



# Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Feb 19, 2018 – 08:39 PM EST

PDB ID : 6BM0  
EMDB ID: : EMD-7114  
Title : Cryo-EM structure of human CPSF-160-WDR33 complex at 3.8 Å resolution  
Authors : Sun, Y.; Zhang, Y.; Hamilton, K.; Walz, T.; Tong, L.  
Deposited on : 2017-11-12  
Resolution : 3.80 Å (reported)

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report  
for a publicly released PDB/EMDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030736

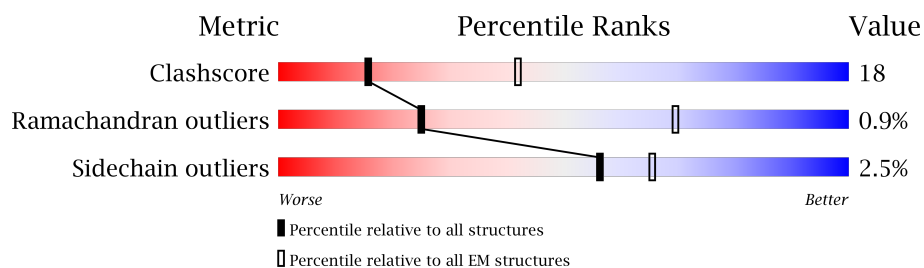
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.80 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	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	A	1443	
2	B	587	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12244 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 Cleavage and polyadenylation specificity factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1175	Total	C	N	O	S	0	0
			9318	5991	1595	1677	55		

- Molecule 2 is a protein called pre-mRNA 3' end processing protein WDR33.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	363	Total	C	N	O	S	0	0
			2926	1850	532	525	19		

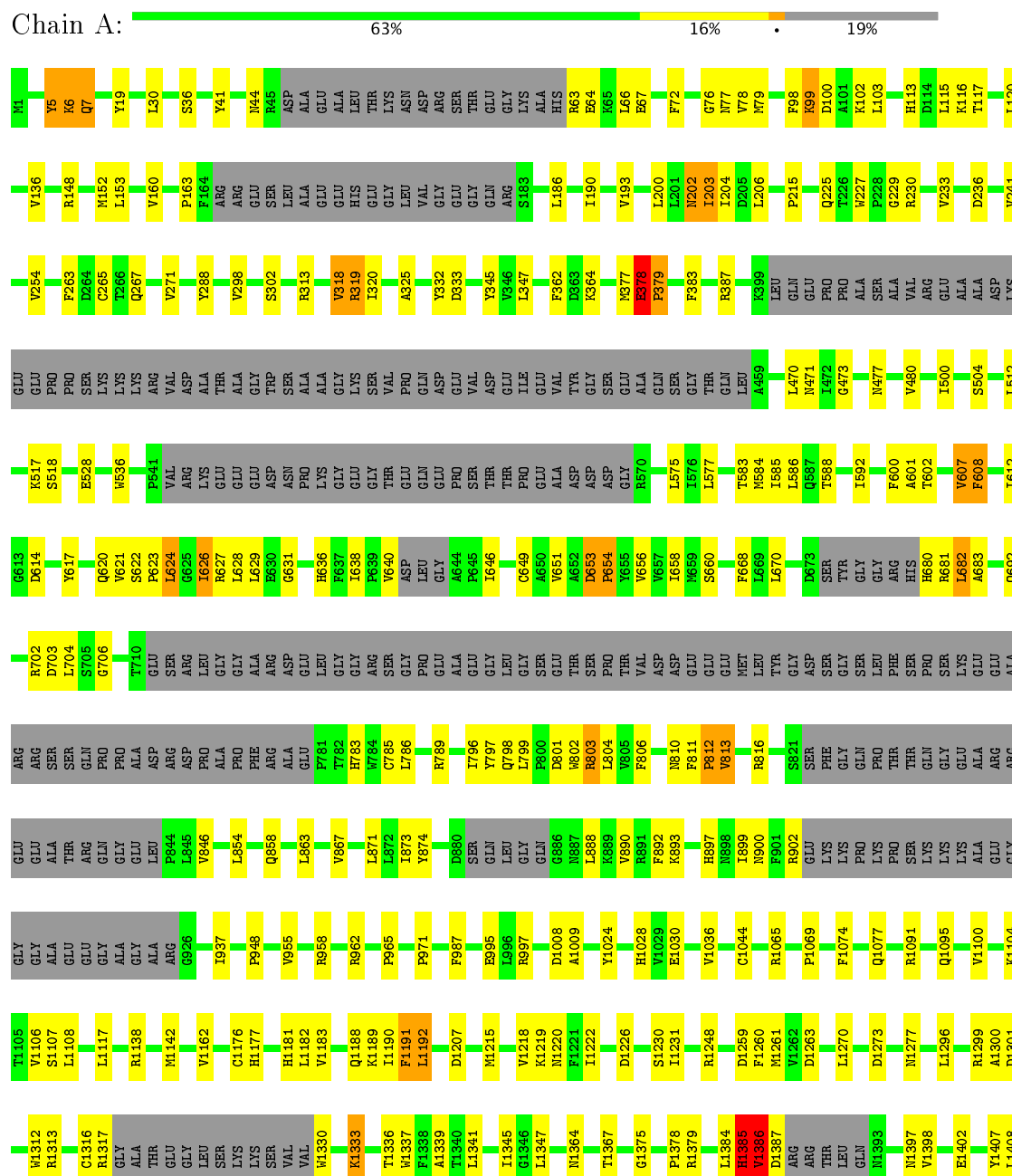
There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	MET	-	expression tag	UNP Q9C0J8
B	-13	GLY	-	expression tag	UNP Q9C0J8
B	-12	SER	-	expression tag	UNP Q9C0J8
B	-11	SER	-	expression tag	UNP Q9C0J8
B	-10	HIS	-	expression tag	UNP Q9C0J8
B	-9	HIS	-	expression tag	UNP Q9C0J8
B	-8	HIS	-	expression tag	UNP Q9C0J8
B	-7	HIS	-	expression tag	UNP Q9C0J8
B	-6	HIS	-	expression tag	UNP Q9C0J8
B	-5	HIS	-	expression tag	UNP Q9C0J8
B	-4	SER	-	expression tag	UNP Q9C0J8
B	-3	SER	-	expression tag	UNP Q9C0J8
B	-2	GLY	-	expression tag	UNP Q9C0J8
B	-1	LEU	-	expression tag	UNP Q9C0J8
B	0	VAL	-	expression tag	UNP Q9C0J8

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

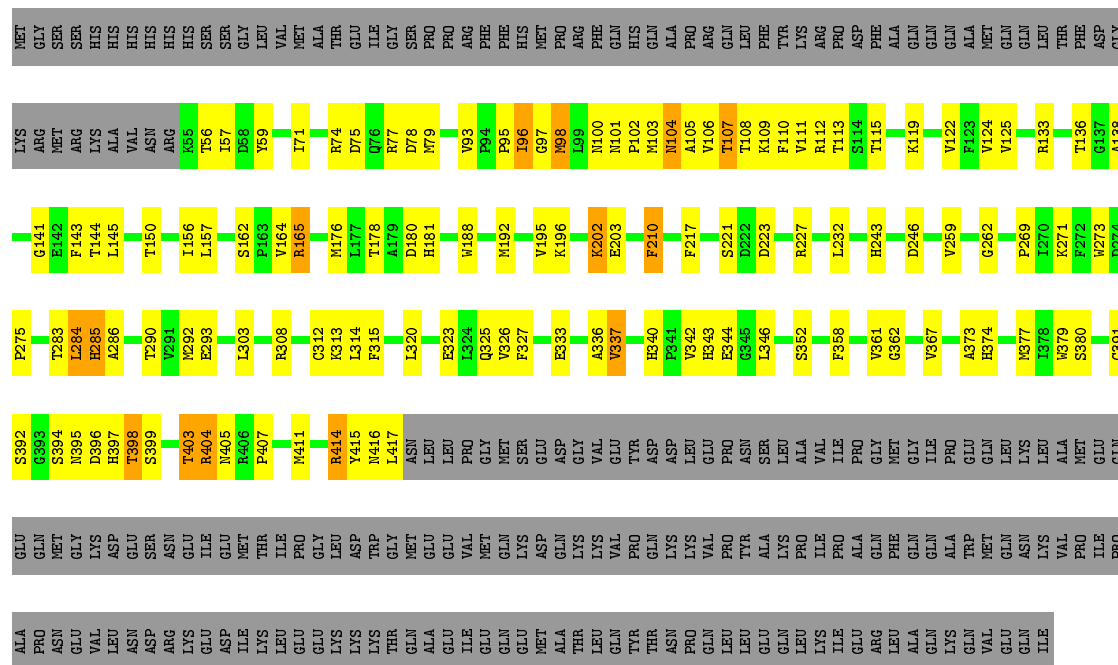
- Molecule 1: Cleavage and polyadenylation specificity factor subunit 1





- Molecule 2: pre-mRNA 3' end processing protein WDR33

Chain B:  41% 19% . 38%



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	205373	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	47	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	38462	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

## 5 Model quality

### 5.1 Standard geometry

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	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	A	0.35	0/9534	0.58	0/12942
2	B	0.37	0/3010	0.61	0/4080
All	All	0.36	0/12544	0.58	0/17022

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9318	0	9366	285	0
2	B	2926	0	2832	168	0
All	All	12244	0	12198	446	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 18.

All (446) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:628:LEU:HD11	1:A:682:LEU:CD2	1.26	1.61
1:A:318:VAL:HG21	1:A:362:PHE:CD2	1.58	1.38

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:626:ILE:HG12	1:A:668:PHE:CE2	1.58	1.36
1:A:617:TYR:HE2	1:A:680:HIS:ND1	1.33	1.26
1:A:816:ARG:HH21	1:A:1410:LEU:CD2	1.52	1.22
1:A:99:LYS:HG3	1:A:1387:ASP:O	1.40	1.21
2:B:374:HIS:NE2	2:B:394:SER:HB2	1.55	1.20
1:A:626:ILE:CG1	1:A:668:PHE:HE2	1.55	1.19
2:B:377:MET:HB3	2:B:395:ASN:HB2	1.19	1.17
2:B:103:MET:O	2:B:106:VAL:HG23	1.42	1.17
1:A:99:LYS:HG3	1:A:1387:ASP:C	1.64	1.16
1:A:628:LEU:CD1	1:A:682:LEU:CD2	2.21	1.16
1:A:378:GLU:HB3	1:A:379:PRO:HD3	1.28	1.15
2:B:103:MET:SD	2:B:367:VAL:HG11	1.87	1.15
1:A:626:ILE:CD1	1:A:638:ILE:HB	1.78	1.13
2:B:377:MET:H	2:B:395:ASN:HB3	1.05	1.12
1:A:651:VAL:HG13	1:A:656:VAL:HG22	1.19	1.11
2:B:103:MET:SD	2:B:367:VAL:CG1	2.38	1.11
2:B:95:PRO:O	2:B:96:ILE:HG13	1.52	1.09
1:A:378:GLU:CB	1:A:379:PRO:CD	2.31	1.09
1:A:1386:VAL:HG23	1:A:1387:ASP:H	1.05	1.09
1:A:1386:VAL:CG2	1:A:1387:ASP:H	1.66	1.08
2:B:374:HIS:CE1	2:B:394:SER:HB2	1.89	1.08
1:A:378:GLU:CB	1:A:379:PRO:HD3	1.81	1.07
1:A:621:VAL:HG22	1:A:626:ILE:CG2	1.84	1.07
1:A:628:LEU:CD1	1:A:682:LEU:HD22	1.85	1.05
1:A:617:TYR:CE2	1:A:680:HIS:ND1	2.25	1.04
1:A:621:VAL:HG22	1:A:626:ILE:HG22	1.39	1.04
2:B:101:ASN:N	2:B:102:PRO:HD3	1.71	1.04
1:A:816:ARG:HH21	1:A:1410:LEU:HD23	0.90	1.04
1:A:378:GLU:HB2	1:A:379:PRO:CD	1.84	1.03
1:A:1386:VAL:HG23	1:A:1387:ASP:N	1.73	1.03
2:B:269:PRO:HG2	2:B:285:HIS:HA	1.37	1.02
1:A:816:ARG:NH2	1:A:1410:LEU:CD2	2.24	1.01
1:A:6:LYS:HB2	1:A:1347:LEU:HD12	1.42	1.01
1:A:626:ILE:HD12	1:A:638:ILE:O	1.58	1.00
1:A:816:ARG:NH2	1:A:1410:LEU:HD23	1.75	1.00
1:A:628:LEU:HD11	1:A:682:LEU:HD23	1.39	1.00
1:A:626:ILE:HD13	1:A:638:ILE:HB	1.42	0.98
1:A:628:LEU:HD11	1:A:682:LEU:HD22	0.99	0.98
2:B:269:PRO:CG	2:B:285:HIS:HA	1.93	0.98
2:B:165:ARG:HH11	2:B:165:ARG:HG2	1.29	0.97
2:B:396:ASP:OD1	2:B:397:HIS:N	1.98	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:626:ILE:HD12	1:A:626:ILE:H	1.28	0.97
1:A:319:ARG:O	1:A:320:ILE:HG23	1.65	0.95
2:B:377:MET:CB	2:B:395:ASN:HB2	1.96	0.94
2:B:292:MET:CG	2:B:308:ARG:HD3	1.97	0.94
1:A:651:VAL:HG22	1:A:656:VAL:HG13	1.48	0.93
1:A:318:VAL:HG21	1:A:362:PHE:HD2	1.12	0.93
1:A:318:VAL:CG2	1:A:362:PHE:CD2	2.51	0.93
1:A:1218:VAL:HG12	1:A:1260:PHE:CE2	2.05	0.91
2:B:95:PRO:O	2:B:96:ILE:CG1	2.18	0.91
2:B:292:MET:SD	2:B:308:ARG:HD3	2.09	0.91
2:B:374:HIS:NE2	2:B:394:SER:CB	2.33	0.91
2:B:107:THR:O	2:B:358:PHE:HE2	1.55	0.90
1:A:153:LEU:HD22	1:A:203:ILE:HG21	1.53	0.89
1:A:628:LEU:HD11	1:A:682:LEU:HD21	1.55	0.89
1:A:72:PHE:CD2	1:A:115:LEU:HD23	2.09	0.88
2:B:377:MET:H	2:B:395:ASN:CB	1.85	0.88
2:B:377:MET:N	2:B:395:ASN:HB3	1.89	0.88
1:A:6:LYS:HB3	1:A:6:LYS:NZ	1.88	0.88
1:A:99:LYS:CG	1:A:1387:ASP:C	2.42	0.87
2:B:377:MET:HB3	2:B:395:ASN:CB	2.04	0.87
1:A:36:SER:HB3	1:A:76:GLY:O	1.74	0.87
1:A:617:TYR:HE2	1:A:680:HIS:HD1	1.19	0.87
2:B:105:ALA:HA	2:B:404:ARG:HG2	1.55	0.87
2:B:333:GLU:OE2	2:B:333:GLU:N	2.08	0.85
1:A:608:PHE:HE2	1:A:651:VAL:HG23	1.42	0.85
1:A:626:ILE:HG12	1:A:668:PHE:HE2	0.70	0.84
2:B:103:MET:SD	2:B:367:VAL:HG13	2.18	0.84
2:B:111:VAL:CG2	2:B:403:THR:HG22	2.08	0.83
1:A:608:PHE:HE2	1:A:651:VAL:CG2	1.92	0.82
1:A:6:LYS:HD3	1:A:1436:THR:CG2	2.08	0.82
2:B:95:PRO:C	2:B:96:ILE:HG13	2.00	0.82
2:B:95:PRO:O	2:B:96:ILE:CB	2.28	0.82
1:A:378:GLU:HB2	1:A:379:PRO:HD2	1.61	0.81
1:A:1106:VAL:HG13	1:A:1177:HIS:HB3	1.62	0.81
1:A:36:SER:CB	1:A:76:GLY:O	2.29	0.81
1:A:651:VAL:HG13	1:A:656:VAL:CG2	2.08	0.81
2:B:101:ASN:N	2:B:102:PRO:CD	2.45	0.80
1:A:621:VAL:HG22	1:A:626:ILE:HG23	1.64	0.79
2:B:374:HIS:CE1	2:B:394:SER:CB	2.66	0.79
1:A:115:LEU:O	1:A:115:LEU:HD12	1.83	0.79
1:A:624:LEU:HD22	1:A:624:LEU:H	1.46	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:111:VAL:CG2	2:B:403:THR:CG2	2.62	0.78
1:A:608:PHE:CE2	1:A:651:VAL:HG23	2.19	0.77
1:A:626:ILE:CD1	1:A:638:ILE:CB	2.62	0.77
2:B:107:THR:O	2:B:358:PHE:CE2	2.37	0.77
1:A:626:ILE:CD1	1:A:638:ILE:O	2.32	0.76
1:A:536:TRP:CZ2	1:A:608:PHE:HA	2.20	0.75
2:B:79:MET:SD	2:B:98:MET:CG	2.74	0.75
1:A:608:PHE:HD2	1:A:649:CYS:SG	2.10	0.74
1:A:1386:VAL:CG2	1:A:1387:ASP:N	2.36	0.73
1:A:318:VAL:HG23	1:A:362:PHE:CB	2.19	0.73
1:A:624:LEU:N	1:A:624:LEU:HD13	2.03	0.72
2:B:377:MET:CB	2:B:395:ASN:CB	2.65	0.72
1:A:797:TYR:HD2	1:A:802:TRP:HZ3	1.34	0.72
2:B:165:ARG:NH1	2:B:165:ARG:HG2	2.03	0.72
2:B:103:MET:O	2:B:104:ASN:C	2.25	0.72
1:A:113:HIS:HB3	1:A:893:LYS:HD2	1.71	0.71
2:B:292:MET:CG	2:B:308:ARG:CD	2.69	0.71
1:A:318:VAL:CG2	1:A:362:PHE:HD2	1.96	0.71
1:A:816:ARG:NH2	1:A:1410:LEU:HD21	2.04	0.71
1:A:1191:PHE:HD1	1:A:1191:PHE:H	1.38	0.71
1:A:377:MET:HE2	1:A:383:PHE:HB2	1.73	0.70
1:A:608:PHE:CD2	1:A:649:CYS:SG	2.84	0.70
2:B:111:VAL:HG21	2:B:403:THR:HG22	1.74	0.70
1:A:202:ASN:O	1:A:203:ILE:HD13	1.92	0.69
2:B:285:HIS:H	2:B:285:HIS:CD2	2.10	0.69
2:B:104:ASN:O	2:B:105:ALA:HB3	1.92	0.69
2:B:396:ASP:OD1	2:B:398:THR:N	2.25	0.69
1:A:6:LYS:HD3	1:A:1436:THR:HG22	1.73	0.69
1:A:681:ARG:HH12	1:A:683:ALA:HB2	1.58	0.69
2:B:373:ALA:HB1	2:B:415:TYR:CD1	2.28	0.69
2:B:103:MET:O	2:B:104:ASN:O	2.11	0.68
1:A:620:GLN:HE21	1:A:627:ARG:HD2	1.57	0.68
2:B:110:PHE:HZ	2:B:113:THR:HG23	1.58	0.68
1:A:636:HIS:HE1	1:A:638:ILE:HD11	1.58	0.68
1:A:626:ILE:HD12	1:A:638:ILE:HB	1.72	0.67
1:A:319:ARG:O	1:A:319:ARG:HG3	1.93	0.67
1:A:621:VAL:CG2	1:A:626:ILE:CG2	2.69	0.67
2:B:124:VAL:HG11	2:B:165:ARG:O	1.95	0.66
2:B:103:MET:C	2:B:106:VAL:HG23	2.16	0.66
1:A:347:LEU:HB2	1:A:362:PHE:HE1	1.61	0.66
2:B:343:HIS:HB3	2:B:346:LEU:HD23	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1301:ASP:CG	1:A:1384:LEU:HD22	2.16	0.66
2:B:119:LYS:O	2:B:397:HIS:CD2	2.49	0.66
1:A:651:VAL:CG1	1:A:656:VAL:HG22	2.12	0.65
1:A:608:PHE:CE2	1:A:651:VAL:CG2	2.78	0.65
2:B:95:PRO:O	2:B:96:ILE:HB	1.95	0.65
1:A:785:CYS:HG	1:A:802:TRP:HH2	1.45	0.65
2:B:56:THR:O	2:B:57:ILE:HD13	1.95	0.65
1:A:621:VAL:CG2	1:A:626:ILE:HG22	2.21	0.64
2:B:124:VAL:CG1	2:B:165:ARG:O	2.44	0.64
1:A:1330:TRP:CH2	1:A:1435:GLU:HB3	2.33	0.64
2:B:292:MET:HG2	2:B:308:ARG:HD3	1.80	0.64
1:A:1044:CYS:HB3	1:A:1069:PRO:HG2	1.80	0.64
2:B:344:GLU:O	2:B:344:GLU:HG3	1.97	0.64
2:B:115:THR:HG22	2:B:398:THR:OG1	1.97	0.64
1:A:797:TYR:CD2	1:A:802:TRP:HZ3	2.15	0.63
2:B:103:MET:CE	2:B:367:VAL:HG21	2.29	0.63
2:B:106:VAL:HG12	2:B:106:VAL:O	1.98	0.63
1:A:785:CYS:HB2	1:A:799:LEU:HD13	1.80	0.63
1:A:298:VAL:HG12	1:A:313:ARG:HB2	1.81	0.63
2:B:333:GLU:CD	2:B:333:GLU:H	2.01	0.63
1:A:797:TYR:HD2	1:A:802:TRP:CZ3	2.15	0.62
2:B:343:HIS:HB3	2:B:346:LEU:CD2	2.29	0.62
2:B:336:ALA:HB2	2:B:379:TRP:O	1.99	0.62
2:B:411:MET:O	2:B:417:LEU:HB2	1.98	0.62
1:A:623:PRO:HA	1:A:646:ILE:CG2	2.29	0.62
2:B:103:MET:SD	2:B:367:VAL:CG2	2.87	0.62
1:A:811:PHE:O	1:A:812:PRO:O	2.17	0.62
2:B:202:LYS:HE2	2:B:227:ARG:HH22	1.62	0.62
2:B:79:MET:SD	2:B:98:MET:HG2	2.39	0.62
1:A:1218:VAL:CG1	1:A:1260:PHE:CE2	2.80	0.62
2:B:110:PHE:HZ	2:B:113:THR:CG2	2.12	0.62
2:B:210:PHE:HB3	2:B:217:PHE:HB3	1.81	0.62
2:B:93:VAL:HG23	2:B:97:GLY:O	1.99	0.61
1:A:302:SER:OG	1:A:302:SER:O	2.17	0.61
1:A:1226:ASP:HB3	1:A:1230:SER:H	1.65	0.61
1:A:318:VAL:HG23	1:A:362:PHE:HB3	1.82	0.61
1:A:1218:VAL:HG13	1:A:1218:VAL:O	2.00	0.61
1:A:318:VAL:HG21	1:A:362:PHE:CG	2.29	0.61
1:A:577:LEU:HB2	1:A:584:MET:HB2	1.81	0.60
2:B:56:THR:CG2	2:B:57:ILE:N	2.63	0.60
1:A:617:TYR:HE2	1:A:680:HIS:CE1	2.12	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:640:VAL:HG12	1:A:640:VAL:O	2.01	0.60
1:A:797:TYR:CD2	1:A:802:TRP:CZ3	2.88	0.60
1:A:319:ARG:CG	1:A:319:ARG:HH11	2.15	0.60
2:B:290:THR:O	2:B:308:ARG:HG2	2.01	0.60
2:B:284:LEU:HD13	2:B:320:LEU:HD22	1.84	0.60
1:A:1277:ASN:HD21	1:A:1385:HIS:HA	1.68	0.59
2:B:336:ALA:O	2:B:337:VAL:C	2.38	0.59
2:B:203:GLU:HG3	2:B:223:ASP:HB3	1.83	0.59
2:B:79:MET:SD	2:B:98:MET:HG3	2.43	0.59
1:A:617:TYR:CE2	1:A:680:HIS:CE1	2.90	0.59
1:A:1188:GLN:NE2	2:B:59:TYR:OH	2.36	0.58
1:A:656:VAL:HB	1:A:668:PHE:HB2	1.84	0.58
2:B:286:ALA:HB1	2:B:315:PHE:HZ	1.67	0.58
1:A:477:ASN:HD22	1:A:1024:TYR:HD1	1.50	0.58
1:A:44:ASN:ND2	1:A:67:GLU:OE1	2.36	0.58
1:A:6:LYS:HZ2	1:A:6:LYS:HB3	1.69	0.58
2:B:325:GLN:HE22	2:B:362:GLY:H	1.51	0.58
2:B:373:ALA:HB1	2:B:415:TYR:HD1	1.67	0.58
1:A:1259:ASP:HB3	1:A:1270:LEU:HB3	1.85	0.58
1:A:626:ILE:HG21	1:A:658:ILE:HD11	1.84	0.58
1:A:607:VAL:HG11	1:A:646:ILE:HG23	1.86	0.58
1:A:1190:ILE:HG22	1:A:1190:ILE:O	2.03	0.58
1:A:6:LYS:HD3	1:A:1436:THR:HG21	1.85	0.58
1:A:6:LYS:HZ1	1:A:6:LYS:HB3	1.67	0.58
1:A:202:ASN:O	1:A:203:ILE:CD1	2.51	0.57
1:A:473:GLY:H	1:A:504:SER:HB2	1.68	0.57
1:A:636:HIS:CE1	1:A:638:ILE:HD11	2.39	0.57
1:A:98:PHE:HB2	1:A:102:LYS:HB2	1.86	0.57
1:A:1191:PHE:N	1:A:1191:PHE:CD1	2.72	0.57
1:A:626:ILE:CG1	1:A:668:PHE:CE2	2.47	0.57
1:A:203:ILE:HG21	1:A:206:LEU:HD23	1.86	0.57
2:B:286:ALA:HB1	2:B:315:PHE:CZ	2.39	0.57
1:A:377:MET:CE	1:A:383:PHE:HB2	2.33	0.57
1:A:347:LEU:HB2	1:A:362:PHE:CE1	2.39	0.57
2:B:95:PRO:C	2:B:96:ILE:CG1	2.64	0.57
1:A:347:LEU:HD13	1:A:362:PHE:CE1	2.40	0.56
1:A:319:ARG:HG2	1:A:319:ARG:NH1	2.19	0.56
2:B:103:MET:SD	2:B:367:VAL:HG21	2.46	0.56
2:B:111:VAL:HG23	2:B:403:THR:HG22	1.84	0.56
1:A:682:LEU:HD13	1:A:682:LEU:N	2.21	0.56
2:B:108:THR:OG1	2:B:405:ASN:OD1	2.23	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:122:VAL:HA	2:B:138:ALA:HA	1.88	0.56
1:A:153:LEU:CD2	1:A:203:ILE:HG21	2.31	0.56
1:A:480:VAL:HG22	1:A:500:ILE:HG22	1.87	0.56
2:B:101:ASN:H	2:B:102:PRO:HD3	1.66	0.56
2:B:303:LEU:HB3	2:B:315:PHE:HB2	1.87	0.55
2:B:210:PHE:HD1	2:B:210:PHE:H	1.54	0.55
2:B:133:ARG:HD3	2:B:145:LEU:HD23	1.87	0.55
1:A:617:TYR:HE2	1:A:680:HIS:CG	2.17	0.55
2:B:157:LEU:HD11	2:B:192:MET:HB3	1.89	0.55
1:A:626:ILE:HD11	1:A:638:ILE:CG2	2.36	0.55
2:B:243:HIS:NE2	2:B:262:GLY:O	2.35	0.55
1:A:626:ILE:N	1:A:626:ILE:HD12	2.07	0.55
2:B:162:SER:HB2	2:B:180:ASP:HB2	1.89	0.55
2:B:292:MET:HG2	2:B:308:ARG:CD	2.36	0.55
1:A:512:LEU:HD11	1:A:1036:VAL:HG21	1.89	0.55
1:A:318:VAL:CG2	1:A:362:PHE:CB	2.84	0.55
1:A:888:LEU:HB3	1:A:890:VAL:HG22	1.89	0.55
2:B:106:VAL:HG13	2:B:358:PHE:CD2	2.42	0.54
2:B:340:HIS:HE1	2:B:342:VAL:HG22	1.72	0.54
2:B:398:THR:HG23	2:B:399:SER:N	2.20	0.54
2:B:210:PHE:N	2:B:210:PHE:CD1	2.72	0.54
2:B:106:VAL:HG13	2:B:358:PHE:HD2	1.73	0.54
1:A:703:ASP:HB3	1:A:706:GLY:HA3	1.89	0.54
1:A:854:LEU:HB3	1:A:955:VAL:HB	1.89	0.54
1:A:1104:LYS:NZ	1:A:1215:MET:O	2.40	0.54
1:A:1263:ASP:OD1	1:A:1333:LYS:NZ	2.41	0.54
1:A:626:ILE:CD1	1:A:668:PHE:CE2	2.90	0.54
2:B:143:PHE:HB2	2:B:157:LEU:HB2	1.90	0.54
1:A:692:GLN:OE1	1:A:789:ARG:NH1	2.41	0.53
2:B:103:MET:C	2:B:104:ASN:O	2.45	0.53
2:B:176:MET:HB3	2:B:188:TRP:HB2	1.90	0.53
2:B:144:THR:HG22	2:B:156:ILE:HG12	1.89	0.53
1:A:319:ARG:O	1:A:320:ILE:CG2	2.47	0.53
1:A:575:LEU:HD23	1:A:586:LEU:HD22	1.91	0.53
1:A:623:PRO:HA	1:A:646:ILE:HG21	1.89	0.53
1:A:1219:LYS:HB3	1:A:1219:LYS:HZ2	1.73	0.53
1:A:387:ARG:O	1:A:471:ASN:ND2	2.38	0.53
1:A:575:LEU:HB3	1:A:586:LEU:HB2	1.90	0.53
1:A:626:ILE:HD13	1:A:638:ILE:CB	2.29	0.53
2:B:340:HIS:CE1	2:B:342:VAL:HG22	2.44	0.53
1:A:470:LEU:HD23	1:A:1009:ALA:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:111:VAL:HG21	2:B:403:THR:CG2	2.34	0.52
2:B:391:CYS:SG	2:B:392:SER:N	2.83	0.52
1:A:1107:SER:HB3	1:A:1117:LEU:HB3	1.91	0.52
2:B:110:PHE:CZ	2:B:113:THR:CG2	2.91	0.52
1:A:1408:LEU:HA	1:A:1415:ARG:HH12	1.74	0.52
1:A:902:ARG:H	1:A:948:PRO:HG3	1.74	0.52
2:B:313:LYS:HG2	2:B:326:VAL:HG12	1.91	0.52
2:B:377:MET:HB2	2:B:395:ASN:ND2	2.24	0.52
1:A:1142:MET:HG2	1:A:1162:VAL:HG22	1.91	0.52
1:A:160:VAL:HG22	1:A:190:ILE:HG12	1.92	0.52
1:A:626:ILE:HD11	1:A:638:ILE:HG22	1.92	0.52
2:B:106:VAL:CG1	2:B:358:PHE:HD2	2.23	0.52
1:A:36:SER:HB2	1:A:76:GLY:O	2.11	0.51
2:B:95:PRO:HB2	2:B:342:VAL:HG21	1.91	0.51
1:A:626:ILE:CG2	1:A:658:ILE:HD11	2.41	0.51
1:A:233:VAL:HG12	2:B:417:LEU:HD11	1.91	0.51
1:A:230:ARG:NH1	2:B:108:THR:OG1	2.42	0.51
1:A:63:ARG:NE	1:A:63:ARG:HA	2.26	0.51
1:A:937:ILE:HD13	1:A:987:PHE:HB3	1.92	0.51
2:B:221:SER:OG	2:B:223:ASP:OD1	2.29	0.51
1:A:646:ILE:HA	1:A:660:SER:HA	1.93	0.51
1:A:626:ILE:CD1	1:A:638:ILE:CG2	2.89	0.51
2:B:119:LYS:O	2:B:397:HIS:HD2	1.92	0.50
1:A:320:ILE:HG12	1:A:345:TYR:HE2	1.75	0.50
2:B:178:THR:HG1	2:B:188:TRP:HE1	1.60	0.50
1:A:120:LEU:HD11	1:A:1375:GLY:HA3	1.93	0.50
2:B:343:HIS:CB	2:B:346:LEU:HD21	2.42	0.50
2:B:56:THR:HG22	2:B:57:ILE:N	2.26	0.50
2:B:97:GLY:O	2:B:98:MET:HB2	2.12	0.50
1:A:319:ARG:CG	1:A:319:ARG:NH1	2.73	0.50
2:B:373:ALA:HB1	2:B:415:TYR:CE1	2.47	0.50
1:A:72:PHE:CE2	1:A:115:LEU:HD23	2.46	0.50
1:A:103:LEU:HD12	1:A:152:MET:HE3	1.94	0.50
2:B:312:CYS:HB2	2:B:327:PHE:HB2	1.94	0.50
1:A:1367:THR:HG23	1:A:1378:PRO:HD2	1.94	0.49
1:A:318:VAL:CG2	1:A:362:PHE:CG	2.93	0.49
1:A:1176:CYS:HB2	1:A:1183:VAL:HB	1.93	0.49
1:A:236:ASP:HA	1:A:263:PHE:HB3	1.94	0.49
2:B:246:ASP:OD1	2:B:246:ASP:N	2.44	0.49
2:B:269:PRO:HG3	2:B:285:HIS:HA	1.88	0.49
2:B:75:ASP:HB2	2:B:77:ARG:HG2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1312:TRP:HB2	1:A:1337:TRP:HB2	1.94	0.49
1:A:19:TYR:OH	1:A:378:GLU:HG3	2.12	0.49
1:A:670:LEU:HA	1:A:682:LEU:HD12	1.95	0.49
1:A:1183:VAL:HG22	1:A:1192:LEU:HG	1.94	0.49
1:A:612:ILE:HD13	1:A:651:VAL:CG1	2.42	0.49
1:A:241:VAL:HG13	1:A:254:VAL:HG13	1.94	0.49
2:B:259:VAL:HG23	2:B:275:PRO:HG3	1.94	0.49
1:A:801:ASP:O	1:A:802:TRP:CD1	2.65	0.49
2:B:343:HIS:CB	2:B:346:LEU:CD2	2.91	0.49
1:A:115:LEU:C	1:A:115:LEU:HD12	2.34	0.49
1:A:202:ASN:O	1:A:203:ILE:CG1	2.61	0.49
1:A:229:GLY:HA2	2:B:407:PRO:HA	1.94	0.49
1:A:622:SER:OG	1:A:623:PRO:HD2	2.13	0.49
1:A:1219:LYS:NZ	1:A:1219:LYS:HB3	2.27	0.48
1:A:267:GLN:NE2	1:A:325:ALA:O	2.46	0.48
2:B:377:MET:N	2:B:395:ASN:CB	2.61	0.48
1:A:1316:CYS:SG	1:A:1317:ARG:N	2.86	0.48
1:A:64:GLU:N	1:A:64:GLU:OE1	2.46	0.48
1:A:136:VAL:HG11	2:B:100:ASN:HB3	1.94	0.48
1:A:653:ASP:HB3	1:A:702:ARG:HD3	1.96	0.48
1:A:803:ARG:HG2	1:A:804:LEU:N	2.28	0.48
1:A:1219:LYS:NZ	1:A:1219:LYS:CB	2.73	0.48
1:A:202:ASN:O	1:A:203:ILE:HG12	2.14	0.48
2:B:125:VAL:HG22	2:B:136:THR:HG23	1.95	0.48
2:B:196:LYS:NZ	2:B:232:LEU:O	2.46	0.48
1:A:302:SER:OG	1:A:1065:ARG:O	2.25	0.48
1:A:1077:GLN:HE22	1:A:1091:ARG:HH21	1.61	0.48
2:B:162:SER:HB3	2:B:181:HIS:HB3	1.96	0.48
2:B:109:LYS:HB3	2:B:403:THR:O	2.14	0.48
2:B:74:ARG:NH1	2:B:78:ASP:OD1	2.47	0.48
1:A:1301:ASP:HB3	1:A:1384:LEU:HD22	1.96	0.47
1:A:863:LEU:HB3	1:A:874:TYR:HB2	1.95	0.47
1:A:318:VAL:HG23	1:A:362:PHE:HB2	1.94	0.47
1:A:1189:LYS:HB2	1:A:1191:PHE:HE1	1.80	0.47
1:A:225:GLN:NE2	2:B:101:ASN:HA	2.29	0.47
2:B:124:VAL:HG13	2:B:165:ARG:O	2.14	0.47
1:A:785:CYS:SG	1:A:802:TRP:HH2	2.37	0.47
1:A:66:LEU:O	1:A:958:ARG:NH1	2.45	0.47
1:A:100:ASP:OD2	1:A:1386:VAL:HG23	2.14	0.47
1:A:1181:HIS:HB3	1:A:1192:LEU:HD23	1.97	0.47
1:A:1385:HIS:ND1	1:A:1386:VAL:HG13	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:63:ARG:HE	1:A:63:ARG:HA	1.80	0.47
1:A:1189:LYS:NZ	1:A:1207:ASP:OD1	2.40	0.47
1:A:783:HIS:HB3	1:A:799:LEU:HD23	1.97	0.47
2:B:336:ALA:O	2:B:337:VAL:O	2.33	0.47
1:A:1177:HIS:HA	1:A:1181:HIS:O	2.15	0.47
1:A:148:ARG:HH21	1:A:215:PRO:CA	2.27	0.46
2:B:314:LEU:HD11	2:B:361:VAL:HG22	1.96	0.46
1:A:629:LEU:HG	1:A:631:GLY:H	1.81	0.46
1:A:517:LYS:HG3	1:A:518:SER:H	1.81	0.46
2:B:284:LEU:O	2:B:284:LEU:HG	2.15	0.46
1:A:1301:ASP:CB	1:A:1384:LEU:HD22	2.45	0.46
1:A:846:VAL:HG22	1:A:867:VAL:HG22	1.98	0.46
1:A:7:GLN:HB3	1:A:1402:GLU:OE2	2.16	0.46
1:A:628:LEU:CD1	1:A:682:LEU:HD23	2.18	0.46
1:A:948:PRO:HA	1:A:971:PRO:HB3	1.97	0.46
1:A:302:SER:CB	1:A:1065:ARG:O	2.64	0.46
1:A:995:GLU:OE1	1:A:997:ARG:NH2	2.49	0.45
1:A:608:PHE:HZ	1:A:651:VAL:HB	1.81	0.45
2:B:103:MET:O	2:B:106:VAL:N	2.49	0.45
2:B:165:ARG:NH1	2:B:165:ARG:CG	2.73	0.45
1:A:874:TYR:HB3	1:A:892:PHE:HB3	1.99	0.45
2:B:336:ALA:CB	2:B:379:TRP:O	2.64	0.45
2:B:113:THR:O	2:B:113:THR:OG1	2.35	0.45
2:B:119:LYS:C	2:B:397:HIS:HD2	2.20	0.45
1:A:148:ARG:HH21	1:A:215:PRO:HA	1.80	0.45
1:A:608:PHE:HE2	1:A:651:VAL:HG21	1.80	0.45
1:A:812:PRO:HB2	1:A:813:VAL:H	1.61	0.45
1:A:1261:MET:HG2	1:A:1270:LEU:HB2	1.98	0.45
2:B:396:ASP:CG	2:B:397:HIS:H	2.08	0.45
1:A:588:THR:HA	1:A:592:ILE:HG22	1.98	0.44
1:A:536:TRP:CE2	1:A:608:PHE:HA	2.52	0.44
2:B:100:ASN:C	2:B:102:PRO:HD3	2.33	0.44
2:B:377:MET:CA	2:B:395:ASN:HB2	2.46	0.44
2:B:119:LYS:C	2:B:397:HIS:CD2	2.91	0.44
1:A:962:ARG:NE	1:A:1008:ASP:O	2.38	0.44
2:B:141:GLY:HA2	2:B:164:VAL:HG23	1.99	0.44
2:B:210:PHE:HB3	2:B:217:PHE:CB	2.45	0.44
1:A:1364:ASN:OD1	1:A:1379:ARG:NH2	2.51	0.44
1:A:623:PRO:HA	1:A:646:ILE:HG22	1.99	0.44
1:A:204:ILE:HG21	1:A:265:CYS:O	2.18	0.43
1:A:319:ARG:HG2	1:A:319:ARG:HH11	1.77	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:785:CYS:SG	1:A:802:TRP:CH2	3.10	0.43
2:B:165:ARG:HH12	2:B:181:HIS:HB2	1.82	0.43
1:A:786:LEU:HD13	1:A:796:ILE:HG12	2.00	0.43
1:A:1316:CYS:SG	1:A:1330:TRP:HB3	2.58	0.43
2:B:165:ARG:HD3	2:B:165:ARG:HA	1.73	0.43
1:A:1300:ALA:HB1	1:A:1398:VAL:HG23	2.00	0.43
1:A:811:PHE:N	1:A:812:PRO:CD	2.81	0.43
2:B:336:ALA:HB1	2:B:380:SER:HA	2.01	0.43
1:A:1341:LEU:HD11	2:B:71:ILE:HG23	2.01	0.43
2:B:292:MET:HG3	2:B:308:ARG:CD	2.46	0.43
1:A:203:ILE:CG2	1:A:206:LEU:HD23	2.48	0.43
2:B:56:THR:OG1	2:B:150:THR:HG22	2.19	0.43
2:B:293:GLU:OE1	2:B:336:ALA:C	2.56	0.43
1:A:1299:ARG:O	1:A:1397:ASN:ND2	2.41	0.43
1:A:1339:ALA:HA	1:A:1345:ILE:HA	2.00	0.43
1:A:271:VAL:HG21	1:A:288:TYR:HE1	1.82	0.43
1:A:583:THR:HB	1:A:602:THR:HA	2.01	0.43
1:A:203:ILE:O	1:A:203:ILE:HG22	2.18	0.43
1:A:628:LEU:CD1	1:A:682:LEU:HD21	2.28	0.43
1:A:1108:LEU:HD21	1:A:1182:LEU:HB2	2.01	0.42
2:B:259:VAL:HB	2:B:273:TRP:HB2	2.01	0.42
1:A:653:ASP:HA	1:A:654:PRO:HD2	1.60	0.42
1:A:704:LEU:HD12	1:A:858:GLN:HG3	2.01	0.42
1:A:798:GLN:OE1	1:A:803:ARG:NH2	2.51	0.42
2:B:103:MET:CA	2:B:106:VAL:HG23	2.49	0.42
2:B:315:PHE:HE1	2:B:323:GLU:HG3	1.84	0.42
1:A:1316:CYS:SG	1:A:1330:TRP:CB	3.07	0.42
1:A:585:ILE:HD11	1:A:600:PHE:HB2	2.01	0.42
1:A:1273:ASP:OD1	1:A:1273:ASP:N	2.51	0.42
1:A:5:TYR:CD2	1:A:5:TYR:O	2.72	0.42
2:B:103:MET:O	2:B:106:VAL:CG2	2.36	0.42
2:B:100:ASN:O	2:B:101:ASN:HB3	2.20	0.42
1:A:1183:VAL:HG11	1:A:1222:ILE:HD13	2.01	0.42
1:A:601:ALA:H	1:A:620:GLN:HE22	1.66	0.42
1:A:1231:ILE:HG21	1:A:1296:LEU:HD12	2.01	0.42
1:A:153:LEU:HB2	1:A:206:LEU:HD21	2.02	0.42
2:B:293:GLU:CD	2:B:336:ALA:HA	2.40	0.42
1:A:163:PRO:HB2	1:A:186:LEU:HB2	2.02	0.42
1:A:900:ASN:HD22	1:A:1434:LEU:HB3	1.84	0.42
2:B:271:LYS:NZ	2:B:283:THR:OG1	2.38	0.42
1:A:1407:TYR:O	1:A:1415:ARG:NH1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:803:ARG:HE	1:A:803:ARG:HB3	1.55	0.41
1:A:871:LEU:HD23	1:A:899:ILE:HG21	2.02	0.41
1:A:518:SER:HB3	1:A:965:PRO:HG2	2.01	0.41
2:B:93:VAL:CG2	2:B:97:GLY:O	2.66	0.41
2:B:115:THR:CG2	2:B:398:THR:OG1	2.65	0.41
1:A:345:TYR:HE1	1:A:364:LYS:HG3	1.85	0.41
1:A:78:VAL:HG22	1:A:98:PHE:HE1	1.85	0.41
1:A:5:TYR:CD2	1:A:5:TYR:C	2.93	0.41
1:A:621:VAL:CG2	1:A:626:ILE:HG23	2.40	0.41
1:A:810:ASN:ND2	1:A:813:VAL:HG21	2.35	0.41
2:B:195:VAL:HG12	2:B:196:LYS:H	1.84	0.41
2:B:202:LYS:CD	2:B:202:LYS:N	2.83	0.41
1:A:528:GLU:HG3	1:A:995:GLU:HG2	2.02	0.41
1:A:99:LYS:HA	1:A:99:LYS:HD2	1.20	0.41
1:A:1411:SER:O	1:A:1415:ARG:N	2.52	0.41
1:A:1313:ARG:HG2	1:A:1336:THR:HG22	2.03	0.41
1:A:193:VAL:HG13	1:A:200:LEU:HD12	2.01	0.41
1:A:202:ASN:C	1:A:203:ILE:HG12	2.40	0.41
1:A:796:ILE:HB	1:A:806:PHE:HB3	2.03	0.41
1:A:1028:HIS:CE1	1:A:1030:GLU:HB2	2.56	0.41
2:B:333:GLU:CD	2:B:352:SER:OG	2.59	0.41
1:A:30:LEU:HB3	1:A:41:TYR:HB2	2.03	0.41
1:A:656:VAL:O	1:A:668:PHE:N	2.43	0.41
1:A:1074:PHE:HD2	1:A:1100:VAL:H	1.69	0.40
1:A:1231:ILE:HG22	1:A:1248:ARG:HA	2.03	0.40
1:A:116:LYS:CG	1:A:117:THR:N	2.85	0.40
1:A:614:ASP:N	1:A:614:ASP:OD1	2.53	0.40
1:A:608:PHE:CZ	1:A:651:VAL:HB	2.56	0.40
1:A:1095:GLN:HE21	1:A:1138:ARG:HH12	1.69	0.40
2:B:333:GLU:OE1	2:B:352:SER:OG	2.36	0.40
1:A:873:ILE:HG12	1:A:897:HIS:NE2	2.35	0.40
2:B:286:ALA:CB	2:B:315:PHE:CZ	3.04	0.40
1:A:77:ASN:O	1:A:79:MET:CE	2.70	0.40
2:B:414:ARG:HE	2:B:414:ARG:HB2	1.71	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	A	1149/1443 (80%)	1045 (91%)	95 (8%)	9 (1%)	22	65
2	B	361/587 (62%)	316 (88%)	40 (11%)	5 (1%)	13	54
All	All	1510/2030 (74%)	1361 (90%)	135 (9%)	14 (1%)	25	62

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	378	GLU
1	A	379	PRO
1	A	654	PRO
1	A	812	PRO
1	A	813	VAL
2	B	96	ILE
2	B	98	MET
2	B	104	ASN
2	B	337	VAL
1	A	1386	VAL
2	B	416	ASN
1	A	203	ILE
1	A	1385	HIS
1	A	653	ASP

### 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	A	1028/1235 (83%)	1005 (98%)	23 (2%)	57	81
2	B	315/514 (61%)	304 (96%)	11 (4%)	41	73
All	All	1343/1749 (77%)	1309 (98%)	34 (2%)	56	79

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	TYR
1	A	6	LYS
1	A	7	GLN
1	A	99	LYS
1	A	202	ASN
1	A	227	TRP
1	A	318	VAL
1	A	319	ARG
1	A	332	TYR
1	A	333	ASP
1	A	378	GLU
1	A	607	VAL
1	A	608	PHE
1	A	624	LEU
1	A	626	ILE
1	A	682	LEU
1	A	803	ARG
1	A	1191	PHE
1	A	1192	LEU
1	A	1220	ASN
1	A	1333	LYS
1	A	1385	HIS
1	A	1386	VAL
2	B	107	THR
2	B	112	ARG
2	B	165	ARG
2	B	202	LYS
2	B	210	PHE
2	B	284	LEU
2	B	285	HIS
2	B	398	THR
2	B	403	THR
2	B	404	ARG
2	B	414	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	246	ASN
1	A	620	GLN
1	A	648	GLN
1	A	664	HIS
1	A	879	HIS
1	A	900	ASN
1	A	1095	GLN
1	A	1188	GLN
1	A	1332	ASN
2	B	69	ASN
2	B	160	HIS
2	B	285	HIS
2	B	325	GLN
2	B	397	HIS
2	B	416	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.