP1:647:ILE:HG13	2.16	0.45
1:CP1:326:LEU:HD23	1:CP1:326:LEU:HA	1.82	0.45
2:FP1:201:GLN:O	2:FP1:205:TYR:HD1	1.99	0.45
2:FP1:697:ILE:HG13	2:FP1:751:TYR:HE2	1.81	0.45
2:FP1:708:LEU:HA	2:GP1:730:MET:HG2	1.97	0.45
2:GP1:55:GLN:NE2	2:GP1:58:GLY:HA3	2.32	0.45
2:GP1:247:THR:HG22	2:GP1:256:PRO:HD2	1.98	0.45
2:HP1:143:TRP:O	2:HP1:147:LEU:HG	2.16	0.45
2:IP1:247:THR:HG22	2:IP1:256:PRO:HD2	1.97	0.45
2:IP1:618:LEU:HD11	2:IP1:619:PHE:CE2	2.51	0.45
2:JP1:740:GLY:HA2	2:JP1:743:VAL:HG12	1.98	0.45
3:OP1:16:ARG:NH1	3:OP1:20:ILE:HG21	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CP1:277:LEU:HD21	1:CP1:281:ARG:HH21	1.81	0.45
1:CP1:292:LEU:HD13	1:DP1:230:PHE:HE1	1.81	0.45
1:DP1:170:LEU:HD12	1:DP1:170:LEU:H	1.81	0.45
2:FP1:28:PRO:HB2	2:FP1:32:ASP:OD2	2.16	0.45
2:FP1:602:LEU:HD23	2:JP1:647:ILE:HD13	1.99	0.45
2:HP1:468:PHE:CE2	2:HP1:930:PHE:HZ	2.34	0.45
2:JP1:103:ILE:HD12	2:JP1:103:ILE:HA	1.88	0.45
1:EP1:353:LYS:HE3	1:EP1:353:LYS:HB3	1.68	0.45
2:HP1:473:LYS:HE3	2:IP1:843:TYR:CZ	2.52	0.45
2:HP1:659:PHE:CE1	2:HP1:707:LEU:HD22	2.51	0.45
1:AP1:105:LYS:HZ3	1:BP1:367:ASN:HA	1.82	0.45
1:BP1:74:VAL:O	1:BP1:78:GLN:HG2	2.16	0.45
1:CP1:81:ALA:CB	1:CP1:378:MET:HE1	2.45	0.45
1:DP1:55:THR:HA	1:EP1:42:TYR:CE1	2.52	0.45
1:DP1:208:ASN:O	1:DP1:212:GLN:HG2	2.17	0.45
2:FP1:103:ILE:N	2:FP1:104:PRO:HD2	2.32	0.45
2:FP1:435:ASN:HA	2:FP1:438:ARG:HD2	1.98	0.45
2:FP1:908:VAL:HG23	2:FP1:909:TYR:HD1	1.82	0.45
2:GP1:290:LEU:HB2	2:GP1:329:ARG:HH12	1.82	0.45
2:JP1:223:ASN:O	2:JP1:227:ARG:HG2	2.16	0.45
1:AP1:328:SER:HA	1:BP1:211:MET:CE	2.46	0.45
1:AP1:417:ILE:O	1:AP1:421:GLU:HG2	2.16	0.45
1:CP1:378:MET:HE3	1:CP1:378:MET:HB2	1.69	0.45
1:DP1:94:MET:HG3	1:EP1:241:SER:HB3	1.98	0.45
1:EP1:248:LEU:HD13	1:EP1:280:ILE:HD11	1.98	0.45
2:FP1:612:CYS:HB2	2:FP1:626:ARG:HE	1.82	0.45
2:GP1:819:TYR:CZ	2:GP1:823:ILE:HD11	2.52	0.45
2:IP1:461:TRP:CZ2	2:IP1:812:PRO:HB3	2.52	0.45
2:JP1:334:ILE:HD12	2:JP1:335:ALA:N	2.32	0.45
1:BP1:343:GLY:HA2	1:BP1:346:ASN:HD22	1.82	0.45
2:GP1:105:LEU:HD12	2:GP1:106:ARG:N	2.32	0.45
2:GP1:326:GLN:O	2:GP1:329:ARG:HB2	2.17	0.45
2:GP1:667:MET:CE	2:GP1:915:ILE:HD12	2.47	0.45
2:HP1:511:ASP:HB3	2:HP1:512:PRO:HA	1.98	0.45
2:HP1:905:TRP:O	2:HP1:908:VAL:HG22	2.16	0.45
2:JP1:330:LEU:O	2:JP1:334:ILE:HG13	2.17	0.45
2:JP1:741:THR:HG23	2:JP1:916:LEU:HG	1.99	0.45
1:AP1:389:SER:HB3	1:AP1:394:GLN:OE1	2.17	0.45
1:DP1:142:ILE:C	1:DP1:142:ILE:HD12	2.42	0.45
1:EP1:104:ASP:HA	1:EP1:109:ASN:ND2	2.32	0.45
2:FP1:288:SER:HA	2:FP1:291:ASN:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:HP1:820:ILE:HA	2:HP1:823:ILE:HG22	1.98	0.45
2:IP1:290:LEU:HB3	2:IP1:329:ARG:NH1	2.31	0.45
2:IP1:648:PHE:HE1	2:IP1:723:PHE:CD2	2.35	0.45
2:JP1:809:PHE:CD1	2:JP1:809:PHE:C	2.95	0.45
1:AP1:385:ASP:H	1:AP1:398:GLN:HE22	1.65	0.45
2:GP1:284:TRP:CD1	2:GP1:332:ARG:HG2	2.52	0.45
2:HP1:628:MET:HA	2:HP1:628:MET:HE2	1.99	0.45
1:BP1:378:MET:HE3	1:BP1:378:MET:HB2	1.65	0.44
1:CP1:389:SER:HB3	1:CP1:394:GLN:OE1	2.17	0.44
1:EP1:141:LEU:H	1:EP1:141:LEU:HD12	1.82	0.44
1:EP1:399:TRP:HE1	1:EP1:414:GLU:CD	2.25	0.44
2:FP1:100:SER:C	3:LP1:16:ARG:HH12	2.25	0.44
2:FP1:713:VAL:HG21	2:GP1:727:LEU:HD12	1.99	0.44
2:GP1:287:ILE:HG13	2:GP1:332:ARG:NH2	2.33	0.44
2:GP1:778:ALA:HB2	2:HP1:943:TRP:CH2	2.52	0.44
2:HP1:191:MET:CE	2:HP1:263:MET:HB3	2.47	0.44
2:HP1:932:LEU:HA	2:HP1:935:HIS:HD2	1.81	0.44
2:IP1:725:PHE:CZ	2:JP1:722:ILE:HG23	2.53	0.44
3:KP1:16:ARG:HA	3:KP1:19:VAL:HG22	1.98	0.44
1:EP1:302:TRP:NE1	1:EP1:306:THR:HG21	2.32	0.44
2:GP1:667:MET:HE2	2:GP1:912:PHE:HD2	1.82	0.44
2:GP1:930:PHE:O	2:GP1:933:ILE:HB	2.17	0.44
1:AP1:421:GLU:O	1:AP1:425:GLN:HG3	2.18	0.44
2:FP1:176:GLY:HA3	2:FP1:492:ASP:HB2	1.99	0.44
2:FP1:472:VAL:HG13	2:FP1:827:TYR:HE1	1.83	0.44
2:JP1:452:PHE:O	2:JP1:455:GLU:HG3	2.17	0.44
2:JP1:689:LEU:HD23	2:JP1:922:TYR:CE2	2.52	0.44
2:FP1:605:MET:HE3	2:FP1:605:MET:HB3	1.81	0.44
2:GP1:563:LEU:HD23	2:GP1:563:LEU:HA	1.82	0.44
2:GP1:639:TYR:CD1	2:GP1:639:TYR:C	2.94	0.44
2:HP1:247:THR:HG22	2:HP1:256:PRO:HD2	2.00	0.44
2:HP1:282:VAL:HA	2:HP1:494:SER:HB3	2.00	0.44
2:IP1:450:ARG:HD2	2:IP1:453:ILE:HD11	1.99	0.44
1:AP1:315:ASN:OD1	1:AP1:318:GLN:HB3	2.17	0.44
1:BP1:43:LEU:HD12	1:CP1:39:LEU:HD13	2.00	0.44
1:EP1:418:LEU:HD12	1:EP1:418:LEU:HA	1.80	0.44
2:FP1:34:SER:HA	2:FP1:462:ILE:HD13	1.99	0.44
2:GP1:213:PRO:O	2:GP1:218:PRO:HB3	2.17	0.44
2:GP1:369:ASP:OD1	2:GP1:369:ASP:N	2.51	0.44
2:GP1:525:ASP:HA	2:GP1:528:ILE:HG22	2.00	0.44
2:HP1:639:TYR:CD1	2:HP1:639:TYR:C	2.94	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:IP1:833:LEU:O	2:IP1:837:PHE:HB2	2.17	0.44
2:FP1:49:LEU:HD22	2:FP1:50:HIS:H	1.83	0.44
2:FP1:77:MET:O	2:FP1:81:MET:HG3	2.17	0.44
2:FP1:331:SER:HA	2:FP1:334:ILE:HD12	1.99	0.44
2:GP1:370:PHE:CD1	2:GP1:377:GLN:HB3	2.52	0.44
2:GP1:651:MET:HE1	2:GP1:655:ILE:HD11	2.00	0.44
2:HP1:753:ILE:HG13	2:HP1:922:TYR:CE2	2.52	0.44
2:IP1:555:GLN:NE2	2:IP1:588:LEU:HD12	2.32	0.44
2:IP1:664:LEU:O	2:IP1:668:LYS:HB2	2.18	0.44
2:JP1:537:VAL:HA	2:JP1:538:PRO:HA	1.86	0.44
3:KP1:40:ARG:HD2	3:KP1:40:ARG:HA	1.78	0.44
1:BP1:359:MET:HB2	1:BP1:367:ASN:OD1	2.18	0.44
1:DP1:104:ASP:HA	1:DP1:109:ASN:ND2	2.33	0.44
1:DP1:424:TYR:CZ	1:DP1:428:LEU:HD11	2.52	0.44
1:DP1:448:LEU:HD11	1:EP1:339:GLN:HB3	1.99	0.44
2:FP1:323:SER:O	2:FP1:326:GLN:HG3	2.18	0.44
2:GP1:766:PHE:CZ	2:HP1:829:GLY:HA3	2.49	0.44
2:IP1:461:TRP:CH2	2:IP1:812:PRO:HB3	2.52	0.44
2:JP1:600:THR:HG22	2:JP1:648:PHE:HE2	1.82	0.44
2:JP1:608:GLN:HG3	2:JP1:633:TYR:CE2	2.52	0.44
1:CP1:174:VAL:HG21	1:DP1:246:ASN:HD21	1.82	0.44
1:DP1:417:ILE:O	1:DP1:421:GLU:HG2	2.17	0.44
2:FP1:272:PHE:HD2	2:FP1:275:LEU:HD12	1.83	0.44
2:GP1:272:PHE:HD2	2:GP1:275:LEU:HD12	1.82	0.44
2:GP1:290:LEU:HD11	2:GP1:437:ILE:HD11	2.00	0.44
2:GP1:939:LYS:HA	2:GP1:939:LYS:HD2	1.86	0.44
2:JP1:240:VAL:HA	2:JP1:333:ALA:HB1	1.99	0.44
1:AP1:128:PRO:HB3	1:AP1:169:TYR:CE2	2.53	0.44
1:AP1:443:MET:HE1	1:EP1:443:MET:CE	2.48	0.44
2:FP1:377:GLN:HE22	2:FP1:402:VAL:HB	1.83	0.44
2:FP1:751:TYR:C	2:FP1:754:PRO:HD2	2.43	0.44
2:HP1:110:GLY:HA3	2:HP1:787:THR:HG22	2.00	0.44
2:HP1:516:LEU:HD23	2:HP1:516:LEU:HA	1.78	0.44
2:HP1:617:ILE:O	2:HP1:618:LEU:C	2.61	0.44
2:IP1:49:LEU:HD13	2:IP1:51:GLY:N	2.33	0.44
1:AP1:435:ARG:NH1	1:BP1:249:ILE:HD11	2.32	0.43
1:DP1:102:VAL:HG21	1:DP1:106:VAL:HG12	2.00	0.43
1:EP1:87:GLY:HA3	1:EP1:118:THR:HG22	2.00	0.43
2:FP1:33:LEU:HD12	2:FP1:459:LYS:O	2.19	0.43
2:FP1:921:MET:HA	2:FP1:924:ILE:HD12	2.00	0.43
2:GP1:188:GLN:O	2:GP1:191:MET:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GP1:335:ALA:HB1	2:GP1:426:TYR:CD1	2.53	0.43
2:GP1:612:CYS:HB3	2:GP1:626:ARG:H	1.83	0.43
2:GP1:704:TRP:CZ2	2:HP1:730:MET:HE3	2.52	0.43
2:GP1:753:ILE:HG13	2:GP1:922:TYR:CE2	2.53	0.43
2:GP1:811:ARG:HE	2:GP1:815:MET:HE2	1.82	0.43
2:IP1:89:HIS:HA	3:NP1:1:MET:HG2	1.99	0.43
2:IP1:452:PHE:CE1	2:IP1:453:ILE:HG13	2.53	0.43
1:CP1:448:LEU:HD11	1:DP1:339:GLN:HB3	2.00	0.43
2:FP1:38:LEU:HD12	2:FP1:38:LEU:HA	1.79	0.43
2:GP1:113:LEU:O	2:GP1:122:CYS:HB3	2.19	0.43
2:HP1:175:SER:HB2	2:HP1:488:GLY:H	1.82	0.43
2:HP1:643:PHE:CZ	2:HP1:647:ILE:HD11	2.53	0.43
1:AP1:419:LEU:HA	1:AP1:419:LEU:HD23	1.80	0.43
1:BP1:401:LYS:HD2	1:BP1:401:LYS:HA	1.75	0.43
1:CP1:33:SER:HB2	1:DP1:31:GLN:OE1	2.17	0.43
1:CP1:206:TYR:CZ	1:CP1:209:LEU:HB2	2.53	0.43
1:DP1:37:SER:O	1:DP1:40:VAL:HG12	2.18	0.43
2:HP1:818:GLY:HA2	2:HP1:936:LEU:HD13	2.01	0.43
2:IP1:667:MET:HE3	2:IP1:696:TYR:OH	2.18	0.43
2:IP1:917:ILE:HD12	2:IP1:917:ILE:HA	1.82	0.43
1:BP1:455:ALA:HB1	1:CP1:293:PRO:HA	2.01	0.43
1:EP1:119:THR:HG21	1:EP1:352:SER:OG	2.19	0.43
2:FP1:73:GLY:O	2:FP1:77:MET:HG3	2.18	0.43
2:FP1:205:TYR:HE2	2:FP1:213:PRO:HG2	1.83	0.43
2:FP1:720:PHE:HD1	2:JP1:716:LEU:HD12	1.83	0.43
2:FP1:766:PHE:CZ	2:GP1:829:GLY:HA2	2.36	0.43
2:GP1:261:LEU:HB2	2:GP1:284:TRP:CZ3	2.52	0.43
2:GP1:725:PHE:O	2:GP1:728:ILE:HG23	2.18	0.43
2:HP1:188:GLN:O	2:HP1:192:LEU:HG	2.18	0.43
2:IP1:334:ILE:HD12	2:IP1:335:ALA:N	2.33	0.43
2:IP1:381:PRO:HD3	2:IP1:573:ASN:HB3	1.99	0.43
2:IP1:756:LEU:O	2:IP1:759:MET:HB2	2.17	0.43
3:OP1:14:ASN:HB3	3:OP1:17:THR:HB	1.99	0.43
1:EP1:115:LEU:HD23	1:EP1:115:LEU:HA	1.79	0.43
1:EP1:123:GLN:NE2	1:EP1:256:THR:HG21	2.33	0.43
2:FP1:645:LEU:HD12	2:FP1:645:LEU:HA	1.84	0.43
2:FP1:716:LEU:HA	2:GP1:723:PHE:CG	2.54	0.43
2:FP1:778:ALA:HB2	2:GP1:943:TRP:CH2	2.53	0.43
2:GP1:79:THR:HA	2:GP1:82:VAL:HG12	2.01	0.43
2:GP1:125:GLN:H	2:GP1:125:GLN:HG2	1.66	0.43
2:HP1:139:ALA:HB2	2:HP1:812:PRO:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:HP1:152:ARG:N	2:HP1:152:ARG:HD3	2.33	0.43
2:HP1:264:PRO:O	2:HP1:276:ASN:ND2	2.51	0.43
2:HP1:434:LEU:O	2:HP1:437:ILE:HG22	2.18	0.43
2:HP1:769:LEU:HD23	2:HP1:769:LEU:HA	1.82	0.43
2:HP1:807:ASN:O	2:HP1:811:ARG:HG2	2.18	0.43
2:JP1:259:PHE:CE2	2:JP1:286:ASN:HB2	2.54	0.43
2:JP1:548:PRO:HD3	2:JP1:568:TYR:HD2	1.82	0.43
2:JP1:586:LYS:HB3	2:JP1:586:LYS:HE3	1.90	0.43
1:BP1:308:LYS:HG2	1:BP1:309:PRO:HD2	2.01	0.43
1:CP1:328:SER:HA	1:DP1:211:MET:CE	2.48	0.43
1:EP1:170:LEU:H	1:EP1:170:LEU:HD12	1.83	0.43
1:EP1:445:LEU:HD13	1:EP1:445:LEU:HA	1.84	0.43
2:GP1:105:LEU:HA	2:GP1:108:THR:HG22	2.00	0.43
2:JP1:45:VAL:HG12	2:JP1:49:LEU:HB2	2.01	0.43
1:CP1:423:ASN:HD21	1:DP1:379:ALA:HA	1.83	0.43
1:EP1:419:LEU:HD23	1:EP1:419:LEU:HA	1.81	0.43
2:GP1:717:ILE:HD12	2:GP1:717:ILE:O	2.19	0.43
2:HP1:377:GLN:HE22	2:HP1:402:VAL:HB	1.83	0.43
2:IP1:383:LYS:HG3	2:IP1:387:GLU:O	2.18	0.43
2:JP1:38:LEU:HD23	2:JP1:38:LEU:HA	1.80	0.43
1:AP1:86:LEU:HA	1:AP1:86:LEU:HD12	1.81	0.43
1:AP1:123:GLN:NE2	1:AP1:256:THR:HG21	2.33	0.43
1:CP1:206:TYR:O	1:CP1:210:VAL:HG12	2.18	0.43
1:EP1:355:LEU:HD23	1:EP1:355:LEU:HA	1.85	0.43
2:FP1:163:PRO:HG2	2:FP1:581:GLY:HA3	1.99	0.43
2:HP1:136:VAL:HG13	2:HP1:461:TRP:HE1	1.84	0.43
2:JP1:399:TRP:CE3	2:JP1:416:GLY:HA3	2.54	0.43
2:JP1:447:LYS:HE2	2:JP1:447:LYS:HB2	1.87	0.43
3:LP1:26:ALA:HA	3:LP1:29:ILE:HG12	2.01	0.43
3:NP1:16:ARG:HA	3:NP1:19:VAL:HG22	2.01	0.43
1:AP1:211:MET:CE	1:EP1:328:SER:HA	2.48	0.43
1:CP1:205:MET:HA	1:CP1:209:LEU:HD23	2.00	0.43
1:CP1:449:LYS:HE2	1:DP1:285:ALA:HB1	1.99	0.43
1:EP1:84:THR:HB	1:EP1:371:GLN:HA	2.01	0.43
2:HP1:103:ILE:HA	2:HP1:106:ARG:HG2	2.01	0.43
2:HP1:922:TYR:HA	2:HP1:925:ILE:HD12	2.00	0.43
2:IP1:766:PHE:HZ	2:JP1:829:GLY:HA2	1.81	0.43
1:AP1:31:GLN:HE22	1:AP1:35:ASN:ND2	2.16	0.43
1:AP1:99:MET:HE2	1:AP1:99:MET:HB2	1.86	0.43
1:EP1:142:ILE:HD13	1:EP1:281:ARG:HD3	2.01	0.43
2:FP1:716:LEU:HA	2:GP1:723:PHE:CD1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:FP1:739:ILE:O	2:FP1:743:VAL:HG22	2.19	0.43
2:GP1:725:PHE:HE1	2:HP1:729:MET:SD	2.42	0.43
2:HP1:503:LYS:HE2	2:HP1:503:LYS:HB2	1.73	0.43
2:IP1:330:LEU:O	2:IP1:334:ILE:HG13	2.19	0.43
2:IP1:612:CYS:HB2	2:IP1:626:ARG:NE	2.27	0.43
2:JP1:573:ASN:HA	2:JP1:576:MET:HE2	2.01	0.43
1:AP1:175:SER:HB3	1:BP1:244:ASN:HD22	1.84	0.42
1:BP1:351:LEU:C	1:BP1:351:LEU:HD23	2.44	0.42
1:DP1:359:MET:HB2	1:DP1:367:ASN:OD1	2.19	0.42
2:FP1:205:TYR:HB3	2:FP1:214:CYS:SG	2.59	0.42
2:GP1:67:ALA:O	2:GP1:71:LEU:HD12	2.18	0.42
2:GP1:125:GLN:HB3	2:GP1:776:MET:SD	2.59	0.42
2:GP1:547:GLN:HA	2:GP1:568:TYR:CD2	2.54	0.42
2:HP1:45:VAL:HG11	2:HP1:129:MET:HG2	2.00	0.42
2:HP1:692:MET:HE3	2:HP1:696:TYR:HE2	1.83	0.42
2:IP1:766:PHE:CG	2:JP1:925:ILE:HD11	2.54	0.42
2:JP1:331:SER:HA	2:JP1:334:ILE:HD11	2.01	0.42
2:JP1:725:PHE:HA	2:JP1:728:ILE:HG22	2.01	0.42
2:HP1:143:TRP:HB2	2:HP1:816:ILE:HG12	2.00	0.42
2:IP1:370:PHE:CE2	2:IP1:562:PRO:HA	2.53	0.42
2:JP1:213:PRO:O	2:JP1:218:PRO:HB3	2.19	0.42
2:JP1:612:CYS:HB2	2:JP1:626:ARG:NE	2.27	0.42
2:JP1:922:TYR:O	2:JP1:925:ILE:HG22	2.19	0.42
1:AP1:172:ASP:HB3	1:AP1:175:SER:OG	2.18	0.42
2:FP1:664:LEU:HD23	2:FP1:664:LEU:HA	1.89	0.42
2:FP1:769:LEU:HA	2:FP1:769:LEU:HD23	1.87	0.42
2:IP1:41:LEU:HD23	2:IP1:42:PHE:CD1	2.54	0.42
2:IP1:708:LEU:HD13	2:JP1:730:MET:HB3	2.01	0.42
2:JP1:525:ASP:OD2	2:JP1:525:ASP:N	2.52	0.42
1:BP1:56:GLN:HB3	1:BP1:59:LYS:HG3	2.01	0.42
1:BP1:445:LEU:HD21	1:CP1:343:GLY:HA3	2.01	0.42
1:CP1:317:VAL:HA	1:DP1:198:TRP:HE1	1.84	0.42
1:DP1:320:LYS:HD2	1:EP1:198:TRP:CE2	2.55	0.42
2:FP1:588:LEU:HD22	2:FP1:665:GLN:HE22	1.83	0.42
2:FP1:817:ILE:HD13	2:JP1:60:MET:HE3	2.00	0.42
2:HP1:33:LEU:HA	2:HP1:36:VAL:HB	2.01	0.42
1:BP1:328:SER:HA	1:CP1:211:MET:CE	2.50	0.42
2:FP1:724:ILE:O	2:FP1:728:ILE:HG22	2.19	0.42
2:GP1:268:LYS:HB3	2:HP1:403:PRO:HB3	2.01	0.42
2:GP1:375:LYS:HE3	2:GP1:375:LYS:HB2	1.91	0.42
2:GP1:391:GLU:OE1	2:GP1:391:GLU:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GP1:461:TRP:CH2	2:GP1:812:PRO:HB3	2.55	0.42
2:GP1:751:TYR:HB3	2:HP1:913:PHE:CD2	2.55	0.42
2:HP1:162:ASP:HB3	2:HP1:165:LYS:HB3	2.02	0.42
2:HP1:299:LYS:H	2:HP1:299:LYS:HG2	1.67	0.42
2:HP1:768:TRP:O	2:HP1:772:VAL:HG12	2.20	0.42
2:HP1:837:PHE:O	2:HP1:841:ILE:HG22	2.18	0.42
1:BP1:33:SER:HB2	1:CP1:31:GLN:OE1	2.20	0.42
1:CP1:54:ILE:HD13	1:CP1:54:ILE:HA	1.87	0.42
1:EP1:216:GLY:HA3	1:EP1:265:SER:O	2.20	0.42
2:FP1:103:ILE:HD11	3:LP1:20:ILE:HD12	2.00	0.42
2:HP1:162:ASP:H	2:HP1:485:PHE:HZ	1.67	0.42
2:HP1:617:ILE:HG22	2:HP1:618:LEU:H	1.85	0.42
2:JP1:101:ILE:O	2:JP1:104:PRO:HD2	2.19	0.42
2:JP1:204:LEU:HD23	2:JP1:204:LEU:HA	1.75	0.42
2:JP1:589:THR:HG23	2:JP1:590:PHE:CD1	2.55	0.42
2:JP1:755:VAL:O	2:JP1:759:MET:HG3	2.19	0.42
2:JP1:936:LEU:N	2:JP1:937:PRO:HD2	2.34	0.42
1:AP1:382:ARG:HB3	1:AP1:399:TRP:CE3	2.55	0.42
1:BP1:204:LEU:HD23	1:BP1:204:LEU:HA	1.82	0.42
1:DP1:308:LYS:HA	1:DP1:308:LYS:HD2	1.75	0.42
2:GP1:35:VAL:HA	2:GP1:38:LEU:HB2	2.02	0.42
2:GP1:524:SER:O	2:GP1:528:ILE:HG22	2.19	0.42
2:GP1:657:MET:O	2:GP1:661:MET:HG2	2.19	0.42
2:GP1:667:MET:HE3	2:GP1:915:ILE:HD12	2.01	0.42
2:HP1:237:VAL:HG13	2:HP1:261:LEU:HD11	2.01	0.42
2:IP1:725:PHE:CE2	2:JP1:722:ILE:HG23	2.55	0.42
3:KP1:24:THR:HA	3:KP1:27:LEU:HD12	2.02	0.42
1:BP1:292:LEU:HD13	1:CP1:230:PHE:CE2	2.55	0.42
2:FP1:187:GLY:HA3	2:FP1:263:MET:HE3	2.02	0.42
2:GP1:334:ILE:HD12	2:GP1:335:ALA:N	2.34	0.42
2:HP1:728:ILE:HD12	2:IP1:730:MET:SD	2.60	0.42
2:IP1:751:TYR:C	2:IP1:754:PRO:HD2	2.45	0.42
2:JP1:804:ILE:O	2:JP1:808:VAL:HG22	2.20	0.42
3:LP1:38:LYS:HA	3:LP1:38:LYS:HD2	1.77	0.42
3:MP1:35:GLY:O	3:MP1:39:ILE:HG13	2.20	0.42
1:AP1:430:ARG:NH2	1:BP1:425:GLN:NE2	2.68	0.42
2:FP1:617:ILE:O	2:FP1:618:LEU:C	2.63	0.42
2:FP1:730:MET:O	2:FP1:733:PRO:HD2	2.20	0.42
2:FP1:759:MET:HE1	2:GP1:917:ILE:HD12	2.01	0.42
2:GP1:240:VAL:HA	2:GP1:333:ALA:HB1	2.01	0.42
2:GP1:573:ASN:O	2:GP1:576:MET:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EP1:96:GLN:OE1	1:EP1:96:GLN:N	2.52	0.42
1:EP1:230:PHE:C	1:EP1:230:PHE:CD2	2.97	0.42
2:FP1:191:MET:HE1	2:FP1:264:PRO:HA	2.02	0.42
2:GP1:41:LEU:HD22	2:GP1:42:PHE:CE2	2.55	0.42
2:GP1:143:TRP:CE2	2:GP1:147:LEU:HD23	2.55	0.42
2:GP1:782:VAL:HG11	2:GP1:801:ALA:HB2	2.02	0.42
2:HP1:667:MET:HE3	2:HP1:911:PHE:HD2	1.84	0.42
2:HP1:799:GLU:HG2	2:HP1:800:PHE:H	1.85	0.42
3:LP1:4:LYS:HB2	3:LP1:4:LYS:HE2	1.83	0.42
1:BP1:303:ASN:HD22	2:GP1:208:GLN:CD	2.28	0.41
1:CP1:219:PRO:HA	1:CP1:220:PRO:HD3	1.91	0.41
1:DP1:298:TYR:HE2	1:EP1:230:PHE:CD1	2.38	0.41
2:FP1:105:LEU:HA	2:FP1:108:THR:HG22	2.02	0.41
2:GP1:703:LEU:O	2:GP1:707:LEU:HG	2.20	0.41
2:HP1:179:LYS:HE3	2:HP1:547:GLN:HE22	1.84	0.41
2:HP1:336:ILE:HD11	2:HP1:491:LEU:HD11	2.01	0.41
2:FP1:59:ASN:HD22	2:GP1:149:TYR:HB2	1.84	0.41
2:GP1:330:LEU:HB3	2:GP1:333:ALA:HB3	2.01	0.41
2:HP1:335:ALA:HB1	2:HP1:426:TYR:CD1	2.55	0.41
2:HP1:448:LYS:HE2	2:HP1:448:LYS:HB2	1.66	0.41
2:HP1:588:LEU:HD22	2:HP1:665:GLN:CD	2.45	0.41
2:IP1:259:PHE:HE1	2:IP1:286:ASN:HB2	1.85	0.41
2:IP1:331:SER:O	2:IP1:334:ILE:HD12	2.19	0.41
2:IP1:837:PHE:CE2	2:IP1:918:TYR:HB2	2.55	0.41
2:JP1:57:MET:SD	2:JP1:61:PHE:HE1	2.43	0.41
2:JP1:137:GLY:O	2:JP1:141:LYS:HG3	2.21	0.41
2:JP1:141:LYS:HA	2:JP1:144:GLU:HG2	2.02	0.41
1:DP1:128:PRO:HB3	1:DP1:169:TYR:CE2	2.55	0.41
1:EP1:215:ILE:HD13	1:EP1:215:ILE:HA	1.75	0.41
1:EP1:253:LEU:HD22	1:EP1:373:LEU:HD22	2.02	0.41
2:HP1:753:ILE:HD13	2:HP1:753:ILE:HA	1.94	0.41
2:HP1:758:TYR:OH	2:IP1:836:GLY:HA3	2.21	0.41
2:JP1:547:GLN:HA	2:JP1:568:TYR:CE2	2.55	0.41
1:AP1:250:ALA:HB3	1:AP1:251:PRO:HD3	2.02	0.41
1:AP1:419:LEU:HD23	1:AP1:422:ILE:HD12	2.02	0.41
2:FP1:136:VAL:HG13	2:FP1:461:TRP:HE1	1.85	0.41
2:GP1:144:GLU:HA	2:GP1:147:LEU:HG	2.01	0.41
2:GP1:329:ARG:HA	2:GP1:329:ARG:HD3	1.81	0.41
2:HP1:105:LEU:HA	2:HP1:108:THR:HG22	2.02	0.41
2:HP1:603:TYR:O	2:HP1:641:TYR:HE2	2.04	0.41
2:HP1:645:LEU:HD23	2:HP1:645:LEU:HA	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:HP1:701:GLY:HA3	2:IP1:905:TRP:CH2	2.55	0.41
2:IP1:131:VAL:HG11	2:IP1:805:LEU:HG	2.01	0.41
2:IP1:600:THR:HB	2:IP1:645:LEU:HD22	2.01	0.41
2:JP1:939:LYS:HE3	2:JP1:939:LYS:HB3	1.86	0.41
3:NP1:21:ILE:HD13	3:NP1:21:ILE:HA	1.84	0.41
1:AP1:104:ASP:OD1	1:AP1:104:ASP:C	2.64	0.41
1:BP1:115:LEU:HD23	1:BP1:115:LEU:HA	1.88	0.41
1:DP1:102:VAL:HG23	1:EP1:253:LEU:HD23	2.01	0.41
1:DP1:302:TRP:O	1:DP1:306:THR:HG22	2.21	0.41
1:DP1:368:ILE:HD13	1:DP1:368:ILE:HA	1.88	0.41
2:FP1:468:PHE:CE1	2:FP1:757:PRO:HG2	2.56	0.41
2:FP1:705:LEU:HD12	2:GP1:594:ILE:HG23	2.03	0.41
2:GP1:147:LEU:HD12	2:GP1:148:SER:N	2.34	0.41
2:GP1:290:LEU:HD12	2:GP1:290:LEU:H	1.85	0.41
2:GP1:671:PHE:CD1	2:GP1:915:ILE:HD11	2.55	0.41
2:GP1:841:ILE:HG13	2:GP1:845:GLN:HG2	2.01	0.41
2:HP1:612:CYS:HB2	2:HP1:626:ARG:HE	1.85	0.41
2:HP1:833:LEU:O	2:HP1:837:PHE:HB2	2.20	0.41
2:IP1:187:GLY:O	2:IP1:191:MET:HG2	2.20	0.41
2:IP1:499:THR:HA	2:IP1:531:GLN:NE2	2.35	0.41
2:IP1:630:ASP:HA	2:IP1:634:ASN:HB2	2.01	0.41
2:JP1:505:PHE:CG	2:JP1:524:SER:HB3	2.56	0.41
3:MP1:36:PHE:O	3:MP1:39:ILE:HD12	2.19	0.41
1:CP1:228:PRO:HG3	1:CP1:234:LYS:HD2	2.01	0.41
2:GP1:184:ILE:HD12	2:GP1:184:ILE:H	1.85	0.41
2:GP1:282:VAL:HA	2:GP1:494:SER:HB3	2.03	0.41
2:GP1:589:THR:HG23	2:GP1:590:PHE:CD1	2.55	0.41
2:GP1:751:TYR:C	2:GP1:754:PRO:HD2	2.46	0.41
2:HP1:210:LYS:HE2	2:HP1:210:LYS:HB2	1.81	0.41
2:IP1:205:TYR:HB3	2:IP1:214:CYS:SG	2.60	0.41
2:IP1:369:ASP:HB3	2:IP1:375:LYS:HA	2.02	0.41
2:IP1:782:VAL:O	2:IP1:786:VAL:HG23	2.20	0.41
2:JP1:685:PRO:HB2	2:JP1:830:VAL:HG11	2.02	0.41
2:JP1:816:ILE:HD13	2:JP1:816:ILE:HA	1.83	0.41
3:MP1:15:THR:HG22	3:MP1:18:ARG:HH22	1.85	0.41
1:AP1:206:TYR:CZ	1:AP1:209:LEU:HB2	2.56	0.41
1:AP1:294:LYS:H	1:AP1:294:LYS:HG2	1.61	0.41
2:GP1:100:SER:HB3	3:KP1:16:ARG:HH12	1.85	0.41
2:GP1:748:VAL:O	2:GP1:753:ILE:HG12	2.20	0.41
2:GP1:803:MET:HE3	2:GP1:804:ILE:N	2.36	0.41
2:HP1:469:PHE:O	2:HP1:473:LYS:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:IP1:691:ASN:HA	2:IP1:694:THR:HG23	2.02	0.41
2:IP1:841:ILE:HG12	2:IP1:914:SER:HB3	2.03	0.41
2:JP1:302:VAL:HB	2:JP1:320:ILE:HG13	2.02	0.41
3:MP1:4:LYS:O	3:MP1:8:LEU:HG	2.20	0.41
3:NP1:16:ARG:O	3:NP1:20:ILE:HG23	2.21	0.41
1:AP1:239:LEU:O	1:AP1:243:LEU:HG	2.21	0.41
1:AP1:339:GLN:HG2	1:AP1:442:ILE:HG23	2.02	0.41
1:AP1:443:MET:HE1	1:EP1:443:MET:HE2	2.01	0.41
1:CP1:70:ASN:HB3	1:CP1:73:VAL:HG22	2.02	0.41
2:FP1:334:ILE:HG13	2:FP1:334:ILE:H	1.69	0.41
2:IP1:98:TRP:CD1	2:IP1:103:ILE:HD11	2.56	0.41
2:JP1:170:ALA:HA	2:JP1:175:SER:H	1.84	0.41
2:JP1:205:TYR:HB3	2:JP1:214:CYS:SG	2.61	0.41
1:AP1:170:LEU:HD12	1:AP1:170:LEU:H	1.86	0.41
1:AP1:326:LEU:HD23	1:AP1:326:LEU:HA	1.81	0.41
1:BP1:104:ASP:OD2	1:BP1:104:ASP:C	2.64	0.41
1:BP1:418:LEU:HD12	1:BP1:418:LEU:HA	1.84	0.41
1:BP1:440:ASN:HB3	1:CP1:439:THR:HG21	2.03	0.41
1:BP1:441:SER:O	1:BP1:445:LEU:HD23	2.19	0.41
1:CP1:448:LEU:HD23	1:CP1:448:LEU:HA	1.77	0.41
1:DP1:292:LEU:HD13	1:DP1:329:TYR:OH	2.21	0.41
1:DP1:360:SER:HB2	1:DP1:366:ALA:HA	2.02	0.41
1:EP1:254:MET:HB3	1:EP1:273:ALA:HB2	2.03	0.41
1:EP1:426:MET:HB2	1:EP1:426:MET:HE3	1.71	0.41
2:FP1:725:PHE:CD2	2:FP1:725:PHE:C	2.98	0.41
2:FP1:725:PHE:CE2	2:GP1:729:MET:HE1	2.55	0.41
2:FP1:937:PRO:HA	2:FP1:940:VAL:HG22	2.03	0.41
2:GP1:56:ILE:O	2:GP1:60:MET:HB2	2.21	0.41
2:GP1:184:ILE:O	2:GP1:188:GLN:HG3	2.20	0.41
2:GP1:287:ILE:HD12	2:GP1:287:ILE:H	1.86	0.41
2:GP1:331:SER:HA	2:GP1:334:ILE:HD11	2.03	0.41
2:GP1:766:PHE:CE2	2:HP1:925:ILE:HG23	2.55	0.41
2:HP1:103:ILE:HG13	2:HP1:104:PRO:CD	2.47	0.41
2:HP1:114:LEU:HD21	2:HP1:783:ALA:HB3	2.03	0.41
2:HP1:301:LEU:HD21	2:HP1:319:ASN:HD21	1.86	0.41
2:HP1:696:TYR:CD1	2:HP1:742:MET:HG2	2.55	0.41
2:HP1:751:TYR:C	2:HP1:754:PRO:HD2	2.46	0.41
2:IP1:28:PRO:HB2	2:IP1:32:ASP:OD2	2.21	0.41
2:IP1:191:MET:HE1	2:IP1:264:PRO:N	2.36	0.41
2:IP1:651:MET:HB2	2:IP1:651:MET:HE2	1.79	0.41
2:IP1:713:VAL:HG11	2:JP1:596:PHE:HE2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:JP1:752:TYR:HE1	2:JP1:756:LEU:HD22	1.86	0.41
1:BP1:284:SER:HB2	1:BP1:344:VAL:HG22	2.03	0.41
1:BP1:419:LEU:HD23	1:BP1:419:LEU:HA	1.84	0.41
1:DP1:43:LEU:HD12	1:DP1:43:LEU:HA	1.92	0.41
2:FP1:210:LYS:HB2	2:FP1:210:LYS:HE2	1.76	0.41
2:IP1:660:LEU:O	2:IP1:663:PRO:HD2	2.21	0.41
2:JP1:704:TRP:CD1	2:JP1:704:TRP:C	3.00	0.41
3:MP1:12:PHE:CZ	3:MP1:22:ILE:HD11	2.56	0.41
1:BP1:120:PHE:CZ	1:BP1:173:PRO:HG3	2.56	0.40
1:BP1:215:ILE:HD12	1:BP1:215:ILE:HA	1.80	0.40
1:EP1:142:ILE:HG22	1:EP1:210:VAL:HG23	2.03	0.40
2:FP1:751:TYR:CE1	2:GP1:910:ALA:HA	2.56	0.40
2:HP1:447:LYS:HD2	2:HP1:447:LYS:H	1.86	0.40
2:IP1:191:MET:CE	2:IP1:263:MET:HB3	2.51	0.40
2:JP1:525:ASP:O	2:JP1:529:GLN:HG3	2.21	0.40
2:JP1:814:LEU:O	2:JP1:817:ILE:HB	2.21	0.40
1:AP1:129:SER:HB3	1:AP1:137:THR:HG21	2.04	0.40
2:FP1:110:GLY:O	2:FP1:114:LEU:HD23	2.21	0.40
2:FP1:296:SER:HA	2:FP1:302:VAL:HG13	2.03	0.40
2:FP1:588:LEU:HD22	2:FP1:665:GLN:NE2	2.35	0.40
2:FP1:708:LEU:O	2:FP1:713:VAL:HG23	2.21	0.40
2:GP1:149:TYR:C	2:GP1:149:TYR:CD2	2.99	0.40
2:GP1:650:GLU:CD	2:GP1:650:GLU:H	2.30	0.40
2:HP1:816:ILE:HD12	2:HP1:816:ILE:HA	1.94	0.40
2:IP1:248:PRO:HD2	2:IP1:256:PRO:HD3	2.03	0.40
2:IP1:597:LYS:HA	2:IP1:597:LYS:HD2	1.79	0.40
2:IP1:725:PHE:O	2:IP1:728:ILE:HG22	2.21	0.40
2:IP1:844:ILE:N	2:IP1:844:ILE:HD13	2.36	0.40
2:JP1:331:SER:O	2:JP1:334:ILE:HD12	2.21	0.40
2:JP1:547:GLN:HA	2:JP1:568:TYR:HE2	1.86	0.40
1:BP1:448:LEU:HD23	1:BP1:448:LEU:HA	1.95	0.40
2:FP1:462:ILE:HG13	2:FP1:463:MET:SD	2.61	0.40
2:FP1:752:TYR:CE1	2:FP1:756:LEU:HB2	2.56	0.40
2:GP1:732:MET:O	2:GP1:736:MET:HB2	2.21	0.40
2:HP1:377:GLN:NE2	2:HP1:402:VAL:H	2.13	0.40
2:IP1:528:ILE:CD1	2:IP1:538:PRO:HD3	2.50	0.40
2:JP1:664:LEU:HD23	2:JP1:664:LEU:HA	1.67	0.40
2:JP1:769:LEU:HD23	2:JP1:769:LEU:HA	1.84	0.40
3:OP1:30:ILE:HD13	3:OP1:30:ILE:HA	1.94	0.40
2:FP1:844:ILE:HD13	2:FP1:844:ILE:N	2.37	0.40
2:HP1:58:GLY:HA2	2:HP1:121:TYR:CE1	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:HP1:370:PHE:HE2	2:HP1:565:SER:HB3	1.87	0.40
2:IP1:290:LEU:HD11	2:IP1:437:ILE:HG12	2.02	0.40
2:JP1:935:HIS:HE1	2:JP1:939:LYS:HD2	1.86	0.40
1:AP1:198:TRP:CD1	1:EP1:317:VAL:HG22	2.56	0.40
1:AP1:401:LYS:HD2	1:AP1:401:LYS:HA	1.70	0.40
1:CP1:35:ASN:O	1:CP1:39:LEU:HD23	2.22	0.40
1:CP1:128:PRO:HG3	1:CP1:169:TYR:CE2	2.56	0.40
1:CP1:295:LEU:HD11	2:FP1:212:PRO:HG3	2.03	0.40
1:EP1:308:LYS:HG2	1:EP1:309:PRO:HD2	2.03	0.40
1:EP1:326:LEU:HD23	1:EP1:326:LEU:HA	1.81	0.40
2:FP1:448:LYS:HA	2:FP1:451:ASP:OD2	2.21	0.40
2:FP1:915:ILE:HD12	2:FP1:915:ILE:HA	1.93	0.40
2:GP1:289:ALA:HB3	2:GP1:437:ILE:HD13	2.04	0.40
2:GP1:500:GLN:HA	2:GP1:503:LYS:HB2	2.02	0.40
2:GP1:800:PHE:HZ	2:HP1:943:TRP:CE2	2.39	0.40
2:GP1:939:LYS:HA	2:GP1:942:ARG:HG3	2.02	0.40
2:HP1:617:ILE:HG22	2:HP1:618:LEU:N	2.37	0.40
2:HP1:619:PHE:HD1	2:HP1:619:PHE:HA	1.76	0.40
2:IP1:93:MET:HE1	3:NP1:17:THR:HG22	2.03	0.40
2:JP1:596:PHE:CD2	2:JP1:656:VAL:HG21	2.56	0.40
3:KP1:5:LYS:HG3	3:KP1:6:GLU:N	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AP1	413/466 (89%)	401 (97%)	12 (3%)	0	100	100
1	BP1	413/466 (89%)	405 (98%)	8 (2%)	0	100	100
1	CP1	413/466 (89%)	406 (98%)	7 (2%)	0	100	100
1	DP1	413/466 (89%)	402 (97%)	11 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	EP1	413/466 (89%)	406 (98%)	7 (2%)	0	100	100
2	FP1	847/1048 (81%)	816 (96%)	31 (4%)	0	100	100
2	GP1	847/1048 (81%)	813 (96%)	34 (4%)	0	100	100
2	HP1	847/1048 (81%)	807 (95%)	40 (5%)	0	100	100
2	IP1	847/1048 (81%)	813 (96%)	34 (4%)	0	100	100
2	JP1	847/1048 (81%)	811 (96%)	36 (4%)	0	100	100
3	KP1	41/1048 (4%)	41 (100%)	0	0	100	100
3	LP1	41/1048 (4%)	41 (100%)	0	0	100	100
3	MP1	41/1048 (4%)	41 (100%)	0	0	100	100
3	NP1	41/1048 (4%)	41 (100%)	0	0	100	100
3	OP1	41/1048 (4%)	41 (100%)	0	0	100	100
All	All	6505/12810 (51%)	6285 (97%)	220 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AP1	360/401 (90%)	347 (96%)	13 (4%)	31	52
1	BP1	360/401 (90%)	350 (97%)	10 (3%)	38	57
1	CP1	360/401 (90%)	350 (97%)	10 (3%)	38	57
1	DP1	360/401 (90%)	350 (97%)	10 (3%)	38	57
1	EP1	360/401 (90%)	352 (98%)	8 (2%)	45	61
2	FP1	715/858 (83%)	683 (96%)	32 (4%)	24	48
2	GP1	715/858 (83%)	683 (96%)	32 (4%)	24	48
2	HP1	715/858 (83%)	674 (94%)	41 (6%)	18	43
2	IP1	715/858 (83%)	678 (95%)	37 (5%)	21	45
2	JP1	715/858 (83%)	677 (95%)	38 (5%)	20	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	KP1	36/765 (5%)	32 (89%)	4 (11%)	6	24
3	LP1	36/765 (5%)	35 (97%)	1 (3%)	38	57
3	MP1	36/765 (5%)	32 (89%)	4 (11%)	6	24
3	NP1	36/765 (5%)	31 (86%)	5 (14%)	3	17
3	OP1	36/765 (5%)	31 (86%)	5 (14%)	3	17
All	All	5555/10120 (55%)	5305 (96%)	250 (4%)	26	48

All (250) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AP1	31	GLN
1	AP1	59	LYS
1	AP1	65	TYR
1	AP1	76	LEU
1	AP1	86	LEU
1	AP1	212	GLN
1	AP1	230	PHE
1	AP1	317	VAL
1	AP1	328	SER
1	AP1	345	SER
1	AP1	346	ASN
1	AP1	381	ARG
1	AP1	447	ASN
1	BP1	43	LEU
1	BP1	71	SER
1	BP1	195	GLN
1	BP1	230	PHE
1	BP1	268	THR
1	BP1	281	ARG
1	BP1	345	SER
1	BP1	374	ASN
1	BP1	426	MET
1	BP1	434	GLU
1	CP1	193	ASN
1	CP1	195	GLN
1	CP1	204	LEU
1	CP1	205	MET
1	CP1	230	PHE
1	CP1	299	SER
1	CP1	345	SER

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Mol	Chain	Res	Type
1	CP1	374	ASN
1	CP1	407	SER
1	CP1	426	MET
1	DP1	172	ASP
1	DP1	193	ASN
1	DP1	195	GLN
1	DP1	203	ASN
1	DP1	210	VAL
1	DP1	298	TYR
1	DP1	303	ASN
1	DP1	345	SER
1	DP1	374	ASN
1	DP1	456	ASP
1	EP1	65	TYR
1	EP1	119	THR
1	EP1	141	LEU
1	EP1	195	GLN
1	EP1	212	GLN
1	EP1	230	PHE
1	EP1	345	SER
1	EP1	387	THR
2	FP1	33	LEU
2	FP1	45	VAL
2	FP1	77	MET
2	FP1	85	MET
2	FP1	127	PHE
2	FP1	140	ASP
2	FP1	141	LYS
2	FP1	191	MET
2	FP1	217	ASN
2	FP1	244	ASN
2	FP1	294	ASN
2	FP1	339	MET
2	FP1	350	MET
2	FP1	402	VAL
2	FP1	427	ASN
2	FP1	508	THR
2	FP1	509	CYS
2	FP1	517	CYS
2	FP1	596	PHE
2	FP1	603	TYR
2	FP1	637	PHE

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Mol	Chain	Res	Type
2	FP1	660	LEU
2	FP1	716	LEU
2	FP1	725	PHE
2	FP1	728	ILE
2	FP1	732	MET
2	FP1	761	PHE
2	FP1	800	PHE
2	FP1	825	LEU
2	FP1	837	PHE
2	FP1	911	PHE
2	FP1	930	PHE
2	GP1	57	MET
2	GP1	127	PHE
2	GP1	140	ASP
2	GP1	149	TYR
2	GP1	191	MET
2	GP1	262	ASP
2	GP1	290	LEU
2	GP1	331	SER
2	GP1	339	MET
2	GP1	486	ASP
2	GP1	508	THR
2	GP1	517	CYS
2	GP1	540	LEU
2	GP1	555	GLN
2	GP1	573	ASN
2	GP1	589	THR
2	GP1	630	ASP
2	GP1	639	TYR
2	GP1	648	PHE
2	GP1	696	TYR
2	GP1	709	ASN
2	GP1	728	ILE
2	GP1	759	MET
2	GP1	761	PHE
2	GP1	807	ASN
2	GP1	825	LEU
2	GP1	837	PHE
2	GP1	915	ILE
2	GP1	916	LEU
2	GP1	931	THR
2	GP1	936	LEU

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Mol	Chain	Res	Type
2	GP1	938	ASP
2	HP1	33	LEU
2	HP1	85	MET
2	HP1	93	MET
2	HP1	125	GLN
2	HP1	127	PHE
2	HP1	140	ASP
2	HP1	147	LEU
2	HP1	149	TYR
2	HP1	196	LYS
2	HP1	262	ASP
2	HP1	285	ASN
2	HP1	295	GLN
2	HP1	299	LYS
2	HP1	325	LEU
2	HP1	326	GLN
2	HP1	348	GLN
2	HP1	368	ASN
2	HP1	369	ASP
2	HP1	393	GLN
2	HP1	430	MET
2	HP1	431	MET
2	HP1	509	CYS
2	HP1	514	SER
2	HP1	515	LEU
2	HP1	530	ILE
2	HP1	540	LEU
2	HP1	557	GLN
2	HP1	564	SER
2	HP1	603	TYR
2	HP1	612	CYS
2	HP1	639	TYR
2	HP1	661	MET
2	HP1	696	TYR
2	HP1	723	PHE
2	HP1	725	PHE
2	HP1	728	ILE
2	HP1	758	TYR
2	HP1	759	MET
2	HP1	837	PHE
2	HP1	911	PHE
2	HP1	936	LEU

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Mol	Chain	Res	Type
2	IP1	33	LEU
2	IP1	38	LEU
2	IP1	42	PHE
2	IP1	50	HIS
2	IP1	57	MET
2	IP1	127	PHE
2	IP1	140	ASP
2	IP1	221	GLU
2	IP1	262	ASP
2	IP1	275	LEU
2	IP1	285	ASN
2	IP1	291	ASN
2	IP1	299	LYS
2	IP1	325	LEU
2	IP1	363	THR
2	IP1	369	ASP
2	IP1	431	MET
2	IP1	450	ARG
2	IP1	452	PHE
2	IP1	509	CYS
2	IP1	543	ASP
2	IP1	546	LYS
2	IP1	564	SER
2	IP1	576	MET
2	IP1	603	TYR
2	IP1	604	TYR
2	IP1	637	PHE
2	IP1	639	TYR
2	IP1	660	LEU
2	IP1	671	PHE
2	IP1	723	PHE
2	IP1	736	MET
2	IP1	761	PHE
2	IP1	776	MET
2	IP1	837	PHE
2	IP1	905	TRP
2	IP1	930	PHE
2	JP1	29	PRO
2	JP1	55	GLN
2	JP1	57	MET
2	JP1	81	MET
2	JP1	93	MET

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Mol	Chain	Res	Type
2	JP1	109	PHE
2	JP1	127	PHE
2	JP1	285	ASN
2	JP1	293	THR
2	JP1	325	LEU
2	JP1	326	GLN
2	JP1	331	SER
2	JP1	359	THR
2	JP1	387	GLU
2	JP1	389	CYS
2	JP1	393	GLN
2	JP1	406	THR
2	JP1	430	MET
2	JP1	457	ASN
2	JP1	525	ASP
2	JP1	547	GLN
2	JP1	564	SER
2	JP1	568	TYR
2	JP1	596	PHE
2	JP1	603	TYR
2	JP1	611	ASP
2	JP1	624	LEU
2	JP1	661	MET
2	JP1	696	TYR
2	JP1	704	TRP
2	JP1	717	ILE
2	JP1	723	PHE
2	JP1	724	ILE
2	JP1	800	PHE
2	JP1	827	TYR
2	JP1	845	GLN
2	JP1	903	THR
2	JP1	941	LEU
3	KP1	12	PHE
3	KP1	16	ARG
3	KP1	36	PHE
3	KP1	38	LYS
3	LP1	12	PHE
3	MP1	7	ASN
3	MP1	12	PHE
3	MP1	37	PHE
3	MP1	40	ARG

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Mol	Chain	Res	Type
3	NP1	11	LEU
3	NP1	12	PHE
3	NP1	16	ARG
3	NP1	36	PHE
3	NP1	37	PHE
3	OP1	1	MET
3	OP1	12	PHE
3	OP1	16	ARG
3	OP1	18	ARG
3	OP1	37	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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

This section contains visualisations of the EMDB entry EMD-49396. 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

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation ⓘ

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

9 Map-model fit ⓘ

This section was not generated.