



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 27, 2024 – 12:46 pm BST

PDB ID : 4AQF  
Title : X-ray crystallographic structure of Crimean-congo haemorrhagic fever virus nucleoprotein  
Authors : Wang, Y.; Dutta, S.; Karlberg, H.; Devignot, S.; Weber, F.; Hao, Q.; Tan, Y.J.; Mirazimi, A.; Kotaka, M.  
Deposited on : 2012-04-17  
Resolution : 3.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

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>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.36.2  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

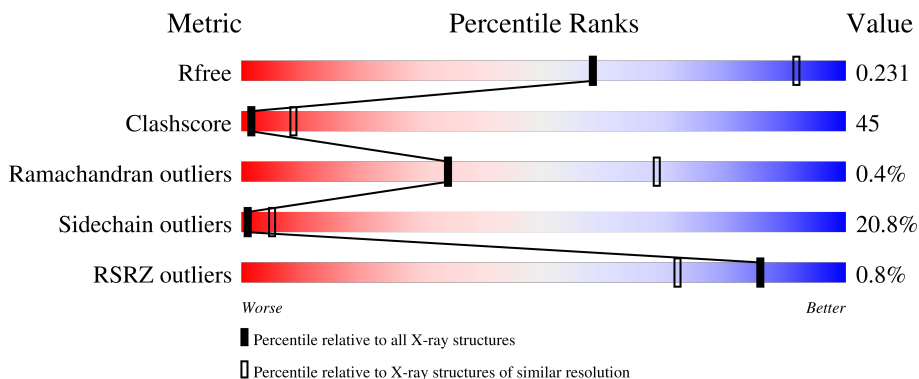
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	483	 43% 42% 11% .
1	B	483	 40% 46% 12% .
2	C	483	 37% 48% 12% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	B	1476	-	-	X	-

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11397 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 NUCLEOPROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	466	3674	2333	626	696	19	0	0	0
1	B	474	3733	2365	641	709	18	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ALA	-	expression tag	UNP P89522
B	0	ALA	-	expression tag	UNP P89522

- Molecule 2 is a protein called NUCLEOPROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	467	3681	2338	629	695	19	0	0	1

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	ALA	-	expression tag	UNP P89522
C	40	ILE	VAL	conflict	UNP P89522

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0

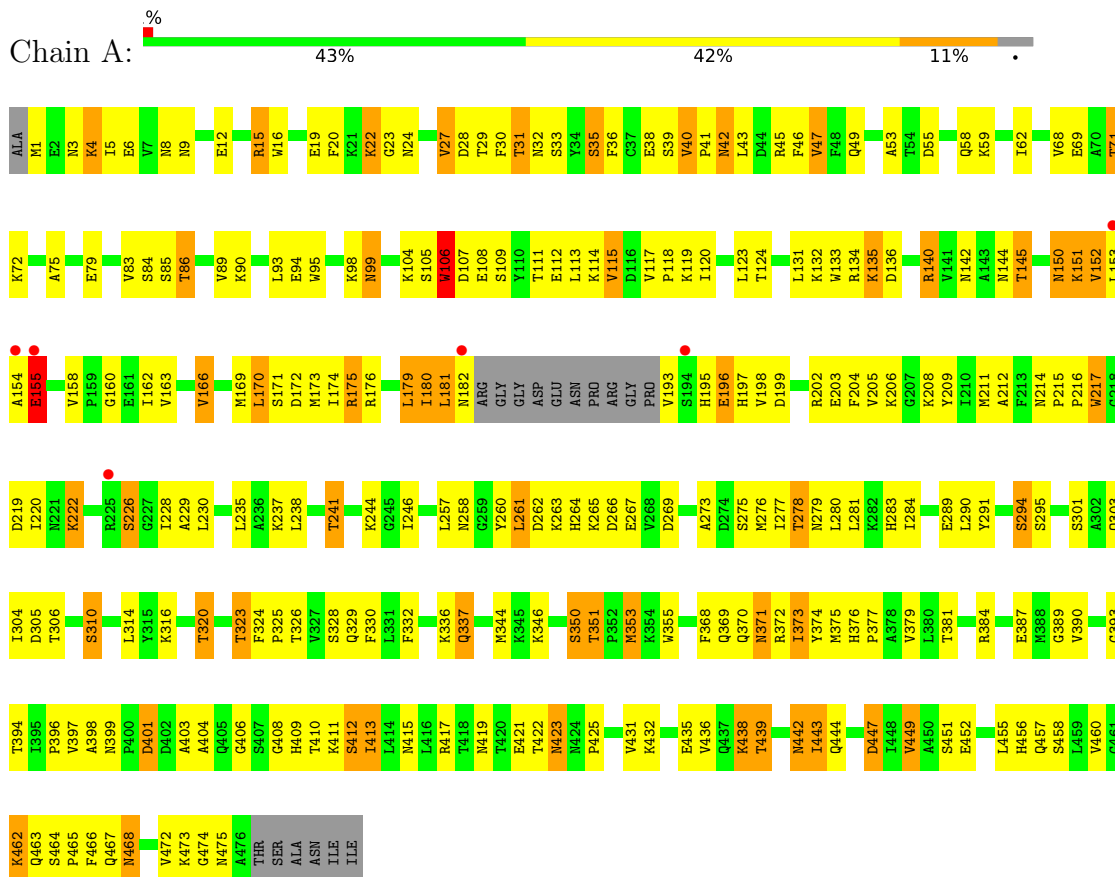
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	112	Total O 112 112	0	0
4	B	99	Total O 99 99	0	0
4	C	78	Total O 78 78	0	0

### 3 Residue-property plots

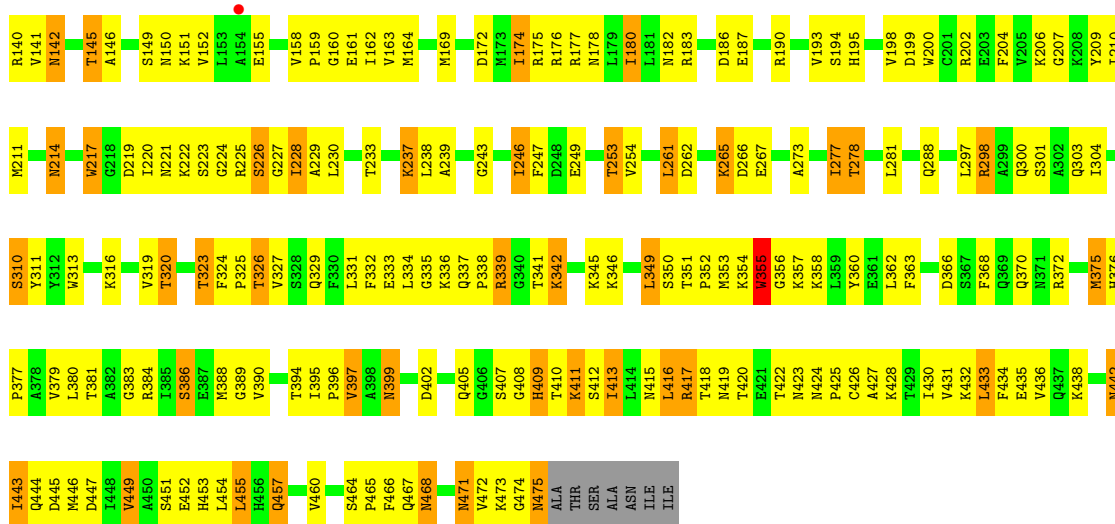
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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: NUCLEOPROTEIN

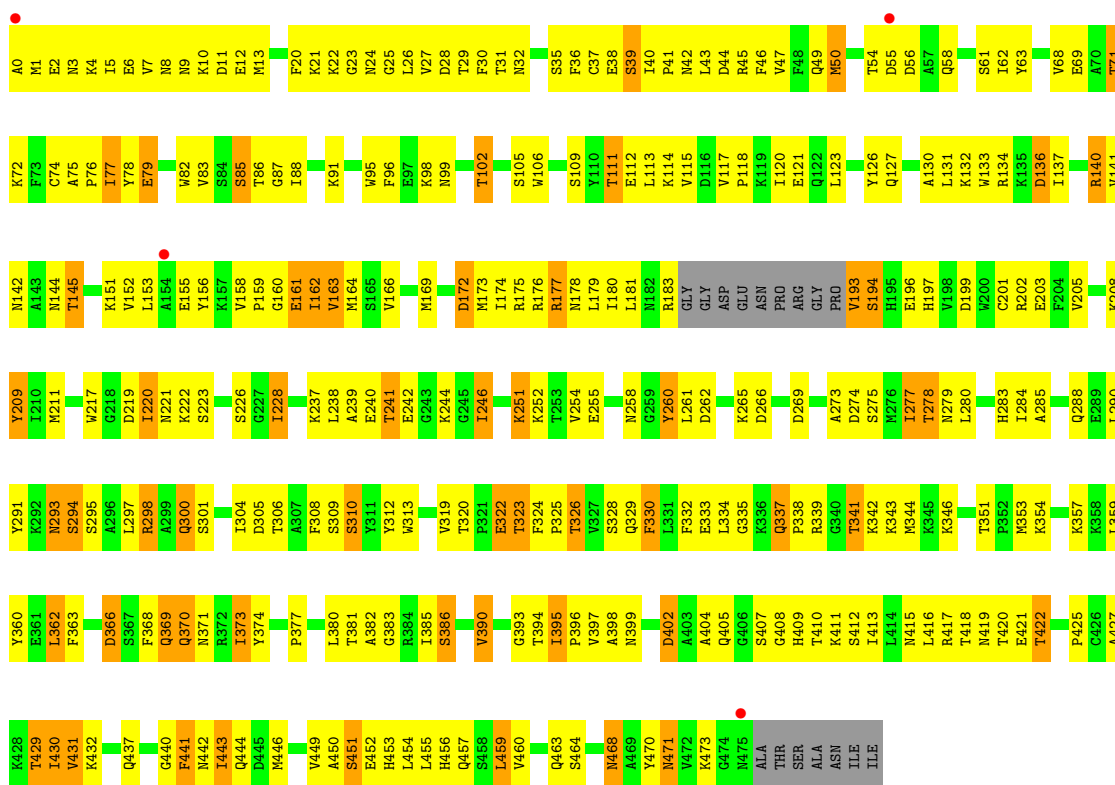


#### • Molecule 1: NUCLEOPROTEIN





● Molecule 2: NUCLEOPROTEIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	133.12Å 133.12Å 289.14Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.24 – 3.10 29.24 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.7 (29.24-3.10) 99.9 (29.24-3.10)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.99 (at 3.11Å)	Xtrriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.170 , 0.233 0.169 , 0.231	Depositor DCC
$R_{free}$ test set	2769 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	93.7	Xtrriage
Anisotropy	0.007	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 73.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.36$	Xtrriage
Estimated twinning fraction	0.003 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	11397	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	96.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.22% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	A	0.70	4/3750 (0.1%)	0.73	0/5061
1	B	0.69	6/3812 (0.2%)	0.71	0/5147
2	C	0.65	4/3757 (0.1%)	0.69	0/5070
All	All	0.68	14/11319 (0.1%)	0.71	0/15278

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	155	GLU	CD-OE1	12.67	1.39	1.25
1	B	155	GLU	CD-OE2	9.54	1.36	1.25
1	A	155	GLU	CD-OE1	9.42	1.36	1.25
1	A	155	GLU	CD-OE2	7.98	1.34	1.25
1	A	155	GLU	CG-CD	7.08	1.62	1.51
1	B	155	GLU	CG-CD	7.01	1.62	1.51
2	C	155	GLU	CD-OE1	6.78	1.33	1.25
2	C	155	GLU	CD-OE2	5.84	1.32	1.25
2	C	313	TRP	CD2-CE2	5.81	1.48	1.41
1	B	200	TRP	CD2-CE2	5.53	1.48	1.41
2	C	106	TRP	CD2-CE2	5.37	1.47	1.41
1	B	217	TRP	CD2-CE2	5.24	1.47	1.41
1	B	355	TRP	CD2-CE2	5.14	1.47	1.41
1	A	106	TRP	CD2-CE2	5.04	1.47	1.41

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	3674	0	3647	310	0
1	B	3733	0	3695	358	3
2	C	3681	0	3664	355	1
3	A	10	0	0	0	0
3	B	10	0	0	2	0
4	A	112	0	0	9	2
4	B	99	0	0	8	0
4	C	78	0	0	8	0
All	All	11397	0	11006	993	3

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 45.

All (993) 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:C:9:ASN:ND2	2:C:12:GLU:HG3	1.39	1.36
1:A:371:ASN:ND2	1:A:447:ASP:OD2	1.60	1.31
2:C:120:ILE:HD11	2:C:298:ARG:NH2	1.46	1.29
1:A:152:VAL:CG2	1:A:474:GLY:HA3	1.62	1.28
2:C:455:LEU:O	2:C:459:LEU:CD1	1.81	1.28
1:A:152:VAL:HG21	1:A:474:GLY:CA	1.64	1.26
1:B:5:ILE:O	1:B:86:THR:HG22	1.29	1.24
1:B:389:GLY:C	1:B:409:HIS:HD2	1.42	1.22
2:C:332:PHE:CD2	2:C:396:PRO:HG3	1.75	1.20
1:B:333:GLU:OE2	1:B:336:LYS:NZ	1.72	1.19
2:C:120:ILE:CD1	2:C:298:ARG:HH21	1.56	1.18
2:C:9:ASN:ND2	2:C:12:GLU:CG	2.04	1.18
1:A:417:ARG:O	1:A:425:PRO:HD2	1.40	1.18
1:A:31:THR:HG22	1:A:415:ASN:ND2	1.59	1.16
1:A:180:ILE:HG22	1:A:181:LEU:HD13	1.27	1.16
1:B:323:THR:O	1:B:326:THR:HG22	1.40	1.15
1:B:226:SER:HB2	1:B:228:ILE:HG13	1.17	1.15
1:B:337:GLN:HB2	1:B:339:ARG:NH1	1.68	1.09
1:B:142:ASN:ND2	1:B:145:THR:HG22	1.68	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:5:ILE:O	2:C:86:THR:CG2	2.01	1.08
1:A:193:VAL:N	1:A:196:GLU:CD	2.05	1.08
1:A:371:ASN:CG	1:A:373:ILE:HD11	1.73	1.07
2:C:180:ILE:HA	2:C:183:ARG:HD2	1.08	1.07
1:A:196:GLU:CD	1:A:196:GLU:H	1.54	1.07
2:C:71:THR:HG21	2:C:409:HIS:O	1.54	1.07
1:A:329:GLN:HB3	1:B:214:ASN:HD21	1.20	1.06
1:B:50:MET:CE	1:B:59:LYS:HG2	1.86	1.06
2:C:449:VAL:HG23	2:C:452:GLU:HB2	1.35	1.06
2:C:459:LEU:HD12	2:C:459:LEU:H	1.21	1.06
1:B:142:ASN:ND2	1:B:145:THR:CG2	2.18	1.05
2:C:0:ALA:CB	2:C:4:LYS:NZ	2.18	1.05
1:A:71:THR:HG22	1:A:409:HIS:O	1.55	1.04
1:B:389:GLY:C	1:B:409:HIS:CD2	2.32	1.03
1:B:5:ILE:O	1:B:86:THR:CG2	2.07	1.03
2:C:275:SER:O	2:C:279:ASN:ND2	1.91	1.03
1:A:214:ASN:HD21	2:C:333:GLU:HG3	1.19	1.02
1:A:179:LEU:H	1:A:179:LEU:HD12	1.19	1.02
1:A:31:THR:CG2	1:A:415:ASN:ND2	2.22	1.01
1:B:417:ARG:O	1:B:425:PRO:HD2	1.60	1.01
2:C:5:ILE:O	2:C:86:THR:HG23	1.56	1.01
1:B:6:GLU:HA	1:B:86:THR:HG21	1.40	1.01
1:A:408:GLY:C	1:A:409:HIS:HD2	1.63	1.00
1:A:460:VAL:CG1	1:A:472:VAL:HG11	1.90	1.00
2:C:425:PRO:O	2:C:429:THR:HG22	1.61	1.00
1:B:71:THR:HG22	1:B:409:HIS:O	1.62	0.99
2:C:332:PHE:CD2	2:C:396:PRO:CG	2.45	0.99
1:B:27:VAL:CG1	1:B:29:THR:HG23	1.91	0.99
2:C:50:MET:SD	2:C:440:GLY:HA3	2.02	0.99
1:B:207:GLY:HA2	1:B:253:THR:HG23	1.44	0.99
2:C:180:ILE:HA	2:C:183:ARG:CD	1.93	0.99
1:A:79:GLU:O	1:A:83:VAL:HG23	1.63	0.98
2:C:82:TRP:O	2:C:85:SER:OG	1.81	0.98
2:C:291:TYR:O	2:C:294:SER:OG	1.80	0.98
1:B:169:MET:HE2	1:B:434:PHE:CD2	1.99	0.97
2:C:71:THR:CG2	2:C:409:HIS:O	2.11	0.97
1:B:85:SER:O	1:B:89:VAL:HG23	1.63	0.97
1:A:460:VAL:HG12	1:A:472:VAL:HG11	1.45	0.97
1:B:438:LYS:HE2	4:B:2095:HOH:O	1.63	0.97
1:A:160:GLY:O	1:A:163:VAL:HG23	1.64	0.97
2:C:193:VAL:HG12	2:C:194:SER:H	1.29	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:380:LEU:HD12	1:B:381:THR:H	1.30	0.96
1:B:58:GLN:O	1:B:62:ILE:HG13	1.64	0.96
1:B:337:GLN:HB2	1:B:339:ARG:HH12	1.18	0.96
2:C:9:ASN:HD21	2:C:12:GLU:HG2	1.31	0.96
1:A:6:GLU:OE2	4:A:2003:HOH:O	1.81	0.96
1:B:226:SER:HB2	1:B:228:ILE:CG1	1.95	0.95
2:C:0:ALA:CB	2:C:4:LYS:HZ1	1.80	0.94
1:A:371:ASN:HD22	1:A:372:ARG:N	1.65	0.94
1:A:409:HIS:O	1:A:412:SER:HB2	1.66	0.94
1:B:79:GLU:O	1:B:83:VAL:HG23	1.66	0.94
1:B:223:SER:HB3	3:B:1476:SO4:O2	1.67	0.93
1:B:323:THR:O	1:B:326:THR:CG2	2.16	0.93
2:C:459:LEU:HD12	2:C:459:LEU:N	1.81	0.93
1:A:438:LYS:HE2	4:A:2109:HOH:O	1.68	0.93
1:A:216:PRO:HB3	2:C:337:GLN:CD	1.89	0.93
2:C:193:VAL:HG12	2:C:194:SER:N	1.83	0.93
1:B:304:ILE:HG22	1:B:377:PRO:CB	1.98	0.93
1:A:432:LYS:O	1:A:436:VAL:HG23	1.69	0.92
1:A:329:GLN:CB	1:B:214:ASN:HD21	1.82	0.92
1:B:261:LEU:N	1:B:261:LEU:HD23	1.83	0.92
1:B:416:LEU:HB3	1:B:426:CYS:HB2	1.50	0.91
1:A:260:TYR:HE2	2:C:1:MET:HG3	1.32	0.91
1:B:380:LEU:HD12	1:B:381:THR:N	1.84	0.91
1:A:71:THR:CG2	1:A:409:HIS:O	2.19	0.91
2:C:9:ASN:HD21	2:C:12:GLU:CG	1.75	0.91
1:A:419:ASN:OD1	1:A:422:THR:HG22	1.71	0.91
1:B:50:MET:HE1	1:B:59:LYS:HG2	1.51	0.91
1:A:42:ASN:OD1	4:A:2019:HOH:O	1.88	0.91
1:B:376:HIS:CD2	1:B:377:PRO:HD2	2.07	0.90
2:C:0:ALA:HB3	2:C:4:LYS:CE	2.01	0.90
2:C:54:THR:HG21	2:C:58:GLN:HE22	1.34	0.90
2:C:183:ARG:NH2	2:C:374:TYR:OH	2.03	0.90
1:A:216:PRO:HB3	2:C:337:GLN:NE2	1.86	0.90
1:A:408:GLY:O	1:A:409:HIS:CD2	2.24	0.90
1:B:169:MET:HE2	1:B:434:PHE:CG	2.05	0.90
2:C:0:ALA:HB1	2:C:4:LYS:HZ3	1.37	0.90
1:A:438:LYS:HA	1:A:443:ILE:HD12	1.53	0.90
1:B:27:VAL:CG1	1:B:29:THR:CG2	2.50	0.90
2:C:0:ALA:HB1	2:C:4:LYS:NZ	1.87	0.90
2:C:332:PHE:CE1	2:C:407:SER:HB2	2.08	0.89
1:A:175:ARG:O	1:A:179:LEU:CD1	2.20	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:261:LEU:HD13	2:C:273:ALA:HB1	1.54	0.89
1:A:371:ASN:HD22	1:A:372:ARG:H	1.20	0.89
1:B:169:MET:CE	1:B:434:PHE:CD2	2.54	0.89
1:B:342:LYS:CD	1:B:342:LYS:H	1.85	0.89
1:A:373:ILE:N	1:A:373:ILE:HD12	1.88	0.89
2:C:449:VAL:HG21	2:C:452:GLU:OE2	1.73	0.88
1:B:27:VAL:HG12	1:B:29:THR:HG23	1.53	0.88
1:B:342:LYS:H	1:B:342:LYS:HD3	1.38	0.88
1:A:408:GLY:C	1:A:409:HIS:CD2	2.46	0.88
2:C:455:LEU:O	2:C:459:LEU:HD11	1.73	0.88
1:A:449:VAL:HG12	1:A:452:GLU:HB2	1.53	0.88
1:A:169:MET:O	1:A:173:MET:HG3	1.72	0.88
1:B:89:VAL:O	1:B:93:LEU:HD12	1.73	0.88
1:A:196:GLU:HA	1:A:199:ASP:HB2	1.55	0.88
1:B:44:ASP:CG	1:B:432:LYS:NZ	2.28	0.87
2:C:50:MET:SD	2:C:440:GLY:CA	2.62	0.87
2:C:209:TYR:HD1	2:C:209:TYR:H	1.21	0.87
1:A:373:ILE:HD12	1:A:373:ILE:H	1.38	0.87
1:B:6:GLU:HA	1:B:86:THR:CG2	2.04	0.86
2:C:455:LEU:O	2:C:459:LEU:HD13	1.74	0.86
2:C:380:LEU:HD12	2:C:381:THR:N	1.91	0.86
1:A:140:ARG:HA	1:A:145:THR:OG1	1.75	0.86
1:B:389:GLY:CA	1:B:409:HIS:CD2	2.59	0.86
2:C:323:THR:O	2:C:326:THR:HG23	1.75	0.85
1:B:337:GLN:O	1:B:339:ARG:HD3	1.76	0.85
1:A:329:GLN:HB3	1:B:214:ASN:ND2	1.91	0.85
2:C:455:LEU:O	2:C:459:LEU:HD12	1.76	0.84
1:B:152:VAL:HG23	1:B:473:LYS:O	1.76	0.84
2:C:459:LEU:CD1	2:C:459:LEU:H	1.90	0.84
1:B:140:ARG:NH1	4:B:2027:HOH:O	2.03	0.84
1:A:4:LYS:HE2	1:A:398:ALA:O	1.78	0.84
1:A:180:ILE:HG22	1:A:181:LEU:CD1	2.07	0.84
1:B:28:ASP:HB3	1:B:34:TYR:CE1	2.13	0.84
1:B:44:ASP:CG	1:B:432:LYS:HZ1	1.78	0.84
1:B:226:SER:CB	1:B:228:ILE:HG13	2.06	0.84
2:C:0:ALA:HB3	2:C:4:LYS:NZ	1.91	0.84
1:A:36:PHE:CZ	1:A:404:ALA:HA	2.13	0.84
1:A:208:LYS:O	1:A:211:MET:HG3	1.77	0.84
2:C:71:THR:HG21	2:C:409:HIS:C	1.98	0.83
1:A:408:GLY:O	1:A:409:HIS:HD2	1.60	0.83
2:C:226:SER:OG	2:C:228:ILE:HG13	1.78	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:455:LEU:HD12	1:B:455:LEU:O	1.77	0.83
1:B:31:THR:OG1	1:B:33:SER:O	1.96	0.83
1:A:449:VAL:CG1	1:A:452:GLU:HB2	2.08	0.83
2:C:449:VAL:HG21	2:C:452:GLU:CD	1.99	0.82
2:C:79:GLU:O	2:C:83:VAL:HG23	1.80	0.82
2:C:114:LYS:O	2:C:368:PHE:HB2	1.80	0.81
2:C:117:VAL:HG12	2:C:118:PRO:HD2	1.62	0.81
1:B:27:VAL:HG11	1:B:29:THR:HG23	1.61	0.81
1:A:71:THR:HG21	1:A:409:HIS:C	2.01	0.81
1:B:351:THR:CG2	1:B:352:PRO:HD2	2.10	0.81
2:C:54:THR:CG2	2:C:58:GLN:NE2	2.44	0.81
1:B:381:THR:OG1	1:B:384:ARG:HG3	1.81	0.81
1:B:44:ASP:OD2	1:B:432:LYS:NZ	2.13	0.81
1:A:175:ARG:O	1:A:179:LEU:HD12	1.80	0.80
1:A:214:ASN:HD21	2:C:333:GLU:CG	1.94	0.80
1:B:50:MET:CE	1:B:59:LYS:CG	2.58	0.80
1:B:419:ASN:HB2	1:B:422:THR:HG22	1.61	0.80
2:C:334:LEU:HD23	2:C:334:LEU:O	1.81	0.80
1:A:291:TYR:O	1:A:294:SER:HB3	1.82	0.80
1:A:196:GLU:CD	1:A:196:GLU:N	2.26	0.80
2:C:54:THR:HG21	2:C:58:GLN:NE2	1.95	0.80
2:C:30:PHE:HE2	2:C:38:GLU:O	1.65	0.80
1:A:71:THR:HB	1:A:408:GLY:CA	2.12	0.80
1:A:162:ILE:O	1:A:166:VAL:HG23	1.81	0.80
1:A:410:THR:O	1:A:413:ILE:HB	1.81	0.80
1:B:63:TYR:CE1	1:B:433:LEU:HD11	2.17	0.79
1:A:260:TYR:CE2	2:C:1:MET:HG3	2.16	0.79
2:C:328:SER:CB	2:C:397:VAL:HG23	2.11	0.79
1:A:95:TRP:O	1:A:99:ASN:ND2	2.16	0.79
1:A:264:HIS:HB3	1:A:267:GLU:OE1	1.83	0.79
1:B:169:MET:CE	1:B:434:PHE:CG	2.66	0.79
1:B:320:THR:HG23	1:B:323:THR:OG1	1.82	0.79
1:A:193:VAL:N	1:A:196:GLU:OE2	2.14	0.79
1:B:95:TRP:HB2	1:B:137:ILE:HD11	1.65	0.79
1:B:351:THR:HG22	1:B:353:MET:H	1.46	0.79
1:B:455:LEU:HD12	1:B:455:LEU:C	2.01	0.79
1:A:152:VAL:HG11	1:A:474:GLY:HA2	1.62	0.78
1:B:142:ASN:HD22	1:B:145:THR:CG2	1.94	0.78
2:C:394:THR:C	2:C:395:ILE:HD12	2.04	0.78
1:A:117:VAL:HG23	1:A:370:GLN:HG2	1.63	0.78
1:A:135:LYS:HE2	4:A:2048:HOH:O	1.84	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:142:ASN:HD22	1:B:142:ASN:N	1.82	0.77
2:C:9:ASN:HD22	2:C:12:GLU:HG3	1.47	0.77
2:C:357:LYS:NZ	4:C:2064:HOH:O	2.17	0.77
1:A:371:ASN:ND2	1:A:373:ILE:HD11	1.99	0.77
2:C:442:ASN:HD21	2:C:444:GLN:HE21	1.31	0.77
2:C:449:VAL:CG2	2:C:452:GLU:HB2	2.13	0.77
1:A:140:ARG:HA	1:A:145:THR:HG1	1.50	0.77
1:B:67:LEU:O	1:B:71:THR:OG1	2.02	0.77
2:C:99:ASN:HB3	2:C:102:THR:OG1	1.85	0.76
1:B:375:MET:CE	1:B:379:VAL:CG1	2.63	0.76
1:B:142:ASN:ND2	1:B:145:THR:HG21	2.01	0.76
1:A:166:VAL:O	1:A:170:LEU:HD12	1.85	0.76
1:A:375:MET:HE2	1:A:379:VAL:HG11	1.68	0.76
1:A:449:VAL:HG11	1:A:452:GLU:CG	2.16	0.76
2:C:111:THR:O	2:C:114:LYS:HB2	1.85	0.76
1:B:141:VAL:HG22	1:B:145:THR:HG21	1.65	0.76
1:B:460:VAL:HG13	1:B:472:VAL:HG11	1.66	0.76
1:A:196:GLU:N	1:A:196:GLU:OE1	2.19	0.76
1:B:134:ARG:NH2	1:B:466:PHE:O	2.17	0.75
1:B:172:ASP:OD2	1:B:176:ARG:NH1	2.19	0.75
1:B:304:ILE:HG22	1:B:377:PRO:HB3	1.68	0.75
1:B:58:GLN:O	1:B:62:ILE:CG1	2.33	0.75
1:B:389:GLY:HA3	1:B:409:HIS:CD2	2.21	0.75
1:B:27:VAL:HG12	1:B:29:THR:CG2	2.16	0.75
1:B:141:VAL:CG2	1:B:142:ASN:ND2	2.49	0.75
1:A:202:ARG:O	1:A:206:LYS:HG3	1.87	0.75
1:B:169:MET:HE1	1:B:434:PHE:CB	2.17	0.75
2:C:179:LEU:O	2:C:183:ARG:HG3	1.86	0.75
1:B:298:ARG:NH1	4:B:2037:HOH:O	2.19	0.74
1:A:438:LYS:NZ	4:A:2057:HOH:O	2.20	0.74
1:B:389:GLY:O	1:B:409:HIS:HD2	1.69	0.74
1:A:71:THR:CG2	1:A:409:HIS:C	2.55	0.74
1:A:214:ASN:ND2	2:C:333:GLU:HB2	2.02	0.74
2:C:208:LYS:HD3	2:C:211:MET:HE3	1.68	0.74
2:C:370:GLN:HA	2:C:370:GLN:HE21	1.50	0.74
1:A:260:TYR:CE2	2:C:1:MET:CG	2.70	0.74
2:C:332:PHE:CG	2:C:396:PRO:HG3	2.22	0.74
1:A:175:ARG:O	1:A:179:LEU:HD11	1.86	0.73
1:A:435:GLU:O	1:A:439:THR:HG22	1.87	0.73
2:C:416:LEU:CD1	2:C:429:THR:HG21	2.18	0.73
1:A:31:THR:CG2	1:A:415:ASN:HD22	2.00	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:417:ARG:HG2	1:B:422:THR:HG21	1.69	0.73
2:C:399:ASN:O	2:C:402:ASP:OD1	2.05	0.73
1:A:329:GLN:HG3	1:B:210:ILE:HG13	1.69	0.73
1:A:134:ARG:NH1	1:A:305:ASP:OD2	2.21	0.73
1:B:152:VAL:HG11	1:B:475:ASN:HB3	1.71	0.73
1:B:431:VAL:O	1:B:435:GLU:HG3	1.88	0.73
1:B:27:VAL:HG11	1:B:29:THR:CG2	2.16	0.73
1:B:95:TRP:CE2	1:B:99:ASN:OD1	2.42	0.72
2:C:193:VAL:CG1	2:C:194:SER:N	2.50	0.72
1:B:349:LEU:HD12	1:B:349:LEU:H	1.54	0.72
2:C:363:PHE:HE1	2:C:382:ALA:HA	1.53	0.72
2:C:370:GLN:HA	2:C:370:GLN:NE2	2.04	0.72
2:C:238:LEU:HD23	2:C:246:ILE:HD12	1.70	0.72
1:B:141:VAL:C	1:B:142:ASN:HD22	1.91	0.72
1:A:72:LYS:NZ	1:A:406:GLY:O	2.22	0.72
1:A:140:ARG:O	1:A:140:ARG:HG3	1.88	0.72
1:B:316:LYS:HE2	4:B:2072:HOH:O	1.90	0.72
1:A:260:TYR:HE2	2:C:1:MET:CG	2.00	0.72
2:C:7:VAL:HG13	2:C:12:GLU:HB2	1.72	0.72
1:A:176:ARG:HA	1:A:179:LEU:CD1	2.20	0.71
1:B:408:GLY:C	1:B:409:HIS:HD1	1.93	0.71
2:C:27:VAL:HG12	2:C:29:THR:H	1.55	0.71
2:C:332:PHE:HE1	2:C:407:SER:HB2	1.53	0.71
2:C:120:ILE:HD11	2:C:298:ARG:HH21	0.66	0.71
1:B:141:VAL:HG23	1:B:142:ASN:ND2	2.05	0.71
2:C:10:LYS:HE3	2:C:141:VAL:O	1.89	0.71
1:B:376:HIS:CD2	1:B:377:PRO:CD	2.74	0.71
2:C:402:ASP:O	2:C:405:GLN:HG3	1.91	0.71
1:A:118:PRO:CG	1:A:123:LEU:HD11	2.21	0.70
1:A:169:MET:CE	1:A:431:VAL:HG22	2.21	0.70
2:C:28:ASP:O	2:C:417:ARG:NH2	2.22	0.70
1:B:195:HIS:CE1	1:B:198:VAL:HG21	2.27	0.70
2:C:390:VAL:HG21	2:C:411:LYS:HB2	1.73	0.70
1:A:195:HIS:O	1:A:199:ASP:CG	2.30	0.70
1:A:306:THR:OG1	1:A:387:GLU:OE1	2.09	0.70
2:C:30:PHE:CE2	2:C:38:GLU:O	2.45	0.70
1:B:176:ARG:O	1:B:180:ILE:HG12	1.91	0.70
2:C:419:ASN:OD1	2:C:422:THR:CG2	2.40	0.70
1:B:351:THR:HG22	1:B:352:PRO:HD2	1.72	0.70
2:C:274:ASP:O	2:C:278:THR:HG23	1.91	0.70
2:C:370:GLN:HE21	2:C:370:GLN:CA	2.04	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:59:LYS:NZ	4:B:2006:HOH:O	2.25	0.70
1:A:40:VAL:HG12	1:A:41:PRO:HD2	1.72	0.70
1:A:45:ARG:NH2	1:A:69:GLU:OE2	2.25	0.70
2:C:0:ALA:CB	2:C:4:LYS:HZ3	1.97	0.70
1:B:389:GLY:O	1:B:409:HIS:CD2	2.44	0.69
2:C:180:ILE:CA	2:C:183:ARG:HD2	2.04	0.69
1:B:337:GLN:CB	1:B:339:ARG:NH1	2.51	0.69
2:C:449:VAL:HG23	2:C:452:GLU:CB	2.19	0.69
1:B:320:THR:HG23	1:B:323:THR:HG1	1.54	0.69
2:C:330:PHE:CD1	2:C:330:PHE:C	2.66	0.69
1:A:30:PHE:CE1	1:A:40:VAL:HG22	2.28	0.68
1:B:399:ASN:O	1:B:402:ASP:HB2	1.92	0.68
2:C:450:ALA:O	2:C:454:LEU:HD12	1.92	0.68
1:A:193:VAL:O	1:A:196:GLU:OE1	2.12	0.68
1:B:45:ARG:NH2	1:B:69:GLU:OE2	2.27	0.68
1:B:141:VAL:H	1:B:145:THR:CG2	2.06	0.67
2:C:394:THR:O	2:C:395:ILE:HD12	1.95	0.67
2:C:160:GLY:O	2:C:163:VAL:HG23	1.95	0.67
1:A:449:VAL:CG1	1:A:449:VAL:O	2.43	0.67
1:B:329:GLN:NE2	1:B:396:PRO:HB3	2.09	0.67
1:A:31:THR:HG21	1:A:35:SER:HB3	1.76	0.67
1:A:389:GLY:O	1:A:393:GLY:N	2.26	0.67
2:C:20:PHE:O	2:C:24:ASN:ND2	2.21	0.67
2:C:68:VAL:O	2:C:72:LYS:HB2	1.94	0.67
2:C:453:HIS:O	2:C:457:GLN:HG3	1.94	0.67
2:C:332:PHE:CD1	2:C:407:SER:HB2	2.29	0.67
2:C:117:VAL:HG13	2:C:374:TYR:HB3	1.77	0.67
2:C:75:ALA:O	2:C:77:ILE:CD1	2.43	0.66
1:A:166:VAL:O	1:A:170:LEU:CD1	2.43	0.66
1:A:180:ILE:CG2	1:A:181:LEU:HD13	2.16	0.66
1:A:435:GLU:O	1:A:439:THR:CG2	2.43	0.66
1:A:449:VAL:HG11	1:A:452:GLU:HG3	1.76	0.66
1:B:375:MET:HE3	1:B:379:VAL:HG11	1.77	0.66
1:A:118:PRO:HB2	1:A:123:LEU:CD1	2.26	0.66
2:C:75:ALA:CB	2:C:394:THR:HG21	2.25	0.66
2:C:351:THR:HG22	2:C:353:MET:HG2	1.77	0.66
2:C:380:LEU:HD12	2:C:381:THR:H	1.61	0.66
1:A:158:VAL:CG1	1:A:162:ILE:HD11	2.26	0.66
1:B:411:LYS:O	1:B:465:PRO:HG3	1.96	0.66
2:C:208:LYS:CD	2:C:211:MET:HE3	2.25	0.66
1:A:22:LYS:HG2	1:A:23:GLY:N	2.11	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:162:ILE:HG21	2:C:431:VAL:HG11	1.78	0.66
2:C:244:LYS:HE2	4:C:2050:HOH:O	1.95	0.66
1:B:442:ASN:ND2	1:B:445:ASP:H	1.93	0.65
2:C:2:GLU:HG2	2:C:3:ASN:N	2.12	0.65
1:A:107:ASP:OD1	1:A:316:LYS:HE2	1.95	0.65
1:B:247:PHE:CD1	1:B:288:GLN:HG2	2.32	0.65
2:C:40:ILE:HG22	2:C:41:PRO:O	1.96	0.65
2:C:363:PHE:CE1	2:C:382:ALA:HA	2.31	0.65
1:A:460:VAL:CG1	1:A:472:VAL:CG1	2.72	0.65
1:A:214:ASN:ND2	2:C:333:GLU:CB	2.59	0.65
1:A:214:ASN:ND2	2:C:333:GLU:HG3	2.02	0.65
1:A:280:LEU:O	1:A:284:ILE:HG13	1.95	0.65
1:B:50:MET:HE1	1:B:59:LYS:CG	2.25	0.65
2:C:402:ASP:OD1	2:C:402:ASP:N	2.26	0.65
2:C:454:LEU:HD12	2:C:454:LEU:H	1.62	0.65
1:B:7:VAL:HG11	1:B:13:MET:HB2	1.78	0.65
1:A:323:THR:O	1:A:326:THR:OG1	2.14	0.65
1:B:152:VAL:HG21	1:B:475:ASN:H	1.61	0.65
1:B:375:MET:CE	1:B:379:VAL:HG12	2.27	0.65
1:A:99:ASN:HD22	1:A:99:ASN:N	1.95	0.64
1:A:320:THR:H	1:A:323:THR:HG22	1.63	0.64
1:B:27:VAL:HG12	1:B:29:THR:H	1.61	0.64
1:B:332:PHE:CG	1:B:396:PRO:HG3	2.32	0.64
1:B:238:LEU:HD23	1:B:246:ILE:HG13	1.79	0.64
2:C:117:VAL:CG1	2:C:118:PRO:HD2	2.27	0.64
2:C:208:LYS:HD3	2:C:211:MET:CE	2.26	0.64
1:A:371:ASN:CG	1:A:373:ILE:CD1	2.59	0.64
2:C:457:GLN:O	2:C:460:VAL:HG23	1.97	0.64
1:B:7:VAL:H	1:B:86:THR:HG23	1.62	0.64
1:B:262:ASP:O	1:B:265:LYS:HG2	1.98	0.64
1:A:449:VAL:CG1	1:A:452:GLU:CB	2.76	0.64
2:C:449:VAL:HG21	2:C:452:GLU:CG	2.27	0.64
1:B:141:VAL:H	1:B:145:THR:HG21	1.63	0.64
1:B:94:GLU:HA	1:B:97:GLU:HG3	1.79	0.64
1:A:353:MET:HG3	1:A:355:TRP:NE1	2.13	0.64
1:A:473:LYS:NZ	4:A:2112:HOH:O	2.07	0.64
2:C:54:THR:CG2	2:C:58:GLN:HE22	2.07	0.64
1:A:31:THR:HG22	1:A:415:ASN:HD21	1.57	0.63
1:B:141:VAL:HG22	1:B:142:ASN:ND2	2.13	0.63
2:C:169:MET:O	2:C:173:MET:HG3	1.98	0.63
2:C:9:ASN:OD1	2:C:11:ASP:N	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:GLU:OE2	4:A:2069:HOH:O	2.15	0.63
1:B:88:ILE:HG22	1:B:311:TYR:OH	1.97	0.63
2:C:410:THR:O	2:C:413:ILE:HG13	1.98	0.63
1:B:375:MET:HE3	1:B:379:VAL:CG1	2.28	0.63
2:C:40:ILE:HG23	2:C:41:PRO:HD2	1.81	0.63
2:C:258:ASN:HB2	2:C:277:ILE:HD12	1.81	0.63
1:A:134:ARG:NH2	1:A:466:PHE:O	2.32	0.63
2:C:457:GLN:O	2:C:460:VAL:CG2	2.47	0.63
1:B:416:LEU:HB3	1:B:426:CYS:CB	2.26	0.62
1:B:383:GLY:O	1:B:386:SER:OG	2.17	0.62
1:A:59:LYS:NZ	4:A:2027:HOH:O	2.31	0.62
1:A:464:SER:HB3	1:A:467:GLN:HG3	1.81	0.62
1:B:50:MET:HE3	1:B:59:LYS:HA	1.82	0.62
1:A:215:PRO:HB2	1:A:217:TRP:NE1	2.14	0.62
1:B:71:THR:CG2	1:B:409:HIS:O	2.45	0.62
1:B:28:ASP:HB3	1:B:34:TYR:CD1	2.34	0.62
2:C:209:TYR:HE2	2:C:260:TYR:HB2	1.65	0.62
2:C:341:THR:O	2:C:344:MET:HB3	1.99	0.62
2:C:180:ILE:O	2:C:183:ARG:HD3	1.99	0.62
2:C:330:PHE:C	2:C:330:PHE:HD1	2.02	0.62
1:A:449:VAL:CG1	1:A:452:GLU:CG	2.77	0.62
1:B:77:ILE:HG23	1:B:395:ILE:HD11	1.82	0.62
1:B:30:PHE:HE2	1:B:38:GLU:O	1.82	0.62
1:B:376:HIS:HB3	1:B:379:VAL:HG23	1.81	0.61
2:C:134:ARG:NH2	2:C:305:ASP:OD1	2.25	0.61
1:A:375:MET:HE2	1:A:379:VAL:CG1	2.30	0.61
1:A:118:PRO:CB	1:A:123:LEU:HD11	2.29	0.61
1:A:387:GLU:O	1:A:390:VAL:HG12	2.00	0.61
2:C:141:VAL:HG22	2:C:145:THR:HG21	1.83	0.61
2:C:419:ASN:OD1	2:C:422:THR:HG22	1.99	0.61
1:A:99:ASN:ND2	1:A:99:ASN:N	2.48	0.61
1:A:449:VAL:HG13	1:A:452:GLU:H	1.65	0.61
1:B:142:ASN:H	1:B:145:THR:HG23	1.64	0.61
1:B:325:PRO:HB3	1:B:397:VAL:CG1	2.30	0.61
1:B:249:GLU:O	1:B:253:THR:OG1	2.19	0.61
1:A:237:LYS:O	1:A:241:THR:HG23	1.99	0.61
1:B:82:TRP:O	1:B:85:SER:HB3	2.01	0.61
1:B:68:VAL:O	1:B:72:LYS:HB2	2.00	0.61
1:B:174:ILE:HG22	1:B:175:ARG:N	2.15	0.61
2:C:371:ASN:OD1	2:C:373:ILE:HG23	2.00	0.61
1:B:442:ASN:HD21	1:B:444:GLN:HB2	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:54:THR:HG23	2:C:58:GLN:NE2	2.15	0.61
1:A:193:VAL:N	1:A:196:GLU:CG	2.63	0.61
1:A:217:TRP:HD1	1:A:219:ASP:O	1.84	0.61
1:A:449:VAL:HG11	1:A:452:GLU:CD	2.19	0.61
2:C:36:PHE:CE2	2:C:404:ALA:HA	2.36	0.61
2:C:109:SER:O	2:C:112:GLU:HG2	2.00	0.61
1:A:179:LEU:HD12	1:A:179:LEU:N	2.01	0.61
1:B:117:VAL:HG23	1:B:370:GLN:NE2	2.16	0.61
1:A:371:ASN:ND2	1:A:373:ILE:CD1	2.63	0.60
1:B:217:TRP:HD1	1:B:219:ASP:O	1.84	0.60
1:B:418:THR:HA	1:B:424:ASN:OD1	2.01	0.60
2:C:161:GLU:HB2	2:C:162:ILE:HD13	1.82	0.60
2:C:203:GLU:OE1	2:C:203:GLU:HA	2.01	0.60
2:C:176:ARG:O	2:C:180:ILE:HG12	2.01	0.60
1:A:118:PRO:HB2	1:A:123:LEU:HD11	1.83	0.60
1:B:351:THR:HG23	1:B:352:PRO:HD2	1.83	0.60
1:B:360:TYR:O	1:B:363:PHE:HD2	1.84	0.60
1:B:172:ASP:OD1	1:B:175:ARG:NH1	2.34	0.60
1:A:30:PHE:O	1:A:417:ARG:HG3	2.01	0.60
1:A:214:ASN:HD22	2:C:333:GLU:HB2	1.66	0.60
1:B:346:LYS:O	1:B:350:SER:OG	2.19	0.60
1:A:123:LEU:HD12	1:A:123:LEU:N	2.17	0.60
1:A:375:MET:CE	1:A:379:VAL:CG1	2.80	0.60
1:B:207:GLY:HA2	1:B:253:THR:CG2	2.26	0.60
1:A:106:TRP:CD1	1:A:106:TRP:N	2.69	0.60
2:C:291:TYR:HA	2:C:294:SER:OG	2.02	0.60
2:C:142:ASN:H	2:C:145:THR:HG23	1.67	0.59
2:C:173:MET:HE2	2:C:452:GLU:HB3	1.83	0.59
1:A:468:ASN:OD1	1:A:468:ASN:C	2.41	0.59
1:A:132:LYS:HE2	1:A:136:ASP:OD2	2.02	0.59
1:A:172:ASP:O	1:A:176:ARG:HG3	2.02	0.59
1:B:103:ILE:HD12	1:B:107:ASP:CB	2.32	0.59
1:B:178:ASN:N	1:B:178:ASN:HD22	2.01	0.59
1:B:247:PHE:CE1	1:B:288:GLN:HG2	2.38	0.59
1:B:375:MET:HE2	1:B:379:VAL:HG12	1.85	0.59
2:C:383:GLY:O	2:C:386:SER:OG	2.19	0.59
2:C:332:PHE:CD2	2:C:396:PRO:HG2	2.37	0.59
1:A:375:MET:HE1	1:A:379:VAL:HG12	1.84	0.59
1:B:304:ILE:HG22	1:B:377:PRO:CA	2.32	0.59
2:C:43:LEU:HB2	2:C:432:LYS:HD2	1.84	0.59
1:B:117:VAL:HG23	1:B:370:GLN:HE21	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:306:THR:O	1:A:310:SER:OG	2.19	0.58
1:B:419:ASN:HB2	1:B:422:THR:CG2	2.32	0.58
1:A:237:LYS:O	1:A:241:THR:CG2	2.51	0.58
1:B:142:ASN:HD22	1:B:145:THR:HG21	1.59	0.58
1:A:260:TYR:CE2	2:C:1:MET:HG2	2.37	0.58
1:A:376:HIS:ND1	1:A:377:PRO:HD2	2.18	0.58
2:C:334:LEU:O	2:C:334:LEU:CD2	2.50	0.58
1:A:71:THR:HB	1:A:408:GLY:HA2	1.86	0.58
1:A:216:PRO:HD2	1:A:217:TRP:CZ2	2.39	0.58
1:B:46:PHE:HE2	1:B:69:GLU:HG3	1.68	0.58
1:B:160:GLY:O	1:B:163:VAL:HG23	2.04	0.58
1:B:177:ARG:HA	1:B:180:ILE:HG13	1.86	0.58
1:B:217:TRP:CD1	1:B:219:ASP:O	2.56	0.58
1:B:332:PHE:CD2	1:B:396:PRO:HG3	2.38	0.58
2:C:158:VAL:HG12	2:C:159:PRO:HD2	1.86	0.58
1:A:438:LYS:CA	1:A:443:ILE:HD12	2.32	0.58
2:C:332:PHE:CE2	2:C:396:PRO:HG2	2.38	0.58
1:A:176:ARG:HA	1:A:179:LEU:HD11	1.85	0.58
1:B:182:ASN:O	1:B:187:GLU:HB2	2.04	0.58
1:A:27:VAL:HG13	1:A:29:THR:H	1.68	0.57
1:A:173:MET:HE1	1:A:456:HIS:HB2	1.86	0.57
1:B:63:TYR:HE1	1:B:433:LEU:HD11	1.65	0.57
2:C:173:MET:HE1	2:C:455:LEU:HB3	1.85	0.57
1:A:117:VAL:HG13	1:A:118:PRO:HD2	1.86	0.57
1:B:474:GLY:C	1:B:475:ASN:HD22	2.08	0.57
2:C:46:PHE:CE2	2:C:69:GLU:HG3	2.39	0.57
1:B:357:LYS:NZ	4:B:2076:HOH:O	2.35	0.57
2:C:306:THR:O	2:C:310:SER:OG	2.21	0.57
1:B:432:LYS:O	1:B:436:VAL:HG23	2.04	0.57
2:C:241:THR:O	2:C:473:LYS:HB3	2.03	0.57
2:C:50:MET:SD	2:C:440:GLY:HA2	2.44	0.57
2:C:75:ALA:HB1	2:C:394:THR:HG21	1.86	0.57
2:C:173:MET:HE2	2:C:452:GLU:CB	2.35	0.57
1:B:142:ASN:ND2	1:B:142:ASN:N	2.53	0.57
1:B:42:ASN:C	1:B:42:ASN:ND2	2.57	0.57
1:B:345:LYS:O	1:B:349:LEU:HD12	2.05	0.57
1:A:158:VAL:HG12	1:A:162:ILE:HD11	1.87	0.57
1:A:417:ARG:O	1:A:425:PRO:CD	2.34	0.57
1:B:223:SER:OG	1:B:227:GLY:HA2	2.04	0.57
2:C:332:PHE:CE2	2:C:396:PRO:CG	2.88	0.57
1:A:261:LEU:HD22	1:A:273:ALA:HB1	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:195:HIS:O	1:B:198:VAL:HG22	2.05	0.56
1:A:375:MET:CE	1:A:379:VAL:HG11	2.35	0.56
2:C:134:ARG:HH21	2:C:305:ASP:CG	2.08	0.56
2:C:158:VAL:CG1	2:C:159:PRO:HD2	2.35	0.56
1:A:216:PRO:CB	2:C:337:GLN:NE2	2.63	0.56
1:A:442:ASN:H	1:A:442:ASN:ND2	2.02	0.56
1:B:46:PHE:CE2	1:B:69:GLU:HG3	2.41	0.56
2:C:2:GLU:HG2	2:C:3:ASN:H	1.70	0.56
2:C:196:GLU:HA	2:C:199:ASP:OD1	2.05	0.56
1:B:50:MET:HE3	1:B:59:LYS:CG	2.35	0.56
1:B:161:GLU:OE1	1:B:428:LYS:NZ	2.34	0.56
1:B:471:ASN:N	1:B:471:ASN:HD22	2.04	0.56
2:C:76:PRO:HB3	2:C:415:ASN:ND2	2.20	0.56
2:C:260:TYR:CD1	2:C:260:TYR:C	2.79	0.56
1:B:390:VAL:HG21	1:B:411:LYS:HB2	1.87	0.56
2:C:183:ARG:NH2	2:C:374:TYR:CZ	2.74	0.56
2:C:328:SER:OG	2:C:397:VAL:HG23	2.06	0.56
1:A:85:SER:O	1:A:89:VAL:HG23	2.05	0.56
1:B:63:TYR:HE1	1:B:433:LEU:CD1	2.18	0.56
1:A:449:VAL:O	1:A:449:VAL:HG13	2.06	0.56
1:B:169:MET:HE1	1:B:434:PHE:HB3	1.87	0.56
2:C:217:TRP:CD1	2:C:219:ASP:O	2.59	0.55
1:A:113:LEU:HD13	1:A:376:HIS:CD2	2.41	0.55
1:A:93:LEU:HD21	1:A:314:LEU:HB3	1.87	0.55
1:B:172:ASP:OD2	1:B:452:GLU:OE2	2.24	0.55
1:B:327:VAL:HG22	1:B:355:TRP:CZ2	2.42	0.55
1:B:44:ASP:OD1	1:B:432:LYS:NZ	2.39	0.55
2:C:7:VAL:HG11	2:C:13:MET:HB2	1.87	0.55
2:C:142:ASN:OD1	2:C:144:ASN:N	2.40	0.55
1:B:120:ILE:HG22	1:B:121:GLU:OE1	2.06	0.55
1:B:442:ASN:HD22	1:B:445:ASP:H	1.54	0.55
2:C:305:ASP:HB3	2:C:308:PHE:HB3	1.88	0.55
2:C:441:PHE:CD1	2:C:441:PHE:N	2.74	0.55
1:A:15:ARG:HG3	1:A:16:TRP:N	2.20	0.55
1:A:36:PHE:CE2	1:A:404:ALA:HA	2.42	0.55
1:A:214:ASN:ND2	2:C:333:GLU:CG	2.66	0.55
1:B:416:LEU:HD23	1:B:426:CYS:HA	1.87	0.55
2:C:78:TYR:HB3	2:C:79:GLU:OE1	2.07	0.55
2:C:220:ILE:HG22	2:C:221:ASN:OD1	2.06	0.55
2:C:261:LEU:HD13	2:C:273:ALA:CB	2.34	0.55
2:C:449:VAL:HG23	2:C:449:VAL:O	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:55:ASP:HB3	1:B:58:GLN:NE2	2.22	0.55
1:B:375:MET:CE	1:B:379:VAL:HG11	2.35	0.55
1:A:49:GLN:HB3	1:A:62:ILE:HD13	1.89	0.55
1:A:152:VAL:HG11	1:A:474:GLY:CA	2.36	0.55
1:A:329:GLN:C	1:B:214:ASN:ND2	2.60	0.55
2:C:10:LYS:O	2:C:13:MET:HB3	2.07	0.55
1:A:31:THR:HG21	1:A:415:ASN:ND2	2.18	0.55
1:A:381:THR:OG1	1:A:384:ARG:HG3	2.06	0.55
1:B:103:ILE:HD12	1:B:107:ASP:HB2	1.89	0.55
2:C:201:CYS:O	2:C:205:VAL:HG13	2.06	0.55
1:A:9:ASN:ND2	1:A:12:GLU:HG3	2.22	0.55
1:B:178:ASN:N	1:B:178:ASN:ND2	2.55	0.55
1:B:413:ILE:O	1:B:416:LEU:HB2	2.06	0.55
2:C:151:LYS:NZ	2:C:242:GLU:OE1	2.40	0.54
2:C:183:ARG:NH2	2:C:374:TYR:CE1	2.76	0.54
1:A:15:ARG:O	1:A:19:GLU:HG2	2.07	0.54
1:B:176:ARG:NH2	1:B:446:MET:O	2.39	0.54
2:C:183:ARG:HH22	2:C:374:TYR:HE1	1.54	0.54
1:B:475:ASN:HD22	1:B:475:ASN:N	2.05	0.54
2:C:127:GLN:NE2	2:C:301:SER:O	2.41	0.54
2:C:162:ILE:HG22	2:C:166:VAL:HG23	1.89	0.54
1:A:409:HIS:CD2	1:A:409:HIS:N	2.75	0.54
1:A:456:HIS:O	1:A:460:VAL:HG23	2.07	0.54
2:C:75:ALA:HB2	2:C:394:THR:HG21	1.88	0.54
2:C:79:GLU:OE1	2:C:79:GLU:N	2.41	0.54
2:C:209:TYR:HD1	2:C:209:TYR:N	1.96	0.54
1:A:175:ARG:NH2	1:A:444:GLN:O	2.40	0.54
2:C:442:ASN:HD21	2:C:444:GLN:NE2	2.01	0.54
1:A:279:ASN:O	1:A:283:HIS:CD2	2.61	0.54
1:B:44:ASP:CG	1:B:432:LYS:HZ3	2.09	0.54
1:B:142:ASN:HD21	1:B:145:THR:CG2	2.17	0.54
1:B:342:LYS:CD	1:B:342:LYS:N	2.63	0.54
2:C:75:ALA:HB2	2:C:394:THR:CG2	2.37	0.54
2:C:320:THR:OG1	2:C:322:GLU:HG2	2.07	0.54
2:C:363:PHE:HE1	2:C:382:ALA:CA	2.18	0.54
1:A:196:GLU:OE1	1:A:197:HIS:N	2.38	0.54
1:B:42:ASN:C	1:B:43:LEU:HD12	2.28	0.54
1:A:154:ALA:O	1:A:155:GLU:OE1	2.25	0.54
1:A:353:MET:HG3	1:A:355:TRP:CD1	2.43	0.54
1:B:310:SER:HA	1:B:313:TRP:CE3	2.43	0.54
1:B:111:THR:O	1:B:114:LYS:HB2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:130:ALA:O	1:B:134:ARG:HG3	2.08	0.54
1:B:433:LEU:O	1:B:433:LEU:HD12	2.08	0.54
2:C:442:ASN:OD1	2:C:444:GLN:HB3	2.08	0.54
1:A:219:ASP:HB2	2:C:346:LYS:HD2	1.89	0.54
2:C:3:ASN:CG	2:C:397:VAL:CG1	2.77	0.54
2:C:132:LYS:O	2:C:136:ASP:OD1	2.25	0.54
2:C:202:ARG:O	2:C:205:VAL:HG22	2.08	0.54
1:B:204:PHE:O	1:B:253:THR:HG21	2.08	0.53
2:C:174:ILE:O	2:C:178:ASN:N	2.28	0.53
2:C:239:ALA:HA	2:C:246:ILE:HD13	1.89	0.53
1:A:263:LYS:HG3	1:A:264:HIS:CD2	2.43	0.53
2:C:351:THR:CG2	2:C:353:MET:HG2	2.37	0.53
1:B:7:VAL:C	1:B:8:ASN:HD22	2.12	0.53
1:B:136:ASP:OD1	1:B:136:ASP:N	2.42	0.53
1:B:319:VAL:HG12	1:B:320:THR:N	2.23	0.53
2:C:419:ASN:OD1	2:C:422:THR:HG23	2.09	0.53
1:B:443:ILE:HD13	1:B:443:ILE:N	2.24	0.53
2:C:7:VAL:HG11	2:C:13:MET:CA	2.39	0.53
2:C:430:ILE:HG22	2:C:431:VAL:N	2.23	0.53
1:B:82:TRP:CE2	1:B:141:VAL:HG11	2.44	0.52
1:B:447:ASP:N	1:B:447:ASP:OD1	2.37	0.52
2:C:429:THR:HA	2:C:432:LYS:HE3	1.91	0.52
1:A:279:ASN:O	1:A:283:HIS:HD2	1.92	0.52
1:A:262:ASP:O	1:A:265:LYS:CG	2.57	0.52
1:B:310:SER:HA	1:B:313:TRP:HE3	1.74	0.52
2:C:176:ARG:NH2	2:C:443:ILE:O	2.43	0.52
1:B:71:THR:HB	1:B:408:GLY:CA	2.40	0.52
2:C:209:TYR:N	2:C:209:TYR:CD1	2.64	0.52
1:A:90:LYS:NZ	1:A:94:GLU:OE1	2.43	0.52
1:B:195:HIS:NE2	1:B:198:VAL:HG21	2.24	0.52
1:B:224:GLY:HA3	1:B:230:LEU:HD21	1.92	0.52
2:C:71:THR:HG22	2:C:412:SER:HB2	1.91	0.52
2:C:449:VAL:CG2	2:C:452:GLU:CG	2.87	0.52
1:A:154:ALA:C	1:A:155:GLU:OE1	2.48	0.52
1:B:331:LEU:HD13	1:B:389:GLY:HA2	1.90	0.52
1:B:351:THR:HG22	1:B:352:PRO:CD	2.38	0.52
2:C:5:ILE:O	2:C:86:THR:HG22	2.02	0.52
1:A:417:ARG:HD3	1:A:419:ASN:HD21	1.75	0.52
1:B:46:PHE:CE1	1:B:65:SER:HB2	2.44	0.52
1:B:326:THR:HG21	1:B:353:MET:HE3	1.91	0.52
1:B:376:HIS:HD2	1:B:377:PRO:CD	2.21	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:136:ASP:OD1	2:C:136:ASP:N	2.41	0.52
1:A:370:GLN:N	1:A:370:GLN:OE1	2.43	0.52
1:B:443:ILE:H	1:B:443:ILE:CD1	2.23	0.52
1:A:47:VAL:HG12	1:A:436:VAL:HG22	1.92	0.52
2:C:142:ASN:OD1	2:C:145:THR:HG22	2.09	0.51
1:B:375:MET:HE2	1:B:379:VAL:CG1	2.40	0.51
2:C:153:LEU:HB2	2:C:459:LEU:O	2.10	0.51
1:A:262:ASP:O	1:A:265:LYS:HG3	2.11	0.51
2:C:335:GLY:HA3	2:C:407:SER:OG	2.10	0.51
1:A:99:ASN:HD22	1:A:99:ASN:H	1.59	0.51
2:C:293:ASN:N	2:C:293:ASN:ND2	2.54	0.51
2:C:217:TRP:HD1	2:C:219:ASP:O	1.94	0.51
2:C:468:ASN:OD1	2:C:468:ASN:C	2.48	0.51
1:A:346:LYS:O	1:A:350:SER:OG	2.19	0.51
1:B:159:PRO:HB2	1:B:161:GLU:HG2	1.93	0.51
2:C:2:GLU:O	2:C:398:ALA:HA	2.11	0.51
2:C:324:PHE:N	2:C:325:PRO:CD	2.74	0.51
1:B:331:LEU:HD11	1:B:388:MET:HB3	1.93	0.51
2:C:6:GLU:HA	2:C:86:THR:HG21	1.92	0.51
2:C:291:TYR:C	2:C:294:SER:OG	2.47	0.51
2:C:442:ASN:ND2	2:C:444:GLN:HE21	2.06	0.51
1:A:257:LEU:HD12	1:A:257:LEU:O	2.10	0.51
1:B:142:ASN:N	1:B:145:THR:HG23	2.25	0.51
2:C:251:LYS:HE3	4:C:2053:HOH:O	2.11	0.51
2:C:416:LEU:HD12	2:C:429:THR:HG21	1.91	0.51
1:A:71:THR:HB	1:A:409:HIS:N	2.25	0.51
1:B:75:ALA:HB1	1:B:394:THR:HG21	1.92	0.51
1:B:410:THR:O	1:B:412:SER:N	2.44	0.51
2:C:49:GLN:HE21	2:C:62:ILE:HG12	1.75	0.51
1:B:427:ALA:O	1:B:431:VAL:HG23	2.11	0.51
2:C:152:VAL:HG23	2:C:473:LYS:O	2.11	0.51
1:A:6:GLU:HA	1:A:86:THR:OG1	2.10	0.50
1:A:373:ILE:H	1:A:373:ILE:CD1	2.02	0.50
1:A:422:THR:O	1:A:423:ASN:CB	2.59	0.50
1:B:30:PHE:CE2	1:B:38:GLU:O	2.64	0.50
1:B:443:ILE:N	1:B:443:ILE:CD1	2.74	0.50
1:B:454:LEU:HA	1:B:457:GLN:HG3	1.92	0.50
2:C:371:ASN:OD1	2:C:371:ASN:C	2.50	0.50
1:B:355:TRP:CE3	1:B:355:TRP:C	2.84	0.50
2:C:142:ASN:OD1	2:C:142:ASN:C	2.50	0.50
1:B:342:LYS:HD3	1:B:342:LYS:N	2.16	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:ILE:HA	1:A:280:LEU:HD12	1.94	0.50
1:B:142:ASN:N	1:B:145:THR:CG2	2.75	0.50
1:B:362:LEU:N	1:B:362:LEU:HD23	2.27	0.50
2:C:21:LYS:HG3	2:C:26:LEU:HB2	1.94	0.50
2:C:172:ASP:O	2:C:176:ARG:HG3	2.12	0.50
1:A:152:VAL:O	1:A:152:VAL:HG22	2.12	0.50
2:C:27:VAL:CG1	2:C:29:THR:OG1	2.59	0.50
2:C:42:ASN:N	4:C:2013:HOH:O	2.43	0.50
2:C:44:ASP:O	2:C:47:VAL:HG12	2.12	0.50
2:C:76:PRO:CA	2:C:415:ASN:ND2	2.75	0.50
2:C:309:SER:O	2:C:312:TYR:HB3	2.11	0.50
2:C:471:ASN:N	2:C:471:ASN:OD1	2.43	0.50
1:B:358:LYS:NZ	4:B:2080:HOH:O	2.44	0.50
2:C:3:ASN:OD1	2:C:397:VAL:HG12	2.11	0.50
1:B:3:ASN:OD1	1:B:5:ILE:N	2.35	0.50
2:C:351:THR:HG22	2:C:353:MET:H	1.76	0.50
1:A:71:THR:HG22	1:A:412:SER:HB2	1.93	0.50
1:B:132:LYS:O	1:B:136:ASP:OD1	2.29	0.50
2:C:300:GLN:NE2	2:C:470:TYR:O	2.38	0.50
1:A:261:LEU:HD11	1:A:277:ILE:HD11	1.92	0.49
2:C:366:ASP:O	2:C:369:GLN:NE2	2.45	0.49
1:B:63:TYR:CE1	1:B:433:LEU:CD1	2.92	0.49
2:C:75:ALA:O	2:C:77:ILE:HD12	2.12	0.49
2:C:280:LEU:O	2:C:284:ILE:HG13	2.12	0.49
1:A:320:THR:HG21	1:B:267:GLU:OE1	2.12	0.49
1:A:376:HIS:ND1	1:A:377:PRO:CD	2.76	0.49
1:B:3:ASN:HA	1:B:397:VAL:HG13	1.94	0.49
1:B:152:VAL:HG21	1:B:475:ASN:N	2.25	0.49
1:B:357:LYS:NZ	4:B:2078:HOH:O	2.45	0.49
2:C:338:PRO:O	2:C:339:ARG:HG2	2.12	0.49
2:C:427:ALA:O	2:C:431:VAL:HG13	2.12	0.49
1:B:27:VAL:CG1	1:B:29:THR:HG22	2.39	0.49
1:B:468:ASN:C	1:B:468:ASN:OD1	2.50	0.49
2:C:7:VAL:C	2:C:8:ASN:HD22	2.15	0.49
2:C:241:THR:HB	2:C:242:GLU:HG2	1.95	0.49
1:B:300:GLN:O	1:B:303:GLN:HG2	2.12	0.49
1:A:123:LEU:CD1	1:A:123:LEU:N	2.76	0.49
1:B:140:ARG:HA	1:B:145:THR:OG1	2.13	0.49
1:B:325:PRO:HA	1:B:397:VAL:CG1	2.43	0.49
1:B:422:THR:O	1:B:423:ASN:HB3	2.12	0.49
1:B:195:HIS:CE1	1:B:198:VAL:CG2	2.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:31:THR:HG21	1:B:35:SER:OG	2.13	0.49
1:A:204:PHE:C	1:A:204:PHE:CD1	2.86	0.48
1:B:449:VAL:O	1:B:449:VAL:HG22	2.12	0.48
2:C:382:ALA:O	2:C:385:ILE:HB	2.13	0.48
2:C:322:GLU:CD	2:C:322:GLU:H	2.16	0.48
2:C:417:ARG:HD2	2:C:419:ASN:HD21	1.78	0.48
1:B:443:ILE:HD13	1:B:444:GLN:H	1.78	0.48
2:C:0:ALA:HB3	2:C:4:LYS:HE3	1.92	0.48
2:C:363:PHE:CE1	2:C:382:ALA:CA	2.95	0.48
1:A:98:LYS:HB2	1:A:99:ASN:ND2	2.28	0.48
1:A:276:MET:O	1:A:280:LEU:HD12	2.13	0.48
1:B:142:ASN:HD21	1:B:145:THR:HG22	1.65	0.48
1:B:355:TRP:HE3	1:B:355:TRP:O	1.96	0.48
2:C:75:ALA:CB	2:C:394:THR:CG2	2.90	0.48
1:A:95:TRP:HZ2	1:A:132:LYS:HG2	1.79	0.48
1:A:398:ALA:CB	1:B:210:ILE:HD11	2.43	0.48
2:C:62:ILE:HG22	2:C:63:TYR:N	2.29	0.48
1:A:117:VAL:HG22	1:A:374:TYR:HB3	1.95	0.48
1:A:305:ASP:OD1	1:A:305:ASP:C	2.52	0.48
1:B:224:GLY:O	1:B:227:GLY:N	2.32	0.48
1:B:333:GLU:OE2	1:B:336:LYS:CE	2.60	0.48
1:B:402:ASP:O	1:B:405:GLN:HG3	2.14	0.48
2:C:1:MET:HA	2:C:398:ALA:HB1	1.96	0.48
2:C:179:LEU:O	2:C:179:LEU:HD23	2.12	0.48
1:A:351:THR:OG1	1:A:353:MET:HB2	2.13	0.48
1:B:324:PHE:N	1:B:325:PRO:CD	2.76	0.48
1:A:95:TRP:CD2	1:A:133:TRP:HD1	2.32	0.48
1:A:3:ASN:OD1	1:A:3:ASN:C	2.52	0.48
1:A:411:LYS:HB3	1:A:465:PRO:HB3	1.96	0.48
1:B:222:LYS:HG3	3:B:1476:SO4:O1	2.13	0.48
2:C:40:ILE:HG23	2:C:41:PRO:CD	2.44	0.48
2:C:173:MET:HG2	2:C:452:GLU:OE1	2.13	0.47
1:A:20:PHE:CE1	1:A:24:ASN:ND2	2.81	0.47
1:B:174:ILE:CG2	1:B:175:ARG:N	2.77	0.47
1:B:417:ARG:O	1:B:425:PRO:CD	2.47	0.47
2:C:237:LYS:HE3	2:C:240:GLU:OE1	2.14	0.47
1:B:2:GLU:HB3	1:B:4:LYS:NZ	2.30	0.47
1:B:237:LYS:HA	1:B:237:LYS:HD3	1.65	0.47
2:C:71:THR:HG22	2:C:409:HIS:O	2.08	0.47
2:C:75:ALA:O	2:C:77:ILE:HD13	2.14	0.47
2:C:175:ARG:O	2:C:179:LEU:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:LEU:HD23	1:A:113:LEU:HA	1.57	0.47
1:A:203:GLU:HA	1:A:206:LYS:HE2	1.97	0.47
1:B:104:LYS:O	1:B:108:GLU:HB2	2.14	0.47
2:C:46:PHE:CZ	2:C:69:GLU:HG3	2.50	0.47
2:C:159:PRO:HB2	2:C:161:GLU:HG3	1.97	0.47
1:A:58:GLN:O	1:A:62:ILE:HG13	2.14	0.47
1:A:353:MET:CG	1:A:355:TRP:NE1	2.77	0.47
1:A:389:GLY:C	1:A:409:HIS:ND1	2.67	0.47
1:B:50:MET:HE2	1:B:59:LYS:HG2	1.89	0.47
1:B:310:SER:HB3	1:B:388:MET:HG2	1.96	0.47
2:C:262:ASP:O	2:C:265:LYS:HB2	2.13	0.47
1:A:193:VAL:O	1:A:197:HIS:HD2	1.98	0.47
1:A:269:ASP:OD1	1:A:269:ASP:C	2.53	0.47
2:C:291:TYR:CA	2:C:294:SER:OG	2.63	0.47
1:A:71:THR:HB	1:A:408:GLY:C	2.35	0.47
1:A:257:LEU:O	1:A:261:LEU:HD12	2.15	0.47
1:A:373:ILE:N	1:A:373:ILE:CD1	2.61	0.47
1:B:152:VAL:CG2	1:B:475:ASN:H	2.25	0.47
1:B:202:ARG:O	1:B:206:LYS:HG3	2.15	0.47
1:B:433:LEU:HD12	1:B:433:LEU:C	2.35	0.47
1:A:115:VAL:HA	1:A:368:PHE:HA	1.97	0.47
1:A:175:ARG:C	1:A:179:LEU:HD11	2.35	0.47
1:A:176:ARG:HA	1:A:179:LEU:HD13	1.96	0.47
1:B:139:PHE:CD1	1:B:139:PHE:C	2.88	0.47
1:A:226:SER:C	1:A:228:ILE:HD12	2.34	0.47
1:A:332:PHE:CE2	1:A:336:LYS:HD2	2.50	0.47
1:A:75:ALA:CB	1:A:394:THR:HG21	2.45	0.47
1:A:176:ARG:CA	1:A:179:LEU:CD1	2.92	0.47
1:B:304:ILE:HG22	1:B:377:PRO:HB2	1.94	0.47
1:B:339:ARG:N	1:B:339:ARG:CD	2.78	0.47
2:C:261:LEU:CD1	2:C:273:ALA:HB1	2.37	0.47
2:C:295:SER:HA	2:C:298:ARG:HG3	1.96	0.47
1:A:1:MET:HB2	1:B:209:TYR:OH	2.15	0.46
1:A:36:PHE:CZ	1:A:404:ALA:CA	2.93	0.46
1:B:113:LEU:HA	1:B:113:LEU:HD23	1.62	0.46
1:B:150:ASN:OD1	1:B:151:LYS:HB3	2.15	0.46
2:C:41:PRO:HA	4:C:2011:HOH:O	2.15	0.46
1:A:278:THR:HG22	1:A:279:ASN:HD22	1.81	0.46
1:B:3:ASN:OD1	1:B:3:ASN:C	2.53	0.46
2:C:9:ASN:HD22	2:C:12:GLU:CG	2.13	0.46
1:A:71:THR:HG21	1:A:409:HIS:CA	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:140:ARG:HG3	1:B:146:ALA:HA	1.96	0.46
2:C:74:CYS:SG	2:C:416:LEU:HD21	2.55	0.46
2:C:328:SER:HB2	2:C:397:VAL:HG23	1.95	0.46
2:C:1:MET:HE1	2:C:329:GLN:HG3	1.97	0.46
2:C:71:THR:HB	2:C:408:GLY:CA	2.45	0.46
2:C:332:PHE:HA	2:C:393:GLY:O	2.16	0.46
2:C:173:MET:HE1	2:C:455:LEU:HD23	1.98	0.46
2:C:443:ILE:HB	2:C:449:VAL:HG11	1.97	0.46
2:C:449:VAL:CG2	2:C:452:GLU:CB	2.86	0.46
1:A:68:VAL:O	1:A:72:LYS:HB2	2.16	0.46
1:A:320:THR:CG2	1:B:267:GLU:OE1	2.63	0.46
1:A:457:GLN:HG2	1:A:462:LYS:HE3	1.98	0.46
1:B:71:THR:HG22	1:B:409:HIS:C	2.34	0.46
2:C:339:ARG:HD2	2:C:343:LYS:HG3	1.98	0.46
1:A:353:MET:HG3	1:A:355:TRP:HE1	1.79	0.46
1:B:104:LYS:HG3	1:B:108:GLU:OE2	2.16	0.46
2:C:3:ASN:OD1	2:C:3:ASN:C	2.54	0.46
1:A:9:ASN:HD21	1:A:12:GLU:HG3	1.80	0.46
1:A:32:ASN:ND2	1:A:463:GLN:HB3	2.30	0.46
1:A:226:SER:HB2	1:A:228:ILE:HD12	1.98	0.46
1:B:8:ASN:N	1:B:12:GLU:OE1	2.46	0.46
1:B:336:LYS:O	1:B:337:GLN:HG2	2.15	0.46
1:A:180:ILE:CG2	1:A:181:LEU:CD1	2.88	0.46
1:A:230:LEU:HD12	1:A:230:LEU:N	2.30	0.46
1:A:389:GLY:O	1:A:393:GLY:CA	2.64	0.45
1:B:71:THR:CG2	1:B:409:HIS:C	2.85	0.45
2:C:279:ASN:O	2:C:283:HIS:CD2	2.69	0.45
1:A:111:THR:O	1:A:114:LYS:HB2	2.16	0.45
2:C:95:TRP:HB2	2:C:137:ILE:HD11	1.98	0.45
1:A:229:ALA:CB	1:A:283:HIS:CE1	2.99	0.45
2:C:3:ASN:CG	2:C:397:VAL:HG11	2.37	0.45
2:C:131:LEU:HD23	2:C:131:LEU:HA	1.85	0.45
1:B:159:PRO:HG2	1:B:162:ILE:HG12	1.99	0.45
1:B:169:MET:CE	1:B:434:PHE:CB	2.86	0.45
1:A:75:ALA:HB1	1:A:394:THR:HG21	1.97	0.45
1:A:173:MET:SD	1:A:455:LEU:HD23	2.56	0.45
1:A:226:SER:CB	1:A:228:ILE:HD12	2.47	0.45
1:B:95:TRP:HZ2	1:B:132:LYS:HG2	1.81	0.45
1:B:325:PRO:HB3	1:B:397:VAL:HG12	1.98	0.45
1:B:339:ARG:HA	1:B:339:ARG:HD2	1.80	0.45
2:C:238:LEU:CD2	2:C:246:ILE:HD12	2.44	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:254:VAL:HG22	2:C:280:LEU:HD13	1.98	0.45
1:A:30:PHE:HE2	1:A:38:GLU:O	1.99	0.45
1:B:261:LEU:HD12	1:B:273:ALA:HB1	1.98	0.45
1:B:357:LYS:O	1:B:360:TYR:HB3	2.16	0.45
2:C:117:VAL:CG1	2:C:374:TYR:HB3	2.43	0.45
2:C:123:LEU:HB3	2:C:301:SER:HB3	1.98	0.45
1:B:75:ALA:CB	1:B:394:THR:HG21	2.47	0.45
1:B:146:ALA:O	1:B:467:GLN:HA	2.17	0.45
1:B:423:ASN:CG	1:B:423:ASN:O	2.54	0.45
2:C:395:ILE:N	2:C:395:ILE:CD1	2.80	0.45
1:A:71:THR:CG2	1:A:409:HIS:N	2.80	0.45
1:A:107:ASP:OD1	1:A:316:LYS:CE	2.62	0.45
1:A:162:ILE:HG13	1:A:166:VAL:CG2	2.47	0.45
1:B:68:VAL:HG21	1:B:338:PRO:HD3	1.98	0.45
1:B:261:LEU:HD23	1:B:261:LEU:H	1.73	0.45
1:B:266:ASP:OD1	1:B:266:ASP:N	2.50	0.45
2:C:140:ARG:HA	2:C:145:THR:OG1	2.17	0.45
1:A:151:LYS:HB2	1:A:151:LYS:HE2	1.64	0.45
1:A:197:HIS:HA	1:A:217:TRP:CH2	2.52	0.45
1:A:329:GLN:NE2	1:A:396:PRO:HB2	2.31	0.45
1:A:118:PRO:HG3	1:A:123:LEU:HD11	1.99	0.44
1:A:123:LEU:HB3	1:A:301:SER:HB3	1.99	0.44
1:A:209:TYR:HB2	1:A:257:LEU:HB2	2.00	0.44
2:C:179:LEU:HD23	2:C:179:LEU:C	2.38	0.44
1:A:179:LEU:H	1:A:179:LEU:CD1	2.04	0.44
1:A:142:ASN:C	1:A:142:ASN:OD1	2.54	0.44
1:B:55:ASP:OD1	1:B:56:ASP:N	2.50	0.44
1:B:335:GLY:HA3	1:B:409:HIS:HE1	1.82	0.44
2:C:280:LEU:HD23	2:C:280:LEU:HA	1.85	0.44
2:C:453:HIS:O	2:C:456:HIS:HB3	2.18	0.44
1:A:456:HIS:ND1	1:A:456:HIS:C	2.70	0.44
1:B:345:LYS:O	1:B:349:LEU:CD1	2.66	0.44
2:C:3:ASN:CG	2:C:397:VAL:HG12	2.38	0.44
1:A:119:LYS:NZ	4:A:2042:HOH:O	2.34	0.44
1:A:324:PHE:N	1:A:325:PRO:CD	2.80	0.44
2:C:40:ILE:CG2	2:C:41:PRO:N	2.80	0.44
1:A:142:ASN:OD1	1:A:144:ASN:N	2.51	0.44
1:A:160:GLY:C	1:A:163:VAL:HG23	2.35	0.44
1:A:216:PRO:HB2	1:A:217:TRP:CE3	2.53	0.44
1:A:262:ASP:O	1:A:265:LYS:HG2	2.18	0.44
2:C:41:PRO:HA	4:C:2013:HOH:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:54:THR:HG23	2:C:58:GLN:HE21	1.81	0.44
2:C:363:PHE:CE1	2:C:382:ALA:N	2.86	0.44
1:A:217:TRP:CD2	1:A:217:TRP:N	2.75	0.44
1:A:330:PHE:N	1:B:214:ASN:ND2	2.66	0.44
1:A:330:PHE:HZ	1:A:344:MET:HG3	1.82	0.44
2:C:209:TYR:HE2	2:C:260:TYR:CB	2.30	0.44
1:B:277:ILE:HG22	1:B:278:THR:N	2.31	0.44
2:C:173:MET:HE3	2:C:452:GLU:HG2	1.99	0.44
1:A:160:GLY:HA2	1:A:163:VAL:CG2	2.47	0.44
1:A:235:LEU:HD12	1:A:235:LEU:HA	1.75	0.44
1:B:152:VAL:CB	1:B:475:ASN:H	2.31	0.44
1:B:319:VAL:CG1	1:B:320:THR:N	2.81	0.44
2:C:30:PHE:C	2:C:417:ARG:HG2	2.38	0.44
1:A:53:ALA:HA	1:A:58:GLN:OE1	2.17	0.43
1:A:222:LYS:O	1:A:230:LEU:HD13	2.17	0.43
1:B:195:HIS:ND1	1:B:199:ASP:OD1	2.47	0.43
2:C:39:SER:OG	4:C:2010:HOH:O	2.21	0.43
2:C:180:ILE:CG2	2:C:183:ARG:NH1	2.81	0.43
1:B:195:HIS:O	1:B:198:VAL:CG2	2.66	0.43
1:B:453:HIS:O	1:B:457:GLN:HG2	2.18	0.43
2:C:162:ILE:CG2	2:C:431:VAL:HG11	2.45	0.43
1:B:355:TRP:CE3	1:B:356:GLY:HA2	2.53	0.43
2:C:22:LYS:CG	2:C:23:GLY:N	2.80	0.43
2:C:324:PHE:CE2	2:C:397:VAL:HG21	2.54	0.43
1:A:376:HIS:ND1	1:A:377:PRO:N	2.67	0.43
1:B:416:LEU:HD12	1:B:416:LEU:HA	1.85	0.43
1:B:141:VAL:C	1:B:142:ASN:ND2	2.67	0.43
2:C:63:TYR:CZ	2:C:437:GLN:NE2	2.86	0.43
2:C:96:PHE:CZ	2:C:312:TYR:HA	2.53	0.43
1:A:55:ASP:OD1	1:A:55:ASP:C	2.57	0.43
1:A:337:GLN:HE22	1:B:193:VAL:HG12	1.83	0.43
1:A:449:VAL:HG12	1:A:449:VAL:O	2.18	0.43
1:B:386:SER:O	1:B:390:VAL:HG23	2.19	0.43
2:C:174:ILE:HA	2:C:177:ARG:HB3	2.01	0.43
1:A:104:LYS:HE2	1:A:108:GLU:OE1	2.18	0.43
1:A:169:MET:HE3	1:A:431:VAL:HG22	1.97	0.43
1:B:101:GLY:O	1:B:104:LYS:CB	2.67	0.43
2:C:290:LEU:HD23	2:C:290:LEU:HA	1.83	0.43
1:B:56:ASP:O	1:B:59:LYS:HB2	2.17	0.43
1:B:141:VAL:HG22	1:B:142:ASN:HD21	1.83	0.43
1:B:416:LEU:CB	1:B:426:CYS:HB2	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:0:ALA:HB2	2:C:4:LYS:HZ1	1.78	0.43
2:C:7:VAL:HG11	2:C:13:MET:CB	2.49	0.43
2:C:31:THR:HG21	2:C:35:SER:CB	2.48	0.43
2:C:285:ALA:HA	2:C:288:GLN:HG3	2.01	0.43
1:A:162:ILE:C	1:A:166:VAL:HG23	2.38	0.43
1:B:230:LEU:HD23	1:B:230:LEU:HA	1.83	0.43
2:C:173:MET:HE2	2:C:452:GLU:CA	2.49	0.43
1:A:3:ASN:OD1	1:A:5:ILE:N	2.50	0.43
1:B:101:GLY:O	1:B:104:LYS:HB3	2.19	0.43
1:B:172:ASP:O	1:B:176:ARG:HG3	2.19	0.43
1:B:325:PRO:CB	1:B:397:VAL:CG1	2.97	0.43
1:B:334:LEU:HD23	1:B:339:ARG:HG2	1.99	0.43
1:B:432:LYS:HA	1:B:435:GLU:HG3	2.01	0.43
2:C:43:LEU:HD11	2:C:69:GLU:CB	2.49	0.43
1:B:75:ALA:CB	1:B:394:THR:CG2	2.97	0.42
1:B:209:TYR:C	1:B:211:MET:N	2.71	0.42
2:C:76:PRO:CB	2:C:415:ASN:ND2	2.82	0.42
2:C:394:THR:C	2:C:395:ILE:CD1	2.82	0.42
2:C:457:GLN:O	2:C:460:VAL:HG22	2.20	0.42
1:A:264:HIS:ND1	1:A:267:GLU:OE1	2.51	0.42
2:C:126:TYR:CD2	2:C:377:PRO:HG2	2.55	0.42
1:A:131:LEU:HD23	1:A:131:LEU:HA	1.89	0.42
1:A:238:LEU:HD23	1:A:246:ILE:HD12	2.01	0.42
1:A:472:VAL:O	1:A:472:VAL:HG12	2.18	0.42
1:B:335:GLY:HA3	1:B:409:HIS:CE1	2.54	0.42
2:C:395:ILE:HD12	2:C:395:ILE:N	2.33	0.42
1:A:212:ALA:O	1:A:215:PRO:HD3	2.20	0.42
1:A:215:PRO:HB2	1:A:217:TRP:CD1	2.55	0.42
1:A:258:ASN:HA	1:A:261:LEU:HD12	2.01	0.42
1:A:267:GLU:O	2:C:354:LYS:HG3	2.20	0.42
2:C:86:THR:OG1	2:C:87:GLY:N	2.51	0.42
1:A:278:THR:HG22	1:A:279:ASN:N	2.33	0.42
1:B:54:THR:OG1	1:B:55:ASP:N	2.53	0.42
2:C:82:TRP:CZ2	2:C:141:VAL:CG1	3.03	0.42
2:C:142:ASN:CG	2:C:145:THR:HG22	2.39	0.42
2:C:220:ILE:HD13	2:C:220:ILE:HA	1.68	0.42
1:A:31:THR:HB	1:A:33:SER:O	2.19	0.42
1:B:221:ASN:O	1:B:222:LYS:C	2.56	0.42
1:B:368:PHE:CE1	1:B:372:ARG:HA	2.54	0.42
2:C:10:LYS:CE	2:C:141:VAL:O	2.65	0.42
2:C:319:VAL:HG12	2:C:320:THR:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:78:TYR:HD1	1:B:78:TYR:C	2.22	0.42
1:B:376:HIS:HD2	1:B:377:PRO:N	2.17	0.42
2:C:360:TYR:HA	2:C:363:PHE:HD2	1.85	0.42
1:A:398:ALA:HB2	1:B:210:ILE:HD11	2.02	0.42
1:B:20:PHE:CD1	1:B:20:PHE:C	2.93	0.42
1:B:126:TYR:CD1	1:B:126:TYR:C	2.93	0.42
1:B:229:ALA:O	1:B:233:THR:HG23	2.20	0.42
1:B:410:THR:C	1:B:412:SER:H	2.23	0.42
2:C:172:ASP:OD1	2:C:172:ASP:C	2.58	0.42
1:A:46:PHE:CE2	1:A:69:GLU:HG3	2.55	0.42
1:A:369:GLN:C	1:A:370:GLN:OE1	2.58	0.42
1:B:3:ASN:CG	1:B:397:VAL:HG22	2.41	0.42
1:B:180:ILE:HG12	1:B:180:ILE:H	1.69	0.42
1:B:442:ASN:ND2	1:B:442:ASN:C	2.73	0.42
2:C:173:MET:CE	2:C:452:GLU:HA	2.50	0.42
2:C:332:PHE:CD1	2:C:407:SER:CB	3.02	0.42
2:C:359:LEU:O	2:C:362:LEU:HB2	2.20	0.41
1:B:50:MET:HE1	1:B:59:LYS:CB	2.49	0.41
1:B:297:LEU:HD12	1:B:297:LEU:HA	1.72	0.41
2:C:50:MET:HA	2:C:62:ILE:CD1	2.50	0.41
1:B:78:TYR:C	1:B:78:TYR:CD1	2.94	0.41
2:C:120:ILE:HG12	2:C:298:ARG:HE	1.85	0.41
1:B:75:ALA:HB2	1:B:394:THR:CG2	2.50	0.41
1:B:118:PRO:HG3	1:B:123:LEU:HD21	2.03	0.41
2:C:50:MET:HE3	2:C:62:ILE:HG21	2.02	0.41
2:C:177:ARG:NH2	4:C:2045:HOH:O	2.37	0.41
1:A:375:MET:HE1	1:A:379:VAL:CG1	2.45	0.41
1:A:464:SER:HB3	1:A:467:GLN:CG	2.48	0.41
1:B:324:PHE:N	1:B:325:PRO:HD3	2.35	0.41
1:B:410:THR:C	1:B:412:SER:N	2.73	0.41
1:B:169:MET:HE1	1:B:434:PHE:HB2	2.00	0.41
1:B:254:VAL:HG11	1:B:281:LEU:HD21	2.02	0.41
1:B:337:GLN:C	1:B:339:ARG:HH11	2.24	0.41
2:C:130:ALA:O	2:C:134:ARG:HG3	2.20	0.41
2:C:363:PHE:HE1	2:C:382:ALA:N	2.19	0.41
1:A:217:TRP:O	2:C:343:LYS:HD2	2.21	0.41
1:A:413:ILE:HD13	1:A:413:ILE:HG21	1.81	0.41
1:B:30:PHE:CD1	1:B:40:VAL:HG12	2.56	0.41
1:B:76:PRO:HB3	1:B:415:ASN:CG	2.40	0.41
1:B:78:TYR:HD1	1:B:78:TYR:O	2.04	0.41
1:B:214:ASN:OD1	1:B:214:ASN:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:376:HIS:CD2	1:B:377:PRO:N	2.89	0.41
2:C:133:TRP:O	2:C:137:ILE:HG12	2.21	0.41
2:C:451:SER:HA	2:C:454:LEU:HD13	2.03	0.41
1:A:31:THR:CG2	1:A:415:ASN:HD21	2.18	0.41
1:A:332:PHE:HA	1:A:393:GLY:O	2.21	0.41
2:C:86:THR:HG23	2:C:86:THR:H	1.60	0.41
2:C:162:ILE:CG2	2:C:166:VAL:HG23	2.50	0.41
2:C:293:ASN:N	2:C:293:ASN:HD22	2.18	0.41
1:B:106:TRP:CD1	1:B:106:TRP:N	2.89	0.40
1:B:325:PRO:HA	1:B:397:VAL:HG12	2.02	0.40
1:B:426:CYS:O	1:B:430:ILE:HG13	2.21	0.40
2:C:366:ASP:OD1	2:C:366:ASP:N	2.46	0.40
1:A:113:LEU:CD1	1:A:376:HIS:CD2	3.03	0.40
1:A:371:ASN:HD22	1:A:371:ASN:C	2.12	0.40
1:A:449:VAL:CG1	1:A:452:GLU:HG3	2.45	0.40
1:B:141:VAL:CG2	1:B:142:ASN:HD22	2.28	0.40
1:B:239:ALA:O	1:B:243:GLY:N	2.53	0.40
2:C:88:ILE:HA	2:C:88:ILE:HD13	1.71	0.40
2:C:183:ARG:NH2	2:C:374:TYR:HH	2.13	0.40
1:A:281:LEU:HD23	1:A:281:LEU:HA	1.87	0.40
1:A:401:ASP:C	1:A:403:ALA:N	2.73	0.40
1:B:304:ILE:CG2	1:B:377:PRO:HB3	2.47	0.40
2:C:32:ASN:ND2	2:C:463:GLN:HB3	2.36	0.40
1:B:3:ASN:ND2	1:B:397:VAL:HG21	2.36	0.40
1:B:43:LEU:O	1:B:46:PHE:N	2.52	0.40
1:B:115:VAL:O	1:B:115:VAL:CG2	2.69	0.40
2:C:91:LYS:HB3	2:C:137:ILE:HD12	2.03	0.40
1:B:454:LEU:HA	1:B:454:LEU:HD23	1.90	0.40
2:C:7:VAL:HG11	2:C:13:MET:HA	2.03	0.40
2:C:77:ILE:CD1	2:C:77:ILE:N	2.85	0.40
2:C:297:LEU:HD12	2:C:297:LEU:HA	1.76	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:ARG:NH2	4:A:2080:HOH:O[4_645]	1.83	0.37
1:B:225:ARG:CZ	4:A:2080:HOH:O[4_645]	1.98	0.22
1:B:354:LYS:NZ	2:C:266:ASP:O[2_645]	2.12	0.08

## 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 X-ray entries followed by that with respect to entries of similar resolution.

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	462/483 (96%)	448 (97%)	11 (2%)	3 (1%)	25	59
1	B	472/483 (98%)	454 (96%)	17 (4%)	1 (0%)	47	79
2	C	463/483 (96%)	445 (96%)	17 (4%)	1 (0%)	47	79
All	All	1397/1449 (96%)	1347 (96%)	45 (3%)	5 (0%)	34	69

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	152	VAL
1	A	150	ASN
2	C	25	GLY
1	A	423	ASN
1	B	411	LYS

### 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 X-ray entries followed by that with respect to entries of similar resolution.

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	395/408 (97%)	310 (78%)	85 (22%)	1	4
1	B	401/408 (98%)	321 (80%)	80 (20%)	1	5
2	C	396/408 (97%)	313 (79%)	83 (21%)	1	5
All	All	1192/1224 (97%)	944 (79%)	248 (21%)	1	5

All (248) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LYS
1	A	8	ASN
1	A	15	ARG
1	A	22	LYS
1	A	27	VAL
1	A	28	ASP
1	A	31	THR
1	A	35	SER
1	A	39	SER
1	A	40	VAL
1	A	42	ASN
1	A	43	LEU
1	A	47	VAL
1	A	71	THR
1	A	84	SER
1	A	86	THR
1	A	99	ASN
1	A	105	SER
1	A	106	TRP
1	A	109	SER
1	A	112	GLU
1	A	115	VAL
1	A	120	ILE
1	A	124	THR
1	A	135	LYS
1	A	140	ARG
1	A	145	THR
1	A	150	ASN
1	A	151	LYS
1	A	153	LEU
1	A	155	GLU
1	A	166	VAL
1	A	170	LEU
1	A	171	SER
1	A	174	ILE
1	A	175	ARG
1	A	179	LEU
1	A	180	ILE
1	A	181	LEU
1	A	182	ASN
1	A	196	GLU
1	A	198	VAL
1	A	205	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	217	TRP
1	A	220	ILE
1	A	222	LYS
1	A	226	SER
1	A	241	THR
1	A	244	LYS
1	A	261	LEU
1	A	266	ASP
1	A	275	SER
1	A	278	THR
1	A	290	LEU
1	A	294	SER
1	A	295	SER
1	A	303	GLN
1	A	304	ILE
1	A	310	SER
1	A	320	THR
1	A	323	THR
1	A	328	SER
1	A	337	GLN
1	A	350	SER
1	A	351	THR
1	A	353	MET
1	A	371	ASN
1	A	373	ILE
1	A	397	VAL
1	A	399	ASN
1	A	401	ASP
1	A	412	SER
1	A	413	ILE
1	A	421	GLU
1	A	438	LYS
1	A	439	THR
1	A	442	ASN
1	A	443	ILE
1	A	447	ASP
1	A	449	VAL
1	A	451	SER
1	A	458	SER
1	A	462	LYS
1	A	468	ASN
1	A	475	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	B	4	LYS
1	B	11	ASP
1	B	28	ASP
1	B	29	THR
1	B	31	THR
1	B	35	SER
1	B	42	ASN
1	B	47	VAL
1	B	52	SER
1	B	54	THR
1	B	62	ILE
1	B	65	SER
1	B	71	THR
1	B	78	TYR
1	B	84	SER
1	B	85	SER
1	B	86	THR
1	B	102	THR
1	B	106	TRP
1	B	109	SER
1	B	120	ILE
1	B	121	GLU
1	B	124	THR
1	B	126	TYR
1	B	136	ASP
1	B	142	ASN
1	B	145	THR
1	B	149	SER
1	B	158	VAL
1	B	164	MET
1	B	174	ILE
1	B	180	ILE
1	B	183	ARG
1	B	186	ASP
1	B	190	ARG
1	B	194	SER
1	B	214	ASN
1	B	220	ILE
1	B	226	SER
1	B	228	ILE
1	B	237	LYS
1	B	246	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	B	253	THR
1	B	261	LEU
1	B	265	LYS
1	B	277	ILE
1	B	278	THR
1	B	298	ARG
1	B	301	SER
1	B	310	SER
1	B	320	THR
1	B	323	THR
1	B	326	THR
1	B	339	ARG
1	B	341	THR
1	B	342	LYS
1	B	349	LEU
1	B	355	TRP
1	B	366	ASP
1	B	375	MET
1	B	386	SER
1	B	397	VAL
1	B	399	ASN
1	B	407	SER
1	B	409	HIS
1	B	413	ILE
1	B	416	LEU
1	B	417	ARG
1	B	420	THR
1	B	433	LEU
1	B	442	ASN
1	B	443	ILE
1	B	449	VAL
1	B	451	SER
1	B	455	LEU
1	B	457	GLN
1	B	464	SER
1	B	468	ASN
1	B	471	ASN
1	B	475	ASN
2	C	37	CYS
2	C	39	SER
2	C	45	ARG
2	C	50	MET

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	C	55	ASP
2	C	56	ASP
2	C	61	SER
2	C	71	THR
2	C	77	ILE
2	C	79	GLU
2	C	85	SER
2	C	98	LYS
2	C	102	THR
2	C	105	SER
2	C	111	THR
2	C	113	LEU
2	C	115	VAL
2	C	121	GLU
2	C	136	ASP
2	C	140	ARG
2	C	145	THR
2	C	156	TYR
2	C	161	GLU
2	C	162	ILE
2	C	163	VAL
2	C	164	MET
2	C	172	ASP
2	C	177	ARG
2	C	181	LEU
2	C	193	VAL
2	C	194	SER
2	C	197	HIS
2	C	209	TYR
2	C	220	ILE
2	C	222	LYS
2	C	223	SER
2	C	228	ILE
2	C	241	THR
2	C	246	ILE
2	C	251	LYS
2	C	252	LYS
2	C	255	GLU
2	C	260	TYR
2	C	269	ASP
2	C	277	ILE
2	C	278	THR

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Mol	Chain	Res	Type
2	C	293	ASN
2	C	294	SER
2	C	298	ARG
2	C	300	GLN
2	C	304	ILE
2	C	310	SER
2	C	322	GLU
2	C	323	THR
2	C	326	THR
2	C	330	PHE
2	C	337	GLN
2	C	341	THR
2	C	342	LYS
2	C	362	LEU
2	C	366	ASP
2	C	369	GLN
2	C	370	GLN
2	C	373	ILE
2	C	386	SER
2	C	390	VAL
2	C	395	ILE
2	C	402	ASP
2	C	418	THR
2	C	420	THR
2	C	421	GLU
2	C	422	THR
2	C	429	THR
2	C	430	ILE
2	C	431	VAL
2	C	441	PHE
2	C	443	ILE
2	C	446	MET
2	C	451	SER
2	C	459	LEU
2	C	464	SER
2	C	468	ASN
2	C	471	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	ASN

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Mol	Chain	Res	Type
1	A	99	ASN
1	A	144	ASN
1	A	197	HIS
1	A	214	ASN
1	A	283	HIS
1	A	329	GLN
1	A	337	GLN
1	A	409	HIS
1	A	415	ASN
1	A	442	ASN
1	A	471	ASN
1	B	8	ASN
1	B	42	ASN
1	B	58	GLN
1	B	99	ASN
1	B	127	GLN
1	B	142	ASN
1	B	178	ASN
1	B	214	ASN
1	B	264	HIS
1	B	329	GLN
1	B	370	GLN
1	B	376	HIS
1	B	409	HIS
1	B	442	ASN
1	B	471	ASN
1	B	475	ASN
2	C	8	ASN
2	C	32	ASN
2	C	49	GLN
2	C	58	GLN
2	C	293	ASN
2	C	303	GLN
2	C	370	GLN
2	C	405	GLN
2	C	437	GLN
2	C	444	GLN
2	C	453	HIS

### 5.3.3 RNA ⓘ

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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	SO4	A	1478	-	4,4,4	0.61	0	6,6,6	0.27	0
3	SO4	B	1477	-	4,4,4	1.66	1 (25%)	6,6,6	0.49	0
3	SO4	A	1477	-	4,4,4	0.49	0	6,6,6	0.24	0
3	SO4	B	1476	-	4,4,4	0.51	0	6,6,6	0.34	0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1477	SO4	O1-S	2.18	1.57	1.46

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1476	SO4	2	0

## 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 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	466/483 (96%)	-0.45	6 (1%) 77 59	53, 88, 141, 174	0
1	B	474/483 (98%)	-0.55	1 (0%) 95 90	61, 90, 136, 161	0
2	C	467/483 (96%)	-0.41	4 (0%) 84 69	56, 98, 156, 202	0
All	All	1407/1449 (97%)	-0.47	11 (0%) 86 72	53, 91, 145, 202	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	194	SER	3.9
2	C	154	ALA	3.6
2	C	0	ALA	3.5
1	B	154	ALA	2.7
1	A	225	ARG	2.6
2	C	475	ASN	2.5
1	A	153	LEU	2.2
1	A	155	GLU	2.2
1	A	154	ALA	2.1
2	C	55	ASP	2.0
1	A	182	ASN	2.0

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

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

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	SO4	A	1477	5/5	0.91	0.15	135,147,174,175	0
3	SO4	B	1476	5/5	0.91	0.13	117,119,123,129	0
3	SO4	A	1478	5/5	0.94	0.18	117,131,141,151	0
3	SO4	B	1477	5/5	0.98	0.25	46,71,87,98	5

## 6.5 Other polymers [i](#)

There are no such residues in this entry.