



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 9, 2017 – 05:06 PM EST

PDB ID : 4NBQ  
Title : Structure of the polynucleotide phosphorylase (CBU\_0852) from *Coxiella burnetii*  
Authors : Rudolph, M.J.; Cheung, J.; Franklin, M.C.; Cassidy, M.; Gary, E.; Burshteyn, F.; Love, J.  
Deposited on : unknown  
Resolution : 2.91 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030345

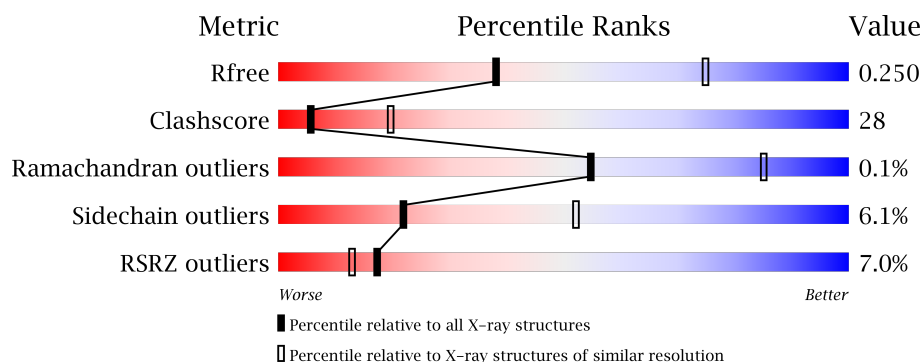
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.91 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))
$R_{free}$	100719	1813 (2.94-2.90)
Clashscore	112137	2045 (2.94-2.90)
Ramachandran outliers	110173	1997 (2.94-2.90)
Sidechain outliers	110143	1999 (2.94-2.90)
RSRZ outliers	101464	1825 (2.94-2.90)

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 on the lower 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  $\leq 5\%$ . 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	715	<div> <div>5%</div> <div> <div></div> <div>54%</div> <div>35%</div> <div>•</div> <div>8%</div> </div> </div>
1	B	715	<div> <div>5%</div> <div> <div></div> <div>53%</div> <div>37%</div> <div>•</div> <div>7%</div> </div> </div>
1	C	715	<div> <div>9%</div> <div> <div></div> <div>44%</div> <div>38%</div> <div>•</div> <div>15%</div> </div> </div>

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
2	SO4	A	701	-	-	X	-
2	SO4	B	701	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14928 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 Polyribonucleotide nucleotidyltransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	659	Total	C	N	O	S	Se	0	1	0
			5072	3189	891	973	3	16			
1	B	668	Total	C	N	O	S	Se	0	0	0
			5121	3220	892	990	3	16			
1	C	607	Total	C	N	O	S	Se	0	0	0
			4658	2930	815	895	3	15			

There are 57 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MSE	-	EXPRESSION TAG	UNP Q83D87
A	-17	HIS	-	EXPRESSION TAG	UNP Q83D87
A	-16	HIS	-	EXPRESSION TAG	UNP Q83D87
A	-15	HIS	-	EXPRESSION TAG	UNP Q83D87
A	-14	HIS	-	EXPRESSION TAG	UNP Q83D87
A	-13	HIS	-	EXPRESSION TAG	UNP Q83D87
A	-12	HIS	-	EXPRESSION TAG	UNP Q83D87
A	-11	HIS	-	EXPRESSION TAG	UNP Q83D87
A	-10	HIS	-	EXPRESSION TAG	UNP Q83D87
A	-9	HIS	-	EXPRESSION TAG	UNP Q83D87
A	-8	HIS	-	EXPRESSION TAG	UNP Q83D87
A	-7	GLU	-	EXPRESSION TAG	UNP Q83D87
A	-6	ASN	-	EXPRESSION TAG	UNP Q83D87
A	-5	LEU	-	EXPRESSION TAG	UNP Q83D87
A	-4	TYR	-	EXPRESSION TAG	UNP Q83D87
A	-3	PHE	-	EXPRESSION TAG	UNP Q83D87
A	-2	GLN	-	EXPRESSION TAG	UNP Q83D87
A	-1	SER	-	EXPRESSION TAG	UNP Q83D87
A	0	ALA	-	EXPRESSION TAG	UNP Q83D87
B	-18	MSE	-	EXPRESSION TAG	UNP Q83D87
B	-17	HIS	-	EXPRESSION TAG	UNP Q83D87
B	-16	HIS	-	EXPRESSION TAG	UNP Q83D87
B	-15	HIS	-	EXPRESSION TAG	UNP Q83D87

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	EXPRESSION TAG	UNP Q83D87
B	-13	HIS	-	EXPRESSION TAG	UNP Q83D87
B	-12	HIS	-	EXPRESSION TAG	UNP Q83D87
B	-11	HIS	-	EXPRESSION TAG	UNP Q83D87
B	-10	HIS	-	EXPRESSION TAG	UNP Q83D87
B	-9	HIS	-	EXPRESSION TAG	UNP Q83D87
B	-8	HIS	-	EXPRESSION TAG	UNP Q83D87
B	-7	GLU	-	EXPRESSION TAG	UNP Q83D87
B	-6	ASN	-	EXPRESSION TAG	UNP Q83D87
B	-5	LEU	-	EXPRESSION TAG	UNP Q83D87
B	-4	TYR	-	EXPRESSION TAG	UNP Q83D87
B	-3	PHE	-	EXPRESSION TAG	UNP Q83D87
B	-2	GLN	-	EXPRESSION TAG	UNP Q83D87
B	-1	SER	-	EXPRESSION TAG	UNP Q83D87
B	0	ALA	-	EXPRESSION TAG	UNP Q83D87
C	-18	MSE	-	EXPRESSION TAG	UNP Q83D87
C	-17	HIS	-	EXPRESSION TAG	UNP Q83D87
C	-16	HIS	-	EXPRESSION TAG	UNP Q83D87
C	-15	HIS	-	EXPRESSION TAG	UNP Q83D87
C	-14	HIS	-	EXPRESSION TAG	UNP Q83D87
C	-13	HIS	-	EXPRESSION TAG	UNP Q83D87
C	-12	HIS	-	EXPRESSION TAG	UNP Q83D87
C	-11	HIS	-	EXPRESSION TAG	UNP Q83D87
C	-10	HIS	-	EXPRESSION TAG	UNP Q83D87
C	-9	HIS	-	EXPRESSION TAG	UNP Q83D87
C	-8	HIS	-	EXPRESSION TAG	UNP Q83D87
C	-7	GLU	-	EXPRESSION TAG	UNP Q83D87
C	-6	ASN	-	EXPRESSION TAG	UNP Q83D87
C	-5	LEU	-	EXPRESSION TAG	UNP Q83D87
C	-4	TYR	-	EXPRESSION TAG	UNP Q83D87
C	-3	PHE	-	EXPRESSION TAG	UNP Q83D87
C	-2	GLN	-	EXPRESSION TAG	UNP Q83D87
C	-1	SER	-	EXPRESSION TAG	UNP Q83D87
C	0	ALA	-	EXPRESSION TAG	UNP Q83D87

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

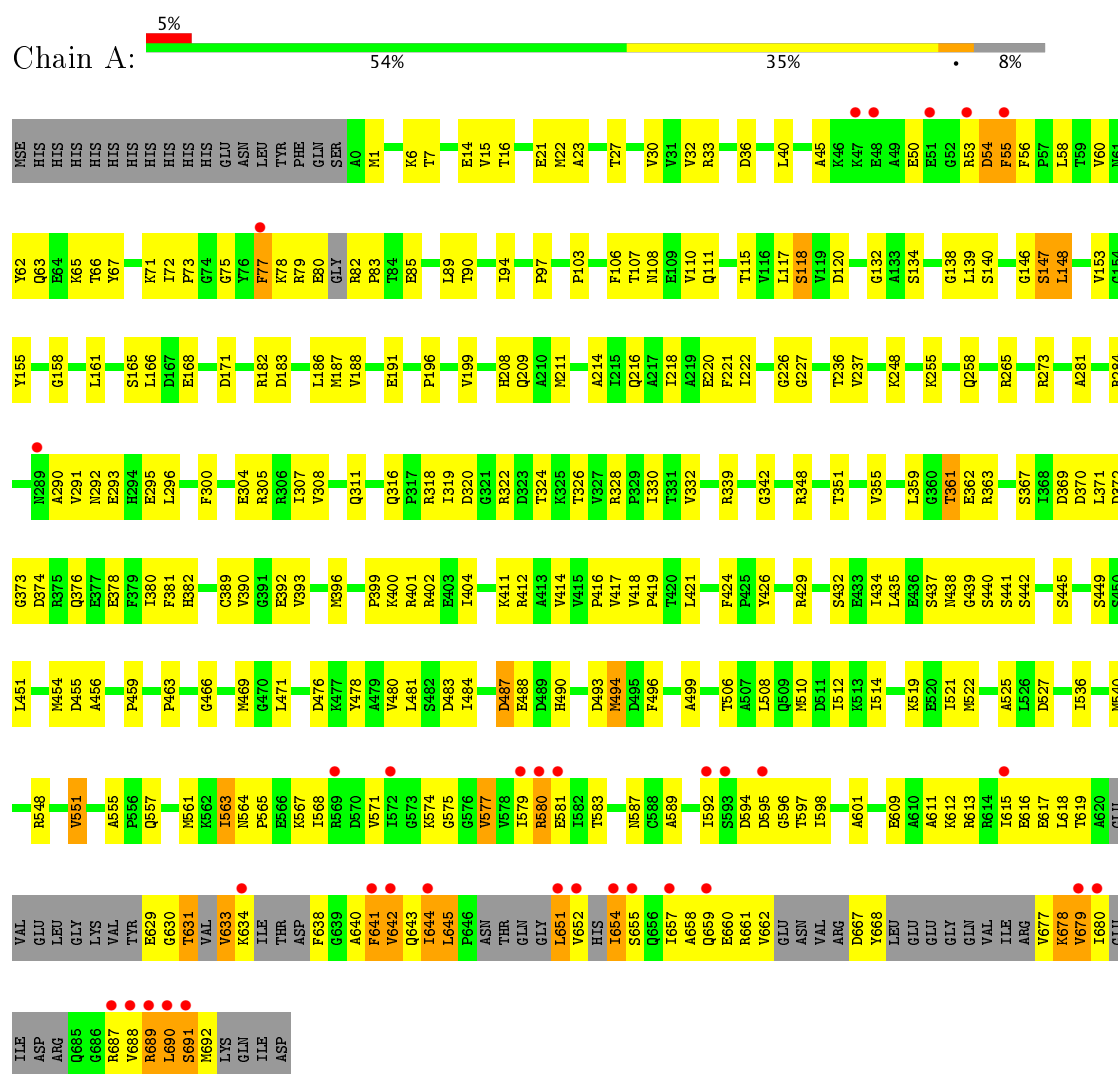
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	9	Total	O	0	0
			9	9		
3	B	3	Total	O	0	0
			3	3		

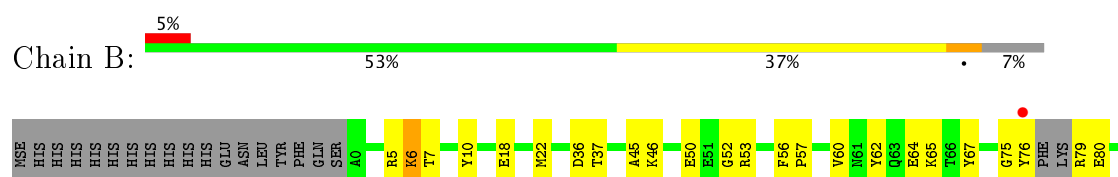
### 3 Residue-property plots

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 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: Polyrribonucleotide nucleotidyltransferase

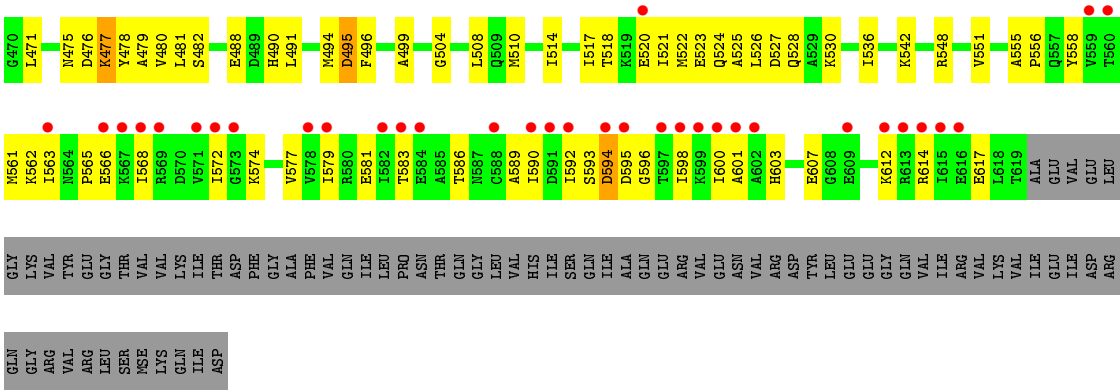


- Molecule 1: Polyrribonucleotide nucleotidyltransferase









## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	99.71Å 111.36Å 219.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.63 – 2.91 49.63 – 2.91	Depositor EDS
% Data completeness (in resolution range)	94.3 (49.63-2.91) 94.1 (49.63-2.91)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.56 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.7.1 _743	Depositor
R, $R_{free}$	0.208 , 0.260 0.200 , 0.250	Depositor DCC
$R_{free}$ test set	2580 reflections (5.07%)	DCC
Wilson B-factor (Å <sup>2</sup> )	67.7	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 64.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	14928	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.78% 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	0.29	0/5124	0.56	1/6887 (0.0%)
1	B	0.26	0/5173	0.51	0/6959
1	C	0.25	0/4714	0.48	0/6348
All	All	0.27	0/15011	0.52	1/20194 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	C	0	1
All	All	0	4

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	679	VAL	CB-CA-C	-6.76	98.56	111.40

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	437	SER	Peptide
1	A	678	LYS	Peptide
1	A	689	ARG	Peptide
1	C	235	PRO	Peptide

## 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	5072	0	5156	297	3
1	B	5121	0	5203	296	2
1	C	4658	0	4737	298	0
2	A	35	0	0	3	0
2	B	20	0	0	4	0
2	C	10	0	0	0	0
3	A	9	0	0	1	0
3	B	3	0	0	1	0
All	All	14928	0	15096	847	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 28.

All (847) 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:C:241:LEU:HD23	1:C:244:TRP:HE1	1.20	1.03
1:A:654:ILE:HG22	1:A:657:ILE:HG22	1.42	1.02
1:B:623:GLU:O	1:B:628:TYR:OH	1.75	1.01
1:A:633:VAL:HG23	1:A:642:VAL:HA	1.39	1.00
1:B:660:GLU:OE2	1:B:668:TYR:OH	1.80	0.99
1:A:658:ALA:HB1	1:A:660:GLU:HG2	1.45	0.98
1:C:260:GLN:HG2	1:C:261:GLU:H	1.28	0.98
1:A:644:ILE:HD12	1:A:645:LEU:H	1.26	0.96
1:A:660:GLU:OE2	1:A:668:TYR:OH	1.81	0.96
1:C:236:THR:O	1:C:238:ASN:ND2	1.99	0.96
1:B:88:THR:HG23	1:B:401:ARG:HG2	1.49	0.95
1:A:691:SER:OG	1:A:692:MSE:N	1.98	0.95
1:A:688:VAL:HG22	1:A:689:ARG:HE	1.30	0.94
1:B:429:ARG:NH2	1:C:80:GLU:OE1	2.01	0.94
1:A:633:VAL:CG2	1:A:642:VAL:HA	1.98	0.93
1:B:643:GLN:OE1	1:B:649:GLN:NE2	2.01	0.93
1:A:292:ASN:HD21	1:A:295:GLU:HB3	1.34	0.93
1:C:43:VAL:HG22	1:C:112:VAL:HG22	1.50	0.92
1:A:402:ARG:NH2	2:A:701:SO4:O1	2.04	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:652:VAL:HG23	1:A:690:LEU:O	1.71	0.91
1:B:566:GLU:O	1:B:569:ARG:HG2	1.70	0.90
1:A:654:ILE:CG2	1:A:657:ILE:HG22	2.01	0.90
1:A:367:SER:OG	1:A:376:GLN:NE2	2.06	0.89
1:B:255:LYS:NZ	1:B:255:LYS:HB2	1.85	0.89
1:B:481:LEU:HB2	1:B:484:ILE:HD11	1.55	0.88
1:B:625:GLY:H	1:B:626:LYS:HB2	1.38	0.86
1:A:688:VAL:CG2	1:A:689:ARG:HE	1.89	0.86
1:A:78:LYS:HE3	1:C:366:GLN:HB2	1.55	0.85
1:A:644:ILE:HG12	1:A:677:VAL:HG21	1.56	0.85
1:B:583:THR:HG22	1:B:590:ILE:HG12	1.59	0.84
1:A:71:LYS:NZ	1:A:369:ASP:OD1	2.11	0.84
1:C:260:GLN:NE2	1:C:261:GLU:OE1	2.10	0.84
1:C:521:ILE:O	1:C:524:GLN:N	2.11	0.84
1:C:251:ALA:HA	1:C:254:LYS:HE2	1.59	0.83
1:A:284:ARG:HH11	1:A:290:ALA:HB1	1.44	0.83
1:C:50:GLU:OE1	1:C:53:ARG:NH2	2.11	0.83
1:B:625:GLY:N	1:B:626:LYS:HB2	1.93	0.83
1:A:305:ARG:NH1	1:A:490:HIS:O	2.13	0.81
1:A:657:ILE:HG23	1:A:658:ALA:H	1.45	0.81
1:B:514:ILE:HG22	1:B:515:GLU:N	1.95	0.81
1:A:641:PHE:H	1:A:651:LEU:HA	1.46	0.81
1:B:625:GLY:HA3	1:B:679:VAL:HB	1.63	0.80
1:C:568:ILE:HD12	1:C:592:ILE:HG21	1.64	0.80
1:A:677:VAL:CG1	1:A:679:VAL:HG13	2.12	0.79
1:B:104:LYS:H	1:B:104:LYS:HD2	1.45	0.79
1:A:630:GLY:HA3	1:A:644:ILE:HG22	1.63	0.79
1:B:661:ARG:O	1:B:662:VAL:HG22	1.82	0.79
1:A:284:ARG:HD3	1:A:290:ALA:HB3	1.65	0.79
1:A:400:LYS:HZ3	1:A:401:ARG:HG2	1.47	0.79
1:A:399:PRO:HB2	1:A:404:ILE:HD11	1.66	0.78
1:A:661:ARG:HG2	1:A:662:VAL:N	1.96	0.78
1:B:514:ILE:HG22	1:B:515:GLU:H	1.49	0.78
1:C:283:GLU:N	1:C:283:GLU:OE1	2.16	0.78
1:C:49:ALA:HB1	1:C:107:THR:HG22	1.66	0.78
1:A:644:ILE:CD1	1:A:645:LEU:H	1.96	0.77
1:A:661:ARG:HG2	1:A:662:VAL:H	1.47	0.77
1:B:50:GLU:H	1:B:53:ARG:HH21	1.29	0.77
1:C:262:LYS:O	1:C:265:ARG:N	2.17	0.77
1:B:277:LEU:HD23	1:B:296:LEU:HD23	1.67	0.77
1:B:632:VAL:HG13	1:B:671:GLU:O	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:156:ARG:O	1:C:159:GLU:HG2	1.85	0.76
1:B:527:ASP:O	1:B:530:LYS:N	2.19	0.75
1:A:54:ASP:N	1:A:54:ASP:OD1	2.18	0.75
1:B:669:LEU:HD23	1:B:670:GLU:N	2.00	0.75
1:C:273:ARG:O	1:C:277:LEU:HB2	1.85	0.75
1:A:434:ILE:HD12	1:A:441:SER:HB2	1.68	0.75
1:B:342:GLY:HA3	1:B:456:ALA:HB2	1.67	0.75
1:B:648:THR:HG22	1:B:649:GLN:H	1.51	0.75
1:A:691:SER:HG	1:A:692:MSE:H	1.33	0.75
1:B:363:ARG:NH2	1:B:584:GLU:OE2	2.20	0.74
1:A:661:ARG:O	1:A:662:VAL:HG23	1.86	0.74
1:A:77:PHE:HE1	1:A:82:ARG:HH12	1.32	0.74
1:B:355:VAL:HG11	1:B:449:SER:HA	1.68	0.74
1:A:644:ILE:CG1	1:A:677:VAL:HG21	2.17	0.74
1:B:46:LYS:HD3	1:B:109:GLU:HG2	1.70	0.74
1:B:661:ARG:HG2	1:B:661:ARG:O	1.88	0.74
1:B:590:ILE:HG23	1:B:600:ILE:HG12	1.71	0.73
1:B:618:LEU:HD23	1:C:574:LYS:NZ	2.03	0.73
1:B:637:ASP:OD2	1:B:639:GLY:N	2.21	0.73
1:C:244:TRP:CH2	1:C:296:LEU:HD21	2.23	0.73
1:C:238:ASN:OD1	1:C:241:LEU:HD12	1.89	0.73
1:C:572:ILE:HA	1:C:579:ILE:HB	1.71	0.73
1:C:242:GLU:O	1:C:245:VAL:HG22	1.89	0.72
1:B:501:THR:HG23	1:B:503:ASN:H	1.54	0.72
1:B:630:GLY:C	1:B:673:GLN:HE22	1.91	0.72
1:C:2:ASN:HA	1:C:3:LYS:HB3	1.70	0.72
1:B:46:LYS:HD3	1:B:109:GLU:CG	2.19	0.72
1:B:481:LEU:HB2	1:B:484:ILE:CD1	2.19	0.72
1:B:551:VAL:HG12	1:B:552:SER:H	1.54	0.72
1:A:454:MSE:HE1	1:A:463:PRO:HD3	1.71	0.72
1:A:53:ARG:HG2	1:A:107:THR:HB	1.72	0.71
1:C:261:GLU:OE2	1:C:262:LYS:N	2.22	0.71
1:C:241:LEU:HD23	1:C:244:TRP:NE1	2.00	0.71
1:C:174:LEU:HD11	1:C:176:LEU:HB2	1.72	0.71
1:A:400:LYS:NZ	1:A:401:ARG:HG2	2.05	0.71
1:B:633:VAL:HG23	1:C:566:GLU:HG2	1.73	0.71
1:B:633:VAL:HG11	1:B:643:GLN:HE21	1.55	0.71
1:B:435:LEU:HD13	1:C:22:MSE:HE3	1.72	0.71
1:A:85:GLU:OE1	1:A:404:ILE:HD12	1.91	0.70
1:A:284:ARG:NH1	1:A:290:ALA:HB1	2.06	0.70
1:B:251:ALA:HB3	1:B:252:PRO:HD3	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:292:ASN:ND2	1:A:295:GLU:HB3	2.04	0.70
1:A:677:VAL:HG13	1:A:679:VAL:CG1	2.22	0.70
1:C:261:GLU:O	1:C:265:ARG:HD3	1.92	0.70
1:A:688:VAL:HG11	1:A:689:ARG:NH2	2.06	0.70
1:B:537:LEU:O	1:B:541:ASN:ND2	2.24	0.70
1:A:644:ILE:HG21	1:A:677:VAL:HG23	1.75	0.69
1:B:50:GLU:H	1:B:53:ARG:NH2	1.90	0.69
1:C:79:ARG:HG2	1:C:80:GLU:H	1.57	0.69
1:A:455:ASP:OD1	1:A:548:ARG:NH1	2.26	0.69
1:B:628:TYR:HD2	1:B:644:ILE:HB	1.57	0.69
1:C:47:LYS:HD3	1:C:47:LYS:H	1.58	0.69
1:B:390:VAL:HG12	1:B:392:GLU:HG3	1.73	0.69
1:A:644:ILE:CD1	1:A:677:VAL:HG21	2.23	0.69
1:A:690:LEU:HD12	1:A:691:SER:O	1.93	0.69
1:B:104:LYS:H	1:B:104:LYS:CD	1.98	0.69
1:B:631:THR:HA	1:B:673:GLN:OE1	1.92	0.69
1:A:361:THR:HG22	1:A:363:ARG:H	1.57	0.69
1:A:575:GLY:O	1:C:614:ARG:NH2	2.26	0.68
1:A:643:GLN:O	1:A:644:ILE:HG13	1.93	0.68
1:B:469:MSE:HE1	1:B:528:GLN:HG2	1.74	0.68
1:C:238:ASN:HB2	1:C:241:LEU:HB2	1.75	0.68
1:C:32:VAL:HG21	1:C:132:GLY:CA	2.24	0.68
1:A:284:ARG:HD3	1:A:290:ALA:CB	2.23	0.68
1:B:618:LEU:HD23	1:C:574:LYS:HZ1	1.59	0.68
1:C:262:LYS:HG3	1:C:263:THR:H	1.56	0.68
1:A:79:ARG:NH2	1:C:384:ASN:OD1	2.24	0.68
1:C:454:MSE:HE1	1:C:463:PRO:HD3	1.74	0.68
1:C:244:TRP:HH2	1:C:296:LEU:HD21	1.56	0.68
1:C:229:LYS:HG2	1:C:230:TRP:N	2.08	0.68
1:A:657:ILE:HG13	1:A:692:MSE:HE1	1.75	0.68
1:B:104:LYS:N	1:B:104:LYS:HD2	2.08	0.68
1:A:677:VAL:HG13	1:A:679:VAL:HG13	1.76	0.68
1:A:581:GLU:OE1	1:B:580:ARG:HD2	1.94	0.67
1:A:401:ARG:HG3	1:A:402:ARG:N	2.09	0.67
1:C:229:LYS:HG2	1:C:230:TRP:H	1.59	0.67
1:C:260:GLN:HG2	1:C:261:GLU:N	2.06	0.67
1:C:328:ARG:HD2	1:C:349:GLY:HA3	1.76	0.67
1:C:378:GLU:HG2	1:C:421:LEU:HD22	1.75	0.67
1:B:681:GLU:HG2	1:B:682:ILE:N	2.10	0.67
1:A:644:ILE:HD12	1:A:645:LEU:N	2.06	0.67
1:C:521:ILE:HG13	1:C:522:MSE:N	2.10	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:487:ASP:N	1:A:487:ASP:OD1	2.25	0.67
1:B:469:MSE:HB2	1:B:496:PHE:HB3	1.76	0.67
1:C:361:THR:HG22	1:C:362:GLU:N	2.09	0.67
1:A:339:ARG:NH1	2:B:701:SO4:O3	2.27	0.67
1:B:196:PRO:HG2	1:B:199:VAL:HG23	1.77	0.67
1:B:527:ASP:N	1:B:527:ASP:OD1	2.28	0.67
1:C:262:LYS:O	1:C:265:ARG:HB2	1.95	0.66
1:A:330:ILE:HD11	1:A:536:ILE:HG12	1.76	0.66
1:A:638:PHE:CE1	1:A:654:ILE:N	2.63	0.66
1:B:208:HIS:HA	1:B:211:MSE:HE3	1.77	0.66
1:B:97:PRO:HB2	1:B:148:LEU:HD23	1.77	0.66
1:A:191:GLU:HB2	1:A:412:ARG:HB2	1.78	0.66
1:C:54:ASP:OD2	1:C:294:HIS:NE2	2.24	0.66
1:C:266:GLN:O	1:C:270:GLN:HB3	1.97	0.65
1:B:514:ILE:CG2	1:B:515:GLU:H	2.09	0.65
1:C:375:ARG:HG2	1:C:376:GLN:N	2.12	0.65
1:C:64:GLU:OE2	1:C:86:LYS:HE3	1.97	0.65
1:A:581:GLU:OE2	1:B:580:ARG:NH1	2.29	0.65
1:A:609:GLU:OE2	1:A:613:ARG:NH1	2.30	0.65
1:C:517:ILE:HG23	1:C:521:ILE:HD11	1.78	0.65
1:B:571:VAL:HA	1:B:618:LEU:HD22	1.78	0.65
1:C:249:SER:O	1:C:252:PRO:HD2	1.97	0.65
1:A:688:VAL:HG21	1:A:689:ARG:HH21	1.60	0.65
1:B:668:TYR:O	1:B:669:LEU:HB2	1.96	0.64
1:C:261:GLU:CG	1:C:262:LYS:H	2.10	0.64
1:A:688:VAL:O	1:A:689:ARG:HG3	1.97	0.64
1:B:312:ILE:HD12	1:B:472:ILE:CD1	2.27	0.64
1:C:83:PRO:HA	1:C:87:GLU:OE2	1.97	0.64
1:A:50:GLU:HG2	1:A:53:ARG:NH2	2.11	0.64
1:A:661:ARG:CG	1:A:662:VAL:H	2.08	0.64
1:C:92:ARG:HG3	1:C:401:ARG:HD3	1.80	0.64
1:A:330:ILE:CD1	1:A:536:ILE:HG12	2.28	0.64
1:B:53:ARG:HD2	1:B:107:THR:HB	1.79	0.64
1:C:254:LYS:HB3	1:C:307:ILE:HD12	1.79	0.64
1:A:611:ALA:O	1:A:615:ILE:HG12	1.97	0.64
1:A:657:ILE:HG23	1:A:658:ALA:N	2.10	0.64
1:C:222:ILE:O	1:C:226:GLY:N	2.30	0.64
1:A:654:ILE:HG22	1:A:657:ILE:CG2	2.22	0.64
1:C:241:LEU:HA	1:C:244:TRP:NE1	2.13	0.64
1:A:519:LYS:HA	1:A:522:MSE:HE3	1.80	0.63
1:B:255:LYS:HB2	1:B:255:LYS:HZ3	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:350:GLU:HB2	1:B:438:ASN:HB2	1.79	0.63
1:B:677:VAL:HG11	1:B:690:LEU:HD13	1.81	0.63
1:C:106:PHE:CE1	1:C:143:PRO:HG2	2.33	0.63
1:B:514:ILE:CG2	1:B:515:GLU:N	2.62	0.63
1:B:625:GLY:CA	1:B:626:LYS:HB2	2.29	0.63
1:B:669:LEU:HD23	1:B:670:GLU:H	1.61	0.63
1:C:6:LYS:NZ	1:C:220:GLU:OE1	2.18	0.63
1:A:592:ILE:HG12	1:A:598:ILE:HG12	1.79	0.63
1:B:471:LEU:HD23	1:B:521:ILE:HG21	1.80	0.63
1:A:77:PHE:CE1	1:A:82:ARG:NH1	2.68	0.62
1:C:2:ASN:HA	1:C:3:LYS:CB	2.29	0.62
1:A:633:VAL:O	1:A:634:LYS:HB2	1.99	0.62
1:A:634:LYS:HE3	1:B:565:PRO:HD2	1.80	0.62
1:A:677:VAL:CG1	1:A:679:VAL:CG1	2.77	0.62
1:B:320:ASP:OD1	1:B:322:ARG:HD3	1.99	0.62
1:C:240:ALA:O	1:C:244:TRP:HD1	1.81	0.62
1:B:312:ILE:HD13	1:B:481:LEU:HD21	1.81	0.62
1:B:310:GLU:O	1:B:314:THR:HG23	1.99	0.62
1:B:558:TYR:HA	1:B:600:ILE:O	1.99	0.62
1:A:581:GLU:HB2	1:B:577:VAL:HG12	1.80	0.62
1:C:32:VAL:HG21	1:C:132:GLY:HA3	1.82	0.62
1:B:667:ASP:O	1:B:668:TYR:HB2	2.00	0.62
1:B:653:HIS:ND1	1:B:655:SER:OG	2.33	0.62
1:C:309:ARG:NH1	1:C:491:LEU:O	2.33	0.62
1:B:97:PRO:HB2	1:B:148:LEU:CD2	2.30	0.62
1:B:570:ASP:HB3	1:C:574:LYS:HZ1	1.64	0.62
1:C:92:ARG:HH11	1:C:401:ARG:HG2	1.64	0.62
1:B:565:PRO:HG3	1:B:595:ASP:HB2	1.82	0.61
1:C:342:GLY:HA3	1:C:456:ALA:HB2	1.80	0.61
1:A:378:GLU:HG2	1:A:421:LEU:HD22	1.80	0.61
1:C:244:TRP:CH2	1:C:245:VAL:HG12	2.35	0.61
1:C:47:LYS:HG2	1:C:48:GLU:H	1.64	0.61
1:A:563:ILE:HG22	1:A:596:GLY:O	2.00	0.61
1:A:652:VAL:CG2	1:A:690:LEU:HD13	2.31	0.61
1:C:443:MSE:HE2	1:C:443:MSE:HA	1.82	0.61
1:C:45:ALA:HB2	1:C:142:ILE:CD1	2.30	0.61
1:A:106:PHE:CZ	1:A:108:ASN:HB2	2.36	0.61
1:A:371:LEU:O	1:A:372:ASP:CG	2.39	0.61
1:C:583:THR:HG22	1:C:590:ILE:HG13	1.83	0.61
1:C:245:VAL:HG11	1:C:299:ILE:CD1	2.30	0.60
1:B:633:VAL:CG2	1:C:566:GLU:HG2	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:614:ARG:NH1	1:C:617:GLU:OE2	2.34	0.60
1:B:218:ILE:O	1:B:222:ILE:HG13	2.02	0.60
1:B:628:TYR:CD2	1:B:644:ILE:HB	2.37	0.60
1:A:651:LEU:HG	1:A:688:VAL:O	2.01	0.60
1:B:45:ALA:HB2	1:B:142:ILE:HD11	1.82	0.60
1:A:658:ALA:CB	1:A:660:GLU:HG2	2.26	0.60
1:B:630:GLY:C	1:B:673:GLN:NE2	2.55	0.60
1:B:659:GLN:O	1:B:660:GLU:HB3	2.01	0.60
1:C:245:VAL:HG11	1:C:299:ILE:HD11	1.83	0.60
1:B:60:VAL:HG22	1:B:112:VAL:HB	1.84	0.60
1:B:191:GLU:HB3	1:B:412:ARG:HB2	1.84	0.60
1:C:250:GLU:HG3	1:C:251:ALA:H	1.65	0.60
1:C:400:LYS:HG3	1:C:401:ARG:H	1.65	0.60
1:A:401:ARG:HG3	1:A:402:ARG:H	1.65	0.60
1:B:552:SER:OG	1:B:554:LEU:HD12	2.01	0.60
1:B:134:SER:HB2	1:B:148:LEU:CD1	2.32	0.60
1:C:65:LYS:HA	1:C:80:GLU:OE2	2.02	0.60
1:A:292:ASN:OD1	1:A:293:GLU:N	2.35	0.60
1:B:607:GLU:O	1:B:610:ALA:N	2.35	0.59
1:C:298:VAL:O	1:C:301:HIS:N	2.35	0.59
1:A:644:ILE:HD12	1:A:645:LEU:HB3	1.82	0.59
1:A:78:LYS:O	1:C:382:HIS:HE1	1.86	0.59
1:B:564:ASN:HB3	1:B:567:LYS:HE2	1.84	0.59
1:A:30:VAL:HG22	1:A:139:LEU:HD12	1.83	0.59
1:B:371:LEU:O	1:B:372:ASP:HB2	2.02	0.59
1:A:644:ILE:HG12	1:A:677:VAL:CG2	2.29	0.59
1:A:494:MSE:HE3	1:A:496:PHE:CE1	2.38	0.59
1:C:522:MSE:O	1:C:526:LEU:HG	2.03	0.59
1:C:134:SER:HB2	1:C:148:LEU:HD12	1.84	0.59
1:A:77:PHE:HE1	1:A:82:ARG:NH1	1.98	0.58
1:A:165:SER:OG	1:A:168:GLU:HG3	2.03	0.58
1:A:643:GLN:C	1:A:644:ILE:HG13	2.24	0.58
1:B:355:VAL:HG11	1:B:449:SER:CA	2.33	0.58
1:C:242:GLU:N	1:C:242:GLU:OE1	2.36	0.58
1:B:607:GLU:HA	1:B:610:ALA:HB3	1.85	0.58
1:C:36:ASP:HB2	1:C:120:ASP:HB2	1.85	0.58
1:B:245:VAL:HG13	1:B:276:LEU:HD11	1.86	0.58
1:C:251:ALA:HB3	1:C:252:PRO:HD3	1.85	0.58
1:A:393:VAL:HG13	1:B:111:GLN:HB2	1.85	0.58
1:C:241:LEU:HA	1:C:244:TRP:HE1	1.67	0.58
1:C:272:ILE:HG22	1:C:276:LEU:HD22	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:261:GLU:CD	1:C:262:LYS:H	2.06	0.58
1:C:614:ARG:O	1:C:617:GLU:HG2	2.04	0.58
1:A:563:ILE:HD11	1:A:619:THR:HG21	1.86	0.58
1:B:673:GLN:OE1	1:B:673:GLN:HA	2.02	0.58
1:B:364:ASP:HB3	1:C:72:ILE:HD12	1.86	0.57
1:A:565:PRO:HA	1:A:568:ILE:HG13	1.85	0.57
1:C:269:ILE:HG13	1:C:270:GLN:H	1.70	0.57
1:B:669:LEU:CD2	1:B:672:GLY:O	2.52	0.57
1:B:554:LEU:H	1:B:554:LEU:HD12	1.69	0.57
1:C:148:LEU:HD23	1:C:186:LEU:HD12	1.86	0.57
1:C:262:LYS:HG3	1:C:263:THR:N	2.19	0.57
1:C:56:PHE:CE2	1:C:58:LEU:HB2	2.39	0.57
1:A:281:ALA:HA	1:A:291:VAL:HG21	1.87	0.57
1:A:273[A]:ARG:HG3	1:A:300:PHE:CE2	2.40	0.57
1:A:389:CYS:HA	1:A:435:LEU:O	2.05	0.57
1:A:22:MSE:CE	1:A:40:LEU:HD22	2.35	0.57
1:C:568:ILE:HD12	1:C:592:ILE:CG2	2.34	0.57
1:A:332:VAL:HG13	1:A:451:LEU:HD13	1.86	0.57
1:A:630:GLY:HA3	1:A:644:ILE:CG2	2.35	0.57
1:B:438:ASN:O	1:B:486:GLY:N	2.32	0.57
1:C:261:GLU:CG	1:C:262:LYS:N	2.68	0.56
1:A:631:THR:C	1:A:642:VAL:HG22	2.25	0.56
1:B:648:THR:HG22	1:B:649:GLN:N	2.19	0.56
1:A:23:ALA:O	3:A:804:HOH:O	2.18	0.56
1:A:629:GLU:N	1:A:677:VAL:N	2.53	0.56
1:B:182:ARG:HG3	1:B:183:ASP:N	2.20	0.56
1:C:257:TYR:OH	1:C:304:GLU:OE2	2.22	0.56
1:C:558:TYR:HA	1:C:600:ILE:O	2.05	0.56
1:A:75:GLY:O	1:A:78:LYS:HA	2.04	0.56
1:B:255:LYS:O	1:B:258:GLN:N	2.30	0.56
1:B:564:ASN:O	1:B:567:LYS:N	2.39	0.56
1:B:660:GLU:O	1:B:661:ARG:HB3	2.04	0.56
1:A:148:LEU:H	1:A:148:LEU:HD12	1.71	0.56
1:A:390:VAL:HG23	1:A:392:GLU:HG2	1.87	0.56
1:B:607:GLU:O	1:B:611:ALA:N	2.39	0.56
1:B:625:GLY:CA	1:B:679:VAL:HB	2.34	0.56
1:C:194:GLU:C	1:C:504:GLY:HA3	2.25	0.56
1:A:551:VAL:CG1	1:A:555:ALA:HB3	2.36	0.56
1:B:420:THR:HG22	1:B:423:LYS:HG3	1.86	0.56
1:C:518:THR:O	1:C:521:ILE:HG12	2.06	0.56
1:A:688:VAL:HG22	1:A:688:VAL:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:165:SER:OG	1:C:168:GLU:HG3	2.04	0.56
1:C:419:PRO:HG3	1:C:459:PRO:O	2.06	0.56
1:B:79:ARG:HG2	1:B:80:GLU:H	1.71	0.55
1:A:638:PHE:CZ	1:A:654:ILE:N	2.74	0.55
1:B:363:ARG:HH22	1:B:584:GLU:CD	2.07	0.55
1:C:53:ARG:HG2	1:C:53:ARG:HH11	1.70	0.55
1:C:375:ARG:HB3	1:C:375:ARG:HH11	1.70	0.55
1:C:562:LYS:HE2	1:C:596:GLY:HA2	1.87	0.55
1:B:623:GLU:HB2	1:B:624:LEU:HG	1.89	0.55
1:B:680:ILE:HD13	1:B:691:SER:HB2	1.88	0.55
1:A:30:VAL:HG22	1:A:139:LEU:CD1	2.36	0.55
1:B:79:ARG:NH2	3:B:802:HOH:O	2.11	0.55
1:C:514:ILE:HD11	1:C:517:ILE:HD11	1.89	0.55
1:B:669:LEU:HD22	1:B:672:GLY:O	2.06	0.55
1:C:293:GLU:C	1:C:295:GLU:H	2.09	0.55
1:B:642:VAL:HG22	1:B:690:LEU:CD1	2.36	0.54
1:C:250:GLU:HG3	1:C:251:ALA:N	2.21	0.54
1:C:318:ARG:NH2	1:C:488:GLU:OE1	2.33	0.54
1:A:382:HIS:CE1	1:A:429:ARG:HE	2.25	0.54
1:B:368:ILE:C	1:B:368:ILE:HD12	2.28	0.54
1:C:361:THR:CG2	1:C:362:GLU:N	2.71	0.54
1:C:97:PRO:HB2	1:C:148:LEU:HD21	1.88	0.54
1:A:78:LYS:HE3	1:C:366:GLN:CB	2.35	0.54
1:C:561:MSE:HB3	1:C:612:LYS:HE2	1.88	0.54
1:A:536:ILE:O	1:A:540:MSE:HG2	2.08	0.54
1:A:640:ALA:O	1:A:641:PHE:CD1	2.60	0.54
1:B:605:THR:O	1:B:609:GLU:HG3	2.08	0.54
1:C:305:ARG:NH1	1:C:490:HIS:O	2.41	0.54
1:A:644:ILE:CG1	1:A:645:LEU:H	2.20	0.54
1:A:638:PHE:HE1	1:A:654:ILE:N	2.04	0.54
1:A:633:VAL:N	1:A:641:PHE:O	2.41	0.54
1:B:636:THR:O	1:B:637:ASP:HB2	2.06	0.54
1:C:41:VAL:HG11	1:C:133:ALA:HA	1.89	0.54
1:C:189:GLU:OE2	1:C:412:ARG:NH1	2.41	0.54
1:C:565:PRO:O	1:C:568:ILE:HG12	2.06	0.54
1:B:632:VAL:HA	1:B:642:VAL:HA	1.90	0.54
1:C:527:ASP:O	1:C:530:LYS:N	2.40	0.54
1:A:657:ILE:CG2	1:A:658:ALA:H	2.19	0.54
1:C:207:GLY:O	1:C:211:MSE:HB2	2.08	0.54
1:A:400:LYS:O	1:A:404:ILE:HG12	2.08	0.54
1:A:22:MSE:HE2	1:A:40:LEU:HD22	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:356:VAL:HG11	1:C:67:TYR:CD1	2.43	0.54
1:B:88:THR:CG2	1:B:401:ARG:HG2	2.30	0.54
1:C:245:VAL:HG23	1:C:246:VAL:N	2.23	0.54
1:C:190:SER:OG	1:C:508:LEU:HB3	2.08	0.54
1:C:592:ILE:HG22	1:C:593:SER:O	2.08	0.54
1:A:577:VAL:HG23	1:B:577:VAL:HG11	1.89	0.53
1:B:237:VAL:HG13	1:B:299:ILE:HD11	1.89	0.53
1:A:440:SER:HA	2:A:701:SO4:O2	2.07	0.53
1:A:691:SER:HG	1:A:692:MSE:N	1.98	0.53
1:C:245:VAL:O	1:C:249:SER:N	2.40	0.53
1:A:348:ARG:HH11	1:A:348:ARG:HG2	1.73	0.53
1:B:102:PHE:HE1	1:B:142:ILE:HG21	1.73	0.53
1:B:421:LEU:HG	1:B:422:ASP:H	1.73	0.53
1:C:244:TRP:CZ3	1:C:245:VAL:HG12	2.43	0.53
1:C:614:ARG:CZ	1:C:617:GLU:OE2	2.57	0.53
1:B:545:ASP:OD1	1:B:546:LYS:HG3	2.08	0.53
1:C:406:HIS:CD2	1:C:442:SER:HB3	2.44	0.53
1:C:454:MSE:O	1:C:548:ARG:HG3	2.09	0.53
1:B:79:ARG:HG2	1:B:80:GLU:N	2.24	0.53
1:A:471:LEU:HD12	1:A:480:VAL:HG22	1.91	0.53
1:B:561:MSE:HG3	1:B:598:ILE:HD12	1.91	0.53
1:B:671:GLU:C	1:C:595:ASP:OD2	2.47	0.53
1:A:182:ARG:NH1	1:A:183:ASP:OD1	2.41	0.52
1:B:440:SER:N	2:B:703:SO4:O4	2.40	0.52
1:C:471:LEU:HD12	1:C:479:ALA:O	2.09	0.52
1:A:688:VAL:CG2	1:A:688:VAL:O	2.57	0.52
1:A:82:ARG:O	1:A:83:PRO:C	2.48	0.52
1:B:471:LEU:CD1	1:B:493:ASP:HB2	2.39	0.52
1:B:682:ILE:O	1:B:683:ASP:C	2.46	0.52
1:C:53:ARG:NH1	1:C:57:PRO:HG2	2.24	0.52
1:B:62:TYR:CD2	1:B:90:THR:HB	2.44	0.52
1:A:454:MSE:HE1	1:A:463:PRO:CD	2.39	0.52
1:B:572:ILE:HD13	1:B:579:ILE:HD12	1.90	0.52
1:C:79:ARG:HG2	1:C:80:GLU:N	2.23	0.52
1:A:66:THR:HG23	1:A:80:GLU:CG	2.40	0.52
1:B:292:ASN:O	1:B:296:LEU:N	2.35	0.52
1:B:371:LEU:O	1:B:372:ASP:CB	2.58	0.52
1:B:484:ILE:HG23	1:B:488:GLU:HB2	1.92	0.52
1:A:382:HIS:CE1	1:B:79:ARG:HB2	2.45	0.52
1:B:630:GLY:HA3	1:B:643:GLN:O	2.10	0.52
1:A:27:THR:O	1:A:140:SER:HA	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:350:GLU:HB2	1:B:438:ASN:CB	2.39	0.52
1:B:551:VAL:HG12	1:B:552:SER:N	2.24	0.52
1:B:565:PRO:O	1:B:568:ILE:HG22	2.10	0.52
1:A:1:MSE:CE	1:A:21:GLU:HG3	2.39	0.52
1:C:521:ILE:HG13	1:C:522:MSE:H	1.73	0.52
1:A:139:LEU:HD23	1:A:226:GLY:HA2	1.91	0.52
1:A:32:VAL:HG21	1:A:132:GLY:CA	2.40	0.52
1:A:97:PRO:HB2	1:A:148:LEU:HD23	1.92	0.52
1:A:118:SER:HB2	1:C:339:ARG:HB2	1.91	0.51
1:A:642:VAL:CG1	1:A:644:ILE:HG23	2.40	0.51
1:B:630:GLY:CA	1:B:673:GLN:HE22	2.22	0.51
1:A:322:ARG:NH2	1:A:483:ASP:O	2.32	0.51
1:A:496:PHE:CZ	1:A:525:ALA:HB1	2.45	0.51
1:A:551:VAL:HG13	1:A:555:ALA:HB3	1.93	0.51
1:C:400:LYS:HG3	1:C:401:ARG:N	2.25	0.51
1:A:311:GLN:HB3	1:A:316:GLN:HG3	1.92	0.51
1:A:471:LEU:HB3	1:A:494:MSE:HG2	1.92	0.51
1:B:341:HIS:CE1	1:B:359:LEU:H	2.29	0.51
1:B:45:ALA:HB2	1:B:110:VAL:HG22	1.90	0.51
1:B:480:VAL:O	1:B:528:GLN:NE2	2.41	0.51
1:C:332:VAL:HG13	1:C:451:LEU:HD13	1.92	0.51
1:A:56:PHE:CE2	1:A:58:LEU:HB2	2.45	0.51
1:B:578:VAL:O	1:B:582:ILE:HG13	2.11	0.51
1:A:320:ASP:OD2	1:A:322:ARG:HD3	2.09	0.51
1:A:75:GLY:O	1:A:78:LYS:N	2.43	0.51
1:A:103:PRO:HA	2:A:705:SO4:O1	2.11	0.51
1:C:390:VAL:HG12	1:C:390:VAL:O	2.11	0.51
1:C:558:TYR:CE2	1:C:601:ALA:HB2	2.46	0.51
1:C:99:ARG:N	1:C:100:PRO:HD2	2.26	0.51
1:B:467:ILE:HG13	1:B:468:ALA:N	2.26	0.51
1:B:650:GLY:HA2	1:B:688:VAL:HG13	1.92	0.51
1:B:659:GLN:O	1:B:660:GLU:CB	2.59	0.51
1:C:38:VAL:HG23	1:C:118:SER:HB3	1.92	0.51
1:C:466:GLY:HA2	1:C:499:ALA:HA	1.93	0.51
1:B:570:ASP:HB3	1:C:574:LYS:NZ	2.25	0.51
1:A:265:ARG:CZ	1:A:319:ILE:HD11	2.41	0.51
1:A:307:ILE:O	1:A:311:GLN:HG3	2.10	0.51
1:B:625:GLY:N	1:B:626:LYS:CB	2.69	0.51
1:C:260:GLN:CG	1:C:261:GLU:H	2.09	0.51
1:C:268:GLN:O	1:C:271:ALA:HB3	2.11	0.51
1:C:328:ARG:O	1:C:330:ILE:HG13	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:154:GLY:HA2	1:B:174:LEU:O	2.11	0.50
1:B:571:VAL:O	1:B:578:VAL:HG23	2.10	0.50
1:B:612:LYS:O	1:B:615:ILE:N	2.42	0.50
1:B:628:TYR:N	1:B:628:TYR:CD1	2.78	0.50
1:A:677:VAL:HG13	1:A:679:VAL:HG12	1.92	0.50
1:C:240:ALA:O	1:C:244:TRP:CD1	2.63	0.50
1:C:415:VAL:N	1:C:416:PRO:HD2	2.27	0.50
1:A:22:MSE:HE3	1:C:435:LEU:CD1	2.41	0.50
1:B:485:LEU:HD12	1:B:487:ASP:H	1.77	0.50
1:C:261:GLU:HG2	1:C:262:LYS:H	1.76	0.50
1:C:272:ILE:CG2	1:C:276:LEU:HD22	2.42	0.50
1:C:520:GLU:OE2	1:C:524:GLN:NE2	2.44	0.50
1:A:255:LYS:HA	1:A:258:GLN:HG3	1.93	0.50
1:C:194:GLU:O	1:C:504:GLY:HA3	2.12	0.50
1:C:106:PHE:CZ	1:C:108:ASN:HB2	2.46	0.50
1:A:642:VAL:HG13	1:A:644:ILE:HG23	1.93	0.49
1:B:380:ILE:HD11	1:B:429:ARG:HG3	1.92	0.49
1:B:564:ASN:CB	1:B:567:LYS:HE2	2.42	0.49
1:B:570:ASP:O	1:B:573:GLY:N	2.45	0.49
1:C:586:THR:O	1:C:607:GLU:HG2	2.12	0.49
1:B:667:ASP:CG	1:B:668:TYR:N	2.65	0.49
1:C:15:VAL:HG22	1:C:34:MSE:HG3	1.92	0.49
1:C:496:PHE:CZ	1:C:525:ALA:HB1	2.47	0.49
1:C:54:ASP:O	1:C:55:PHE:HB3	2.13	0.49
1:C:97:PRO:HB2	1:C:148:LEU:CD2	2.41	0.49
1:A:1:MSE:HE3	1:A:21:GLU:HA	1.93	0.49
1:B:312:ILE:HG21	1:B:481:LEU:HD21	1.94	0.49
1:C:521:ILE:CG1	1:C:522:MSE:N	2.75	0.49
1:A:378:GLU:HG2	1:A:421:LEU:CD2	2.42	0.49
1:A:494:MSE:HE3	1:A:496:PHE:CD1	2.48	0.49
1:B:435:LEU:CD1	1:C:22:MSE:HE3	2.41	0.49
1:C:411:LYS:O	1:C:415:VAL:HG23	2.13	0.49
1:C:469:MSE:HB2	1:C:496:PHE:CZ	2.48	0.49
1:A:633:VAL:HG22	1:A:642:VAL:HG23	1.94	0.49
1:B:380:ILE:HD13	1:B:382:HIS:CE1	2.48	0.49
1:C:361:THR:CG2	1:C:362:GLU:H	2.26	0.49
1:A:401:ARG:CG	1:A:402:ARG:N	2.75	0.49
1:A:563:ILE:HG23	1:A:564:ASN:N	2.28	0.49
1:A:589:ALA:HB3	1:A:601:ALA:HB3	1.93	0.49
1:A:401:ARG:CG	1:A:402:ARG:H	2.25	0.49
1:A:679:VAL:HG23	1:A:679:VAL:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:194:GLU:OE2	1:B:501:THR:HG21	2.13	0.49
1:B:623:GLU:OE1	1:B:623:GLU:N	2.46	0.49
1:B:96:ARG:HB2	1:B:97:PRO:HD3	1.93	0.49
1:B:312:ILE:HD12	1:B:472:ILE:HD13	1.94	0.49
1:B:657:ILE:O	1:B:658:ALA:C	2.51	0.49
1:A:36:ASP:O	1:A:118:SER:OG	2.30	0.49
1:A:634:LYS:HE3	1:B:565:PRO:CD	2.42	0.49
1:B:604:THR:OG1	1:B:606:GLU:N	2.45	0.49
1:C:266:GLN:HA	1:C:269:ILE:CG1	2.43	0.49
1:C:269:ILE:HD12	1:C:270:GLN:N	2.27	0.49
1:C:282:ALA:HB3	1:C:283:GLU:OE1	2.13	0.49
1:A:208:HIS:HA	1:A:211:MSE:HE3	1.94	0.48
1:B:360:GLY:HA2	1:B:556:PRO:HG2	1.94	0.48
1:B:92:ARG:HH21	1:B:402:ARG:CD	2.26	0.48
1:C:3:LYS:HE3	1:C:18:GLU:OE1	2.13	0.48
1:B:380:ILE:HD11	1:B:429:ARG:HD2	1.95	0.48
1:A:138:GLY:HA3	1:A:222:ILE:HD13	1.95	0.48
1:A:680:ILE:C	1:A:680:ILE:HD12	2.33	0.48
1:C:378:GLU:HG2	1:C:421:LEU:CD2	2.42	0.48
1:A:633:VAL:N	1:A:640:ALA:O	2.46	0.48
1:B:381:PHE:HB3	1:B:411:LYS:HB2	1.93	0.48
1:C:252:PRO:HB2	1:C:272:ILE:HD12	1.95	0.48
1:C:361:THR:HG22	1:C:362:GLU:H	1.76	0.48
1:C:562:LYS:NZ	1:C:563:ILE:O	2.43	0.48
1:C:330:ILE:CD1	1:C:536:ILE:HG12	2.44	0.48
1:A:148:LEU:HD13	1:A:148:LEU:O	2.13	0.48
1:C:32:VAL:HG21	1:C:132:GLY:HA2	1.96	0.48
1:B:434:ILE:HD12	1:B:441:SER:HB2	1.95	0.48
1:B:662:VAL:HA	1:B:668:TYR:HE2	1.78	0.48
1:C:8:PHE:CE1	1:C:15:VAL:HB	2.49	0.48
1:C:328:ARG:HH22	1:C:439:GLY:HA3	1.79	0.48
1:A:6:LYS:O	1:A:16:THR:HA	2.13	0.48
1:A:374:ASP:OD1	1:A:374:ASP:O	2.32	0.48
1:B:648:THR:HG22	1:B:649:GLN:OE1	2.13	0.48
1:A:381:PHE:HB3	1:A:411:LYS:HD2	1.96	0.48
1:C:563:ILE:HD11	1:C:568:ILE:HD13	1.96	0.48
1:A:414:VAL:O	1:A:417:VAL:HG22	2.14	0.47
1:B:316:GLN:HB3	1:B:317:PRO:HD2	1.95	0.47
1:B:519:LYS:O	1:B:523:GLU:N	2.40	0.47
1:C:229:LYS:CG	1:C:230:TRP:N	2.77	0.47
1:A:236:THR:HG22	1:A:237:VAL:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:ARG:HH22	1:A:439:GLY:HA3	1.78	0.47
1:B:467:ILE:HG12	1:B:469:MSE:SE	2.64	0.47
1:B:573:GLY:HA3	1:B:578:VAL:HG22	1.95	0.47
1:B:681:GLU:HG2	1:B:682:ILE:H	1.77	0.47
1:B:75:GLY:C	1:B:76:TYR:HD1	2.17	0.47
1:C:140:SER:HB2	1:C:142:ILE:HG13	1.97	0.47
1:C:143:PRO:HA	1:C:229:LYS:HE3	1.95	0.47
1:B:628:TYR:HD1	1:B:628:TYR:N	2.12	0.47
1:B:631:THR:HA	1:B:673:GLN:CD	2.35	0.47
1:C:191:GLU:HB2	1:C:412:ARG:HB2	1.97	0.47
1:C:53:ARG:HG2	1:C:53:ARG:NH1	2.29	0.47
1:A:466:GLY:HA2	1:A:499:ALA:HA	1.97	0.47
1:B:323:ASP:OD1	1:B:323:ASP:N	2.48	0.47
1:B:471:LEU:CD2	1:B:521:ILE:HG21	2.44	0.47
1:A:36:ASP:HB2	1:A:120:ASP:HB2	1.97	0.47
1:A:89:LEU:HG	1:A:404:ILE:HG22	1.96	0.47
1:A:342:GLY:HA3	1:A:456:ALA:HB2	1.97	0.47
1:A:630:GLY:CA	1:A:644:ILE:HG22	2.40	0.47
1:A:644:ILE:CG1	1:A:645:LEU:N	2.78	0.47
1:B:581:GLU:CB	1:C:577:VAL:HG12	2.44	0.47
1:C:406:HIS:HD2	1:C:442:SER:HB3	1.79	0.47
1:A:72:ILE:HG23	1:C:429:ARG:HD2	1.97	0.47
1:C:480:VAL:O	1:C:528:GLN:NE2	2.43	0.47
1:A:32:VAL:HG21	1:A:132:GLY:HA3	1.97	0.47
1:A:594:ASP:O	1:A:595:ASP:OD1	2.33	0.47
1:B:327:VAL:HG12	1:B:328:ARG:O	2.15	0.47
1:C:382:HIS:HB2	1:C:431:VAL:HG22	1.96	0.47
1:C:417:VAL:HG21	1:C:464:VAL:CG2	2.45	0.47
1:A:292:ASN:O	1:A:293:GLU:HB3	2.15	0.47
1:A:633:VAL:HG22	1:A:642:VAL:HA	1.94	0.47
1:B:383:TYR:CD1	1:B:383:TYR:C	2.88	0.47
1:C:45:ALA:HB2	1:C:142:ILE:HD11	1.96	0.47
1:C:92:ARG:HG3	1:C:401:ARG:CD	2.44	0.47
1:B:469:MSE:O	1:B:496:PHE:N	2.44	0.47
1:C:261:GLU:HG2	1:C:262:LYS:N	2.30	0.47
1:A:153:VAL:HA	1:A:161:LEU:O	2.15	0.46
1:C:3:LYS:HD3	1:C:21:GLU:HB2	1.97	0.46
1:C:595:ASP:OD1	1:C:595:ASP:O	2.32	0.46
1:C:592:ILE:HG13	1:C:598:ILE:HG12	1.96	0.46
1:A:146:GLY:HA3	1:A:147:SER:HA	1.73	0.46
1:A:328:ARG:HH22	1:A:439:GLY:CA	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:30:VAL:HG23	1:C:136:ALA:HA	1.96	0.46
1:C:57:PRO:HB2	1:C:109:GLU:HG3	1.96	0.46
1:A:631:THR:O	1:A:644:ILE:N	2.45	0.46
1:A:678:LYS:NZ	1:A:692:MSE:O	2.46	0.46
1:A:688:VAL:HG11	1:A:689:ARG:CZ	2.45	0.46
1:A:134:SER:HB3	1:A:218:ILE:HD13	1.97	0.46
1:A:594:ASP:C	1:A:595:ASP:OD1	2.53	0.46
1:B:421:LEU:HG	1:B:422:ASP:N	2.31	0.46
1:B:572:ILE:O	1:B:576:GLY:HA2	2.15	0.46
1:B:633:VAL:CG2	1:B:634:LYS:N	2.78	0.46
1:B:248:LYS:HD2	1:B:276:LEU:HD23	1.97	0.46
1:B:660:GLU:HG2	1:B:660:GLU:O	2.16	0.46
1:B:661:ARG:O	1:B:662:VAL:CG2	2.61	0.46
1:B:93:LEU:HD11	1:B:187:MSE:HE1	1.98	0.46
1:C:274:ASP:O	1:C:277:LEU:N	2.48	0.46
1:A:351:THR:OG1	1:A:439:GLY:HA3	2.15	0.46
1:A:574:LYS:O	1:A:577:VAL:HG13	2.16	0.46
1:A:633:VAL:O	1:A:634:LYS:CB	2.63	0.46
1:A:435:LEU:HD11	1:B:22:MSE:HE3	1.97	0.46
1:C:238:ASN:O	1:C:242:GLU:OE1	2.33	0.46
1:B:396:MSE:HE2	1:C:63:GLN:OE1	2.16	0.46
1:A:304:GLU:O	1:A:308:VAL:HG23	2.16	0.46
1:C:318:ARG:HH21	1:C:488:GLU:CD	2.18	0.46
1:A:609:GLU:OE2	1:A:613:ARG:CZ	2.63	0.46
1:C:245:VAL:O	1:C:249:SER:HB2	2.15	0.46
1:C:316:GLN:HB3	1:C:317:PRO:HD2	1.98	0.46
1:A:139:LEU:HD11	1:A:221:PHE:HE2	1.80	0.46
1:B:519:LYS:O	1:B:523:GLU:HB2	2.16	0.46
1:C:82:ARG:O	1:C:83:PRO:C	2.52	0.46
1:A:248:LYS:HD3	1:A:248:LYS:HA	1.77	0.46
1:B:365:ALA:HB2	1:B:427:VAL:HG21	1.97	0.46
1:B:191:GLU:HB3	1:B:412:ARG:HD2	1.97	0.46
1:B:655:SER:HG	1:B:655:SER:H	1.51	0.46
1:B:677:VAL:HG13	1:B:690:LEU:HB3	1.98	0.46
1:C:469:MSE:HB2	1:C:496:PHE:CE1	2.51	0.46
1:A:27:THR:HG22	1:A:140:SER:HB2	1.98	0.45
1:A:273[A]:ARG:HG3	1:A:300:PHE:CZ	2.51	0.45
1:A:281:ALA:HA	1:A:291:VAL:CG2	2.46	0.45
1:A:6:LYS:HB2	1:A:221:PHE:HD1	1.80	0.45
1:B:244:TRP:CZ3	1:B:276:LEU:HD22	2.51	0.45
1:B:590:ILE:CD1	1:B:600:ILE:HG23	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:366:GLN:HG3	1:C:78:LYS:HG2	1.98	0.45
1:A:400:LYS:HG3	1:A:401:ARG:N	2.31	0.45
1:B:37:THR:HA	1:B:118:SER:O	2.17	0.45
1:B:62:TYR:OH	1:B:64:GLU:OE2	2.32	0.45
1:A:372:ASP:OD1	1:A:372:ASP:O	2.33	0.45
1:B:434:ILE:CD1	1:B:441:SER:HB2	2.46	0.45
1:B:550:GLN:NE2	2:B:702:SO4:O3	2.49	0.45
1:C:127:ILE:N	1:C:128:PRO:HD2	2.31	0.45
1:C:303:LEU:HA	1:C:306:ARG:HD2	1.97	0.45
1:B:57:PRO:HB2	1:B:109:GLU:CB	2.47	0.45
1:B:312:ILE:HD13	1:B:481:LEU:CD2	2.46	0.45
1:B:92:ARG:HH21	1:B:402:ARG:HD2	1.81	0.45
1:C:471:LEU:HD11	1:C:478:TYR:HB2	1.99	0.45
1:A:273[A]:ARG:CG	1:A:300:PHE:CE2	3.00	0.45
1:A:644:ILE:HD12	1:A:645:LEU:CB	2.46	0.45
1:A:72:ILE:HG23	1:A:73:PRO:HD2	1.99	0.45
1:B:681:GLU:CG	1:B:682:ILE:N	2.79	0.45
1:C:229:LYS:CG	1:C:230:TRP:H	2.28	0.45
1:C:417:VAL:HG21	1:C:464:VAL:HG21	1.99	0.45
1:A:419:PRO:HG3	1:A:459:PRO:O	2.16	0.45
1:A:478:TYR:CE2	1:A:521:ILE:HG12	2.52	0.45
1:A:595:ASP:HA	1:A:596:GLY:HA2	1.66	0.45
1:B:45:ALA:CB	1:B:110:VAL:HG22	2.46	0.45
1:B:167:ASP:O	1:B:170:LYS:HB2	2.16	0.45
1:B:518:THR:HG23	1:B:520:GLU:HB2	1.99	0.45
1:B:563:ILE:CG1	1:B:598:ILE:HD11	2.47	0.45
1:B:615:ILE:O	1:B:615:ILE:HG22	2.16	0.45
1:C:256:ALA:HA	1:C:259:ILE:HD11	1.98	0.45
1:C:27:THR:HB	1:C:43:VAL:O	2.17	0.45
1:A:679:VAL:CG2	1:A:679:VAL:O	2.58	0.45
1:C:261:GLU:CD	1:C:261:GLU:N	2.69	0.45
1:A:216:GLN:O	1:A:220:GLU:HG2	2.17	0.45
1:A:688:VAL:HG22	1:A:689:ARG:HG3	1.99	0.45
1:B:36:ASP:HB2	1:B:120:ASP:HB2	1.99	0.45
1:B:97:PRO:HD3	1:B:187:MSE:HG2	1.99	0.45
1:B:388:PHE:C	1:B:388:PHE:CD1	2.90	0.45
1:B:194:GLU:O	1:B:504:GLY:HA3	2.17	0.45
1:C:82:ARG:HG3	1:C:82:ARG:O	2.16	0.45
1:A:355:VAL:HG11	1:A:449:SER:HA	1.99	0.45
1:A:561:MSE:HE1	1:A:616:GLU:HG3	1.97	0.45
1:B:662:VAL:HA	1:B:668:TYR:CE2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:366:GLN:CG	1:C:368:ILE:HG23	2.47	0.45
1:C:146:GLY:HA3	1:C:147:SER:HA	1.60	0.44
1:C:478:TYR:OH	1:C:521:ILE:HG22	2.18	0.44
1:C:92:ARG:HH11	1:C:401:ARG:CG	2.30	0.44
1:A:15:VAL:HA	1:A:33:ARG:O	2.17	0.44
1:C:107:THR:O	1:C:107:THR:HG23	2.17	0.44
1:C:78:LYS:HD3	1:C:78:LYS:HA	1.71	0.44
1:A:421:LEU:HA	1:A:421:LEU:HD12	1.85	0.44
1:B:45:ALA:CB	1:B:142:ILE:HD11	2.47	0.44
1:A:21:GLU:OE2	1:C:333:LYS:NZ	2.26	0.44
1:C:244:TRP:CZ3	1:C:248:LYS:HD2	2.53	0.44
1:B:657:ILE:HG22	1:B:658:ALA:N	2.32	0.44
1:C:106:PHE:HE1	1:C:143:PRO:HG2	1.81	0.44
1:C:477:LYS:HA	1:C:477:LYS:HD2	1.49	0.44
1:A:471:LEU:HD13	1:A:494:MSE:HE2	1.98	0.44
1:A:687:ARG:HA	1:A:687:ARG:HD3	1.66	0.44
1:C:245:VAL:HG11	1:C:299:ILE:HD12	2.00	0.44
1:C:478:TYR:CZ	1:C:521:ILE:HG22	2.53	0.44
1:A:613:ARG:O	1:A:617:GLU:HG2	2.17	0.44
1:A:77:PHE:CE1	1:A:82:ARG:NH2	2.86	0.44
1:C:246:VAL:HG12	1:C:247:GLU:N	2.32	0.44
1:C:471:LEU:HD22	1:C:494:MSE:HE2	2.00	0.44
1:B:641:PHE:CE2	1:B:651:LEU:HD13	2.52	0.44
1:C:3:LYS:H	1:C:20:GLY:HA3	1.81	0.44
1:A:324:THR:HG22	1:A:481:LEU:CD2	2.47	0.44
1:A:361:THR:CG2	1:A:362:GLU:N	2.80	0.44
1:A:508:LEU:HD11	1:A:510:MSE:HE3	2.00	0.44
1:A:652:VAL:C	1:A:654:ILE:CD1	2.87	0.44
1:B:152:ARG:HG2	1:B:164:PRO:HD2	1.99	0.44
1:C:138:GLY:HA3	1:C:222:ILE:HD11	1.99	0.44
1:C:387:PRO:HB2	1:C:392:GLU:O	2.17	0.44
1:A:493:ASP:HB3	1:A:514:ILE:CG2	2.48	0.43
1:A:188:VAL:HB	1:A:510:MSE:HB2	2.00	0.43
1:B:519:LYS:HA	1:B:522:MSE:HE3	2.00	0.43
1:B:361:THR:CG2	1:B:601:ALA:HB1	2.48	0.43
1:C:119:VAL:HG11	1:C:371:LEU:HG	2.00	0.43
1:A:645:LEU:HD12	1:A:645:LEU:C	2.38	0.43
1:B:5:ARG:NH1	1:B:18:GLU:OE2	2.50	0.43
1:B:363:ARG:NH1	1:B:584:GLU:OE2	2.50	0.43
1:C:269:ILE:CG1	1:C:270:GLN:N	2.81	0.43
1:C:375:ARG:NH1	1:C:375:ARG:HB3	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:393:VAL:HG13	1:B:111:GLN:CB	2.48	0.43
1:A:641:PHE:N	1:A:651:LEU:HA	2.25	0.43
1:B:309:ARG:HH22	1:B:493:ASP:CG	2.21	0.43
1:B:194:GLU:OE2	1:B:501:THR:CG2	2.67	0.43
1:C:279:ASP:O	1:C:283:GLU:OE1	2.37	0.43
1:B:279:ASP:O	1:B:283:GLU:OE1	2.37	0.43
1:B:454:MSE:HE2	1:B:547:PRO:HD3	1.99	0.43
1:C:355:VAL:HG22	1:C:432:SER:HA	1.99	0.43
1:C:361:THR:CG2	1:C:589:ALA:HB2	2.48	0.43
1:B:581:GLU:HB2	1:C:577:VAL:HG12	2.00	0.43
1:B:146:GLY:HA3	1:B:147:SER:HA	1.80	0.43
1:B:588:CYS:SG	1:B:607:GLU:HB3	2.59	0.43
1:B:96:ARG:HB2	1:B:97:PRO:CD	2.48	0.43
1:C:155:TYR:CZ	1:C:158:GLY:HA2	2.53	0.43
1:A:494:MSE:HB2	1:A:512:ILE:HG12	2.00	0.43
1:B:52:GLY:HA2	1:B:294:HIS:CG	2.54	0.43
1:B:669:LEU:HD21	1:B:672:GLY:O	2.19	0.43
1:C:274:ASP:O	1:C:278:ALA:N	2.43	0.43
1:A:416:PRO:HG2	1:A:506:THR:HB	2.00	0.43
1:A:50:GLU:HG2	1:A:53:ARG:CZ	2.48	0.43
1:A:644:ILE:HD13	1:A:677:VAL:HG21	1.96	0.43
1:B:435:LEU:HD22	1:C:40:LEU:CD2	2.48	0.43
1:B:563:ILE:HG12	1:B:598:ILE:HD11	2.00	0.43
1:C:244:TRP:HE3	1:C:248:LYS:CE	2.32	0.43
1:C:440:SER:HB3	1:C:468:ALA:HB2	2.01	0.43
1:C:475:ASN:ND2	1:C:476:ASP:OD1	2.52	0.43
1:A:273[B]:ARG:HH12	1:A:296:LEU:HD23	1.84	0.43
1:B:550:GLN:OE1	1:B:550:GLN:N	2.52	0.43
1:C:269:ILE:CG1	1:C:270:GLN:H	2.31	0.43
1:C:188:VAL:HB	1:C:510:MSE:HB2	2.01	0.43
1:A:580:ARG:NH2	1:C:581:GLU:OE2	2.52	0.43
1:A:196:PRO:HG2	1:A:199:VAL:HG23	2.01	0.43
1:A:469:MSE:HG3	1:A:496:PHE:CE2	2.54	0.43
1:A:451:LEU:HG	1:A:540:MSE:HE3	2.01	0.43
1:B:414:VAL:O	1:B:417:VAL:HG22	2.18	0.43
1:B:650:GLY:CA	1:B:688:VAL:HG13	2.49	0.43
1:A:236:THR:CG2	1:A:237:VAL:N	2.81	0.42
1:B:384:ASN:HB3	1:C:79:ARG:HH21	1.84	0.42
1:B:471:LEU:HD23	1:B:521:ILE:CG2	2.48	0.42
1:C:271:ALA:O	1:C:275:GLN:NE2	2.51	0.42
1:A:166:LEU:HD11	1:A:372:ASP:OD2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:414:VAL:HG12	1:B:418:VAL:HG23	2.01	0.42
1:A:63:GLN:HG3	1:A:115:THR:HG23	2.01	0.42
1:A:6:LYS:HB2	1:A:221:PHE:CD1	2.55	0.42
1:A:424:PHE:CE2	1:A:426:TYR:HB2	2.54	0.42
1:B:260:GLN:OE1	1:B:320:ASP:O	2.37	0.42
1:B:332:VAL:HG13	1:B:451:LEU:HD13	2.00	0.42
1:C:195:LEU:HD13	1:C:199:VAL:HG11	2.01	0.42
1:C:319:ILE:HA	1:C:319:ILE:HD12	1.90	0.42
1:C:495:ASP:C	1:C:495:ASP:OD1	2.57	0.42
1:A:186:LEU:HA	1:A:186:LEU:HD23	1.79	0.42
1:B:627:VAL:O	1:B:627:VAL:HG22	2.18	0.42
1:C:62:TYR:CD2	1:C:90:THR:HB	2.54	0.42
1:A:424:PHE:O	1:A:426:TYR:N	2.49	0.42
1:A:493:ASP:CB	1:A:514:ILE:HD13	2.49	0.42
1:B:291:VAL:O	1:B:294:HIS:HB3	2.19	0.42
1:B:498:VAL:HG22	1:B:508:LEU:HD13	2.00	0.42
1:C:209:GLN:HG3	1:C:210:ALA:N	2.35	0.42
1:C:298:VAL:O	1:C:300:PHE:N	2.53	0.42
1:C:47:LYS:H	1:C:47:LYS:CD	2.30	0.42
1:C:73:PRO:O	1:C:78:LYS:HD3	2.19	0.42
1:A:111:GLN:HB2	1:C:393:VAL:HG13	2.01	0.42
1:A:155:TYR:CZ	1:A:158:GLY:HA2	2.54	0.42
1:A:641:PHE:H	1:A:651:LEU:CA	2.23	0.42
1:B:572:ILE:CD1	1:B:579:ILE:HD12	2.49	0.42
1:C:593:SER:O	1:C:594:ASP:C	2.57	0.42
1:A:442:SER:O	1:A:445:SER:HB3	2.19	0.42
1:A:62:TYR:CD2	1:A:90:THR:HB	2.55	0.42
1:A:652:VAL:C	1:A:654:ILE:HD12	2.40	0.42
1:A:678:LYS:HB2	1:A:690:LEU:CD1	2.50	0.42
1:A:60:VAL:HG11	1:A:94:ILE:HB	2.01	0.42
1:B:579:ILE:O	1:B:583:THR:HG23	2.19	0.42
1:C:244:TRP:CE3	1:C:248:LYS:NZ	2.85	0.42
1:A:89:LEU:HG	1:A:404:ILE:CG2	2.50	0.42
1:A:493:ASP:HB3	1:A:514:ILE:HG23	2.01	0.42
1:B:626:LYS:HD3	1:B:626:LYS:HA	1.80	0.42
1:B:633:VAL:HG11	1:B:643:GLN:NE2	2.30	0.42
1:C:188:VAL:HG21	1:C:204:VAL:HG22	2.01	0.42
1:C:555:ALA:HB1	1:C:556:PRO:HD2	2.01	0.42
1:A:65:LYS:HG3	1:A:67:TYR:CZ	2.54	0.42
1:A:7:THR:HG21	1:A:14:GLU:OE2	2.20	0.42
1:B:126:ASP:OD1	1:B:127:ILE:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:148:LEU:HD13	1:B:148:LEU:O	2.20	0.42
1:B:339:ARG:HA	1:B:339:ARG:HD3	1.83	0.42
1:B:380:ILE:HD11	1:B:429:ARG:CG	2.50	0.42
1:B:382:HIS:CE1	1:C:79:ARG:HB2	2.55	0.42
1:C:262:LYS:CG	1:C:263:THR:N	2.81	0.42
1:C:245:VAL:HG23	1:C:246:VAL:H	1.83	0.42
1:C:265:ARG:O	1:C:269:ILE:HG13	2.20	0.42
1:C:469:MSE:SE	1:C:482:SER:HA	2.70	0.42
1:B:578:VAL:HA	1:C:577:VAL:HG11	2.01	0.42
1:B:45:ALA:HB2	1:B:142:ILE:CD1	2.49	0.41
1:A:370:ASP:O	1:A:373:GLY:N	2.53	0.41
1:A:612:LYS:O	1:A:615:ILE:HB	2.20	0.41
1:A:78:LYS:HE3	1:C:366:GLN:CD	2.41	0.41
1:B:484:ILE:HG22	1:B:485:LEU:N	2.35	0.41
1:B:530:LYS:HA	1:B:533:ARG:NH1	2.34	0.41
1:B:6:LYS:HG3	1:B:7:THR:N	2.35	0.41
1:A:380:ILE:O	1:A:429:ARG:HA	2.20	0.41
1:B:192:ALA:O	1:B:506:THR:HA	2.20	0.41
1:B:625:GLY:CA	1:B:626:LYS:CB	2.96	0.41
1:C:140:SER:CB	1:C:142:ILE:HG13	2.51	0.41
1:C:542:LYS:HB3	1:C:542:LYS:HE3	1.82	0.41
1:C:561:MSE:HG2	1:C:598:ILE:HB	2.02	0.41
1:A:359:LEU:CD1	1:A:551:VAL:HG22	2.51	0.41
1:C:47:LYS:HG2	1:C:48:GLU:N	2.32	0.41
1:C:318:ARG:NE	1:C:481:LEU:HD22	2.35	0.41
1:C:92:ARG:HH11	1:C:401:ARG:HD3	1.83	0.41
1:A:117:LEU:HA	1:A:117:LEU:HD23	1.68	0.41
1:A:138:GLY:HA3	1:A:222:ILE:CD1	2.51	0.41
1:B:332:VAL:CG1	1:B:451:LEU:HD13	2.51	0.41
1:B:567:LYS:HD2	1:B:619:THR:HB	2.02	0.41
1:C:480:VAL:HG12	1:C:528:GLN:NE2	2.36	0.41
1:A:214:ALA:O	1:A:218:ILE:HG13	2.20	0.41
1:A:418:VAL:HA	1:A:419:PRO:HD3	1.86	0.41
1:A:564:ASN:HB2	1:A:567:LYS:HD2	2.03	0.41
1:B:99:ARG:N	1:B:100:PRO:HD2	2.36	0.41
1:C:234:PRO:HA	1:C:235:PRO:HD2	1.92	0.41
1:C:33:ARG:HA	1:C:37:THR:O	2.20	0.41
1:A:634:LYS:O	1:A:641:PHE:CD1	2.74	0.41
1:B:330:ILE:HA	1:B:347:THR:O	2.20	0.41
1:B:527:ASP:C	1:B:529:ALA:N	2.71	0.41
1:C:408:ARG:O	1:C:412:ARG:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:496:PHE:HB2	1:C:510:MSE:HG2	2.03	0.41
1:A:557:GLN:OE1	1:A:557:GLN:HA	2.21	0.41
1:B:65:LYS:HB3	1:B:67:TYR:CE2	2.55	0.41
1:C:185:VAL:HG23	1:C:208:HIS:ND1	2.36	0.41
1:A:563:ILE:HD11	1:A:571:VAL:HG21	2.03	0.41
1:A:633:VAL:HG23	1:A:642:VAL:CA	2.28	0.41
1:B:134:SER:HB2	1:B:148:LEU:HD12	2.03	0.41
1:B:253:LEU:HD12	1:B:303:LEU:HG	2.03	0.41
1:B:595:ASP:HA	1:B:596:GLY:HA2	1.63	0.41
1:C:293:GLU:C	1:C:295:GLU:N	2.75	0.41
1:A:236:THR:CG2	1:A:237:VAL:H	2.34	0.41
1:A:631:THR:O	1:A:642:VAL:HG13	2.21	0.41
1:A:688:VAL:HG13	1:A:689:ARG:NE	2.36	0.41
1:B:566:GLU:O	1:B:569:ARG:CG	2.56	0.41
1:C:143:PRO:HA	1:C:229:LYS:CE	2.50	0.41
1:C:165:SER:O	1:C:169:LEU:HG	2.21	0.41
1:C:350:GLU:O	1:C:436:GLU:HB3	2.20	0.41
1:C:458:VAL:O	1:C:460:THR:N	2.54	0.41
1:C:521:ILE:O	1:C:523:GLU:N	2.54	0.41
1:C:64:GLU:OE1	1:C:371:LEU:HD22	2.20	0.41
1:A:85:GLU:OE1	1:A:404:ILE:HG23	2.20	0.40
1:A:55:PHE:CD1	1:A:55:PHE:N	2.88	0.40
1:A:583:THR:O	1:A:587:ASN:N	2.54	0.40
1:B:138:GLY:HA3	1:B:222:ILE:HD13	2.03	0.40
1:B:121:SER:HB3	2:B:701:SO4:O4	2.21	0.40
1:C:298:VAL:C	1:C:300:PHE:N	2.73	0.40
1:B:671:GLU:HB3	1:C:595:ASP:OD2	2.22	0.40
1:A:318:ARG:NH2	1:A:484:ILE:HA	2.36	0.40
1:A:45:ALA:HB2	1:A:110:VAL:HG22	2.03	0.40
1:A:657:ILE:CG2	1:A:658:ALA:N	2.78	0.40
1:B:56:PHE:HA	1:B:57:PRO:HD3	1.84	0.40
1:C:253:LEU:HD23	1:C:256:ALA:HB3	2.03	0.40
1:C:418:VAL:HA	1:C:419:PRO:HD3	1.93	0.40
1:C:46:LYS:HG2	1:C:47:LYS:HD3	2.03	0.40
1:C:56:PHE:HA	1:C:57:PRO:HD3	1.81	0.40
1:A:568:ILE:HD12	1:A:594:ASP:O	2.22	0.40
1:B:276:LEU:HD23	1:B:276:LEU:HA	1.73	0.40
1:B:453:LEU:O	1:B:458:VAL:HG23	2.20	0.40
1:B:618:LEU:H	1:B:618:LEU:HD12	1.86	0.40
1:C:476:ASP:N	1:C:476:ASP:OD1	2.52	0.40
1:A:678:LYS:HB2	1:A:690:LEU:HD11	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:435:LEU:CD1	1:B:22:MSE:HE3	2.51	0.40
1:B:248:LYS:HD2	1:B:276:LEU:CD2	2.51	0.40
1:B:369:ASP:O	1:B:370:ASP:HB3	2.21	0.40
1:C:368:ILE:HG13	1:C:368:ILE:O	2.22	0.40
1:C:521:ILE:CG1	1:C:522:MSE:H	2.32	0.40
1:A:476:ASP:N	1:A:476:ASP:OD1	2.51	0.40
1:A:579:ILE:O	1:A:583:THR:HG23	2.21	0.40
1:C:235:PRO:O	1:C:237:VAL:N	2.54	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:A:171:ASP:OD2	1:B:661:ARG:NH1[4_445]	1.96	0.24
1:A:284:ARG:O	1:B:653:HIS:NE2[2_555]	2.10	0.10
1:A:227:GLY:O	1:A:661:ARG:NH1[2_555]	2.17	0.03

## 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	640/715 (90%)	606 (95%)	33 (5%)	1 (0%)	51	81
1	B	650/715 (91%)	617 (95%)	32 (5%)	1 (0%)	51	81
1	C	599/715 (84%)	547 (91%)	52 (9%)	0	100	100
All	All	1889/2145 (88%)	1770 (94%)	117 (6%)	2 (0%)	55	85

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	644	ILE
1	B	627	VAL

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	543/577 (94%)	508 (94%)	35 (6%)	20	50
1	B	550/577 (95%)	516 (94%)	34 (6%)	21	51
1	C	499/577 (86%)	471 (94%)	28 (6%)	25	56
All	All	1592/1731 (92%)	1495 (94%)	97 (6%)	22	52

All (97) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	ASP
1	A	55	PHE
1	A	77	PHE
1	A	118	SER
1	A	147	SER
1	A	148	LEU
1	A	187	MSE
1	A	209	GLN
1	A	326	THR
1	A	361	THR
1	A	396	MSE
1	A	432	SER
1	A	438	ASN
1	A	487	ASP
1	A	488	GLU
1	A	494	MSE
1	A	527	ASP
1	A	551	VAL
1	A	563	ILE
1	A	577	VAL
1	A	580	ARG
1	A	597	THR
1	A	618	LEU
1	A	631	THR
1	A	633	VAL
1	A	641	PHE

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Mol	Chain	Res	Type
1	A	642	VAL
1	A	645	LEU
1	A	651	LEU
1	A	654	ILE
1	A	655	SER
1	A	659	GLN
1	A	667	ASP
1	A	690	LEU
1	A	691	SER
1	B	6	LYS
1	B	10	TYR
1	B	104	LYS
1	B	148	LEU
1	B	156	ARG
1	B	187	MSE
1	B	194	GLU
1	B	255	LYS
1	B	263	THR
1	B	273	ARG
1	B	343	SER
1	B	368	ILE
1	B	375	ARG
1	B	381	PHE
1	B	383	TYR
1	B	388	PHE
1	B	421	LEU
1	B	429	ARG
1	B	471	LEU
1	B	527	ASP
1	B	549	SER
1	B	554	LEU
1	B	569	ARG
1	B	571	VAL
1	B	594	ASP
1	B	604	THR
1	B	624	LEU
1	B	628	TYR
1	B	632	VAL
1	B	633	VAL
1	B	655	SER
1	B	660	GLU
1	B	667	ASP

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Mol	Chain	Res	Type
1	B	669	LEU
1	C	1	MSE
1	C	10	TYR
1	C	24	ARG
1	C	47	LYS
1	C	80	GLU
1	C	92	ARG
1	C	107	THR
1	C	121	SER
1	C	148	LEU
1	C	171	ASP
1	C	187	MSE
1	C	236	THR
1	C	237	VAL
1	C	239	THR
1	C	253	LEU
1	C	259	ILE
1	C	261	GLU
1	C	293	GLU
1	C	294	HIS
1	C	296	LEU
1	C	371	LEU
1	C	420	THR
1	C	441	SER
1	C	477	LYS
1	C	495	ASP
1	C	551	VAL
1	C	594	ASP
1	C	603	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	GLN
1	A	376	GLN
1	B	209	GLN
1	B	384	ASN
1	B	535	HIS
1	B	541	ASN
1	B	673	GLN
1	C	145	ASN
1	C	366	GLN

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Mol	Chain	Res	Type
1	C	382	HIS
1	C	406	HIS
1	C	603	HIS

### 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 ⓘ

13 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	$\# Z  > 2$
2	SO4	A	701	-	4,4,4	0.15	0	6,6,6	0.18	0
2	SO4	A	702	-	4,4,4	0.16	0	6,6,6	0.06	0
2	SO4	A	703	-	4,4,4	0.14	0	6,6,6	0.15	0
2	SO4	A	704	-	4,4,4	0.15	0	6,6,6	0.09	0
2	SO4	A	705	-	4,4,4	0.14	0	6,6,6	0.07	0
2	SO4	A	706	-	4,4,4	0.15	0	6,6,6	0.07	0
2	SO4	A	707	-	4,4,4	0.13	0	6,6,6	0.11	0
2	SO4	B	701	-	4,4,4	0.15	0	6,6,6	0.10	0
2	SO4	B	702	-	4,4,4	0.15	0	6,6,6	0.06	0
2	SO4	B	703	-	4,4,4	0.17	0	6,6,6	0.13	0
2	SO4	B	704	-	4,4,4	0.15	0	6,6,6	0.09	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	C	701	-	4,4,4	0.14	0	6,6,6	0.10	0
2	SO4	C	702	-	4,4,4	0.16	0	6,6,6	0.07	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	A	701	-	-	0/0/0/0	0/0/0/0
2	SO4	A	702	-	-	0/0/0/0	0/0/0/0
2	SO4	A	703	-	-	0/0/0/0	0/0/0/0
2	SO4	A	704	-	-	0/0/0/0	0/0/0/0
2	SO4	A	705	-	-	0/0/0/0	0/0/0/0
2	SO4	A	706	-	-	0/0/0/0	0/0/0/0
2	SO4	A	707	-	-	0/0/0/0	0/0/0/0
2	SO4	B	701	-	-	0/0/0/0	0/0/0/0
2	SO4	B	702	-	-	0/0/0/0	0/0/0/0
2	SO4	B	703	-	-	0/0/0/0	0/0/0/0
2	SO4	B	704	-	-	0/0/0/0	0/0/0/0
2	SO4	C	701	-	-	0/0/0/0	0/0/0/0
2	SO4	C	702	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	SO4	2	0
2	A	705	SO4	1	0
2	B	701	SO4	2	0
2	B	702	SO4	1	0
2	B	703	SO4	1	0

## 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.



## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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	643/715 (89%)	0.17	33 (5%) 29 25	32, 53, 133, 198	0
1	B	652/715 (91%)	0.30	37 (5%) 24 20	37, 75, 123, 156	0
1	C	592/715 (82%)	0.52	63 (10%) 7 5	43, 83, 139, 184	0
All	All	1887/2145 (87%)	0.32	133 (7%) 17 13	32, 73, 132, 198	0

All (133) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	597	THR	6.2
1	C	571	VAL	6.1
1	B	575	GLY	6.1
1	C	583	THR	6.0
1	C	150	ALA	5.4
1	C	591	ASP	5.4
1	C	582	ILE	5.3
1	C	573	GLY	5.3
1	B	571	VAL	5.1
1	C	229	LYS	4.8
1	A	687	ARG	4.6
1	B	420	THR	4.6
1	C	279	ASP	4.5
1	C	272	ILE	4.5
1	C	278	ALA	4.5
1	A	691	SER	4.5
1	B	633	VAL	4.5
1	C	579	ILE	4.4
1	A	77	PHE	4.3
1	B	594	ASP	4.2
1	C	275	GLN	4.1
1	C	276	LEU	4.1
1	C	601	ALA	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	655	SER	4.1
1	A	679	VAL	3.9
1	B	465	ALA	3.9
1	C	297	ALA	3.8
1	A	689	ARG	3.8
1	C	273	ARG	3.8
1	C	296	LEU	3.8
1	B	642	VAL	3.8
1	B	422	ASP	3.8
1	B	658	ALA	3.8
1	B	650	GLY	3.7
1	A	659	GLN	3.7
1	C	560	THR	3.6
1	C	572	ILE	3.6
1	A	48	GLU	3.5
1	B	615	ILE	3.4
1	B	635	ILE	3.4
1	C	602	ALA	3.4
1	C	566	GLU	3.4
1	B	562	LYS	3.3
1	C	613	ARG	3.2
1	C	600	ILE	3.2
1	C	595	ASP	3.1
1	A	51	GLU	3.1
1	A	289	ASN	3.1
1	A	55	PHE	3.1
1	C	569	ARG	3.1
1	C	563	ILE	3.1
1	B	563	ILE	3.0
1	C	568	ILE	3.0
1	B	574	LYS	3.0
1	C	616	GLU	2.9
1	B	641	PHE	2.9
1	B	595	ASP	2.9
1	C	584	GLU	2.9
1	B	573	GLY	2.9
1	B	572	ILE	2.9
1	B	632	VAL	2.9
1	B	426	TYR	2.8
1	C	590	ILE	2.8
1	C	615	ILE	2.8
1	A	690	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	599	LYS	2.8
1	B	598	ILE	2.8
1	A	688	VAL	2.8
1	C	264	ALA	2.8
1	A	579	ILE	2.8
1	C	559	VAL	2.7
1	C	592	ILE	2.7
1	C	266	GLN	2.7
1	C	578	VAL	2.7
1	A	642	VAL	2.7
1	C	254	LYS	2.7
1	C	609	GLU	2.7
1	A	634	LYS	2.7
1	C	149	GLY	2.7
1	B	639	GLY	2.7
1	C	39	LEU	2.6
1	B	419	PRO	2.6
1	A	593	SER	2.6
1	B	644	ILE	2.6
1	A	569	ARG	2.6
1	C	588	CYS	2.5
1	C	282	ALA	2.5
1	C	612	LYS	2.5
1	B	671	GLU	2.4
1	C	244	TRP	2.4
1	B	76	TYR	2.3
1	A	641	PHE	2.3
1	A	47	LYS	2.3
1	A	581	GLU	2.3
1	A	644	ILE	2.3
1	C	299	ILE	2.3
1	A	53	ARG	2.3
1	A	680	ILE	2.3
1	C	614	ARG	2.3
1	A	595	ASP	2.3
1	B	618	LEU	2.3
1	C	598	ILE	2.3
1	C	300	PHE	2.3
1	C	236	THR	2.3
1	B	590	ILE	2.3
1	C	105	GLY	2.3
1	B	417	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	559	VAL	2.2
1	A	652	VAL	2.2
1	B	500	GLY	2.2
1	A	592	ILE	2.2
1	C	388	PHE	2.2
1	C	162	LEU	2.2
1	C	9	GLN	2.2
1	B	425	PRO	2.2
1	B	155	TYR	2.2
1	A	657	ILE	2.2
1	C	399	PRO	2.2
1	B	464	VAL	2.2
1	A	651	LEU	2.2
1	A	572	ILE	2.2
1	A	654	ILE	2.1
1	C	15	VAL	2.1
1	A	615	ILE	2.1
1	B	569	ARG	2.1
1	A	580	ARG	2.1
1	C	520	GLU	2.1
1	C	10	TYR	2.1
1	C	567	LYS	2.1
1	C	594	ASP	2.0
1	B	578	VAL	2.0
1	C	148	LEU	2.0
1	C	186	LEU	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	B	703	5/5	0.85	0.24	1.25	95,106,109,110	0
2	SO4	C	701	5/5	0.93	0.12	-1.13	103,106,110,110	0
2	SO4	A	703	5/5	0.96	0.15	-1.19	71,74,79,82	0
2	SO4	A	701	5/5	0.95	0.12	-2.39	82,84,86,89	0
2	SO4	B	704	5/5	0.97	0.09	-2.91	96,99,103,103	0
2	SO4	A	702	5/5	0.90	0.13	-	112,116,117,120	0
2	SO4	A	704	5/5	0.95	0.15	-	95,101,102,105	0
2	SO4	A	707	5/5	0.93	0.31	-	122,125,127,128	0
2	SO4	B	702	5/5	0.89	0.21	-	139,140,140,140	0
2	SO4	A	706	5/5	0.88	0.35	-	149,150,153,154	0
2	SO4	A	705	5/5	0.86	0.22	-	140,142,143,143	0
2	SO4	B	701	5/5	0.91	0.19	-	119,121,123,123	0
2	SO4	C	702	5/5	0.87	0.28	-	136,137,137,137	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.