



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:17 AM GMT

PDB ID : 3A8Q  
Title : Low-resolution crystal structure of the Tiam2 PHCCEX domain  
Authors : Terawaki, S.; Kitano, K.; Mori, T.; Zhai, Y.; Higuchi, Y.; Itoh, N.; Watanabe, T.; Kaibuchi, K.; Hakoshima, T.  
Deposited on : 2009-10-07  
Resolution : 3.20 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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

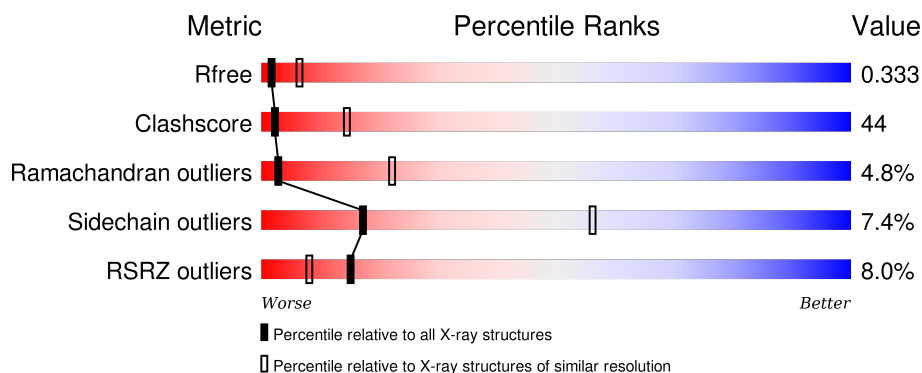
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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))
$R_{free}$	91344	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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	263	<div> <div>9%</div> <div>41% 38% 7% • 12%</div> </div>
1	B	263	<div> <div>7%</div> <div>40% 41% 7% • 12%</div> </div>
1	C	263	<div> <div>9%</div> <div>40% 40% 8% • 12%</div> </div>
1	D	263	<div> <div>3%</div> <div>40% 40% 7% • 12%</div> </div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 7412 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 T-lymphoma invasion and metastasis-inducing protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	231	Total	C	N	O	S	0	0	0
			1853	1182	330	329	12			
1	B	231	Total	C	N	O	S	0	0	0
			1853	1182	330	329	12			
1	C	231	Total	C	N	O	S	0	0	0
			1853	1182	330	329	12			
1	D	231	Total	C	N	O	S	0	0	0
			1853	1182	330	329	12			

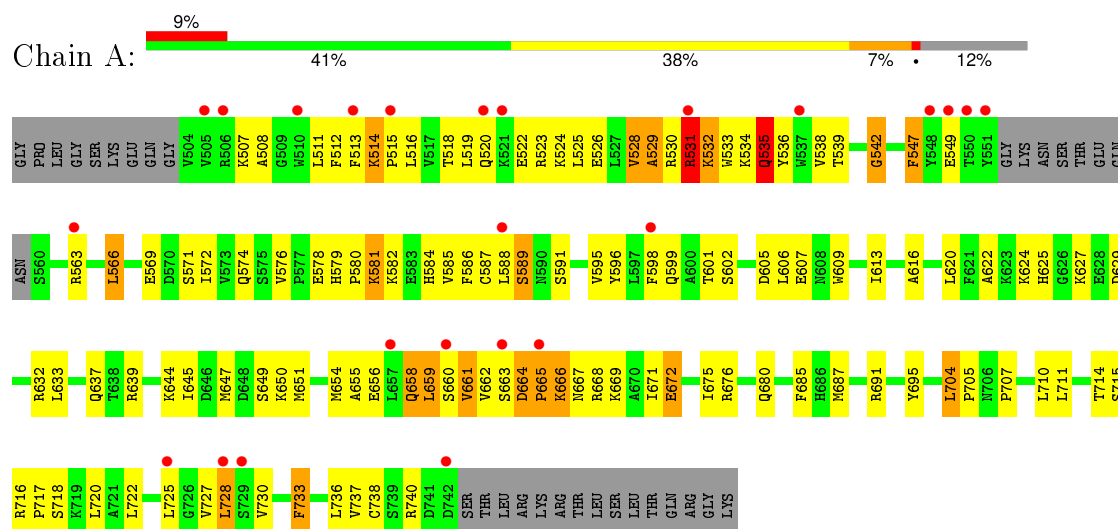
There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	495	GLY	-	EXPRESSION TAG	UNP Q6ZPF3
A	496	PRO	-	EXPRESSION TAG	UNP Q6ZPF3
A	497	LEU	-	EXPRESSION TAG	UNP Q6ZPF3
A	498	GLY	-	EXPRESSION TAG	UNP Q6ZPF3
A	499	SER	-	EXPRESSION TAG	UNP Q6ZPF3
B	495	GLY	-	EXPRESSION TAG	UNP Q6ZPF3
B	496	PRO	-	EXPRESSION TAG	UNP Q6ZPF3
B	497	LEU	-	EXPRESSION TAG	UNP Q6ZPF3
B	498	GLY	-	EXPRESSION TAG	UNP Q6ZPF3
B	499	SER	-	EXPRESSION TAG	UNP Q6ZPF3
C	495	GLY	-	EXPRESSION TAG	UNP Q6ZPF3
C	496	PRO	-	EXPRESSION TAG	UNP Q6ZPF3
C	497	LEU	-	EXPRESSION TAG	UNP Q6ZPF3
C	498	GLY	-	EXPRESSION TAG	UNP Q6ZPF3
C	499	SER	-	EXPRESSION TAG	UNP Q6ZPF3
D	495	GLY	-	EXPRESSION TAG	UNP Q6ZPF3
D	496	PRO	-	EXPRESSION TAG	UNP Q6ZPF3
D	497	LEU	-	EXPRESSION TAG	UNP Q6ZPF3
D	498	GLY	-	EXPRESSION TAG	UNP Q6ZPF3
D	499	SER	-	EXPRESSION TAG	UNP Q6ZPF3

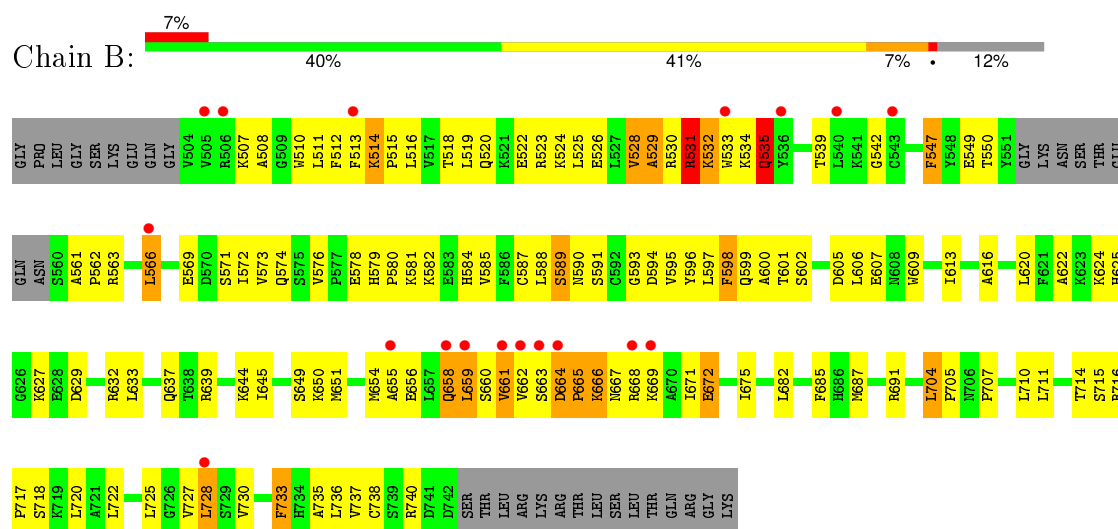
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: T-lymphoma invasion and metastasis-inducing protein 2

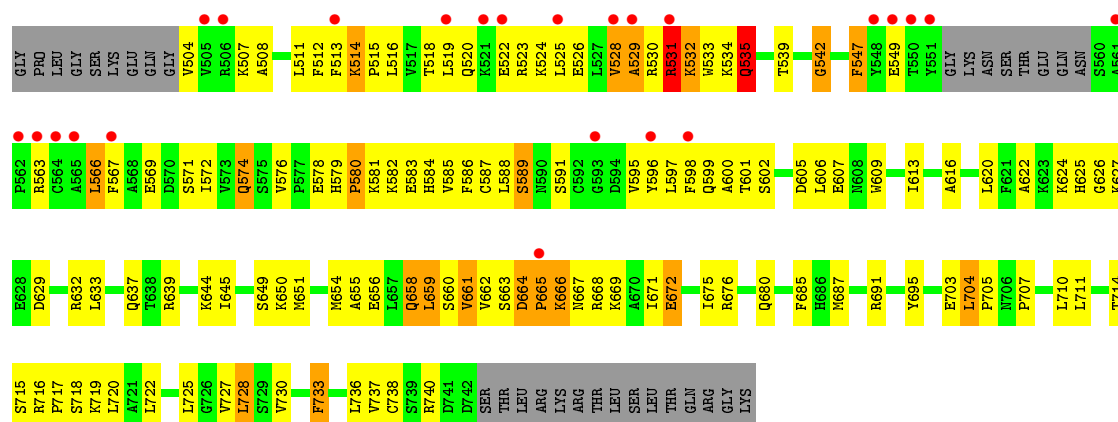


- Molecule 1: T-lymphoma invasion and metastasis-inducing protein 2

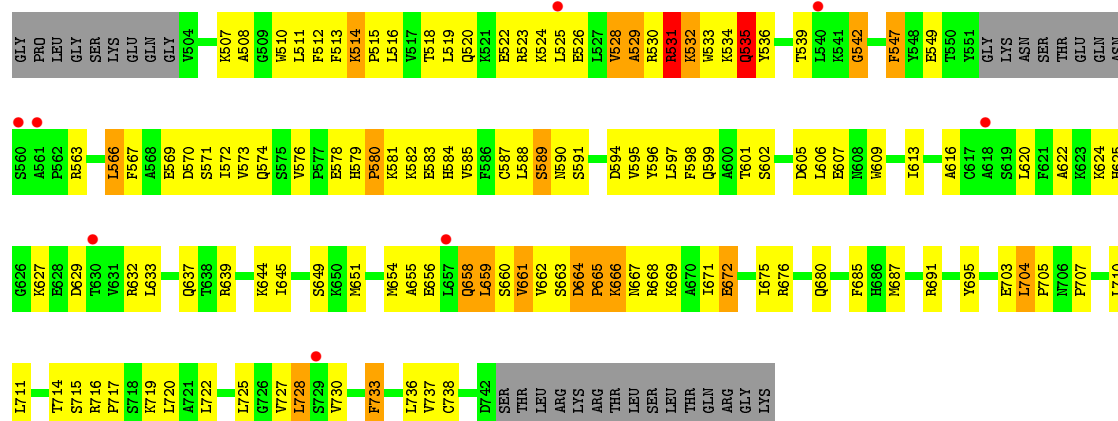


- Molecule 1: T-lymphoma invasion and metastasis-inducing protein 2





• Molecule 1: T-lymphoma invasion and metastasis-inducing protein 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.56 Å 105.56 Å 287.58 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.56 – 3.20 45.56 – 3.19	Depositor EDS
% Data completeness (in resolution range)	91.9 (45.56-3.20) 91.6 (45.56-3.19)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.51 (at 3.19 Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.283 , 0.332 0.286 , 0.333	Depositor DCC
$R_{free}$ test set	2518 reflections (9.88%)	DCC
Wilson B-factor (Å <sup>2</sup> )	109.9	Xtriage
Anisotropy	0.565	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 99.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 25554 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	7412	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	144.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.83% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.43	0/1890	0.60	0/2544
1	B	0.38	0/1890	0.58	0/2544
1	C	0.41	0/1890	0.59	0/2544
1	D	0.43	0/1890	0.60	0/2544
All	All	0.41	0/7560	0.59	0/10176

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1853	0	1901	167	0
1	B	1853	0	1901	160	0
1	C	1853	0	1901	176	0
1	D	1853	0	1901	164	0
All	All	7412	0	7604	656	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 44.

All (656) 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:B:716:ARG:HH12	1:B:720:LEU:HD11	1.13	1.11
1:A:716:ARG:HH12	1:A:720:LEU:HD11	1.13	1.07
1:C:716:ARG:HH12	1:C:720:LEU:HD11	1.15	1.06
1:D:716:ARG:HH12	1:D:720:LEU:HD11	1.18	1.03
1:A:666:LYS:HZ2	1:A:666:LYS:HB3	1.26	1.01
1:D:520:GLN:HG3	1:D:526:GLU:HG3	1.45	0.98
1:B:520:GLN:HG3	1:B:526:GLU:HG3	1.46	0.98
1:C:520:GLN:HG3	1:C:526:GLU:HG3	1.47	0.96
1:A:520:GLN:HG3	1:A:526:GLU:HG3	1.46	0.95
1:C:654:MET:HA	1:C:654:MET:HE2	1.51	0.93
1:B:588:LEU:HD23	1:B:589:SER:N	1.85	0.92
1:D:579:HIS:HE1	1:D:581:LYS:HG2	1.34	0.91
1:B:579:HIS:HE1	1:B:581:LYS:HG2	1.34	0.91
1:C:579:HIS:HE1	1:C:581:LYS:HG2	1.36	0.90
1:D:520:GLN:HG3	1:D:526:GLU:CG	2.02	0.90
1:C:520:GLN:HG3	1:C:526:GLU:CG	2.02	0.89
1:A:520:GLN:HG3	1:A:526:GLU:CG	2.02	0.88
1:B:520:GLN:HG3	1:B:526:GLU:CG	2.03	0.88
1:A:518:THR:HG22	1:A:528:VAL:HG22	1.55	0.88
1:C:518:THR:HG22	1:C:528:VAL:HG22	1.56	0.86
1:A:579:HIS:HE1	1:A:581:LYS:HG2	1.40	0.86
1:C:722:LEU:HD21	1:C:736:LEU:HB2	1.58	0.85
1:D:518:THR:HG22	1:D:528:VAL:HG22	1.58	0.85
1:C:588:LEU:HD23	1:C:589:SER:N	1.91	0.84
1:D:588:LEU:HD23	1:D:589:SER:N	1.91	0.84
1:A:651:MET:SD	1:C:654:MET:CE	2.65	0.84
1:A:588:LEU:HD23	1:A:589:SER:N	1.93	0.84
1:B:518:THR:HG22	1:B:528:VAL:HG22	1.60	0.83
1:A:722:LEU:HD21	1:A:736:LEU:HB2	1.60	0.83
1:A:666:LYS:NZ	1:A:666:LYS:HB3	1.93	0.83
1:B:716:ARG:NH1	1:B:720:LEU:HD11	1.95	0.82
1:B:549:GLU:HB2	1:B:563:ARG:HH11	1.45	0.81
1:D:579:HIS:CE1	1:D:581:LYS:HG2	2.15	0.81
1:D:549:GLU:HB2	1:D:563:ARG:HH11	1.46	0.80
1:B:579:HIS:CE1	1:B:581:LYS:HG2	2.16	0.79
1:C:579:HIS:CE1	1:C:581:LYS:HG2	2.16	0.79
1:D:666:LYS:HB3	1:D:666:LYS:NZ	1.97	0.79
1:A:549:GLU:HB2	1:A:563:ARG:HH11	1.47	0.79
1:C:549:GLU:HB2	1:C:563:ARG:HH11	1.47	0.78
1:A:716:ARG:NH1	1:A:720:LEU:HD11	1.95	0.78
1:A:579:HIS:CE1	1:A:581:LYS:HG2	2.19	0.78
1:D:722:LEU:HD21	1:D:736:LEU:HB2	1.63	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:666:LYS:HB3	1:C:666:LYS:NZ	1.98	0.78
1:B:722:LEU:HD21	1:B:736:LEU:HB2	1.64	0.78
1:B:666:LYS:HB3	1:B:666:LYS:NZ	1.98	0.77
1:A:669:LYS:NZ	1:A:669:LYS:HB3	2.00	0.77
1:D:513:PHE:CE2	1:D:515:PRO:HD3	2.21	0.76
1:D:659:LEU:HD11	1:D:672:GLU:HG3	1.68	0.76
1:B:659:LEU:HD11	1:B:672:GLU:HG3	1.66	0.76
1:B:513:PHE:CE2	1:B:515:PRO:HD3	2.21	0.75
1:C:659:LEU:HD11	1:C:672:GLU:HG3	1.67	0.75
1:B:704:LEU:HD13	1:B:705:PRO:HD2	1.68	0.75
1:A:722:LEU:HD11	1:A:733:PHE:HA	1.70	0.74
1:C:666:LYS:HZ3	1:C:667:ASN:H	1.35	0.74
1:B:669:LYS:NZ	1:B:669:LYS:HB3	2.01	0.74
1:C:669:LYS:HB3	1:C:669:LYS:NZ	2.03	0.74
1:C:716:ARG:NH1	1:C:720:LEU:HD11	1.97	0.74
1:C:513:PHE:CE2	1:C:515:PRO:HD3	2.23	0.74
1:D:666:LYS:HZ2	1:D:667:ASN:H	1.36	0.74
1:A:659:LEU:HD11	1:A:672:GLU:HG3	1.70	0.74
1:D:722:LEU:HD11	1:D:733:PHE:HA	1.71	0.73
1:A:513:PHE:CE2	1:A:515:PRO:HD3	2.24	0.73
1:C:722:LEU:HD11	1:C:733:PHE:HA	1.69	0.73
1:C:664:ASP:HB2	1:C:666:LYS:NZ	2.03	0.73
1:A:664:ASP:HB2	1:A:666:LYS:NZ	2.04	0.73
1:D:584:HIS:CE1	1:D:602:SER:HA	2.24	0.73
1:D:629:ASP:OD2	1:D:632:ARG:HB2	1.89	0.72
1:D:533:TRP:HE1	1:D:581:LYS:HE3	1.55	0.72
1:C:584:HIS:CE1	1:C:602:SER:HA	2.24	0.72
1:D:716:ARG:NH1	1:D:720:LEU:HD11	2.00	0.72
1:C:533:TRP:HE1	1:C:581:LYS:HE3	1.55	0.72
1:B:722:LEU:HD11	1:B:733:PHE:HA	1.72	0.72
1:B:664:ASP:HB2	1:B:666:LYS:NZ	2.04	0.72
1:B:666:LYS:HZ3	1:B:667:ASN:H	1.38	0.72
1:B:584:HIS:CE1	1:B:602:SER:HA	2.25	0.72
1:D:669:LYS:NZ	1:D:669:LYS:HB3	2.03	0.72
1:D:704:LEU:HD13	1:D:705:PRO:HD2	1.72	0.71
1:B:629:ASP:OD2	1:B:632:ARG:HB2	1.90	0.71
1:A:651:MET:SD	1:C:654:MET:HE1	2.30	0.71
1:C:606:LEU:HD23	1:C:607:GLU:N	2.05	0.71
1:B:659:LEU:HD12	1:B:671:ILE:HB	1.73	0.71
1:A:584:HIS:CE1	1:A:602:SER:HA	2.26	0.71
1:A:533:TRP:HE1	1:A:581:LYS:HE3	1.55	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:622:ALA:HA	1:A:633:LEU:CD2	2.20	0.70
1:D:622:ALA:HA	1:D:633:LEU:HD23	1.73	0.70
1:C:704:LEU:HD13	1:C:705:PRO:HD2	1.74	0.70
1:B:533:TRP:HE1	1:B:581:LYS:HE3	1.55	0.70
1:B:736:LEU:O	1:B:736:LEU:HD12	1.91	0.70
1:B:622:ALA:HA	1:B:633:LEU:HD23	1.72	0.70
1:C:659:LEU:C	1:C:659:LEU:HD23	2.11	0.70
1:D:659:LEU:HD23	1:D:659:LEU:C	2.12	0.70
1:D:645:ILE:O	1:D:649:SER:HB2	1.92	0.70
1:A:629:ASP:OD2	1:A:632:ARG:HB2	1.92	0.70
1:D:664:ASP:HB2	1:D:666:LYS:NZ	2.06	0.69
1:A:622:ALA:HA	1:A:633:LEU:HD23	1.73	0.69
1:A:606:LEU:HD23	1:A:607:GLU:N	2.05	0.69
1:A:704:LEU:HD13	1:A:705:PRO:HD2	1.74	0.69
1:D:622:ALA:HA	1:D:633:LEU:CD2	2.21	0.69
1:B:622:ALA:HA	1:B:633:LEU:CD2	2.22	0.69
1:A:727:VAL:HG22	1:A:728:LEU:N	2.06	0.69
1:B:666:LYS:HZ2	1:B:666:LYS:HB3	1.57	0.69
1:C:622:ALA:HA	1:C:633:LEU:CD2	2.23	0.68
1:D:659:LEU:HD12	1:D:671:ILE:HB	1.75	0.68
1:A:736:LEU:HD12	1:A:736:LEU:O	1.93	0.67
1:C:629:ASP:OD2	1:C:632:ARG:HB2	1.95	0.67
1:C:664:ASP:O	1:C:666:LYS:N	2.27	0.67
1:B:645:ILE:O	1:B:649:SER:HB2	1.95	0.67
1:C:622:ALA:HA	1:C:633:LEU:HD23	1.77	0.67
1:A:645:ILE:O	1:A:649:SER:HB2	1.94	0.67
1:D:566:LEU:HD21	1:D:596:TYR:CE2	2.30	0.66
1:A:659:LEU:HD23	1:A:659:LEU:C	2.15	0.66
1:D:736:LEU:O	1:D:736:LEU:HD12	1.96	0.66
1:A:659:LEU:HD12	1:A:671:ILE:HB	1.77	0.66
1:B:591:SER:HA	1:B:738:CYS:SG	2.35	0.66
1:A:658:GLN:OE1	1:A:659:LEU:N	2.28	0.66
1:B:659:LEU:C	1:B:659:LEU:HD23	2.15	0.65
1:B:727:VAL:HG22	1:B:728:LEU:N	2.11	0.65
1:D:513:PHE:CD1	1:D:547:PHE:HE1	2.15	0.65
1:B:716:ARG:HH11	1:B:716:ARG:HG2	1.62	0.65
1:C:727:VAL:HG22	1:C:728:LEU:N	2.11	0.65
1:C:716:ARG:HG2	1:C:716:ARG:HH11	1.62	0.64
1:A:566:LEU:HD21	1:A:596:TYR:CE2	2.32	0.64
1:C:659:LEU:HD12	1:C:671:ILE:HB	1.78	0.64
1:D:659:LEU:HB2	1:D:671:ILE:HG21	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:727:VAL:HG22	1:A:728:LEU:H	1.61	0.64
1:D:669:LYS:HB3	1:D:669:LYS:HZ2	1.61	0.64
1:C:519:LEU:HD11	1:C:523:ARG:HA	1.80	0.64
1:A:664:ASP:O	1:A:666:LYS:N	2.30	0.64
1:A:582:LYS:HD3	1:A:599:GLN:HE22	1.62	0.64
1:B:513:PHE:CD1	1:B:547:PHE:HE1	2.16	0.63
1:C:513:PHE:CD1	1:C:547:PHE:HE1	2.16	0.63
1:A:669:LYS:HZ2	1:A:669:LYS:HB3	1.63	0.63
1:A:534:LYS:HG3	1:A:534:LYS:O	1.97	0.63
1:D:727:VAL:HG22	1:D:728:LEU:N	2.13	0.63
1:D:666:LYS:HB3	1:D:666:LYS:HZ1	1.60	0.63
1:A:513:PHE:CD1	1:A:547:PHE:HE1	2.16	0.63
1:D:549:GLU:CB	1:D:563:ARG:HH11	2.11	0.63
1:B:651:MET:O	1:B:654:MET:HB2	1.98	0.63
1:B:549:GLU:CB	1:B:563:ARG:HH11	2.11	0.63
1:B:669:LYS:HZ3	1:B:669:LYS:HB3	1.63	0.63
1:C:719:LYS:NZ	1:D:583:GLU:HG3	2.14	0.63
1:B:606:LEU:HD23	1:B:607:GLU:N	2.14	0.63
1:D:606:LEU:HD23	1:D:607:GLU:N	2.13	0.62
1:C:582:LYS:HD3	1:C:599:GLN:HE22	1.64	0.62
1:D:664:ASP:O	1:D:666:LYS:N	2.32	0.62
1:D:714:THR:HG1	1:D:733:PHE:HE2	1.46	0.62
1:C:534:LYS:O	1:C:534:LYS:HG3	1.98	0.62
1:A:519:LEU:HD11	1:A:523:ARG:HA	1.81	0.62
1:A:716:ARG:HG2	1:A:716:ARG:HH11	1.64	0.62
1:A:620:LEU:HD12	1:A:620:LEU:O	1.98	0.62
1:D:662:VAL:O	1:D:662:VAL:HG13	1.98	0.62
1:C:645:ILE:O	1:C:649:SER:HB2	1.99	0.62
1:A:549:GLU:CB	1:A:563:ARG:HH11	2.12	0.62
1:D:733:PHE:O	1:D:737:VAL:HG23	2.00	0.62
1:D:519:LEU:HD11	1:D:523:ARG:HA	1.82	0.62
1:C:513:PHE:O	1:C:514:LYS:HB2	1.98	0.62
1:B:659:LEU:HB2	1:B:671:ILE:HG21	1.81	0.62
1:C:581:LYS:HG3	1:C:582:LYS:H	1.65	0.62
1:A:513:PHE:O	1:A:514:LYS:HB2	1.99	0.62
1:B:566:LEU:HD21	1:B:596:TYR:CE2	2.35	0.62
1:D:513:PHE:O	1:D:514:LYS:HB2	1.99	0.62
1:A:662:VAL:HG13	1:A:662:VAL:O	2.00	0.61
1:B:582:LYS:HD3	1:B:599:GLN:HE22	1.63	0.61
1:C:736:LEU:HD12	1:C:736:LEU:O	1.99	0.61
1:C:716:ARG:HG2	1:C:716:ARG:NH1	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:658:GLN:O	1:A:661:VAL:HB	2.01	0.61
1:C:566:LEU:HD21	1:C:596:TYR:CE2	2.35	0.61
1:C:733:PHE:O	1:C:737:VAL:HG23	2.00	0.61
1:D:534:LYS:HG3	1:D:534:LYS:O	2.00	0.61
1:C:549:GLU:CB	1:C:563:ARG:HH11	2.13	0.61
1:B:716:ARG:NH1	1:B:716:ARG:HG2	2.16	0.61
1:D:716:ARG:HG2	1:D:716:ARG:HH11	1.65	0.61
1:B:664:ASP:O	1:B:666:LYS:N	2.33	0.61
1:D:581:LYS:HG3	1:D:582:LYS:H	1.66	0.61
1:C:662:VAL:O	1:C:662:VAL:HG13	2.01	0.60
1:A:666:LYS:HD2	1:A:667:ASN:N	2.16	0.60
1:B:666:LYS:HD2	1:B:667:ASN:N	2.17	0.60
1:C:666:LYS:HD2	1:C:667:ASN:N	2.16	0.60
1:C:651:MET:O	1:C:654:MET:HB2	2.02	0.60
1:B:535:GLN:HE22	1:C:626:GLY:HA3	1.66	0.60
1:D:582:LYS:HD3	1:D:599:GLN:HE22	1.66	0.60
1:C:644:LYS:HB3	1:C:685:PHE:CE2	2.37	0.60
1:B:637:GLN:HA	1:B:637:GLN:NE2	2.17	0.60
1:C:637:GLN:HA	1:C:637:GLN:NE2	2.17	0.60
1:B:519:LEU:HD11	1:B:523:ARG:HA	1.83	0.60
1:C:529:ALA:O	1:C:531:ARG:N	2.36	0.59
1:C:522:GLU:O	1:C:524:LYS:HG3	2.03	0.59
1:D:522:GLU:O	1:D:524:LYS:HG3	2.02	0.59
1:B:581:LYS:HG3	1:B:582:LYS:H	1.67	0.59
1:A:637:GLN:NE2	1:A:637:GLN:HA	2.18	0.59
1:B:513:PHE:O	1:B:514:LYS:HB2	2.02	0.59
1:C:606:LEU:HD23	1:C:606:LEU:C	2.23	0.59
1:B:532:LYS:N	1:B:532:LYS:HD2	2.18	0.59
1:D:716:ARG:NH1	1:D:716:ARG:HG2	2.18	0.59
1:D:620:LEU:HD12	1:D:620:LEU:O	2.02	0.59
1:D:666:LYS:HD2	1:D:667:ASN:N	2.17	0.58
1:B:662:VAL:HG13	1:B:662:VAL:O	2.03	0.58
1:C:664:ASP:HB2	1:C:666:LYS:HZ2	1.65	0.58
1:D:651:MET:O	1:D:654:MET:HB2	2.04	0.58
1:C:664:ASP:C	1:C:666:LYS:H	2.07	0.58
1:A:644:LYS:HB3	1:A:685:PHE:CE2	2.38	0.58
1:D:532:LYS:N	1:D:532:LYS:HD2	2.18	0.58
1:D:529:ALA:O	1:D:531:ARG:N	2.37	0.58
1:A:518:THR:HG22	1:A:528:VAL:CG2	2.31	0.58
1:C:659:LEU:HB2	1:C:671:ILE:HG21	1.86	0.58
1:D:644:LYS:HE2	1:D:685:PHE:CZ	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:581:LYS:HG3	1:A:582:LYS:H	1.68	0.58
1:B:522:GLU:O	1:B:524:LYS:HG3	2.04	0.58
1:B:733:PHE:O	1:B:737:VAL:HG23	2.04	0.58
1:A:644:LYS:HE2	1:A:685:PHE:CZ	2.39	0.58
1:A:651:MET:O	1:A:654:MET:HB2	2.03	0.57
1:A:733:PHE:O	1:A:737:VAL:HG23	2.04	0.57
1:B:620:LEU:O	1:B:620:LEU:HD12	2.04	0.57
1:A:529:ALA:O	1:A:531:ARG:N	2.37	0.57
1:B:664:ASP:HB2	1:B:666:LYS:HZ2	1.69	0.57
1:B:522:GLU:CG	1:B:524:LYS:HE3	2.34	0.57
1:C:625:HIS:O	1:C:627:LYS:HG2	2.03	0.57
1:B:625:HIS:O	1:B:627:LYS:HG2	2.04	0.57
1:D:727:VAL:HG22	1:D:728:LEU:H	1.70	0.57
1:C:522:GLU:CG	1:C:524:LYS:HE3	2.34	0.57
1:B:529:ALA:O	1:B:531:ARG:N	2.37	0.57
1:D:644:LYS:HB3	1:D:685:PHE:CE2	2.40	0.57
1:A:659:LEU:HB2	1:A:671:ILE:HG21	1.86	0.57
1:B:532:LYS:H	1:B:532:LYS:HD2	1.70	0.57
1:A:625:HIS:O	1:A:627:LYS:HG2	2.05	0.57
1:C:644:LYS:HE2	1:C:685:PHE:CZ	2.39	0.57
1:D:710:LEU:HD23	1:D:730:VAL:HG13	1.86	0.57
1:C:727:VAL:HG22	1:C:728:LEU:H	1.69	0.57
1:B:714:THR:HG1	1:B:733:PHE:HE2	1.49	0.56
1:C:518:THR:HG22	1:C:528:VAL:CG2	2.31	0.56
1:D:637:GLN:NE2	1:D:637:GLN:HA	2.20	0.56
1:D:532:LYS:H	1:D:532:LYS:HD2	1.71	0.56
1:A:532:LYS:N	1:A:532:LYS:HD2	2.20	0.56
1:A:727:VAL:CG2	1:A:728:LEU:H	2.19	0.56
1:A:716:ARG:HG2	1:A:716:ARG:NH1	2.18	0.56
1:C:525:LEU:HB3	1:C:725:LEU:HD11	1.87	0.56
1:D:606:LEU:HD23	1:D:606:LEU:C	2.26	0.56
1:A:522:GLU:O	1:A:524:LYS:HG3	2.06	0.56
1:D:625:HIS:O	1:D:627:LYS:HG2	2.05	0.56
1:A:710:LEU:HD23	1:A:730:VAL:HG13	1.87	0.55
1:D:664:ASP:HB2	1:D:666:LYS:HZ1	1.71	0.55
1:B:664:ASP:C	1:B:666:LYS:H	2.10	0.55
1:C:532:LYS:N	1:C:532:LYS:HD2	2.21	0.55
1:A:666:LYS:HZ3	1:A:667:ASN:H	1.54	0.55
1:B:582:LYS:HD3	1:B:599:GLN:NE2	2.21	0.55
1:D:522:GLU:CG	1:D:524:LYS:HE3	2.35	0.55
1:A:591:SER:HA	1:A:738:CYS:SG	2.46	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:658:GLN:OE1	1:D:659:LEU:N	2.39	0.55
1:B:644:LYS:HE2	1:B:685:PHE:CZ	2.41	0.55
1:B:727:VAL:HG22	1:B:728:LEU:H	1.69	0.55
1:B:534:LYS:HG3	1:B:534:LYS:O	2.07	0.55
1:C:572:ILE:CG1	1:C:691:ARG:HD3	2.37	0.55
1:A:664:ASP:C	1:A:666:LYS:H	2.09	0.55
1:A:525:LEU:HB3	1:A:725:LEU:HD11	1.88	0.55
1:A:662:VAL:O	1:A:668:ARG:HD3	2.07	0.55
1:B:606:LEU:C	1:B:606:LEU:HD23	2.27	0.55
1:A:714:THR:HG1	1:A:733:PHE:HE2	1.55	0.55
1:D:664:ASP:C	1:D:666:LYS:H	2.11	0.55
1:C:637:GLN:HE21	1:C:637:GLN:HA	1.72	0.54
1:C:658:GLN:O	1:C:661:VAL:HB	2.07	0.54
1:B:512:PHE:O	1:B:598:PHE:HA	2.08	0.54
1:D:525:LEU:HB3	1:D:725:LEU:HD11	1.88	0.54
1:D:687:MET:CE	1:D:710:LEU:HD21	2.37	0.54
1:C:620:LEU:HD12	1:C:620:LEU:O	2.06	0.54
1:A:687:MET:CE	1:A:710:LEU:HD21	2.37	0.54
1:C:710:LEU:HD23	1:C:730:VAL:HG13	1.90	0.54
1:C:525:LEU:CB	1:C:725:LEU:HD11	2.38	0.54
1:D:518:THR:HG22	1:D:528:VAL:CG2	2.34	0.54
1:A:606:LEU:HD23	1:A:606:LEU:C	2.27	0.54
1:D:591:SER:HA	1:D:738:CYS:SG	2.47	0.54
1:C:511:LEU:HD11	1:C:609:TRP:CE2	2.43	0.54
1:B:637:GLN:HE21	1:B:637:GLN:HA	1.73	0.54
1:C:591:SER:HA	1:C:738:CYS:SG	2.48	0.54
1:D:508:ALA:HB1	1:D:539:THR:HG22	1.90	0.53
1:B:687:MET:CE	1:B:710:LEU:HD21	2.38	0.53
1:A:727:VAL:CG2	1:A:728:LEU:N	2.71	0.53
1:A:508:ALA:HB1	1:A:539:THR:HG22	1.90	0.53
1:D:512:PHE:O	1:D:598:PHE:HA	2.09	0.53
1:C:714:THR:HG1	1:C:733:PHE:HE2	1.53	0.53
1:B:658:GLN:OE1	1:B:659:LEU:N	2.41	0.53
1:C:601:THR:HG23	1:C:605:ASP:OD2	2.08	0.53
1:A:581:LYS:CG	1:A:582:LYS:H	2.21	0.53
1:C:532:LYS:HD2	1:C:532:LYS:H	1.74	0.53
1:A:647:MET:HE3	1:C:650:LYS:HD3	1.91	0.53
1:C:582:LYS:HD3	1:C:599:GLN:NE2	2.23	0.53
1:B:644:LYS:HB3	1:B:685:PHE:CE2	2.44	0.53
1:A:718:SER:OG	1:A:740:ARG:NH2	2.42	0.53
1:C:666:LYS:HZ2	1:C:666:LYS:HB3	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:525:LEU:HB3	1:B:725:LEU:HD11	1.90	0.52
1:D:581:LYS:CG	1:D:582:LYS:H	2.21	0.52
1:C:581:LYS:CG	1:C:582:LYS:H	2.22	0.52
1:B:710:LEU:HD23	1:B:730:VAL:HG13	1.92	0.52
1:A:651:MET:SD	1:C:654:MET:HE3	2.47	0.52
1:B:518:THR:HG22	1:B:528:VAL:CG2	2.36	0.52
1:A:582:LYS:HD3	1:A:599:GLN:NE2	2.23	0.52
1:D:571:SER:HB3	1:D:588:LEU:HD21	1.92	0.52
1:A:522:GLU:CG	1:A:524:LYS:HE3	2.38	0.52
1:B:581:LYS:CG	1:B:582:LYS:H	2.22	0.52
1:A:637:GLN:HE21	1:A:637:GLN:HA	1.72	0.52
1:C:719:LYS:HZ1	1:D:583:GLU:HG3	1.74	0.52
1:C:658:GLN:OE1	1:C:659:LEU:N	2.42	0.52
1:B:508:ALA:HB1	1:B:539:THR:HG22	1.92	0.52
1:A:512:PHE:CZ	1:A:535:GLN:HG3	2.45	0.51
1:A:532:LYS:HD2	1:A:532:LYS:H	1.73	0.51
1:A:576:VAL:HB	1:A:585:VAL:HB	1.92	0.51
1:A:511:LEU:HD11	1:A:609:TRP:CE2	2.45	0.51
1:B:588:LEU:HD23	1:B:588:LEU:C	2.31	0.51
1:C:659:LEU:CD1	1:C:672:GLU:HG3	2.36	0.51
1:A:659:LEU:HA	1:A:662:VAL:HG12	1.92	0.51
1:A:659:LEU:CD1	1:A:672:GLU:HG3	2.40	0.51
1:D:531:ARG:H	1:D:531:ARG:CD	2.24	0.51
1:B:714:THR:OG1	1:B:733:PHE:HE2	1.93	0.51
1:B:662:VAL:O	1:B:668:ARG:HD3	2.10	0.51
1:D:513:PHE:HE2	1:D:515:PRO:HD3	1.71	0.51
1:B:514:LYS:CG	1:B:531:ARG:HH21	2.23	0.51
1:B:658:GLN:O	1:B:661:VAL:HB	2.10	0.51
1:C:662:VAL:O	1:C:668:ARG:HD3	2.10	0.51
1:D:601:THR:HG23	1:D:605:ASP:OD2	2.11	0.51
1:D:662:VAL:O	1:D:668:ARG:HD3	2.11	0.51
1:B:659:LEU:CD1	1:B:672:GLU:HG3	2.38	0.51
1:B:511:LEU:HD11	1:B:609:TRP:CE2	2.46	0.51
1:A:663:SER:HA	1:A:668:ARG:HE	1.76	0.51
1:B:601:THR:HG23	1:B:605:ASP:OD2	2.10	0.51
1:D:525:LEU:CB	1:D:725:LEU:HD11	2.40	0.51
1:A:525:LEU:CB	1:A:725:LEU:HD11	2.41	0.50
1:C:512:PHE:CZ	1:C:535:GLN:HG3	2.47	0.50
1:D:659:LEU:CD1	1:D:672:GLU:HG3	2.40	0.50
1:D:513:PHE:CD2	1:D:515:PRO:HD3	2.46	0.50
1:A:514:LYS:CG	1:A:531:ARG:HH21	2.24	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:669:LYS:HB3	1:C:669:LYS:HZ2	1.73	0.50
1:A:512:PHE:O	1:A:598:PHE:HA	2.11	0.50
1:B:707:PRO:CB	1:B:730:VAL:HG21	2.41	0.50
1:D:637:GLN:HE21	1:D:637:GLN:HA	1.76	0.50
1:C:508:ALA:HB1	1:C:539:THR:HG22	1.93	0.50
1:C:507:LYS:HG3	1:C:508:ALA:N	2.27	0.50
1:D:656:GLU:C	1:D:658:GLN:H	2.16	0.50
1:C:512:PHE:O	1:C:598:PHE:HA	2.11	0.50
1:C:666:LYS:HZ3	1:C:666:LYS:HB3	1.75	0.50
1:B:512:PHE:CZ	1:B:535:GLN:HG3	2.46	0.49
1:D:663:SER:HA	1:D:668:ARG:HE	1.77	0.49
1:C:663:SER:HA	1:C:668:ARG:HE	1.77	0.49
1:D:727:VAL:CG2	1:D:728:LEU:H	2.25	0.49
1:B:550:THR:OG1	1:C:624:LYS:HD3	2.12	0.49
1:A:572:ILE:CG1	1:A:691:ARG:HD3	2.42	0.49
1:C:576:VAL:HB	1:C:585:VAL:HB	1.94	0.49
1:A:513:PHE:CD2	1:A:515:PRO:HD3	2.47	0.49
1:B:507:LYS:HG3	1:B:508:ALA:N	2.26	0.49
1:A:579:HIS:CD2	1:A:585:VAL:HG21	2.47	0.49
1:A:512:PHE:CE1	1:A:535:GLN:HG3	2.48	0.49
1:C:571:SER:HB3	1:C:588:LEU:HD21	1.94	0.49
1:D:658:GLN:O	1:D:661:VAL:HB	2.12	0.49
1:C:512:PHE:CE1	1:C:535:GLN:HG3	2.48	0.49
1:B:665:PRO:HA	1:B:668:ARG:HB2	1.95	0.49
1:C:669:LYS:HB3	1:C:669:LYS:HZ3	1.76	0.49
1:A:651:MET:SD	1:C:654:MET:SD	3.10	0.49
1:C:513:PHE:CD2	1:C:515:PRO:HD3	2.48	0.49
1:C:664:ASP:CB	1:C:666:LYS:HZ2	2.24	0.49
1:B:727:VAL:CG2	1:B:728:LEU:H	2.26	0.49
1:D:707:PRO:CB	1:D:730:VAL:HG21	2.43	0.49
1:D:582:LYS:HD3	1:D:599:GLN:NE2	2.26	0.49
1:B:513:PHE:CD2	1:B:515:PRO:HD3	2.47	0.49
1:B:576:VAL:HB	1:B:585:VAL:HB	1.94	0.49
1:C:547:PHE:N	1:C:547:PHE:HD2	2.10	0.49
1:C:727:VAL:CG2	1:C:728:LEU:N	2.75	0.49
1:B:645:ILE:CG1	1:B:685:PHE:HB3	2.43	0.49
1:C:727:VAL:CG2	1:C:728:LEU:H	2.26	0.49
1:D:715:SER:HB2	1:D:717:PRO:HD2	1.95	0.49
1:C:664:ASP:C	1:C:666:LYS:N	2.66	0.49
1:B:633:LEU:O	1:B:637:GLN:HG2	2.13	0.49
1:C:531:ARG:CD	1:C:531:ARG:H	2.24	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:650:LYS:O	1:B:654:MET:HG2	2.13	0.48
1:C:687:MET:CE	1:C:710:LEU:HD21	2.42	0.48
1:D:511:LEU:HD11	1:D:609:TRP:CE2	2.47	0.48
1:D:659:LEU:HA	1:D:662:VAL:HG12	1.95	0.48
1:A:645:ILE:CG1	1:A:685:PHE:HB3	2.42	0.48
1:C:707:PRO:CB	1:C:730:VAL:HG21	2.43	0.48
1:A:654:MET:CE	1:A:654:MET:HA	2.43	0.48
1:B:513:PHE:HE2	1:B:515:PRO:HD3	1.73	0.48
1:B:514:LYS:HE2	1:B:531:ARG:NH2	2.29	0.48
1:A:581:LYS:HG3	1:A:582:LYS:HG3	1.95	0.48
1:B:663:SER:HA	1:B:668:ARG:HE	1.78	0.48
1:B:531:ARG:CD	1:B:531:ARG:H	2.26	0.48
1:B:547:PHE:CD2	1:B:547:PHE:N	2.82	0.48
1:C:514:LYS:CG	1:C:531:ARG:HH21	2.27	0.48
1:A:531:ARG:H	1:A:531:ARG:CD	2.26	0.48
1:C:714:THR:OG1	1:C:733:PHE:HE2	1.95	0.48
1:B:549:GLU:CB	1:B:563:ARG:NH1	2.77	0.48
1:C:716:ARG:N	1:C:717:PRO:CD	2.76	0.48
1:A:664:ASP:C	1:A:666:LYS:N	2.66	0.48
1:B:512:PHE:HB2	1:B:599:GLN:HB3	1.95	0.48
1:A:707:PRO:CB	1:A:730:VAL:HG21	2.44	0.48
1:D:665:PRO:HA	1:D:668:ARG:HB2	1.95	0.48
1:A:601:THR:HG23	1:A:605:ASP:OD2	2.13	0.48
1:B:525:LEU:CB	1:B:725:LEU:HD11	2.43	0.48
1:D:569:GLU:OE2	1:D:624:LYS:HD2	2.13	0.48
1:B:727:VAL:CG2	1:B:728:LEU:N	2.75	0.48
1:B:716:ARG:N	1:B:717:PRO:CD	2.77	0.48
1:A:514:LYS:HE2	1:A:531:ARG:NH2	2.28	0.48
1:B:571:SER:HB3	1:B:588:LEU:HD21	1.96	0.47
1:D:512:PHE:CZ	1:D:535:GLN:HG3	2.49	0.47
1:A:512:PHE:HB2	1:A:599:GLN:HB3	1.96	0.47
1:B:547:PHE:HD2	1:B:547:PHE:N	2.12	0.47
1:B:659:LEU:HA	1:B:662:VAL:HG12	1.96	0.47
1:A:516:LEU:O	1:A:516:LEU:HD12	2.15	0.47
1:B:542:GLY:O	1:B:616:ALA:HB1	2.14	0.47
1:B:715:SER:HB2	1:B:717:PRO:HD2	1.97	0.47
1:D:533:TRP:HE1	1:D:581:LYS:CE	2.26	0.47
1:B:512:PHE:CE1	1:B:535:GLN:HG3	2.49	0.47
1:C:533:TRP:HE1	1:C:581:LYS:CE	2.25	0.47
1:C:664:ASP:N	1:C:664:ASP:OD2	2.47	0.47
1:C:659:LEU:HD23	1:C:660:SER:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:533:TRP:HE1	1:A:581:LYS:CE	2.24	0.47
1:D:507:LYS:HG3	1:D:508:ALA:N	2.29	0.47
1:B:572:ILE:HG12	1:B:691:ARG:HD3	1.96	0.47
1:D:716:ARG:N	1:D:717:PRO:CD	2.78	0.47
1:B:664:ASP:C	1:B:666:LYS:N	2.68	0.47
1:A:587:CYS:SG	1:A:595:VAL:HG13	2.54	0.47
1:A:547:PHE:HD2	1:A:547:PHE:N	2.13	0.47
1:D:645:ILE:CG1	1:D:685:PHE:HB3	2.43	0.47
1:A:507:LYS:HG3	1:A:508:ALA:N	2.30	0.47
1:A:547:PHE:CD2	1:A:547:PHE:N	2.83	0.47
1:A:659:LEU:HD23	1:A:660:SER:N	2.29	0.47
1:D:549:GLU:CB	1:D:563:ARG:NH1	2.76	0.47
1:D:639:ARG:NH1	1:D:639:ARG:HB2	2.30	0.47
1:D:512:PHE:CE1	1:D:535:GLN:HG3	2.50	0.47
1:B:533:TRP:HE1	1:B:581:LYS:CE	2.27	0.47
1:C:547:PHE:N	1:C:547:PHE:CD2	2.80	0.47
1:A:658:GLN:C	1:A:658:GLN:OE1	2.53	0.47
1:C:715:SER:HB2	1:C:717:PRO:HD2	1.97	0.46
1:B:707:PRO:HB2	1:B:730:VAL:HG21	1.97	0.46
1:D:514:LYS:HE2	1:D:531:ARG:NH2	2.30	0.46
1:C:513:PHE:HE2	1:C:515:PRO:HD3	1.75	0.46
1:D:664:ASP:C	1:D:666:LYS:N	2.68	0.46
1:A:714:THR:OG1	1:A:733:PHE:HE2	1.97	0.46
1:D:727:VAL:CG2	1:D:728:LEU:N	2.76	0.46
1:C:645:ILE:CG1	1:C:685:PHE:HB3	2.44	0.46
1:C:718:SER:OG	1:C:740:ARG:NH2	2.47	0.46
1:C:650:LYS:O	1:C:654:MET:HG2	2.14	0.46
1:D:576:VAL:HG12	1:D:576:VAL:O	2.15	0.46
1:C:572:ILE:HD11	1:C:691:ARG:HB2	1.97	0.46
1:B:569:GLU:OE2	1:B:624:LYS:HD2	2.15	0.46
1:C:520:GLN:HG3	1:C:526:GLU:CB	2.45	0.46
1:D:514:LYS:CG	1:D:531:ARG:HH21	2.28	0.46
1:A:609:TRP:O	1:A:613:ILE:HG13	2.15	0.46
1:C:665:PRO:HA	1:C:668:ARG:HB2	1.98	0.46
1:D:707:PRO:HB2	1:D:730:VAL:HG21	1.97	0.46
1:D:691:ARG:HD2	1:D:695:TYR:OH	2.16	0.46
1:B:664:ASP:OD2	1:B:664:ASP:N	2.49	0.46
1:A:715:SER:HB2	1:A:717:PRO:HD2	1.98	0.46
1:D:547:PHE:N	1:D:547:PHE:CD2	2.83	0.46
1:D:547:PHE:N	1:D:547:PHE:HD2	2.13	0.46
1:D:576:VAL:HB	1:D:585:VAL:HB	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:512:PHE:HB2	1:C:599:GLN:HB3	1.97	0.46
1:D:714:THR:OG1	1:D:733:PHE:HE2	1.98	0.46
1:A:586:PHE:HB3	1:A:606:LEU:CD1	2.46	0.46
1:A:572:ILE:HD11	1:A:691:ARG:HB2	1.98	0.46
1:A:664:ASP:N	1:A:664:ASP:OD2	2.49	0.45
1:B:535:GLN:NE2	1:C:626:GLY:HA3	2.31	0.45
1:C:659:LEU:HA	1:C:662:VAL:HG12	1.97	0.45
1:C:637:GLN:HE21	1:C:637:GLN:CA	2.28	0.45
1:C:514:LYS:NZ	1:C:581:LYS:NZ	2.64	0.45
1:C:579:HIS:CD2	1:C:585:VAL:HG21	2.51	0.45
1:A:665:PRO:HA	1:A:668:ARG:HB2	1.98	0.45
1:B:716:ARG:HB3	1:B:717:PRO:HD3	1.98	0.45
1:A:520:GLN:HG3	1:A:526:GLU:CB	2.45	0.45
1:D:513:PHE:CD1	1:D:547:PHE:CE1	3.01	0.45
1:A:549:GLU:CB	1:A:563:ARG:NH1	2.78	0.45
1:B:656:GLU:C	1:B:658:GLN:H	2.19	0.45
1:B:637:GLN:CA	1:B:637:GLN:NE2	2.78	0.45
1:A:711:LEU:HD13	1:A:728:LEU:HD12	1.96	0.45
1:C:722:LEU:HG	1:C:736:LEU:CD2	2.47	0.45
1:C:586:PHE:HB3	1:C:606:LEU:CD1	2.46	0.45
1:A:513:PHE:CD1	1:A:547:PHE:CE1	3.01	0.45
1:B:654:MET:CE	1:B:654:MET:HA	2.46	0.45
1:D:572:ILE:CG1	1:D:691:ARG:HD3	2.46	0.45
1:A:676:ARG:NH2	1:A:680:GLN:HG3	2.32	0.45
1:B:588:LEU:HD12	1:B:613:ILE:HD13	1.99	0.45
1:D:659:LEU:CD2	1:D:659:LEU:C	2.82	0.45
1:B:572:ILE:CG1	1:B:691:ARG:HD3	2.46	0.45
1:C:516:LEU:O	1:C:516:LEU:HD12	2.17	0.45
1:C:639:ARG:HB2	1:C:639:ARG:NH1	2.32	0.45
1:B:514:LYS:HG2	1:B:531:ARG:NH2	2.31	0.45
1:C:656:GLU:C	1:C:658:GLN:H	2.20	0.45
1:C:572:ILE:HG12	1:C:691:ARG:HD3	1.98	0.45
1:B:513:PHE:CD1	1:B:547:PHE:CE1	3.01	0.44
1:D:588:LEU:HD23	1:D:588:LEU:C	2.38	0.44
1:A:572:ILE:HG12	1:A:691:ARG:HD3	1.99	0.44
1:C:513:PHE:CD1	1:C:547:PHE:CE1	3.02	0.44
1:A:514:LYS:HG2	1:A:531:ARG:NH2	2.33	0.44
1:C:549:GLU:CB	1:C:563:ARG:NH1	2.78	0.44
1:C:711:LEU:HD13	1:C:728:LEU:HD12	1.99	0.44
1:B:639:ARG:HB2	1:B:639:ARG:NH1	2.31	0.44
1:A:637:GLN:NE2	1:A:637:GLN:CA	2.79	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:633:LEU:O	1:C:637:GLN:HG2	2.17	0.44
1:D:520:GLN:HG3	1:D:526:GLU:CB	2.47	0.44
1:D:659:LEU:HD23	1:D:660:SER:N	2.32	0.44
1:D:707:PRO:HB2	1:D:730:VAL:CG2	2.47	0.44
1:C:569:GLU:OE2	1:C:624:LYS:HD2	2.18	0.44
1:B:516:LEU:O	1:B:516:LEU:HD12	2.17	0.44
1:D:633:LEU:O	1:D:637:GLN:HG2	2.17	0.44
1:C:707:PRO:HB2	1:C:730:VAL:HG21	1.99	0.44
1:D:512:PHE:HB2	1:D:599:GLN:HB3	1.99	0.44
1:A:669:LYS:HZ3	1:A:669:LYS:HB3	1.82	0.44
1:A:639:ARG:NH1	1:A:639:ARG:HB2	2.32	0.44
1:C:654:MET:HA	1:C:654:MET:CE	2.37	0.44
1:B:664:ASP:CB	1:B:666:LYS:HZ2	2.30	0.44
1:A:664:ASP:HB2	1:A:666:LYS:HZ1	1.78	0.44
1:D:581:LYS:HG3	1:D:582:LYS:HG3	1.99	0.44
1:A:716:ARG:N	1:A:717:PRO:CD	2.81	0.44
1:A:633:LEU:O	1:A:637:GLN:HG2	2.17	0.44
1:B:707:PRO:HB2	1:B:730:VAL:CG2	2.48	0.44
1:A:569:GLU:OE2	1:A:624:LYS:HD2	2.18	0.44
1:C:513:PHE:O	1:C:514:LYS:CB	2.66	0.43
1:B:659:LEU:HD23	1:B:660:SER:N	2.33	0.43
1:D:516:LEU:O	1:D:516:LEU:HD12	2.17	0.43
1:A:576:VAL:HG12	1:A:576:VAL:O	2.19	0.43
1:C:609:TRP:O	1:C:613:ILE:HG13	2.18	0.43
1:B:722:LEU:HG	1:B:736:LEU:CD2	2.48	0.43
1:A:645:ILE:HG12	1:A:685:PHE:HB3	2.00	0.43
1:D:572:ILE:HG12	1:D:691:ARG:HD3	2.01	0.43
1:C:520:GLN:CG	1:C:526:GLU:HB2	2.48	0.43
1:B:597:LEU:C	1:B:598:PHE:CD2	2.91	0.43
1:A:579:HIS:CG	1:A:585:VAL:HG21	2.53	0.43
1:A:687:MET:HE2	1:A:710:LEU:HD11	2.01	0.43
1:D:664:ASP:CB	1:D:666:LYS:HZ1	2.31	0.43
1:A:716:ARG:HB3	1:A:717:PRO:HD3	2.00	0.43
1:C:531:ARG:CD	1:C:531:ARG:N	2.82	0.43
1:D:522:GLU:HB3	1:D:524:LYS:HE3	2.01	0.43
1:B:587:CYS:SG	1:B:595:VAL:HG13	2.58	0.43
1:A:659:LEU:C	1:A:659:LEU:CD2	2.83	0.43
1:B:711:LEU:HD13	1:B:728:LEU:HD12	2.00	0.43
1:D:711:LEU:HD13	1:D:728:LEU:HD12	1.99	0.43
1:D:676:ARG:NH2	1:D:680:GLN:HG3	2.34	0.43
1:A:542:GLY:O	1:A:616:ALA:HB1	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:520:GLN:CG	1:A:526:GLU:HB2	2.48	0.43
1:A:588:LEU:C	1:A:588:LEU:HD23	2.37	0.43
1:B:534:LYS:HE3	1:B:534:LYS:HB2	1.79	0.43
1:B:520:GLN:HG3	1:B:526:GLU:CB	2.47	0.43
1:B:510:TRP:CE3	1:B:535:GLN:NE2	2.87	0.43
1:A:588:LEU:HD12	1:A:613:ILE:HD13	2.01	0.43
1:C:574:GLN:HE21	1:C:574:GLN:HB3	1.71	0.43
1:D:587:CYS:SG	1:D:595:VAL:HG13	2.58	0.43
1:C:576:VAL:HG12	1:C:576:VAL:O	2.19	0.43
1:C:597:LEU:C	1:C:598:PHE:CD2	2.92	0.43
1:A:707:PRO:HB2	1:A:730:VAL:CG2	2.49	0.42
1:D:654:MET:CE	1:D:654:MET:HA	2.48	0.42
1:D:637:GLN:CA	1:D:637:GLN:HE21	2.32	0.42
1:C:707:PRO:HB2	1:C:730:VAL:CG2	2.49	0.42
1:D:514:LYS:NZ	1:D:581:LYS:NZ	2.68	0.42
1:D:531:ARG:N	1:D:531:ARG:CD	2.82	0.42
1:A:514:LYS:CE	1:A:531:ARG:NH2	2.83	0.42
1:A:658:GLN:OE1	1:A:659:LEU:CA	2.67	0.42
1:A:508:ALA:CB	1:A:539:THR:HG22	2.49	0.42
1:D:597:LEU:C	1:D:598:PHE:CD2	2.93	0.42
1:A:656:GLU:C	1:A:658:GLN:H	2.22	0.42
1:C:528:VAL:HG12	1:C:529:ALA:N	2.34	0.42
1:C:581:LYS:HG3	1:C:582:LYS:HG3	2.01	0.42
1:D:573:VAL:HG22	1:D:588:LEU:HG	2.02	0.42
1:D:664:ASP:N	1:D:664:ASP:OD2	2.51	0.42
1:C:716:ARG:HB3	1:C:717:PRO:HD3	2.01	0.42
1:D:534:LYS:HE2	1:D:536:TYR:CE2	2.54	0.42
1:A:722:LEU:HG	1:A:736:LEU:CD2	2.48	0.42
1:C:659:LEU:HD11	1:C:672:GLU:CG	2.43	0.42
1:B:601:THR:OG1	1:B:602:SER:N	2.53	0.42
1:A:676:ARG:HA	1:A:676:ARG:HD2	1.90	0.42
1:D:513:PHE:O	1:D:514:LYS:CB	2.67	0.42
1:B:579:HIS:CD2	1:B:585:VAL:HG21	2.55	0.42
1:C:514:LYS:HG2	1:C:531:ARG:NH2	2.35	0.42
1:D:609:TRP:O	1:D:613:ILE:HG13	2.20	0.42
1:A:571:SER:HB3	1:A:588:LEU:HD21	2.02	0.42
1:A:534:LYS:HE2	1:A:536:TYR:CE2	2.54	0.42
1:D:520:GLN:CG	1:D:526:GLU:HB2	2.50	0.42
1:C:518:THR:CG2	1:C:528:VAL:HG22	2.39	0.42
1:D:703:GLU:HG2	1:D:704:LEU:N	2.35	0.42
1:C:703:GLU:HG2	1:C:704:LEU:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:514:LYS:HE2	1:C:531:ARG:NH2	2.34	0.42
1:A:528:VAL:HG12	1:A:529:ALA:N	2.34	0.42
1:C:668:ARG:HG3	1:C:668:ARG:HH11	1.85	0.42
1:D:579:HIS:CD2	1:D:585:VAL:HG21	2.55	0.41
1:B:514:LYS:CE	1:B:531:ARG:NH2	2.83	0.41
1:A:637:GLN:HE21	1:A:637:GLN:CA	2.28	0.41
1:B:593:GLY:HA2	1:B:735:ALA:HA	2.01	0.41
1:D:655:ALA:HB3	1:D:675:ILE:CD1	2.50	0.41
1:B:581:LYS:HG3	1:B:582:LYS:HG3	2.01	0.41
1:C:529:ALA:O	1:C:531:ARG:HG3	2.20	0.41
1:A:529:ALA:O	1:A:531:ARG:HG3	2.20	0.41
1:C:511:LEU:HD23	1:C:600:ALA:HA	2.02	0.41
1:D:722:LEU:HG	1:D:736:LEU:CD2	2.50	0.41
1:B:522:GLU:HB3	1:B:524:LYS:HE3	2.02	0.41
1:C:687:MET:HE2	1:C:710:LEU:HD11	2.01	0.41
1:B:655:ALA:HB3	1:B:675:ILE:CD1	2.50	0.41
1:D:580:PRO:HG2	1:D:581:LYS:H	1.85	0.41
1:B:718:SER:OG	1:B:740:ARG:NH2	2.51	0.41
1:D:510:TRP:CE3	1:D:535:GLN:NE2	2.89	0.41
1:A:687:MET:HE3	1:A:733:PHE:CD1	2.56	0.41
1:A:601:THR:OG1	1:A:602:SER:N	2.53	0.41
1:C:522:GLU:HB3	1:C:524:LYS:HE3	2.03	0.41
1:A:691:ARG:HD2	1:A:695:TYR:OH	2.21	0.41
1:D:569:GLU:HG2	1:D:570:ASP:OD2	2.20	0.41
1:B:655:ALA:HB3	1:B:675:ILE:HD11	2.03	0.41
1:D:542:GLY:O	1:D:616:ALA:HB1	2.19	0.41
1:C:655:ALA:HB3	1:C:675:ILE:CD1	2.51	0.41
1:C:504:VAL:O	1:C:542:GLY:N	2.42	0.41
1:A:664:ASP:HB2	1:A:666:LYS:HZ2	1.83	0.41
1:B:533:TRP:NE1	1:B:581:LYS:HE3	2.31	0.41
1:C:580:PRO:HG2	1:C:581:LYS:H	1.85	0.41
1:D:508:ALA:CB	1:D:539:THR:HG22	2.49	0.41
1:C:542:GLY:O	1:C:616:ALA:HB1	2.20	0.41
1:B:520:GLN:CG	1:B:526:GLU:HB2	2.50	0.41
1:D:588:LEU:HD12	1:D:613:ILE:HD13	2.03	0.41
1:B:590:ASN:OD1	1:B:594:ASP:HB2	2.21	0.41
1:A:514:LYS:NZ	1:A:581:LYS:NZ	2.68	0.41
1:A:513:PHE:HE2	1:A:515:PRO:HD3	1.77	0.41
1:A:660:SER:C	1:A:661:VAL:HG23	2.41	0.41
1:A:508:ALA:HA	1:A:538:VAL:O	2.19	0.41
1:B:573:VAL:HG22	1:B:588:LEU:HG	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:533:TRP:NE1	1:D:581:LYS:HE3	2.30	0.41
1:B:529:ALA:O	1:B:531:ARG:HG3	2.21	0.41
1:B:576:VAL:O	1:B:576:VAL:HG12	2.21	0.41
1:B:514:LYS:NZ	1:B:581:LYS:NZ	2.69	0.41
1:B:531:ARG:CD	1:B:531:ARG:N	2.84	0.41
1:B:645:ILE:HG12	1:B:685:PHE:HB3	2.03	0.41
1:D:534:LYS:HE3	1:D:534:LYS:HB2	1.80	0.41
1:D:587:CYS:HB2	1:D:597:LEU:HD23	2.02	0.41
1:D:566:LEU:HD12	1:D:567:PHE:N	2.35	0.41
1:C:691:ARG:HD2	1:C:695:TYR:OH	2.21	0.41
1:B:511:LEU:HD23	1:B:600:ALA:HA	2.03	0.41
1:B:528:VAL:HG12	1:B:529:ALA:N	2.35	0.40
1:C:588:LEU:HD12	1:C:613:ILE:HD13	2.02	0.40
1:B:508:ALA:CB	1:B:539:THR:HG22	2.51	0.40
1:C:587:CYS:SG	1:C:595:VAL:HG13	2.62	0.40
1:D:601:THR:OG1	1:D:602:SER:N	2.54	0.40
1:C:601:THR:OG1	1:C:602:SER:N	2.53	0.40
1:C:584:HIS:ND1	1:C:602:SER:HA	2.36	0.40
1:C:676:ARG:NH2	1:C:680:GLN:HG3	2.36	0.40
1:D:513:PHE:CD2	1:D:514:LYS:N	2.89	0.40
1:D:656:GLU:C	1:D:658:GLN:N	2.74	0.40
1:D:656:GLU:O	1:D:658:GLN:N	2.39	0.40
1:B:561:ALA:HA	1:B:562:PRO:HD3	1.91	0.40
1:C:583:GLU:HG3	1:D:719:LYS:NZ	2.36	0.40
1:D:590:ASN:OD1	1:D:594:ASP:HB2	2.22	0.40
1:A:650:LYS:O	1:A:654:MET:HG2	2.19	0.40
1:D:529:ALA:O	1:D:531:ARG:HG3	2.22	0.40
1:C:514:LYS:NZ	1:C:581:LYS:HZ3	2.18	0.40
1:A:531:ARG:N	1:A:531:ARG:CD	2.84	0.40
1:C:588:LEU:C	1:C:588:LEU:HD23	2.38	0.40
1:A:707:PRO:HB2	1:A:730:VAL:HG21	2.01	0.40
1:D:645:ILE:HG12	1:D:685:PHE:HB3	2.03	0.40
1:C:566:LEU:HD12	1:C:567:PHE:N	2.36	0.40
1:A:655:ALA:HB3	1:A:675:ILE:CD1	2.52	0.40
1:B:682:LEU:HD23	1:B:682:LEU:HA	1.90	0.40
1:B:715:SER:HG	1:B:718:SER:HB2	1.86	0.40
1:D:535:GLN:O	1:D:536:TYR:CG	2.75	0.40
1:C:519:LEU:HD13	1:C:525:LEU:HD23	2.03	0.40
1:D:519:LEU:HD13	1:D:525:LEU:HD23	2.03	0.40
1:A:522:GLU:HB3	1:A:524:LYS:HE3	2.02	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	227/263 (86%)	183 (81%)	32 (14%)	12 (5%)	2	19
1	B	227/263 (86%)	185 (82%)	32 (14%)	10 (4%)	3	24
1	C	227/263 (86%)	184 (81%)	32 (14%)	11 (5%)	3	22
1	D	227/263 (86%)	185 (82%)	31 (14%)	11 (5%)	3	22
All	All	908/1052 (86%)	737 (81%)	127 (14%)	44 (5%)	3	22

All (44) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	528	VAL
1	A	530	ARG
1	B	528	VAL
1	B	530	ARG
1	C	528	VAL
1	C	530	ARG
1	D	528	VAL
1	D	530	ARG
1	A	514	LYS
1	A	529	ALA
1	A	535	GLN
1	A	661	VAL
1	B	514	LYS
1	B	529	ALA
1	B	661	VAL
1	C	514	LYS
1	C	529	ALA
1	C	535	GLN
1	C	661	VAL
1	D	514	LYS
1	D	529	ALA
1	D	535	GLN

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Mol	Chain	Res	Type
1	D	661	VAL
1	A	531	ARG
1	A	665	PRO
1	A	672	GLU
1	B	531	ARG
1	B	535	GLN
1	B	665	PRO
1	C	531	ARG
1	C	665	PRO
1	C	672	GLU
1	D	531	ARG
1	D	665	PRO
1	D	672	GLU
1	B	672	GLU
1	A	580	PRO
1	B	580	PRO
1	D	580	PRO
1	A	581	LYS
1	C	580	PRO
1	D	542	GLY
1	C	542	GLY
1	A	542	GLY

### 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	205/233 (88%)	190 (93%)	15 (7%)	17	57
1	B	205/233 (88%)	189 (92%)	16 (8%)	16	53
1	C	205/233 (88%)	190 (93%)	15 (7%)	17	57
1	D	205/233 (88%)	190 (93%)	15 (7%)	17	57
All	All	820/932 (88%)	759 (93%)	61 (7%)	17	56

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	531	ARG
1	A	532	LYS
1	A	535	GLN
1	A	547	PHE
1	A	566	LEU
1	A	574	GLN
1	A	578	GLU
1	A	589	SER
1	A	658	GLN
1	A	659	LEU
1	A	664	ASP
1	A	666	LYS
1	A	704	LEU
1	A	728	LEU
1	A	733	PHE
1	B	531	ARG
1	B	532	LYS
1	B	535	GLN
1	B	547	PHE
1	B	566	LEU
1	B	574	GLN
1	B	578	GLU
1	B	589	SER
1	B	598	PHE
1	B	658	GLN
1	B	659	LEU
1	B	664	ASP
1	B	666	LYS
1	B	704	LEU
1	B	728	LEU
1	B	733	PHE
1	C	531	ARG
1	C	532	LYS
1	C	535	GLN
1	C	547	PHE
1	C	566	LEU
1	C	574	GLN
1	C	578	GLU
1	C	589	SER
1	C	658	GLN
1	C	659	LEU
1	C	664	ASP
1	C	666	LYS

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Mol	Chain	Res	Type
1	C	704	LEU
1	C	728	LEU
1	C	733	PHE
1	D	531	ARG
1	D	532	LYS
1	D	535	GLN
1	D	547	PHE
1	D	566	LEU
1	D	574	GLN
1	D	578	GLU
1	D	589	SER
1	D	658	GLN
1	D	659	LEU
1	D	664	ASP
1	D	666	LYS
1	D	704	LEU
1	D	728	LEU
1	D	733	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	535	GLN
1	A	574	GLN
1	A	599	GLN
1	A	608	ASN
1	A	637	GLN
1	A	673	ASN
1	A	674	GLN
1	A	680	GLN
1	A	681	ASN
1	B	535	GLN
1	B	574	GLN
1	B	599	GLN
1	B	608	ASN
1	B	637	GLN
1	B	673	ASN
1	B	674	GLN
1	B	680	GLN
1	B	681	ASN
1	B	686	HIS
1	C	535	GLN

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Mol	Chain	Res	Type
1	C	574	GLN
1	C	579	HIS
1	C	599	GLN
1	C	608	ASN
1	C	637	GLN
1	C	673	ASN
1	C	674	GLN
1	C	680	GLN
1	C	681	ASN
1	C	686	HIS
1	D	535	GLN
1	D	574	GLN
1	D	579	HIS
1	D	599	GLN
1	D	608	ASN
1	D	637	GLN
1	D	673	ASN
1	D	674	GLN
1	D	680	GLN
1	D	681	ASN
1	D	686	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 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	231/263 (87%)	0.62	24 (10%) 8 5	87, 141, 197, 200	0
1	B	231/263 (87%)	0.49	18 (7%) 16 9	93, 151, 194, 200	0
1	C	231/263 (87%)	0.60	24 (10%) 8 5	87, 139, 191, 200	0
1	D	231/263 (87%)	0.40	8 (3%) 48 32	91, 130, 185, 200	0
All	All	924/1052 (87%)	0.53	74 (8%) 15 8	87, 141, 192, 200	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	551	TYR	9.6
1	A	513	PHE	8.0
1	A	657	LEU	6.8
1	A	550	THR	5.9
1	A	551	TYR	5.3
1	B	668	ARG	4.7
1	C	565	ALA	4.7
1	C	550	THR	4.6
1	B	506	ARG	4.4
1	B	669	LYS	4.3
1	B	663	SER	4.3
1	B	662	VAL	4.3
1	A	548	TYR	4.2
1	A	725	LEU	3.8
1	A	506	ARG	3.6
1	C	525	LEU	3.6
1	A	505	VAL	3.5
1	B	659	LEU	3.5
1	A	515	PRO	3.4
1	B	543	CYS	3.4
1	C	593	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	655	ALA	3.3
1	C	531	ARG	3.3
1	A	660	SER	3.3
1	C	563	ARG	3.3
1	B	536	TYR	3.2
1	B	728	LEU	3.2
1	C	506	ARG	3.1
1	D	630	THR	3.1
1	A	549	GLU	3.1
1	A	531	ARG	3.1
1	C	596	TYR	3.0
1	D	525	LEU	3.0
1	A	742	ASP	2.9
1	C	529	ALA	2.9
1	D	561	ALA	2.9
1	A	521	LYS	2.9
1	C	665	PRO	2.8
1	C	567	PHE	2.8
1	D	560	SER	2.8
1	A	537	TRP	2.7
1	A	563	ARG	2.7
1	C	561	ALA	2.7
1	C	528	VAL	2.7
1	B	658	GLN	2.6
1	A	520	GLN	2.6
1	C	562	PRO	2.6
1	C	513	PHE	2.6
1	C	522	GLU	2.5
1	A	665	PRO	2.5
1	C	598	PHE	2.4
1	D	618	ALA	2.4
1	B	661	VAL	2.4
1	D	657	LEU	2.4
1	C	505	VAL	2.3
1	C	564	CYS	2.3
1	D	540	LEU	2.3
1	C	521	LYS	2.3
1	A	729	SER	2.3
1	A	663	SER	2.2
1	A	588	LEU	2.2
1	C	548	TYR	2.2
1	A	598	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	566	LEU	2.2
1	B	540	LEU	2.1
1	B	505	VAL	2.1
1	B	533	TRP	2.1
1	A	728	LEU	2.1
1	C	519	LEU	2.1
1	D	729	SER	2.1
1	B	513	PHE	2.1
1	C	549	GLU	2.0
1	A	510	TRP	2.0
1	B	664	ASP	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.