



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:25 PM GMT

PDB ID : 1FL9  
Title : THE YJEE PROTEIN  
Authors : Teplyakov, A.; Gilliland, G.L.; Structure 2 Function Project (S2F)  
Deposited on : 2000-08-13  
Resolution : 2.50 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) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

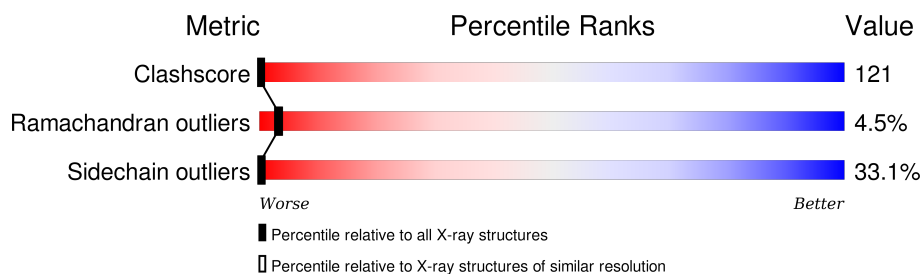
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	161	
1	B	161	
1	C	161	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3799 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 HYPOTHETICAL PROTEIN HI0065.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	157	Total	C	N	O	S	0	0	0
			1255	806	201	241	7			
1	B	157	Total	C	N	O	S	0	0	0
			1255	806	201	241	7			
1	C	157	Total	C	N	O	S	0	0	0
			1255	806	201	241	7			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	SEE REMARK 999	UNP P44492
B	-1	SER	-	SEE REMARK 999	UNP P44492
C	0	HIS	-	SEE REMARK 999	UNP P44492

- Molecule 2 is MERCURY (II) ION (three-letter code: HG) (formula: Hg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Hg	0	0
			1	1		
2	A	1	Total	Hg	0	0
			1	1		
2	C	1	Total	Hg	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	12	Total	O	0	0
			12	12		
3	B	7	Total	O	0	0
			7	7		

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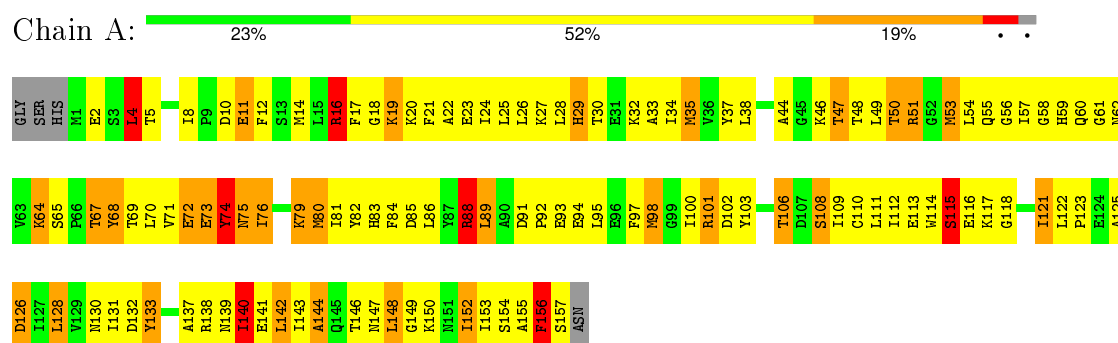
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	12	Total	O	0	0
			12	12		

### 3 Residue-property plots [i](#)

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.

Note EDS was not executed.

#### • Molecule 1: HYPOTHETICAL PROTEIN HI0065



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.40 Å   73.00 Å   96.80 Å 90.00°   110.20°   90.00°	Depositor
Resolution (Å)	10.00 – 2.50	Depositor
% Data completeness (in resolution range)	95.0 (10.00-2.50)	Depositor
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.220 , 0.285	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3799	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.70	0/1279	1.58	16/1726 (0.9%)
1	B	0.79	0/1279	1.81	34/1726 (2.0%)
1	C	0.90	3/1279 (0.2%)	1.71	23/1726 (1.3%)
All	All	0.80	3/3837 (0.1%)	1.70	73/5178 (1.4%)

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	C	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	113	GLU	CD-OE1	-12.39	1.12	1.25
1	C	113	GLU	CD-OE2	8.46	1.34	1.25
1	C	113	GLU	CG-CD	5.17	1.59	1.51

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	16	ARG	CD-NE-CZ	11.61	139.85	123.60
1	B	103	TYR	CB-CG-CD1	-9.62	115.23	121.00
1	C	16	ARG	NE-CZ-NH1	-9.36	115.62	120.30
1	A	156	PHE	CB-CG-CD1	9.32	127.32	120.80
1	A	51	ARG	NE-CZ-NH2	-9.05	115.78	120.30
1	B	141	GLU	OE1-CD-OE2	-8.77	112.77	123.30
1	B	21	PHE	CB-CG-CD1	8.38	126.67	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	66	PRO	N-CA-C	8.29	133.66	112.10
1	C	88	ARG	NE-CZ-NH1	8.17	124.39	120.30
1	A	16	ARG	N-CA-CB	7.97	124.95	110.60
1	A	16	ARG	CG-CD-NE	7.78	128.13	111.80
1	C	7	TYR	CB-CG-CD1	-7.71	116.38	121.00
1	B	103	TYR	CB-CG-CD2	7.66	125.60	121.00
1	C	123	PRO	N-CD-CG	7.43	114.34	103.20
1	B	102	ASP	CA-CB-CG	7.36	129.59	113.40
1	C	84	PHE	CB-CG-CD1	-7.34	115.66	120.80
1	B	37	TYR	CB-CG-CD1	-7.24	116.66	121.00
1	B	66	PRO	CA-C-N	7.04	132.70	117.20
1	B	105	ASN	N-CA-C	7.02	129.95	111.00
1	C	82	TYR	CB-CG-CD1	-6.91	116.86	121.00
1	C	84	PHE	CB-CG-CD2	6.67	125.47	120.80
1	B	83	HIS	CA-CB-CG	6.63	124.86	113.60
1	B	100	ILE	N-CA-C	6.56	128.70	111.00
1	B	124	GLU	OE1-CD-OE2	-6.44	115.57	123.30
1	C	123	PRO	CA-N-CD	-6.37	102.58	111.50
1	B	16	ARG	NE-CZ-NH1	-6.35	117.13	120.30
1	C	133	TYR	CB-CG-CD1	6.30	124.78	121.00
1	C	75	ASN	N-CA-CB	6.27	121.89	110.60
1	C	31	GLU	OE1-CD-OE2	-6.24	115.82	123.30
1	B	53	MET	CA-CB-CG	6.21	123.85	113.30
1	C	88	ARG	CD-NE-CZ	6.20	132.28	123.60
1	A	140	ILE	CB-CA-C	-6.15	99.30	111.60
1	A	156	PHE	CA-CB-CG	6.12	128.59	113.90
1	C	61	GLY	N-CA-C	-5.99	98.13	113.10
1	B	26	LEU	CA-CB-CG	5.99	129.07	115.30
1	C	16	ARG	CD-NE-CZ	-5.96	115.26	123.60
1	B	136	ASP	N-CA-CB	5.94	121.30	110.60
1	B	67	THR	N-CA-C	5.92	127.00	111.00
1	A	51	ARG	CD-NE-CZ	5.89	131.85	123.60
1	A	74	TYR	CB-CG-CD2	5.62	124.37	121.00
1	A	88	ARG	NE-CZ-NH1	5.60	123.10	120.30
1	B	101	ARG	N-CA-CB	5.59	120.67	110.60
1	B	7	TYR	CB-CG-CD1	-5.58	117.65	121.00
1	C	63	VAL	CG1-CB-CG2	-5.58	101.97	110.90
1	B	74	TYR	CB-CG-CD2	-5.58	117.65	121.00
1	B	144	ALA	O-C-N	5.52	131.54	122.70
1	A	74	TYR	CB-CG-CD1	-5.52	117.69	121.00
1	B	30	THR	CA-C-N	-5.45	105.21	117.20
1	C	101	ARG	NE-CZ-NH2	5.44	123.02	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	144	ALA	N-CA-CB	-5.43	102.50	110.10
1	A	157	SER	N-CA-CB	-5.42	102.36	110.50
1	A	142	LEU	CA-CB-CG	5.42	127.76	115.30
1	C	133	TYR	CB-CG-CD2	-5.37	117.78	121.00
1	C	66	PRO	N-CA-C	5.36	126.05	112.10
1	C	113	GLU	OE1-CD-OE2	5.35	129.72	123.30
1	C	115	SER	N-CA-CB	-5.34	102.48	110.50
1	B	76	ILE	CB-CA-C	5.34	122.28	111.60
1	B	147	ASN	CB-CG-OD1	-5.34	110.93	121.60
1	B	114	TRP	N-CA-C	5.26	125.20	111.00
1	A	88	ARG	NE-CZ-NH2	-5.26	117.67	120.30
1	B	33	ALA	C-N-CA	5.23	134.79	121.70
1	A	16	ARG	CA-CB-CG	5.19	124.81	113.40
1	C	4	LEU	CA-CB-CG	5.18	127.22	115.30
1	C	88	ARG	CA-CB-CG	5.14	124.70	113.40
1	B	83	HIS	CB-CA-C	5.13	120.66	110.40
1	B	37	TYR	CA-CB-CG	-5.12	103.67	113.40
1	B	134	TYR	CA-CB-CG	5.11	123.11	113.40
1	C	111	LEU	CA-C-O	5.08	130.77	120.10
1	B	57	ILE	CB-CA-C	5.08	121.75	111.60
1	B	24	ILE	CB-CA-C	-5.06	101.49	111.60
1	B	114	TRP	CA-CB-CG	-5.02	104.17	113.70
1	B	104	PHE	O-C-N	-5.01	114.68	122.70
1	B	47	THR	N-CA-CB	5.01	119.82	110.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	101	ARG	Mainchain
1	C	143	ILE	Mainchain
1	C	63	VAL	Mainchain

## 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	1255	0	1244	246	0
1	B	1255	0	1244	375	0
1	C	1255	0	1244	336	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	12	0	0	1	0
3	B	7	0	0	1	0
3	C	12	0	0	3	0
All	All	3799	0	3732	904	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 121.

All (904) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:LYS:HD3	1:A:109:ILE:CD1	1.66	1.24
1:B:89:LEU:HD11	1:B:95:LEU:CD2	1.67	1.23
1:B:21:PHE:HA	1:B:156:PHE:CZ	1.75	1.21
1:B:7:TYR:CE1	1:B:137:ALA:HB1	1.78	1.19
1:A:71:VAL:HG13	1:A:84:PHE:CE1	1.77	1.18
1:A:26:LEU:HA	1:A:79:LYS:CE	1.75	1.17
1:C:8:ILE:HD12	1:C:140:ILE:HG12	1.19	1.17
1:C:42:LEU:HD21	1:C:114:TRP:CZ2	1.80	1.16
1:C:57:ILE:CG2	1:C:76:ILE:HG21	1.74	1.15
1:B:121:ILE:N	1:B:121:ILE:HD12	1.61	1.15
1:A:16:ARG:NH2	1:C:135:ASP:HB2	1.59	1.15
1:B:121:ILE:H	1:B:121:ILE:CD1	1.54	1.14
1:B:20:LYS:O	1:B:24:ILE:HD13	1.45	1.14
1:C:8:ILE:CG2	1:C:138:ARG:HB2	1.78	1.13
1:B:139:ASN:HD21	1:C:51:ARG:NH2	1.46	1.12
1:B:146:THR:HG22	1:B:147:ASN:N	1.61	1.11
1:C:35:MET:HE2	1:C:104:PHE:CE1	1.86	1.11
1:B:37:TYR:CE1	1:B:125:ALA:HB2	1.87	1.10
1:C:35:MET:CE	1:C:104:PHE:HE1	1.64	1.09
1:B:7:TYR:HE1	1:B:137:ALA:HB1	0.99	1.09
1:A:16:ARG:HH21	1:C:135:ASP:HB2	1.11	1.09
1:C:94:GLU:HA	1:C:97:PHE:CD2	1.88	1.08
1:C:57:ILE:HG22	1:C:76:ILE:HG21	1.13	1.08
1:C:8:ILE:HG22	1:C:138:ARG:HB2	1.29	1.07
1:B:69:THR:HG22	1:B:70:LEU:H	0.91	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:ILE:HD11	1:A:156:PHE:HD1	1.10	1.06
1:B:20:LYS:HD2	1:B:24:ILE:HD11	1.36	1.05
1:C:42:LEU:HD21	1:C:114:TRP:HZ2	0.91	1.05
1:A:88:ARG:HG3	1:A:88:ARG:HH11	1.18	1.05
1:B:95:LEU:HD13	1:B:122:LEU:CD1	1.87	1.04
1:B:64:LYS:HG3	1:B:72:GLU:HG2	1.39	1.04
1:B:82:TYR:HE2	1:B:103:TYR:HA	1.19	1.04
1:C:35:MET:CE	1:C:104:PHE:CE1	2.40	1.04
1:B:20:LYS:CD	1:B:24:ILE:HD11	1.88	1.04
1:A:73:GLU:HB3	1:A:82:TYR:CD1	1.93	1.03
1:B:69:THR:HG22	1:B:70:LEU:N	1.73	1.03
1:A:79:LYS:CD	1:A:109:ILE:HD11	1.89	1.03
1:A:24:ILE:HG21	1:A:155:ALA:CB	1.87	1.03
1:B:89:LEU:HD11	1:B:95:LEU:HD21	1.38	1.03
1:A:146:THR:HG22	1:A:147:ASN:H	1.24	1.03
1:C:8:ILE:CD1	1:C:140:ILE:HG12	1.87	1.03
1:C:34:ILE:HG22	1:C:110:CYS:H	1.20	1.03
1:C:50:THR:HG22	1:C:54:LEU:HD13	1.38	1.02
1:B:95:LEU:HD13	1:B:122:LEU:HD12	1.40	1.02
1:B:6:GLN:H	1:B:140:ILE:HG22	1.19	1.02
1:C:131:ILE:HD13	1:C:131:ILE:N	1.72	1.02
1:B:146:THR:CG2	1:B:147:ASN:H	1.73	1.01
1:B:146:THR:HG22	1:B:147:ASN:H	1.10	1.01
1:B:2:GLU:HA	1:B:2:GLU:OE1	1.59	1.01
1:A:24:ILE:HD11	1:A:156:PHE:CD1	1.95	1.00
1:A:17:PHE:CE2	1:A:156:PHE:HE2	1.78	1.00
1:B:82:TYR:CE2	1:B:103:TYR:HA	1.95	1.00
1:C:42:LEU:CD2	1:C:114:TRP:HZ2	1.74	1.00
1:B:118:GLY:HA3	1:B:122:LEU:HD12	1.43	1.00
1:A:26:LEU:CA	1:A:79:LYS:HE3	1.91	0.99
1:C:24:ILE:CD1	1:C:152:ILE:HG23	1.91	0.99
1:A:73:GLU:HB3	1:A:82:TYR:HD1	1.19	0.99
1:C:15:LEU:HD21	1:C:48:THR:HG22	1.42	0.99
1:B:89:LEU:O	1:B:117:LYS:HG2	1.62	0.98
1:C:15:LEU:HD21	1:C:48:THR:CG2	1.93	0.98
1:A:89:LEU:HD11	1:A:94:GLU:HB2	1.45	0.98
1:A:12:PHE:CE1	1:C:137:ALA:HB1	1.98	0.98
1:A:17:PHE:CE2	1:A:156:PHE:CE2	2.52	0.97
1:B:133:TYR:HA	1:C:12:PHE:CZ	1.99	0.97
1:A:17:PHE:HE2	1:A:156:PHE:HE2	1.02	0.97
1:B:69:THR:CG2	1:B:70:LEU:H	1.77	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:29:HIS:ND1	1:C:30:THR:N	2.12	0.97
1:B:14:MET:HE2	1:B:49:LEU:HG	1.45	0.97
1:B:103:TYR:N	1:B:103:TYR:CD1	2.27	0.96
1:A:132:ASP:HB2	1:A:139:ASN:CB	1.95	0.96
1:B:125:ALA:O	1:B:145:GLN:NE2	1.98	0.96
1:C:99:GLY:HA2	1:C:103:TYR:HB2	1.46	0.96
1:A:33:ALA:HB1	1:A:108:SER:O	1.65	0.96
1:B:148:LEU:HD23	1:B:149:GLY:H	1.30	0.96
1:C:35:MET:HE2	1:C:123:PRO:HD2	1.45	0.96
1:C:41:ASP:HB3	1:C:133:TYR:HE1	1.31	0.95
1:B:7:TYR:HE1	1:B:137:ALA:CB	1.79	0.95
1:C:144:ALA:HB2	1:C:153:ILE:HG13	1.48	0.95
1:B:95:LEU:HD23	1:B:95:LEU:N	1.80	0.95
1:B:82:TYR:OH	1:B:102:ASP:HB2	1.66	0.95
1:C:21:PHE:CE1	1:C:25:LEU:HD11	2.01	0.95
1:B:139:ASN:HD21	1:C:51:ARG:HH22	1.15	0.94
1:A:71:VAL:HG22	1:A:84:PHE:CZ	2.02	0.94
1:B:139:ASN:ND2	1:C:51:ARG:NH2	2.14	0.94
1:A:24:ILE:HG21	1:A:155:ALA:HB1	1.47	0.94
1:A:26:LEU:HA	1:A:79:LYS:HE3	0.94	0.94
1:B:132:ASP:O	1:B:139:ASN:N	2.01	0.94
1:C:94:GLU:HA	1:C:97:PHE:HD2	1.28	0.94
1:B:66:PRO:HG3	1:B:72:GLU:HB2	1.49	0.93
1:B:19:LYS:HE3	1:B:23:GLU:CD	1.88	0.93
1:A:67:THR:HG22	1:A:68:TYR:N	1.83	0.93
1:A:71:VAL:CG2	1:A:84:PHE:CZ	2.52	0.93
1:B:89:LEU:CD1	1:B:95:LEU:CD2	2.46	0.93
1:C:104:PHE:HZ	1:C:122:LEU:HD13	1.34	0.93
1:B:89:LEU:HD11	1:B:95:LEU:HD23	1.49	0.93
1:A:132:ASP:HB2	1:A:139:ASN:HB3	1.48	0.92
1:A:71:VAL:HG22	1:A:84:PHE:CE2	2.04	0.92
1:B:37:TYR:HD2	1:B:115:SER:HB3	1.33	0.92
1:B:7:TYR:CE1	1:B:137:ALA:CB	2.53	0.92
1:C:30:THR:HG21	1:C:107:ASP:H	1.33	0.92
1:B:148:LEU:HA	1:B:151:ASN:ND2	1.83	0.92
1:C:21:PHE:HE1	1:C:25:LEU:HD11	1.30	0.92
1:B:89:LEU:HD21	1:B:95:LEU:HD21	1.50	0.91
1:B:64:LYS:HG3	1:B:72:GLU:CG	2.00	0.91
1:A:71:VAL:CG1	1:A:84:PHE:CE1	2.53	0.91
1:A:79:LYS:HD3	1:A:109:ILE:HD11	0.92	0.91
1:C:37:TYR:CD1	1:C:125:ALA:HB2	2.05	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:37:TYR:CD2	1:B:115:SER:HB3	2.05	0.90
1:B:121:ILE:H	1:B:121:ILE:HD12	0.75	0.90
1:C:57:ILE:HG22	1:C:76:ILE:CG2	2.00	0.90
1:A:60:GLN:HA	1:C:6:GLN:NE2	1.87	0.90
1:C:50:THR:CG2	1:C:54:LEU:HD13	2.01	0.90
1:A:10:ASP:OD1	1:A:11:GLU:N	2.06	0.89
1:C:24:ILE:HD11	1:C:152:ILE:HG23	1.54	0.89
1:B:51:ARG:HA	1:B:63:VAL:HG11	1.55	0.89
1:C:144:ALA:HB2	1:C:153:ILE:CG1	2.03	0.89
1:B:26:LEU:HD22	1:B:77:ALA:HB3	1.55	0.88
1:B:103:TYR:H	1:B:103:TYR:HD1	1.20	0.88
1:B:95:LEU:CD1	1:B:122:LEU:HD12	2.02	0.88
1:B:6:GLN:HB2	1:B:140:ILE:CG2	2.04	0.88
1:B:67:THR:HB	1:B:85:ASP:OD2	1.72	0.88
1:B:7:TYR:O	1:B:9:PRO:HD3	1.74	0.88
1:C:15:LEU:CD2	1:C:48:THR:HG22	2.04	0.88
1:B:136:ASP:H	1:C:16:ARG:HH12	1.22	0.88
1:A:86:LEU:HD21	1:A:95:LEU:HD21	1.55	0.87
1:C:127:ILE:HG22	1:C:128:LEU:H	1.39	0.87
1:B:20:LYS:HD2	1:B:24:ILE:CD1	2.04	0.87
1:B:9:PRO:HG2	1:C:56:GLY:HA2	1.56	0.87
1:A:88:ARG:HD3	1:A:88:ARG:O	1.75	0.86
1:C:144:ALA:HB2	1:C:153:ILE:CD1	2.05	0.86
1:A:60:GLN:HA	1:C:6:GLN:HE22	1.40	0.86
1:A:86:LEU:CD2	1:A:89:LEU:HD22	2.05	0.86
1:C:70:LEU:O	1:C:71:VAL:CG2	2.23	0.86
1:B:6:GLN:HB2	1:B:140:ILE:HG21	1.58	0.85
1:A:35:MET:HB3	1:A:125:ALA:HA	1.58	0.85
1:A:71:VAL:HG13	1:A:84:PHE:HE1	1.40	0.85
1:A:25:LEU:HD23	1:A:34:ILE:HD13	1.57	0.85
1:C:125:ALA:HB1	1:C:127:ILE:O	1.77	0.85
1:C:15:LEU:HD23	1:C:15:LEU:N	1.92	0.85
1:C:41:ASP:HB3	1:C:133:TYR:CE1	2.11	0.85
1:A:24:ILE:CG2	1:A:155:ALA:HB1	2.07	0.84
1:B:14:MET:CE	1:B:49:LEU:HG	2.06	0.84
1:B:103:TYR:N	1:B:103:TYR:HD1	1.73	0.84
1:A:25:LEU:CD2	1:A:34:ILE:HD13	2.06	0.84
1:B:21:PHE:HZ	1:B:36:VAL:HG11	1.40	0.83
1:B:6:GLN:N	1:B:140:ILE:HG22	1.92	0.83
1:C:6:GLN:HG3	1:C:17:PHE:CE1	2.13	0.83
1:A:118:GLY:HA3	1:A:122:LEU:CD1	2.08	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:79:LYS:HG2	1:C:109:ILE:HG13	1.61	0.83
1:B:139:ASN:ND2	1:C:51:ARG:HH22	1.76	0.83
1:B:54:LEU:HD12	1:B:74:TYR:CE2	2.14	0.83
1:B:133:TYR:CD1	1:B:133:TYR:O	2.32	0.82
1:C:144:ALA:CB	1:C:153:ILE:CD1	2.57	0.82
1:C:1:MET:HB2	1:C:150:LYS:HE2	1.60	0.82
1:C:24:ILE:HD12	1:C:152:ILE:HG23	1.60	0.82
1:B:18:GLY:O	1:B:53:MET:HG3	1.78	0.82
1:B:70:LEU:O	1:B:84:PHE:HA	1.80	0.82
1:B:8:ILE:HD12	1:B:14:MET:SD	2.20	0.82
1:C:35:MET:CE	1:C:123:PRO:HD2	2.10	0.82
1:B:19:LYS:HB2	1:B:56:GLY:HA3	1.62	0.81
1:B:57:ILE:HG23	1:B:76:ILE:HG21	1.62	0.81
1:C:1:MET:CB	1:C:150:LYS:HE2	2.10	0.81
1:B:2:GLU:HB2	1:B:144:ALA:CB	2.09	0.81
1:B:42:LEU:HG	1:B:114:TRP:HH2	1.45	0.81
1:B:21:PHE:HA	1:B:156:PHE:HZ	1.35	0.81
1:B:133:TYR:HA	1:C:12:PHE:HZ	1.43	0.81
1:A:94:GLU:HA	1:A:97:PHE:CD2	2.15	0.81
1:B:97:PHE:N	1:B:97:PHE:HD1	1.79	0.81
1:B:95:LEU:H	1:B:95:LEU:HD23	1.43	0.81
1:B:19:LYS:HE3	1:B:23:GLU:OE2	1.80	0.80
1:B:89:LEU:CD1	1:B:95:LEU:HD21	2.10	0.80
1:C:59:HIS:CE1	1:C:64:LYS:HE3	2.17	0.80
1:B:92:PRO:HA	1:B:95:LEU:HG	1.64	0.80
1:A:37:TYR:CE2	1:A:115:SER:HB2	2.17	0.80
1:B:24:ILE:H	1:B:24:ILE:CD1	1.95	0.80
1:A:33:ALA:CB	1:A:108:SER:O	2.30	0.79
1:C:82:TYR:HB3	1:C:84:PHE:HE1	1.47	0.79
1:C:4:LEU:HD13	1:C:5:THR:H	1.46	0.79
1:C:94:GLU:CA	1:C:97:PHE:HD2	1.95	0.79
1:B:24:ILE:HG23	1:B:155:ALA:HB1	1.64	0.78
1:B:8:ILE:CD1	1:B:14:MET:SD	2.71	0.78
1:B:69:THR:HG22	1:B:71:VAL:H	1.48	0.78
1:B:9:PRO:CG	1:C:56:GLY:HA2	2.12	0.78
1:B:136:ASP:N	1:C:16:ARG:HH12	1.80	0.78
1:A:14:MET:HG2	1:A:48:THR:HG22	1.64	0.78
1:B:53:MET:HE1	1:B:111:LEU:HD21	1.63	0.78
1:C:1:MET:HG2	1:C:145:GLN:HA	1.65	0.78
1:A:57:ILE:HG22	1:A:76:ILE:HG21	1.65	0.78
1:A:14:MET:HG2	1:A:48:THR:CG2	2.14	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:47:THR:CG2	1:A:48:THR:N	2.46	0.78
1:B:19:LYS:NZ	1:B:56:GLY:O	2.12	0.77
1:A:140:ILE:O	1:A:140:ILE:HG22	1.82	0.77
1:C:51:ARG:O	1:C:55:GLN:HB2	1.84	0.77
1:B:148:LEU:HD23	1:B:149:GLY:N	1.99	0.77
1:B:4:LEU:HD23	1:B:153:ILE:HG23	1.65	0.77
1:B:2:GLU:HB2	1:B:144:ALA:HB3	1.64	0.77
1:C:35:MET:HE1	1:C:104:PHE:HE1	1.50	0.77
1:B:136:ASP:H	1:C:16:ARG:NH1	1.83	0.77
1:C:37:TYR:CE1	1:C:125:ALA:HB2	2.20	0.77
1:B:89:LEU:HD12	1:B:94:GLU:HB2	1.67	0.77
1:B:82:TYR:CE2	1:B:103:TYR:CG	2.73	0.77
1:C:53:MET:SD	1:C:111:LEU:HD11	2.25	0.77
1:B:4:LEU:HD21	1:C:62:ASN:HD21	1.50	0.77
1:A:57:ILE:CG2	1:A:76:ILE:HG21	2.16	0.76
1:C:109:ILE:O	1:C:109:ILE:HG22	1.85	0.76
1:B:54:LEU:HD12	1:B:74:TYR:CD2	2.20	0.76
1:B:25:LEU:HD13	1:B:109:ILE:HD13	1.65	0.76
1:A:79:LYS:CD	1:A:109:ILE:CD1	2.58	0.76
1:C:128:LEU:O	1:C:142:LEU:HA	1.84	0.76
1:C:70:LEU:C	1:C:71:VAL:HG23	2.05	0.76
1:B:20:LYS:HD3	1:B:24:ILE:HD11	1.67	0.76
1:C:104:PHE:CZ	1:C:122:LEU:HD13	2.20	0.76
1:B:34:ILE:O	1:B:34:ILE:HG22	1.85	0.76
1:A:19:LYS:HG3	1:A:56:GLY:HA3	1.68	0.76
1:C:34:ILE:CG2	1:C:110:CYS:H	1.96	0.76
1:C:30:THR:CG2	1:C:107:ASP:H	1.97	0.76
1:A:19:LYS:HG3	1:A:56:GLY:CA	2.16	0.76
1:C:70:LEU:O	1:C:71:VAL:HG23	1.86	0.75
1:B:97:PHE:N	1:B:97:PHE:CD1	2.54	0.75
1:B:25:LEU:HD13	1:B:109:ILE:CD1	2.16	0.75
1:B:118:GLY:HA3	1:B:122:LEU:CD1	2.16	0.75
1:C:41:ASP:O	1:C:44:ALA:N	2.19	0.75
1:C:144:ALA:CB	1:C:153:ILE:HG13	2.15	0.75
1:C:15:LEU:HA	1:C:52:GLY:HA3	1.69	0.75
1:B:2:GLU:HG2	1:B:150:LYS:HG3	1.69	0.75
1:C:30:THR:HG21	1:C:107:ASP:N	2.00	0.75
1:B:82:TYR:CE2	1:B:103:TYR:CA	2.70	0.74
1:A:8:ILE:HG22	1:A:8:ILE:O	1.87	0.74
1:A:47:THR:HG22	1:A:48:THR:H	1.52	0.74
1:B:26:LEU:HD23	1:B:79:LYS:HB2	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:95:LEU:HD13	1:B:122:LEU:HD11	1.67	0.74
1:C:8:ILE:HD12	1:C:140:ILE:CG1	2.09	0.74
1:A:118:GLY:HA3	1:A:122:LEU:HD12	1.69	0.74
1:B:84:PHE:HD1	1:B:84:PHE:H	1.35	0.74
1:B:143:ILE:HG22	1:B:144:ALA:O	1.87	0.74
1:B:2:GLU:O	1:B:143:ILE:HA	1.87	0.74
1:C:29:HIS:CG	1:C:30:THR:H	2.06	0.74
1:B:54:LEU:CD1	1:B:74:TYR:CD2	2.71	0.73
1:A:17:PHE:HE2	1:A:156:PHE:CE2	1.92	0.73
1:C:1:MET:CG	1:C:145:GLN:HA	2.18	0.73
1:A:37:TYR:CD1	1:A:125:ALA:HB2	2.24	0.73
1:B:21:PHE:CA	1:B:156:PHE:CZ	2.65	0.73
1:C:131:ILE:HD12	1:C:140:ILE:HD12	1.70	0.73
1:B:7:TYR:OH	1:B:137:ALA:HB2	1.88	0.73
1:B:151:ASN:O	1:B:155:ALA:HB2	1.88	0.73
1:B:19:LYS:HD2	1:B:56:GLY:CA	2.19	0.73
1:B:133:TYR:HB2	1:B:138:ARG:HG3	1.71	0.73
1:B:89:LEU:CD2	1:B:95:LEU:HD21	2.18	0.73
1:A:35:MET:CB	1:A:125:ALA:HA	2.18	0.73
1:B:19:LYS:HB2	1:B:52:GLY:O	1.89	0.72
1:A:4:LEU:HD12	1:A:153:ILE:HG23	1.70	0.72
1:A:24:ILE:CD1	1:A:156:PHE:HD1	1.98	0.72
1:B:54:LEU:N	1:B:54:LEU:HD23	2.03	0.72
1:C:1:MET:HB2	1:C:144:ALA:O	1.87	0.72
1:B:95:LEU:HD12	1:B:121:ILE:HD13	1.70	0.72
1:A:101:ARG:HB2	1:A:103:TYR:CE1	2.25	0.72
1:A:25:LEU:HD21	1:A:34:ILE:HG21	1.72	0.72
1:B:151:ASN:O	1:B:155:ALA:CB	2.38	0.72
1:B:84:PHE:N	1:B:84:PHE:CD1	2.55	0.71
1:C:83:HIS:HD2	1:C:84:PHE:N	1.88	0.71
1:C:91:ASP:HB2	1:C:92:PRO:HD2	1.73	0.71
1:C:129:VAL:HG12	1:C:131:ILE:HD11	1.72	0.71
1:C:102:ASP:O	1:C:103:TYR:CD1	2.44	0.70
1:C:49:LEU:O	1:C:53:MET:CB	2.39	0.70
1:C:94:GLU:HA	1:C:97:PHE:CE2	2.26	0.70
1:A:83:HIS:NE2	1:A:113:GLU:OE2	2.25	0.70
1:C:103:TYR:O	1:C:110:CYS:SG	2.50	0.70
1:C:8:ILE:HG21	1:C:138:ARG:HB2	1.73	0.70
1:C:70:LEU:O	1:C:71:VAL:HG22	1.91	0.70
1:C:8:ILE:HG22	1:C:8:ILE:O	1.90	0.70
1:B:24:ILE:HD13	1:B:24:ILE:H	1.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:83:HIS:HD2	1:C:84:PHE:H	1.39	0.69
1:C:144:ALA:HB2	1:C:153:ILE:HD11	1.74	0.69
1:B:37:TYR:CE1	1:B:125:ALA:CB	2.73	0.69
1:A:12:PHE:CD1	1:C:137:ALA:HB1	2.28	0.69
1:B:21:PHE:HD1	1:B:156:PHE:HE2	1.40	0.69
1:B:89:LEU:CD1	1:B:94:GLU:HB2	2.23	0.69
1:A:118:GLY:HA3	1:A:122:LEU:HD13	1.75	0.69
1:C:66:PRO:HG3	1:C:72:GLU:HB2	1.73	0.69
1:B:104:PHE:CE2	1:B:123:PRO:CD	2.76	0.69
1:C:84:PHE:HB3	1:C:86:LEU:HD13	1.73	0.69
1:C:46:LYS:HD2	1:C:113:GLU:HG2	1.74	0.69
1:C:62:ASN:N	1:C:62:ASN:HD22	1.90	0.68
1:C:74:TYR:O	1:C:80:MET:HA	1.93	0.68
1:B:82:TYR:CE2	1:B:103:TYR:CD2	2.82	0.68
1:B:14:MET:HB3	1:B:48:THR:HG22	1.76	0.68
1:A:37:TYR:CE2	1:A:115:SER:CB	2.77	0.68
1:C:84:PHE:HZ	1:C:103:TYR:CD2	2.09	0.68
1:A:19:LYS:NZ	1:A:56:GLY:O	2.26	0.68
1:A:144:ALA:HB1	1:A:149:GLY:C	2.13	0.68
1:B:104:PHE:CE2	1:B:123:PRO:HD3	2.28	0.68
1:B:86:LEU:HD13	1:B:122:LEU:CD1	2.24	0.68
1:B:21:PHE:CA	1:B:156:PHE:HZ	2.03	0.68
1:B:8:ILE:O	1:B:8:ILE:HG22	1.93	0.68
1:B:7:TYR:HB3	1:C:55:GLN:HB3	1.76	0.68
1:C:57:ILE:HG21	1:C:76:ILE:HG21	1.73	0.68
1:B:73:GLU:HG2	1:B:82:TYR:CE1	2.28	0.68
1:A:50:THR:HG21	1:A:83:HIS:CE1	2.28	0.68
1:A:74:TYR:CD1	1:A:81:ILE:HG22	2.28	0.68
1:C:11:GLU:HA	1:C:138:ARG:HH12	1.58	0.68
1:C:131:ILE:CD1	1:C:131:ILE:H	2.03	0.68
1:C:8:ILE:CD1	1:C:140:ILE:CG1	2.69	0.68
1:B:136:ASP:CA	1:C:16:ARG:HH12	2.06	0.68
1:A:4:LEU:HD23	1:A:5:THR:N	2.08	0.68
1:A:71:VAL:HG11	1:A:103:TYR:HE2	1.58	0.68
1:B:2:GLU:O	1:B:143:ILE:HG23	1.94	0.68
1:A:19:LYS:CG	1:A:56:GLY:HA3	2.23	0.67
1:A:61:GLY:H	1:C:6:GLN:HE21	1.40	0.67
1:B:5:THR:O	1:B:5:THR:HG23	1.95	0.67
1:C:49:LEU:HD22	1:C:53:MET:CE	2.24	0.67
1:A:24:ILE:HG21	1:A:155:ALA:HB3	1.73	0.67
1:C:144:ALA:HB3	1:C:153:ILE:HD12	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:ARG:NH2	1:C:135:ASP:CB	2.50	0.67
1:C:148:LEU:HD23	1:C:148:LEU:C	2.14	0.67
1:C:5:THR:HA	1:C:140:ILE:O	1.95	0.67
1:B:26:LEU:O	1:B:79:LYS:NZ	2.28	0.66
1:B:86:LEU:HD13	1:B:122:LEU:HD11	1.76	0.66
1:B:89:LEU:HD21	1:B:95:LEU:CD2	2.25	0.66
1:C:127:ILE:HG22	1:C:128:LEU:N	2.09	0.66
1:A:118:GLY:CA	1:A:122:LEU:HD12	2.26	0.66
1:B:35:MET:CE	1:B:112:ILE:HD11	2.25	0.66
1:A:71:VAL:HG21	1:A:84:PHE:CZ	2.29	0.66
1:B:37:TYR:CD2	1:B:115:SER:CB	2.78	0.66
1:A:88:ARG:CG	1:A:88:ARG:HH11	2.01	0.66
1:C:128:LEU:HB2	1:C:143:ILE:O	1.96	0.66
1:A:146:THR:HG22	1:A:147:ASN:N	2.04	0.66
1:B:4:LEU:N	1:B:142:LEU:O	2.29	0.66
1:B:25:LEU:CD1	1:B:109:ILE:HD13	2.26	0.66
1:B:35:MET:HE2	1:B:112:ILE:HD11	1.78	0.66
1:C:148:LEU:HD23	1:C:148:LEU:O	1.96	0.66
1:B:25:LEU:HD21	1:B:34:ILE:HG21	1.76	0.66
1:B:24:ILE:N	1:B:24:ILE:CD1	2.58	0.66
1:B:137:ALA:H	1:C:16:ARG:NH1	1.94	0.66
1:B:149:GLY:HA2	1:B:152:ILE:HD12	1.79	0.65
1:A:132:ASP:HB2	1:A:139:ASN:HB2	1.78	0.65
1:C:142:LEU:HD23	1:C:142:LEU:N	2.11	0.65
1:B:57:ILE:CG2	1:B:76:ILE:HG21	2.26	0.65
1:C:82:TYR:HB3	1:C:84:PHE:CE1	2.29	0.65
1:A:74:TYR:CD1	1:A:74:TYR:N	2.65	0.65
1:C:102:ASP:HA	1:C:105:ASN:ND2	2.12	0.65
1:B:37:TYR:CE2	1:B:115:SER:CB	2.79	0.65
1:B:84:PHE:N	1:B:84:PHE:HD1	1.90	0.65
1:A:89:LEU:HD11	1:A:94:GLU:CB	2.24	0.65
1:A:46:LYS:HB2	3:A:206:HOH:O	1.97	0.65
1:C:53:MET:SD	1:C:111:LEU:CD1	2.84	0.65
1:C:6:GLN:O	1:C:139:ASN:HA	1.97	0.65
1:C:89:LEU:HD23	1:C:117:LYS:HB3	1.79	0.65
1:C:106:THR:HG23	1:C:107:ASP:OD1	1.97	0.65
1:B:11:GLU:O	1:B:15:LEU:HD12	1.96	0.64
1:B:6:GLN:HG3	1:B:17:PHE:CE1	2.33	0.64
1:C:35:MET:HG2	1:C:123:PRO:CG	2.27	0.64
1:C:4:LEU:CD1	1:C:5:THR:H	2.09	0.64
1:A:34:ILE:HD12	1:A:109:ILE:HG12	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:LEU:O	1:A:117:LYS:HG2	1.97	0.64
1:A:86:LEU:HD21	1:A:89:LEU:HD22	1.78	0.64
1:A:21:PHE:HE2	1:A:142:LEU:HD21	1.63	0.64
1:C:34:ILE:HA	1:C:126:ASP:OD2	1.98	0.64
1:C:146:THR:HG22	1:C:147:ASN:N	2.11	0.64
1:A:115:SER:OG	1:A:115:SER:O	2.15	0.64
1:A:57:ILE:CG2	1:A:76:ILE:CG2	2.76	0.64
1:B:57:ILE:HG23	1:B:76:ILE:CG2	2.27	0.64
1:A:12:PHE:CE1	1:C:137:ALA:CB	2.77	0.64
1:A:67:THR:CG2	1:A:68:TYR:N	2.54	0.64
1:C:14:MET:HG2	1:C:138:ARG:NH1	2.13	0.64
1:C:144:ALA:HB3	1:C:153:ILE:CD1	2.28	0.64
1:A:35:MET:HB3	1:A:125:ALA:CA	2.28	0.63
1:C:49:LEU:O	1:C:53:MET:HB3	1.98	0.63
1:C:75:ASN:C	1:C:76:ILE:HD12	2.18	0.63
1:C:89:LEU:HD22	1:C:95:LEU:HD21	1.80	0.63
1:B:6:GLN:HG3	1:B:17:PHE:HE1	1.62	0.63
1:B:115:SER:OG	1:B:116:GLU:N	2.31	0.63
1:A:89:LEU:CD1	1:A:94:GLU:HB2	2.27	0.63
1:B:40:GLY:HA3	1:B:46:LYS:HD3	1.80	0.63
1:A:4:LEU:O	1:A:141:GLU:HA	1.98	0.63
1:C:35:MET:HG2	1:C:123:PRO:HG2	1.81	0.63
1:B:20:LYS:O	1:B:24:ILE:CD1	2.35	0.62
1:B:126:ASP:HB3	1:B:146:THR:OG1	1.99	0.62
1:B:146:THR:HG21	1:B:148:LEU:HD22	1.79	0.62
1:B:19:LYS:CE	1:B:23:GLU:OE2	2.47	0.62
1:B:148:LEU:O	1:B:152:ILE:HG13	1.98	0.62
1:C:70:LEU:C	1:C:71:VAL:CG2	2.66	0.62
1:A:8:ILE:CG2	1:A:138:ARG:HB2	2.28	0.62
1:A:8:ILE:CG2	1:A:8:ILE:O	2.48	0.62
1:B:37:TYR:CD1	1:B:125:ALA:HB2	2.34	0.62
1:B:139:ASN:HD21	1:C:51:ARG:HH21	1.43	0.62
1:C:41:ASP:CB	1:C:133:TYR:HE1	2.11	0.62
1:B:24:ILE:CG2	1:B:155:ALA:HB1	2.29	0.62
1:B:55:GLN:HG2	1:B:59:HIS:O	1.99	0.62
1:B:95:LEU:CD2	1:B:95:LEU:N	2.57	0.62
1:A:17:PHE:CE2	1:A:156:PHE:CZ	2.87	0.62
1:B:82:TYR:CZ	1:B:103:TYR:CD2	2.88	0.62
1:B:146:THR:HB	1:B:148:LEU:HD23	1.80	0.62
1:B:21:PHE:CZ	1:B:36:VAL:HG11	2.31	0.62
1:C:57:ILE:CG2	1:C:76:ILE:CG2	2.67	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:47:THR:CG2	1:A:48:THR:H	2.09	0.62
1:B:100:ILE:N	1:B:100:ILE:HD13	2.14	0.62
1:C:74:TYR:N	1:C:74:TYR:CD1	2.68	0.61
1:A:10:ASP:CG	1:A:11:GLU:H	2.02	0.61
1:C:2:GLU:O	1:C:153:ILE:CD1	2.48	0.61
1:B:82:TYR:HH	1:B:102:ASP:HB2	1.61	0.61
1:A:59:HIS:HE1	1:A:62:ASN:O	1.82	0.61
1:B:6:GLN:HB2	1:B:140:ILE:HG22	1.82	0.61
1:B:152:ILE:HA	1:B:155:ALA:HB3	1.83	0.61
1:C:60:GLN:NE2	1:C:60:GLN:H	1.98	0.61
1:A:117:LYS:HD2	1:A:117:LYS:N	2.16	0.61
1:B:37:TYR:CD1	1:B:125:ALA:CB	2.83	0.61
1:C:24:ILE:HG13	1:C:152:ILE:HD12	1.82	0.61
1:B:8:ILE:N	1:B:138:ARG:O	2.30	0.61
1:C:126:ASP:O	1:C:145:GLN:N	2.30	0.61
1:C:83:HIS:CD2	1:C:84:PHE:N	2.66	0.61
1:B:2:GLU:HB2	1:B:144:ALA:HB2	1.83	0.61
1:B:25:LEU:HD21	1:B:34:ILE:HD13	1.83	0.61
1:C:144:ALA:CB	1:C:153:ILE:HD11	2.29	0.61
1:A:121:ILE:HG22	1:A:122:LEU:N	2.16	0.61
1:A:47:THR:HG23	1:A:48:THR:N	2.14	0.61
1:A:64:LYS:CB	1:A:72:GLU:OE1	2.49	0.61
1:B:151:ASN:O	1:B:155:ALA:N	2.30	0.60
1:C:36:VAL:C	1:C:37:TYR:HD1	2.05	0.60
1:A:88:ARG:HG3	1:A:88:ARG:NH1	1.97	0.60
1:C:95:LEU:HD11	1:C:118:GLY:HA2	1.82	0.60
1:B:29:HIS:CG	1:B:30:THR:N	2.67	0.60
1:A:57:ILE:HG22	1:A:76:ILE:CG2	2.30	0.60
1:B:126:ASP:O	1:B:145:GLN:N	2.34	0.60
1:B:26:LEU:HD22	1:B:77:ALA:CB	2.30	0.60
1:C:132:ASP:O	1:C:138:ARG:HA	2.01	0.60
1:A:61:GLY:H	1:C:6:GLN:NE2	1.98	0.60
1:A:24:ILE:CD1	1:A:156:PHE:CD1	2.78	0.60
1:B:36:VAL:HG12	1:B:129:VAL:HG23	1.83	0.60
1:B:19:LYS:HE3	1:B:23:GLU:OE1	2.01	0.60
1:B:69:THR:HG22	1:B:71:VAL:N	2.15	0.60
1:C:153:ILE:O	1:C:156:PHE:HB2	2.01	0.60
1:B:88:ARG:HH11	1:B:88:ARG:HG3	1.67	0.60
1:B:82:TYR:HE2	1:B:103:TYR:CA	2.05	0.60
1:B:2:GLU:CA	1:B:2:GLU:OE1	2.41	0.60
1:B:137:ALA:O	1:C:12:PHE:HE1	1.85	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:VAL:CG2	1:A:84:PHE:CE2	2.80	0.60
1:B:133:TYR:CB	1:B:138:ARG:HG3	2.31	0.60
1:C:84:PHE:HB2	1:C:112:ILE:HG12	1.84	0.60
1:A:25:LEU:CD2	1:A:34:ILE:HG21	2.32	0.59
1:B:73:GLU:HG2	1:B:82:TYR:HE1	1.67	0.59
1:A:71:VAL:HG11	1:A:103:TYR:CE2	2.37	0.59
1:C:129:VAL:CG1	1:C:131:ILE:HD11	2.32	0.59
1:C:94:GLU:CA	1:C:97:PHE:CD2	2.71	0.59
1:A:5:THR:HB	1:A:141:GLU:HG3	1.82	0.59
1:A:24:ILE:HD13	1:A:155:ALA:CB	2.32	0.59
1:C:112:ILE:HD11	1:C:122:LEU:HD12	1.83	0.59
1:C:28:LEU:HD13	1:C:152:ILE:CD1	2.32	0.59
1:A:34:ILE:HG12	1:A:148:LEU:HD21	1.84	0.59
1:A:24:ILE:CG2	1:A:155:ALA:CB	2.68	0.59
1:C:35:MET:HE2	1:C:123:PRO:CD	2.26	0.59
1:B:82:TYR:CE1	1:B:103:TYR:CE2	2.91	0.59
1:C:8:ILE:HB	1:C:138:ARG:O	2.03	0.59
1:B:84:PHE:CZ	1:B:104:PHE:HE1	2.19	0.59
1:B:143:ILE:CG2	1:B:144:ALA:N	2.66	0.59
1:B:82:TYR:CD2	1:B:103:TYR:CD2	2.90	0.59
1:C:80:MET:SD	1:C:82:TYR:OH	2.56	0.58
1:A:88:ARG:O	1:A:88:ARG:CD	2.51	0.58
1:A:121:ILE:CG2	1:A:122:LEU:N	2.67	0.58
1:C:59:HIS:HE1	1:C:64:LYS:HE3	1.64	0.58
1:B:86:LEU:CD1	1:B:122:LEU:CD1	2.81	0.58
1:A:14:MET:CG	1:A:48:THR:HG22	2.33	0.58
1:C:35:MET:HB3	1:C:125:ALA:HA	1.85	0.58
1:A:12:PHE:CD1	1:C:137:ALA:CB	2.86	0.58
1:C:37:TYR:OH	1:C:123:PRO:O	2.21	0.58
1:C:131:ILE:CD1	1:C:140:ILE:HD12	2.34	0.58
1:B:19:LYS:HA	1:B:53:MET:HA	1.86	0.58
1:C:21:PHE:C	1:C:21:PHE:CD1	2.77	0.58
1:B:25:LEU:HD22	1:B:25:LEU:O	2.04	0.58
1:C:35:MET:HE1	1:C:104:PHE:CE1	2.31	0.58
1:A:24:ILE:HD13	1:A:155:ALA:HB3	1.86	0.58
1:C:73:GLU:HA	1:C:81:ILE:O	2.04	0.58
1:B:21:PHE:HD1	1:B:156:PHE:CE2	2.22	0.57
1:A:14:MET:O	1:A:18:GLY:N	2.37	0.57
1:B:86:LEU:CD1	1:B:122:LEU:HD11	2.34	0.57
1:C:62:ASN:N	1:C:62:ASN:ND2	2.52	0.57
1:B:143:ILE:HG22	1:B:144:ALA:N	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:ASN:O	1:A:140:ILE:HG13	2.04	0.57
1:C:1:MET:HG2	1:C:145:GLN:HG3	1.86	0.57
1:B:24:ILE:HD12	1:B:24:ILE:N	2.18	0.57
1:C:2:GLU:O	1:C:153:ILE:HD12	2.04	0.57
1:A:75:ASN:OD1	1:A:75:ASN:C	2.43	0.57
1:C:64:LYS:H	1:C:64:LYS:HD2	1.70	0.57
1:A:132:ASP:CB	1:A:139:ASN:HB3	2.30	0.57
1:B:10:ASP:OD1	1:B:11:GLU:N	2.35	0.57
1:A:64:LYS:HB2	1:A:72:GLU:OE1	2.04	0.57
1:A:29:HIS:HE1	1:A:106:THR:HG23	1.69	0.57
1:B:104:PHE:HE2	1:B:123:PRO:HD3	1.68	0.57
1:B:139:ASN:ND2	1:C:51:ARG:HH21	1.97	0.57
1:C:8:ILE:N	1:C:138:ARG:O	2.38	0.57
1:B:115:SER:O	1:B:117:LYS:N	2.37	0.56
1:B:37:TYR:CD1	1:B:37:TYR:N	2.74	0.56
1:A:35:MET:N	1:A:35:MET:CE	2.68	0.56
1:A:26:LEU:HG	1:A:79:LYS:HD2	1.87	0.56
1:C:131:ILE:CD1	1:C:131:ILE:N	2.40	0.56
1:A:60:GLN:CD	1:C:20:LYS:HD3	2.26	0.56
1:A:152:ILE:O	1:A:155:ALA:HB3	2.05	0.56
1:A:76:ILE:N	1:A:79:LYS:O	2.33	0.56
1:B:133:TYR:CA	1:C:12:PHE:CZ	2.82	0.56
1:C:76:ILE:N	1:C:76:ILE:HD12	2.21	0.56
1:B:51:ARG:HG3	1:B:63:VAL:CG1	2.36	0.56
1:C:112:ILE:CD1	1:C:122:LEU:HD12	2.34	0.56
1:A:35:MET:CA	1:A:35:MET:CE	2.83	0.56
1:A:21:PHE:HE2	1:A:142:LEU:CD2	2.18	0.56
1:A:153:ILE:O	1:A:155:ALA:N	2.39	0.56
1:B:51:ARG:HG3	1:B:63:VAL:HG13	1.87	0.56
1:B:55:GLN:HA	1:B:59:HIS:H	1.70	0.55
1:B:4:LEU:HB3	1:B:142:LEU:HB2	1.88	0.55
1:C:22:ALA:HA	1:C:25:LEU:HD12	1.86	0.55
1:A:29:HIS:CG	1:A:30:THR:H	2.24	0.55
1:B:51:ARG:HA	1:B:63:VAL:CG1	2.34	0.55
1:C:82:TYR:CD2	1:C:103:TYR:O	2.58	0.55
1:C:93:GLU:O	1:C:97:PHE:CE2	2.59	0.55
1:B:146:THR:CG2	1:B:147:ASN:N	2.33	0.55
1:C:112:ILE:HD11	1:C:122:LEU:CD1	2.37	0.55
1:C:131:ILE:HG23	1:C:140:ILE:CD1	2.36	0.55
1:B:25:LEU:CD2	1:B:25:LEU:O	2.54	0.55
1:A:70:LEU:O	1:A:84:PHE:HA	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:20:LYS:O	1:B:21:PHE:C	2.44	0.55
1:C:1:MET:HB3	1:C:150:LYS:NZ	2.22	0.55
1:B:133:TYR:CG	1:B:133:TYR:O	2.57	0.55
1:B:148:LEU:HA	1:B:151:ASN:HD21	1.65	0.55
1:A:38:LEU:HB2	1:A:113:GLU:HG3	1.88	0.55
1:A:133:TYR:O	1:A:133:TYR:CD1	2.60	0.55
1:A:50:THR:HG21	1:A:83:HIS:NE2	2.22	0.55
1:B:21:PHE:CB	1:B:156:PHE:HZ	2.19	0.55
1:C:131:ILE:HG23	1:C:140:ILE:HD11	1.86	0.55
1:C:1:MET:HB3	1:C:150:LYS:HE2	1.86	0.55
1:B:63:VAL:HG23	1:B:63:VAL:O	2.06	0.55
1:B:8:ILE:HB	1:B:138:ARG:HB2	1.89	0.55
1:B:136:ASP:OD2	1:C:16:ARG:NH1	2.39	0.55
1:A:74:TYR:HD1	1:A:81:ILE:HG22	1.72	0.55
1:B:53:MET:C	1:B:54:LEU:HD23	2.27	0.55
1:B:92:PRO:CA	1:B:95:LEU:HG	2.34	0.55
1:A:126:ASP:O	1:A:149:GLY:HA3	2.07	0.55
1:C:10:ASP:HB3	3:C:202:HOH:O	2.05	0.55
1:C:6:GLN:HG3	1:C:17:PHE:HE1	1.68	0.55
1:B:14:MET:HE3	1:B:14:MET:HA	1.89	0.54
1:A:35:MET:HE2	1:A:35:MET:N	2.23	0.54
1:B:22:ALA:HB2	1:B:53:MET:HG2	1.88	0.54
1:B:148:LEU:O	1:B:152:ILE:CD1	2.56	0.54
1:B:14:MET:HA	1:B:14:MET:CE	2.38	0.54
1:B:19:LYS:HD2	1:B:56:GLY:C	2.27	0.54
1:C:21:PHE:CD1	1:C:25:LEU:HD11	2.43	0.54
1:B:7:TYR:N	1:C:55:GLN:OE1	2.26	0.54
1:C:59:HIS:ND1	1:C:63:VAL:CG2	2.71	0.54
1:B:5:THR:HA	1:B:140:ILE:O	2.07	0.54
1:A:46:LYS:O	1:A:50:THR:OG1	2.24	0.54
1:B:24:ILE:CG2	1:B:155:ALA:CB	2.86	0.54
1:B:8:ILE:HG21	1:B:138:ARG:HD3	1.90	0.53
1:B:133:TYR:CA	1:C:12:PHE:HZ	2.16	0.53
1:A:60:GLN:CA	1:C:6:GLN:HE22	2.17	0.53
1:C:131:ILE:HD12	1:C:140:ILE:CD1	2.38	0.53
1:B:136:ASP:CB	1:C:16:ARG:HH12	2.20	0.53
1:C:49:LEU:HD22	1:C:53:MET:HE3	1.90	0.53
1:A:62:ASN:ND2	1:C:4:LEU:HD22	2.23	0.53
1:C:146:THR:HG22	1:C:147:ASN:H	1.74	0.53
1:A:4:LEU:C	1:A:4:LEU:CD2	2.77	0.53
1:B:41:ASP:O	1:B:42:LEU:C	2.46	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:LEU:HB3	1:A:153:ILE:HD12	1.91	0.53
1:C:33:ALA:HB2	1:C:104:PHE:O	2.08	0.53
1:B:96:GLU:OE1	1:B:96:GLU:HA	2.09	0.53
1:B:9:PRO:HB3	1:C:19:LYS:CE	2.39	0.53
1:C:73:GLU:C	1:C:74:TYR:CD1	2.82	0.53
1:C:8:ILE:CG2	1:C:138:ARG:CB	2.70	0.53
1:A:88:ARG:NH1	1:A:88:ARG:CG	2.65	0.53
1:A:101:ARG:HB2	1:A:103:TYR:CD1	2.44	0.53
1:C:105:ASN:O	1:C:108:SER:HB2	2.09	0.53
1:C:50:THR:CG2	1:C:54:LEU:CD1	2.82	0.53
1:C:24:ILE:CG1	1:C:152:ILE:HD12	2.39	0.53
1:A:49:LEU:HD12	1:A:131:ILE:HD11	1.91	0.53
1:B:29:HIS:ND1	1:B:30:THR:N	2.57	0.53
1:B:128:LEU:CD1	1:B:145:GLN:OE1	2.57	0.53
1:C:1:MET:HB3	1:C:150:LYS:CE	2.38	0.53
1:A:92:PRO:O	1:A:95:LEU:N	2.40	0.53
1:B:42:LEU:HG	1:B:114:TRP:CH2	2.36	0.53
1:B:86:LEU:HD22	1:B:89:LEU:HD22	1.91	0.52
1:C:87:TYR:O	1:C:87:TYR:CD1	2.62	0.52
1:B:67:THR:HA	1:B:85:ASP:HB3	1.91	0.52
1:C:49:LEU:HD13	1:C:129:VAL:HG11	1.91	0.52
1:B:38:LEU:CD2	1:B:129:VAL:HG11	2.39	0.52
1:B:54:LEU:N	1:B:54:LEU:CD2	2.71	0.52
1:C:2:GLU:HB2	1:C:150:LYS:HD2	1.90	0.52
1:B:47:THR:HG22	1:B:63:VAL:HG21	1.92	0.52
1:B:6:GLN:NE2	1:C:60:GLN:HA	2.24	0.52
1:C:144:ALA:CB	1:C:153:ILE:CG1	2.77	0.52
1:A:64:LYS:HB3	1:A:72:GLU:OE1	2.09	0.52
1:B:84:PHE:CE1	1:B:112:ILE:HG12	2.44	0.52
1:C:89:LEU:CD2	1:C:95:LEU:HD21	2.39	0.52
1:A:16:ARG:O	1:A:20:LYS:HG3	2.10	0.52
1:A:80:MET:O	1:A:81:ILE:HG13	2.10	0.52
1:C:24:ILE:HD12	1:C:152:ILE:CD1	2.40	0.52
1:A:71:VAL:CG1	1:A:82:TYR:HB3	2.41	0.51
1:C:64:LYS:HD2	1:C:74:TYR:CE2	2.44	0.51
1:B:2:GLU:CB	1:B:144:ALA:HB2	2.39	0.51
1:A:101:ARG:CB	1:A:103:TYR:CE1	2.94	0.51
1:B:37:TYR:CE2	1:B:115:SER:HB2	2.44	0.51
1:C:35:MET:CG	1:C:123:PRO:HG2	2.40	0.51
1:C:37:TYR:HD1	1:C:37:TYR:N	2.08	0.51
1:C:39:ASN:O	1:C:130:ASN:HA	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:95:LEU:CD1	1:B:118:GLY:CA	2.88	0.51
1:A:89:LEU:HD21	1:A:95:LEU:HG	1.93	0.51
1:B:97:PHE:HD1	1:B:97:PHE:H	1.51	0.51
1:A:73:GLU:HB3	1:A:82:TYR:CE1	2.43	0.51
1:A:4:LEU:C	1:A:4:LEU:HD23	2.30	0.51
1:B:50:THR:HG22	1:B:54:LEU:HG	1.92	0.51
1:A:34:ILE:HG23	1:A:148:LEU:CD2	2.40	0.51
1:B:52:GLY:O	1:B:56:GLY:HA3	2.11	0.51
1:B:75:ASN:C	1:B:76:ILE:HG12	2.31	0.51
1:B:2:GLU:O	1:B:143:ILE:CA	2.57	0.51
1:B:2:GLU:CB	1:B:144:ALA:CB	2.87	0.51
1:A:4:LEU:HD13	1:A:142:LEU:HD12	1.92	0.51
1:B:140:ILE:O	1:B:140:ILE:HG22	2.10	0.51
1:A:23:GLU:O	1:A:27:LYS:HG3	2.11	0.51
1:C:115:SER:HB3	3:C:201:HOH:O	2.11	0.51
1:C:94:GLU:C	1:C:97:PHE:HD2	2.13	0.50
1:A:116:GLU:HB2	1:A:117:LYS:HD2	1.93	0.50
1:B:8:ILE:HD13	1:B:14:MET:HA	1.94	0.50
1:B:5:THR:O	1:B:5:THR:CG2	2.59	0.50
1:C:35:MET:HB3	1:C:37:TYR:HE1	1.76	0.50
1:A:8:ILE:HG22	1:A:138:ARG:HB2	1.92	0.50
1:C:37:TYR:N	1:C:37:TYR:CD1	2.80	0.50
1:B:9:PRO:HG3	1:C:56:GLY:HA2	1.91	0.50
1:B:82:TYR:CZ	1:B:103:TYR:CE2	2.99	0.50
1:B:20:LYS:HG3	1:B:21:PHE:N	2.25	0.50
1:B:7:TYR:OH	1:B:137:ALA:CB	2.59	0.50
1:C:49:LEU:CD1	1:C:129:VAL:HG11	2.41	0.50
1:B:126:ASP:HB3	1:B:146:THR:CB	2.42	0.50
1:B:14:MET:HB3	1:B:48:THR:CG2	2.41	0.50
1:B:150:LYS:O	1:B:154:SER:OG	2.30	0.50
1:B:66:PRO:O	1:B:69:THR:HB	2.12	0.50
1:C:94:GLU:O	1:C:97:PHE:HD2	1.94	0.50
1:A:54:LEU:CD2	1:A:81:ILE:HG21	2.41	0.50
1:B:148:LEU:CD2	1:B:149:GLY:N	2.73	0.50
1:B:84:PHE:CE2	1:B:104:PHE:HE1	2.29	0.50
1:B:84:PHE:CE2	1:B:104:PHE:CE1	3.00	0.50
1:C:11:GLU:O	1:C:14:MET:HB2	2.11	0.50
1:B:18:GLY:HA2	1:B:49:LEU:CD2	2.42	0.49
1:C:14:MET:CG	1:C:138:ARG:NH1	2.75	0.49
1:B:92:PRO:CB	1:B:121:ILE:HD11	2.42	0.49
1:B:37:TYR:HD1	1:B:37:TYR:N	2.10	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:ARG:HH21	1:C:135:ASP:CB	2.03	0.49
1:C:127:ILE:CG2	1:C:128:LEU:H	2.18	0.49
1:C:146:THR:HG22	1:C:148:LEU:H	1.78	0.49
1:C:1:MET:CB	1:C:150:LYS:CE	2.87	0.49
1:C:89:LEU:HD11	1:C:91:ASP:O	2.12	0.49
1:A:21:PHE:CE2	1:A:142:LEU:HD21	2.45	0.49
1:B:37:TYR:HE2	1:B:115:SER:CB	2.23	0.49
1:C:146:THR:O	1:C:150:LYS:N	2.32	0.49
1:C:64:LYS:HD2	1:C:74:TYR:HE2	1.77	0.49
1:A:22:ALA:O	1:A:25:LEU:HB2	2.12	0.49
1:C:34:ILE:O	1:C:110:CYS:HB2	2.12	0.49
1:C:76:ILE:HD13	1:C:81:ILE:HD11	1.95	0.49
1:B:95:LEU:CD1	1:B:118:GLY:HA2	2.43	0.49
1:C:44:ALA:HA	1:C:133:TYR:CD1	2.47	0.49
1:A:44:ALA:HA	1:A:133:TYR:CD2	2.47	0.49
1:B:139:ASN:OD1	1:B:140:ILE:N	2.46	0.49
1:B:38:LEU:HD23	1:B:129:VAL:CG1	2.42	0.49
1:A:57:ILE:HG21	1:A:76:ILE:CG2	2.41	0.49
1:A:57:ILE:HG21	1:A:76:ILE:HG21	1.92	0.49
1:A:146:THR:CG2	1:A:147:ASN:H	2.06	0.49
1:B:104:PHE:CE2	1:B:123:PRO:HD2	2.48	0.49
1:C:36:VAL:CG2	1:C:127:ILE:HD13	2.43	0.49
1:B:2:GLU:HB3	1:B:153:ILE:HD12	1.95	0.49
1:A:144:ALA:CB	1:A:149:GLY:C	2.80	0.49
1:A:141:GLU:HB3	1:A:143:ILE:HG13	1.94	0.48
1:B:19:LYS:HD2	1:B:56:GLY:O	2.13	0.48
1:C:26:LEU:HD11	1:C:57:ILE:HG23	1.95	0.48
1:C:62:ASN:HB2	3:C:210:HOH:O	2.12	0.48
1:B:25:LEU:HD21	1:B:34:ILE:CD1	2.44	0.48
1:A:17:PHE:C	1:A:17:PHE:CD1	2.87	0.48
1:B:21:PHE:CD2	1:B:53:MET:SD	3.06	0.48
1:B:19:LYS:CB	1:B:52:GLY:O	2.60	0.48
1:C:146:THR:CG2	1:C:147:ASN:N	2.76	0.48
1:B:8:ILE:HB	1:B:138:ARG:O	2.14	0.48
1:B:92:PRO:HB3	1:B:121:ILE:HD11	1.94	0.48
1:C:22:ALA:O	1:C:25:LEU:HB2	2.14	0.48
1:C:38:LEU:HD11	1:C:111:LEU:HD21	1.93	0.48
1:B:146:THR:HG22	1:B:148:LEU:H	1.79	0.48
1:C:54:LEU:HD11	1:C:111:LEU:HD13	1.96	0.48
1:C:69:THR:O	1:C:70:LEU:CB	2.62	0.48
1:A:131:ILE:HG22	1:A:131:ILE:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:104:PHE:HZ	1:B:122:LEU:HD23	1.79	0.48
1:C:59:HIS:ND1	1:C:63:VAL:HG22	2.28	0.48
1:A:64:LYS:HE3	1:A:64:LYS:HB2	1.48	0.48
1:B:7:TYR:CD2	1:C:52:GLY:HA2	2.49	0.48
1:C:102:ASP:HA	1:C:105:ASN:HD21	1.77	0.48
1:A:37:TYR:CE1	1:A:125:ALA:HB2	2.48	0.47
1:B:89:LEU:CD2	1:B:95:LEU:CD2	2.89	0.47
1:A:8:ILE:HG21	1:A:138:ARG:HB2	1.95	0.47
1:B:137:ALA:H	1:C:16:ARG:CZ	2.26	0.47
1:B:146:THR:HB	1:B:148:LEU:CD2	2.42	0.47
1:C:9:PRO:HD2	1:C:13:SER:OG	2.14	0.47
1:C:14:MET:HG2	1:C:138:ARG:HH11	1.76	0.47
1:B:13:SER:C	1:B:15:LEU:N	2.66	0.47
1:B:21:PHE:HZ	1:B:36:VAL:CG1	2.19	0.47
1:C:95:LEU:CD1	1:C:118:GLY:HA2	2.43	0.47
1:C:49:LEU:O	1:C:53:MET:HB2	2.14	0.47
1:A:139:ASN:O	1:A:140:ILE:CG1	2.61	0.47
1:B:133:TYR:CB	1:B:138:ARG:HA	2.44	0.47
1:B:89:LEU:CG	1:B:95:LEU:HD21	2.43	0.47
1:B:9:PRO:HB3	1:C:19:LYS:NZ	2.30	0.47
1:C:82:TYR:HE2	1:C:108:SER:OG	1.97	0.47
1:C:21:PHE:C	1:C:21:PHE:HD1	2.17	0.47
1:C:23:GLU:HA	1:C:26:LEU:HD12	1.96	0.47
1:B:140:ILE:CG2	1:B:140:ILE:O	2.63	0.47
1:C:26:LEU:HD11	1:C:57:ILE:HD13	1.96	0.47
1:B:82:TYR:CD2	1:B:103:TYR:CB	2.98	0.47
1:B:29:HIS:CG	1:B:30:THR:H	2.33	0.47
1:A:51:ARG:NH2	1:C:139:ASN:HD21	2.13	0.47
1:C:37:TYR:CD1	1:C:125:ALA:CB	2.89	0.47
1:A:47:THR:O	1:A:48:THR:C	2.53	0.47
1:B:21:PHE:HB2	1:B:156:PHE:HZ	1.80	0.47
1:B:54:LEU:O	1:B:59:HIS:HB2	2.14	0.47
1:A:126:ASP:OD1	1:A:126:ASP:N	2.47	0.46
1:A:84:PHE:HB2	1:A:112:ILE:HA	1.97	0.46
1:A:118:GLY:CA	1:A:122:LEU:CD1	2.87	0.46
1:B:95:LEU:CD1	1:B:118:GLY:HA3	2.45	0.46
1:A:130:ASN:O	1:A:140:ILE:HA	2.15	0.46
1:A:25:LEU:HD22	1:A:34:ILE:HD13	1.90	0.46
1:B:36:VAL:HG12	1:B:129:VAL:CG2	2.45	0.46
1:B:81:ILE:CG2	1:B:111:LEU:HD12	2.46	0.46
1:C:60:GLN:C	1:C:61:GLY:O	2.53	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:LEU:HD22	1:A:53:MET:HE2	1.97	0.46
1:C:34:ILE:HG22	1:C:34:ILE:O	2.16	0.46
1:C:50:THR:HG23	1:C:54:LEU:HD13	1.94	0.46
1:A:118:GLY:O	1:A:122:LEU:HB3	2.15	0.46
1:B:10:ASP:O	1:B:13:SER:N	2.42	0.46
1:B:19:LYS:NZ	1:B:23:GLU:OE2	2.48	0.46
1:B:82:TYR:CE2	1:B:103:TYR:CB	2.98	0.46
1:B:74:TYR:HB2	1:B:81:ILE:HB	1.97	0.46
1:C:35:MET:HE2	1:C:104:PHE:CZ	2.44	0.46
1:A:25:LEU:CD2	1:A:34:ILE:CD1	2.89	0.46
1:C:21:PHE:CE2	1:C:129:VAL:CG2	2.99	0.46
1:A:26:LEU:CA	1:A:79:LYS:CE	2.69	0.45
1:A:33:ALA:O	1:A:35:MET:CE	2.65	0.45
1:B:7:TYR:CZ	1:B:137:ALA:CB	2.99	0.45
1:B:20:LYS:CD	1:B:24:ILE:CD1	2.74	0.45
1:C:82:TYR:CE2	1:C:103:TYR:HA	2.51	0.45
1:B:95:LEU:HD12	1:B:122:LEU:HD12	1.96	0.45
1:B:126:ASP:HB3	1:B:146:THR:HB	1.97	0.45
1:B:38:LEU:HD23	1:B:129:VAL:HG11	1.97	0.45
1:B:8:ILE:O	1:B:8:ILE:CG2	2.63	0.45
1:C:21:PHE:CD1	1:C:21:PHE:O	2.69	0.45
1:A:25:LEU:HD22	1:A:34:ILE:CD1	2.47	0.45
1:A:73:GLU:H	1:A:73:GLU:HG3	1.40	0.45
1:A:54:LEU:HD22	1:A:81:ILE:HG21	1.98	0.45
1:B:37:TYR:O	1:B:129:VAL:HB	2.16	0.45
1:C:35:MET:HG2	1:C:123:PRO:CD	2.46	0.45
1:C:81:ILE:HG12	1:C:81:ILE:H	1.39	0.45
1:C:82:TYR:HB2	1:C:110:CYS:HA	1.99	0.45
1:C:28:LEU:HD13	1:C:152:ILE:HD11	1.98	0.45
1:A:98:MET:O	1:A:101:ARG:N	2.50	0.45
1:A:24:ILE:O	1:A:25:LEU:C	2.54	0.45
1:B:14:MET:CG	1:B:48:THR:HG22	2.47	0.45
1:A:34:ILE:HG23	1:A:148:LEU:HD23	1.98	0.45
1:A:24:ILE:HD13	1:A:24:ILE:HG21	1.66	0.45
1:A:60:GLN:O	1:A:60:GLN:HG3	2.17	0.45
1:C:35:MET:SD	1:C:110:CYS:HB3	2.56	0.45
1:B:86:LEU:HD13	1:B:122:LEU:HD13	1.97	0.45
1:B:10:ASP:CG	1:B:11:GLU:H	2.19	0.45
1:A:128:LEU:N	1:A:143:ILE:O	2.46	0.45
1:C:76:ILE:CD1	1:C:76:ILE:N	2.80	0.45
1:A:117:LYS:HD2	1:A:117:LYS:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:148:LEU:O	1:B:152:ILE:CG1	2.65	0.44
1:B:86:LEU:CD1	1:B:122:LEU:HD13	2.46	0.44
1:C:36:VAL:HG22	1:C:127:ILE:HD13	1.99	0.44
1:B:19:LYS:CA	1:B:52:GLY:O	2.65	0.44
1:C:35:MET:SD	1:C:104:PHE:HE1	2.38	0.44
1:C:87:TYR:HB2	1:C:114:TRP:CD1	2.53	0.44
1:B:118:GLY:O	1:B:122:LEU:HB2	2.18	0.44
1:B:146:THR:HG21	1:B:148:LEU:CD2	2.44	0.44
1:C:11:GLU:HA	1:C:138:ARG:NH1	2.30	0.44
1:A:122:LEU:HA	1:A:123:PRO:HD3	1.77	0.44
1:A:22:ALA:HA	1:A:25:LEU:HB2	1.99	0.44
1:A:59:HIS:CE1	1:A:62:ASN:O	2.67	0.44
1:C:23:GLU:O	1:C:26:LEU:HB2	2.17	0.44
1:C:17:PHE:CD2	1:C:17:PHE:C	2.90	0.44
1:C:98:MET:HG2	1:C:99:GLY:N	2.33	0.44
1:B:18:GLY:O	1:B:21:PHE:HB3	2.18	0.44
1:B:8:ILE:HD13	1:B:14:MET:CA	2.48	0.44
1:A:86:LEU:CD2	1:A:89:LEU:CD2	2.89	0.44
1:B:30:THR:O	1:B:107:ASP:HA	2.18	0.44
1:C:142:LEU:HD23	1:C:142:LEU:H	1.81	0.44
1:A:30:THR:HG21	1:A:34:ILE:HG13	2.00	0.43
1:A:53:MET:HB2	1:A:53:MET:HE2	1.78	0.43
1:C:84:PHE:HB2	1:C:112:ILE:CG1	2.47	0.43
1:A:97:PHE:N	1:A:97:PHE:CD1	2.76	0.43
1:A:79:LYS:HD3	1:A:109:ILE:HD12	1.81	0.43
1:B:128:LEU:HD11	1:B:145:GLN:OE1	2.18	0.43
1:C:37:TYR:CG	1:C:125:ALA:HB2	2.49	0.43
1:C:59:HIS:ND1	1:C:63:VAL:HG23	2.32	0.43
1:A:144:ALA:HB1	1:A:149:GLY:HA3	2.00	0.43
1:A:71:VAL:CG1	1:A:84:PHE:CZ	2.98	0.43
1:A:71:VAL:HA	1:A:83:HIS:O	2.18	0.43
1:B:63:VAL:O	1:B:63:VAL:CG2	2.67	0.43
1:C:130:ASN:HB2	1:C:141:GLU:CB	2.48	0.43
1:C:86:LEU:O	1:C:117:LYS:HG3	2.18	0.43
1:B:25:LEU:CD2	1:B:34:ILE:HD13	2.48	0.43
1:A:144:ALA:HB1	1:A:149:GLY:CA	2.46	0.43
1:A:100:ILE:O	1:A:100:ILE:HG22	2.18	0.43
1:A:60:GLN:O	1:A:60:GLN:CG	2.66	0.43
1:C:22:ALA:O	1:C:25:LEU:N	2.52	0.43
1:A:61:GLY:N	1:C:6:GLN:HE21	2.13	0.43
1:A:139:ASN:C	1:A:140:ILE:HG13	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:34:ILE:C	1:A:35:MET:HE1	2.39	0.43
1:A:4:LEU:O	1:A:142:LEU:N	2.38	0.43
1:B:8:ILE:CG2	1:B:138:ARG:HD3	2.48	0.43
1:B:146:THR:CG2	1:B:148:LEU:CD2	2.96	0.43
1:C:35:MET:HG3	1:C:37:TYR:CE1	2.53	0.43
1:C:75:ASN:O	1:C:76:ILE:HD12	2.18	0.43
1:A:74:TYR:HB2	1:A:81:ILE:CG2	2.49	0.43
1:C:37:TYR:CE1	1:C:125:ALA:CB	2.98	0.43
1:B:35:MET:HE1	1:B:112:ILE:HD11	1.99	0.43
1:B:26:LEU:HD11	1:B:57:ILE:HG13	1.99	0.43
1:C:84:PHE:CZ	1:C:103:TYR:CD2	2.99	0.43
1:C:50:THR:HG23	1:C:54:LEU:CD1	2.49	0.43
1:C:146:THR:CG2	1:C:147:ASN:H	2.31	0.43
1:B:82:TYR:CD2	1:B:103:TYR:HB3	2.53	0.43
1:C:116:GLU:HG2	1:C:116:GLU:H	1.67	0.43
1:A:44:ALA:O	1:A:131:ILE:HG21	2.18	0.43
1:C:8:ILE:HD11	1:C:140:ILE:HG12	1.90	0.43
1:B:88:ARG:HG3	1:B:88:ARG:NH1	2.29	0.43
1:A:83:HIS:CE1	1:A:113:GLU:OE2	2.72	0.43
1:A:53:MET:O	1:A:57:ILE:HG13	2.18	0.43
1:B:66:PRO:HG2	1:B:83:HIS:O	2.19	0.43
1:C:150:LYS:HB2	1:C:150:LYS:HE3	1.77	0.43
1:C:41:ASP:O	1:C:43:GLY:N	2.52	0.43
1:B:132:ASP:HB2	3:B:206:HOH:O	2.18	0.42
1:B:133:TYR:CB	1:B:138:ARG:CG	2.96	0.42
1:C:131:ILE:HG23	1:C:131:ILE:HD12	1.73	0.42
1:C:37:TYR:O	1:C:39:ASN:N	2.51	0.42
1:C:7:TYR:HA	1:C:139:ASN:HD22	1.84	0.42
1:B:8:ILE:HD11	1:B:14:MET:HE3	2.00	0.42
1:B:47:THR:HG23	1:B:50:THR:HB	2.00	0.42
1:B:6:GLN:O	1:B:139:ASN:OD1	2.37	0.42
1:C:34:ILE:CG2	1:C:110:CYS:N	2.75	0.42
1:B:108:SER:O	1:B:109:ILE:HG12	2.20	0.42
1:B:18:GLY:HA2	1:B:49:LEU:HD23	2.01	0.42
1:B:82:TYR:CE1	1:B:103:TYR:CD2	3.07	0.42
1:C:2:GLU:CB	1:C:150:LYS:HD2	2.49	0.42
1:C:60:GLN:NE2	1:C:60:GLN:N	2.66	0.42
1:A:55:GLN:C	1:A:57:ILE:H	2.22	0.42
1:B:133:TYR:HA	1:C:12:PHE:CE1	2.50	0.42
1:B:84:PHE:HE2	1:B:104:PHE:CE1	2.38	0.42
1:C:102:ASP:CB	1:C:105:ASN:HD22	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:7:TYR:CE1	1:C:15:LEU:HB3	2.54	0.42
1:A:64:LYS:O	1:A:65:SER:C	2.57	0.42
1:B:10:ASP:OD1	1:B:11:GLU:HB3	2.20	0.42
1:B:26:LEU:HD23	1:B:79:LYS:CB	2.46	0.42
1:B:37:TYR:HE2	1:B:115:SER:HB2	1.82	0.42
1:B:18:GLY:CA	1:B:49:LEU:HD23	2.50	0.42
1:C:80:MET:CE	1:C:82:TYR:OH	2.67	0.42
1:C:28:LEU:HD13	1:C:152:ILE:HD13	2.01	0.42
1:C:35:MET:HG3	1:C:37:TYR:HE1	1.84	0.42
1:A:144:ALA:HB2	1:A:149:GLY:O	2.20	0.42
1:A:98:MET:O	1:A:101:ARG:HB2	2.19	0.42
1:C:122:LEU:HD23	1:C:122:LEU:N	2.35	0.42
1:B:2:GLU:O	1:B:144:ALA:N	2.52	0.42
1:B:25:LEU:CD2	1:B:25:LEU:C	2.88	0.42
1:A:50:THR:O	1:A:53:MET:HB3	2.19	0.42
1:B:136:ASP:H	1:C:16:ARG:CZ	2.33	0.42
1:A:144:ALA:CB	1:A:149:GLY:O	2.68	0.42
1:A:98:MET:O	1:A:101:ARG:CB	2.68	0.41
1:A:44:ALA:HB1	1:A:133:TYR:CG	2.55	0.41
1:B:137:ALA:H	1:C:16:ARG:HH12	1.68	0.41
1:B:55:GLN:NE2	1:B:61:GLY:O	2.51	0.41
1:C:17:PHE:CE1	1:C:156:PHE:HE2	2.38	0.41
1:C:80:MET:HG3	1:C:80:MET:H	1.67	0.41
1:B:133:TYR:CE1	1:B:133:TYR:O	2.71	0.41
1:A:8:ILE:O	1:A:137:ALA:HB1	2.20	0.41
1:C:15:LEU:HD22	1:C:52:GLY:CA	2.50	0.41
1:A:23:GLU:H	1:A:23:GLU:HG3	1.65	0.41
1:A:92:PRO:O	1:A:93:GLU:C	2.57	0.41
1:B:24:ILE:O	1:B:28:LEU:HG	2.19	0.41
1:B:69:THR:C	1:B:70:LEU:HG	2.40	0.41
1:A:67:THR:HG22	1:A:68:TYR:CD1	2.56	0.41
1:C:8:ILE:HG21	1:C:138:ARG:CB	2.42	0.41
1:B:115:SER:O	1:B:116:GLU:C	2.59	0.41
1:B:92:PRO:HA	1:B:95:LEU:CG	2.41	0.41
1:A:141:GLU:HB3	1:A:143:ILE:CG1	2.51	0.41
1:C:14:MET:O	1:C:15:LEU:C	2.57	0.41
1:C:91:ASP:HB2	1:C:92:PRO:CD	2.48	0.41
1:B:53:MET:O	1:B:57:ILE:HB	2.21	0.41
1:B:7:TYR:CZ	1:B:137:ALA:HB2	2.55	0.41
1:C:5:THR:HG22	1:C:6:GLN:N	2.36	0.41
1:B:82:TYR:CD2	1:B:103:TYR:CG	3.07	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:14:MET:CB	1:B:48:THR:HG22	2.45	0.40
1:C:22:ALA:HA	1:C:25:LEU:CD1	2.51	0.40
1:C:5:THR:CG2	1:C:6:GLN:N	2.85	0.40
1:B:142:LEU:HA	1:B:142:LEU:HD23	1.91	0.40
1:B:85:ASP:HA	1:B:113:GLU:HB3	2.02	0.40
1:A:4:LEU:CD1	1:A:153:ILE:HG23	2.45	0.40
1:A:76:ILE:HG13	1:A:81:ILE:HD12	2.02	0.40
1:A:83:HIS:O	1:A:84:PHE:CD1	2.74	0.40
1:C:128:LEU:HD13	1:C:145:GLN:OE1	2.21	0.40
1:A:114:TRP:O	1:A:116:GLU:N	2.55	0.40
1:C:29:HIS:CG	1:C:30:THR:N	2.72	0.40
1:B:87:TYR:CD1	1:B:114:TRP:CZ3	3.09	0.40
1:A:111:LEU:H	1:A:111:LEU:HD23	1.86	0.40
1:B:136:ASP:CB	1:C:16:ARG:NH1	2.82	0.40
1:A:60:GLN:CA	1:C:6:GLN:NE2	2.69	0.40
1:B:4:LEU:CD2	1:C:62:ASN:HD21	2.29	0.40
1:B:37:TYR:HE1	1:B:125:ALA:HB2	1.67	0.40
1:B:70:LEU:HD12	1:B:70:LEU:N	2.37	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	155/161 (96%)	118 (76%)	30 (19%)	7 (4%)	3	3
1	B	155/161 (96%)	127 (82%)	23 (15%)	5 (3%)	5	6
1	C	155/161 (96%)	116 (75%)	30 (19%)	9 (6%)	2	2
All	All	465/483 (96%)	361 (78%)	83 (18%)	21 (4%)	3	3

All (21) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	B	116	GLU
1	C	115	SER
1	A	115	SER
1	A	140	ILE
1	A	154	SER
1	B	31	GLU
1	C	38	LEU
1	C	118	GLY
1	A	4	LEU
1	B	58	GLY
1	C	33	ALA
1	C	57	ILE
1	C	142	LEU
1	B	67	THR
1	B	115	SER
1	C	9	PRO
1	C	66	PRO
1	A	11	GLU
1	A	29	HIS
1	C	156	PHE
1	A	58	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	135/138 (98%)	95 (70%)	40 (30%)	0	0
1	B	135/138 (98%)	82 (61%)	53 (39%)	0	0
1	C	135/138 (98%)	94 (70%)	41 (30%)	0	0
All	All	405/414 (98%)	271 (67%)	134 (33%)	0	0

All (134) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	A	4	LEU

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Mol	Chain	Res	Type
1	A	16	ARG
1	A	19	LYS
1	A	28	LEU
1	A	32	LYS
1	A	35	MET
1	A	47	THR
1	A	50	THR
1	A	53	MET
1	A	64	LYS
1	A	67	THR
1	A	68	TYR
1	A	69	THR
1	A	72	GLU
1	A	73	GLU
1	A	74	TYR
1	A	75	ASN
1	A	76	ILE
1	A	79	LYS
1	A	80	MET
1	A	85	ASP
1	A	88	ARG
1	A	89	LEU
1	A	91	ASP
1	A	98	MET
1	A	101	ARG
1	A	102	ASP
1	A	106	THR
1	A	108	SER
1	A	110	CYS
1	A	115	SER
1	A	121	ILE
1	A	126	ASP
1	A	128	LEU
1	A	133	TYR
1	A	148	LEU
1	A	150	LYS
1	A	152	ILE
1	A	156	PHE
1	B	2	GLU
1	B	4	LEU
1	B	12	PHE
1	B	14	MET

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Mol	Chain	Res	Type
1	B	20	LYS
1	B	24	ILE
1	B	25	LEU
1	B	26	LEU
1	B	27	LYS
1	B	30	THR
1	B	32	LYS
1	B	36	VAL
1	B	46	LYS
1	B	48	THR
1	B	49	LEU
1	B	54	LEU
1	B	57	ILE
1	B	64	LYS
1	B	65	SER
1	B	70	LEU
1	B	76	ILE
1	B	79	LYS
1	B	80	MET
1	B	81	ILE
1	B	84	PHE
1	B	85	ASP
1	B	88	ARG
1	B	89	LEU
1	B	95	LEU
1	B	97	PHE
1	B	100	ILE
1	B	103	TYR
1	B	106	THR
1	B	108	SER
1	B	113	GLU
1	B	117	LYS
1	B	119	GLN
1	B	121	ILE
1	B	126	ASP
1	B	127	ILE
1	B	128	LEU
1	B	131	ILE
1	B	133	TYR
1	B	134	TYR
1	B	136	ASP
1	B	138	ARG

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Mol	Chain	Res	Type
1	B	140	ILE
1	B	150	LYS
1	B	151	ASN
1	B	152	ILE
1	B	154	SER
1	B	156	PHE
1	B	157	SER
1	C	3	SER
1	C	4	LEU
1	C	11	GLU
1	C	12	PHE
1	C	13	SER
1	C	14	MET
1	C	16	ARG
1	C	19	LYS
1	C	20	LYS
1	C	34	ILE
1	C	35	MET
1	C	37	TYR
1	C	41	ASP
1	C	42	LEU
1	C	46	LYS
1	C	49	LEU
1	C	60	GLN
1	C	62	ASN
1	C	64	LYS
1	C	72	GLU
1	C	73	GLU
1	C	74	TYR
1	C	80	MET
1	C	81	ILE
1	C	88	ARG
1	C	98	MET
1	C	100	ILE
1	C	106	THR
1	C	107	ASP
1	C	109	ILE
1	C	112	ILE
1	C	122	LEU
1	C	127	ILE
1	C	128	LEU
1	C	131	ILE

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Mol	Chain	Res	Type
1	C	141	GLU
1	C	142	LEU
1	C	145	GLN
1	C	150	LYS
1	C	156	PHE
1	C	157	SER

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	29	HIS
1	A	59	HIS
1	A	147	ASN
1	B	6	GLN
1	B	75	ASN
1	B	151	ASN
1	C	6	GLN
1	C	60	GLN
1	C	62	ASN
1	C	83	HIS
1	C	105	ASN
1	C	139	ASN

### 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](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.