



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 08:42 PM GMT

PDB ID : 2H6R
Title : Crystal Structure of triosephosphate isomerase (TIM) from Methanocaldococcus jannaschii
Authors : Gayathri, P.; Banerjee, M.; Vijayalakshmi, A.; Balaram, H.; Balaram, P.; Murthy, M.R.N.
Deposited on : 2006-06-01
Resolution : 2.30 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

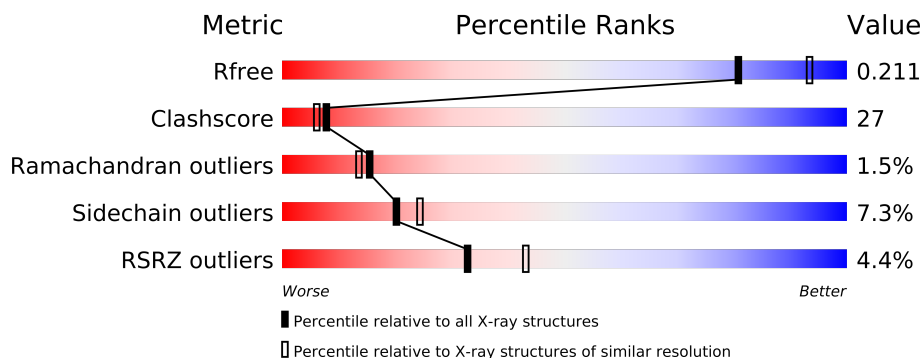
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.30 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}	66092	2929 (2.30-2.30)
Clashscore	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (2.30-2.30)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	219	
1	B	219	
1	C	219	
1	D	219	
1	E	219	
1	F	219	
1	G	219	
1	H	219	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12422 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Triosephosphate isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	203	Total	C	N	O	S	0	0	0
			1504	943	258	294	9			
1	B	209	Total	C	N	O	S	0	0	0
			1548	971	265	303	9			
1	C	204	Total	C	N	O	S	0	0	0
			1508	946	260	293	9			
1	D	200	Total	C	N	O	S	0	0	0
			1480	927	255	289	9			
1	E	207	Total	C	N	O	S	0	0	0
			1538	966	264	299	9			
1	F	201	Total	C	N	O	S	0	0	0
			1490	934	257	290	9			
1	G	200	Total	C	N	O	S	0	0	0
			1477	925	254	289	9			
1	H	201	Total	C	N	O	S	0	0	0
			1493	937	257	290	9			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	VAL	LEU	ENGINEERED	UNP Q58923
A	134	CYS	TYR	ENGINEERED	UNP Q58923
B	2	VAL	LEU	ENGINEERED	UNP Q58923
B	134	CYS	TYR	ENGINEERED	UNP Q58923
C	2	VAL	LEU	ENGINEERED	UNP Q58923
C	134	CYS	TYR	ENGINEERED	UNP Q58923
D	2	VAL	LEU	ENGINEERED	UNP Q58923
D	134	CYS	TYR	ENGINEERED	UNP Q58923
E	2	VAL	LEU	ENGINEERED	UNP Q58923
E	134	CYS	TYR	ENGINEERED	UNP Q58923
F	2	VAL	LEU	ENGINEERED	UNP Q58923
F	134	CYS	TYR	ENGINEERED	UNP Q58923
G	2	VAL	LEU	ENGINEERED	UNP Q58923

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Chain	Residue	Modelled	Actual	Comment	Reference
G	134	CYS	TYR	ENGINEERED	UNP Q58923
H	2	VAL	LEU	ENGINEERED	UNP Q58923
H	134	CYS	TYR	ENGINEERED	UNP Q58923

- Molecule 2 is water.

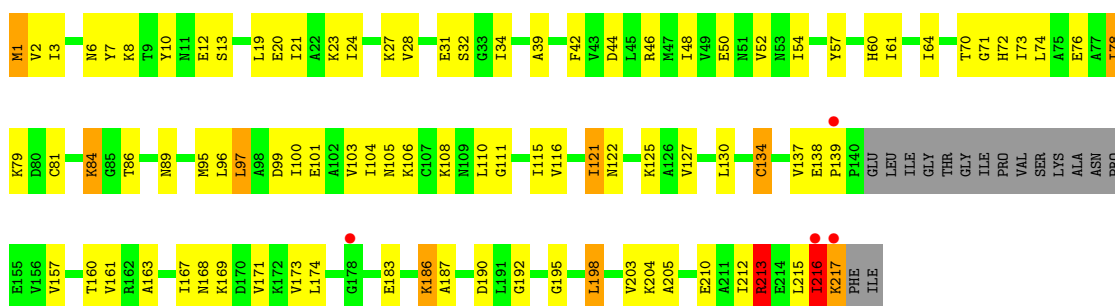
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	58	Total	O	0	0
			58	58		
2	B	55	Total	O	0	0
			55	55		
2	C	45	Total	O	0	0
			45	45		
2	D	46	Total	O	0	0
			46	46		
2	E	53	Total	O	0	0
			53	53		
2	F	34	Total	O	0	0
			34	34		
2	G	36	Total	O	0	0
			36	36		
2	H	57	Total	O	0	0
			57	57		

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.

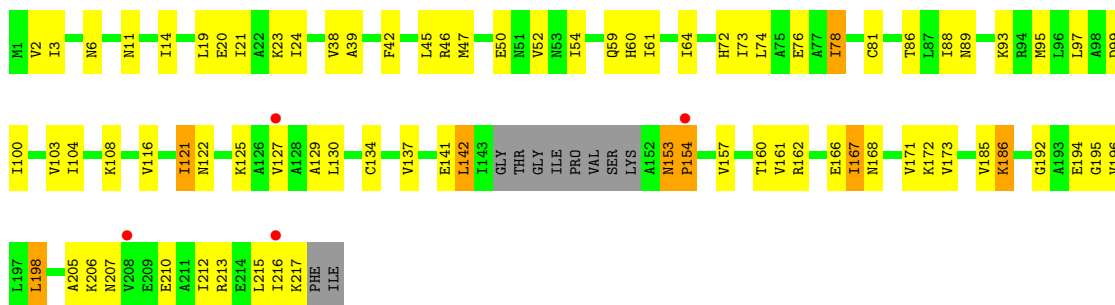
- Molecule 1: Triosephosphate isomerase

Chain A:



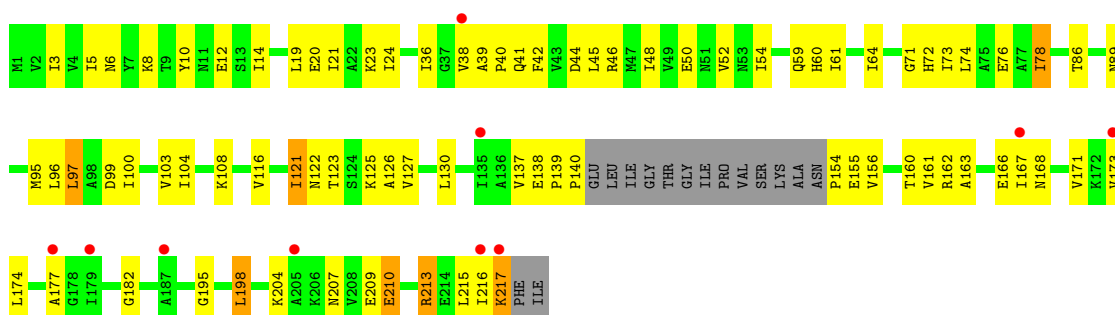
- Molecule 1: Triosephosphate isomerase

Chain B:



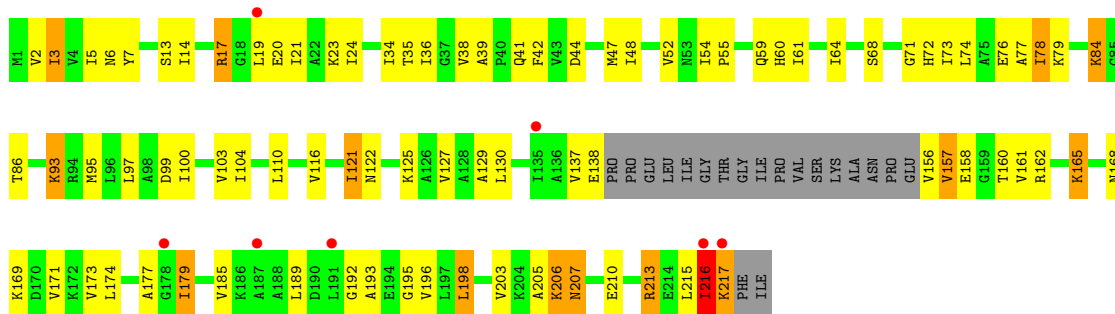
- Molecule 1: Triosephosphate isomerase

Chain C:



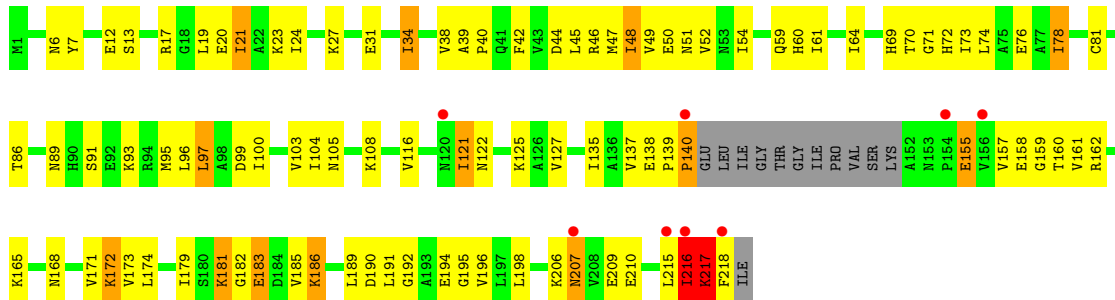
- Molecule 1: Triosephosphate isomerase

Chain D:



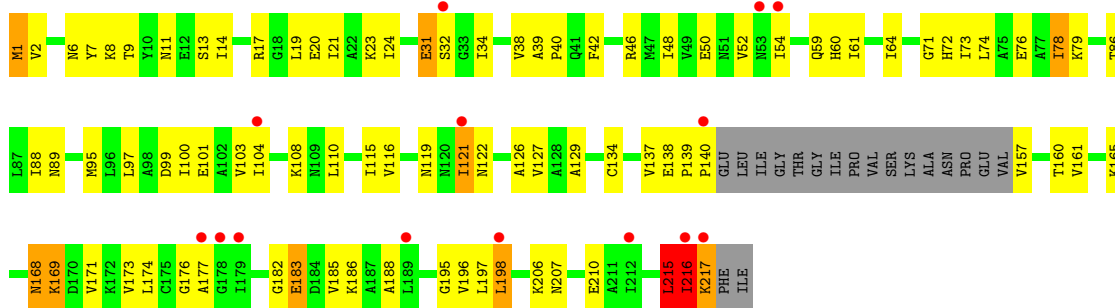
- Molecule 1: Triosephosphate isomerase

Chain E:



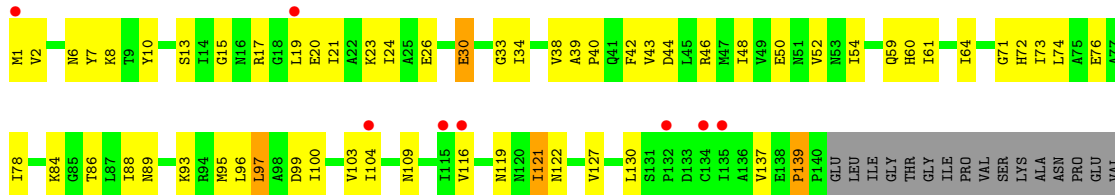
- Molecule 1: Triosephosphate isomerase

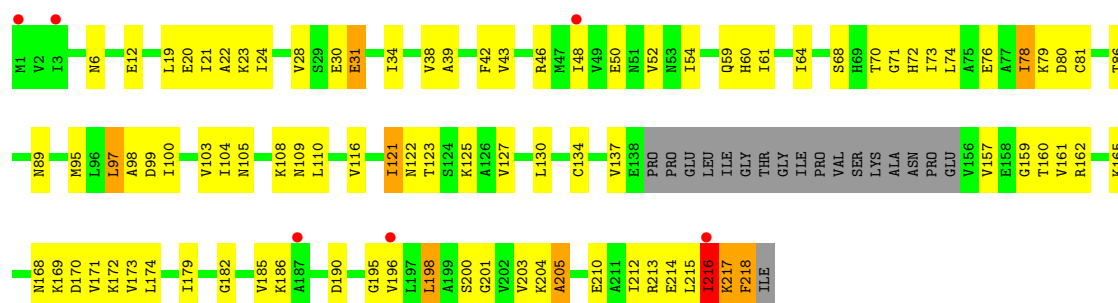
Chain F:



- Molecule 1: Triosephosphate isomerase

Chain G:





4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	139.34Å 139.34Å 80.89Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.28 – 2.30 34.98 – 2.30	Depositor EDS
% Data completeness (in resolution range)	92.7 (34.28-2.30) 96.2 (34.98-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.56 (at 2.29Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.213 , 0.278 0.207 , 0.211	Depositor DCC
R_{free} test set	3415 reflections (4.75%)	DCC
Wilson B-factor (Å ²)	29.9	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 20.4	EDS
Estimated twinning fraction	0.250 for h,k,l 0.250 for k,h,-l 0.250 for -k,-h,-l 0.250 for -h,-k,l 0.467 for -h,-k,l 0.426 for h,-h-k,-l 0.420 for -k,-h,-l	Xtriage
Reported twinning fraction	0.250 for h,k,l 0.250 for k,h,-l 0.250 for -k,-h,-l 0.250 for -h,-k,l	Depositor
L-test for twinning	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Outliers	0 of 75331 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	12422	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.30	0/1516	1.01	8/2051 (0.4%)
1	B	0.23	0/1561	0.58	1/2114 (0.0%)
1	C	0.28	0/1521	0.60	1/2058 (0.0%)
1	D	0.30	0/1490	0.81	5/2014 (0.2%)
1	E	0.27	0/1552	0.58	0/2100
1	F	0.29	0/1502	0.64	2/2031 (0.1%)
1	G	0.24	0/1489	0.57	0/2015
1	H	0.31	1/1504 (0.1%)	0.64	4/2032 (0.2%)
All	All	0.28	1/12135 (0.0%)	0.69	21/16415 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	216	ILE	C-O	-5.05	1.13	1.23

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	213	ARG	NE-CZ-NH1	-21.76	109.42	120.30
1	A	213	ARG	NE-CZ-NH2	21.27	130.94	120.30
1	D	216	ILE	CA-C-N	-16.48	80.94	117.20
1	A	216	ILE	CA-C-N	-13.72	87.02	117.20
1	D	216	ILE	C-N-CA	12.72	153.51	121.70
1	D	216	ILE	O-C-N	11.35	140.86	122.70
1	A	213	ARG	CD-NE-CZ	10.54	138.36	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	216	ILE	N-CA-C	9.43	136.46	111.00
1	H	216	ILE	O-C-N	-8.59	108.95	122.70
1	A	216	ILE	C-N-CA	7.85	141.33	121.70
1	H	216	ILE	C-N-CA	-7.78	102.24	121.70
1	F	215	LEU	CA-CB-CG	7.20	131.86	115.30
1	A	216	ILE	O-C-N	6.88	133.71	122.70
1	F	216	ILE	N-CA-C	-6.39	93.74	111.00
1	D	216	ILE	CA-C-O	6.18	133.09	120.10
1	A	216	ILE	CA-C-O	5.93	132.56	120.10
1	H	216	ILE	CA-C-N	5.87	130.12	117.20
1	D	213	ARG	NE-CZ-NH2	-5.63	117.48	120.30
1	C	213	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	B	213	ARG	NE-CZ-NH2	-5.57	117.51	120.30
1	H	213	ARG	NE-CZ-NH2	-5.45	117.57	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	216	ILE	Mainchain

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1504	0	1560	98	0
1	B	1548	0	1604	67	0
1	C	1508	0	1569	75	0
1	D	1480	0	1537	96	0
1	E	1538	0	1596	105	0
1	F	1490	0	1552	111	0
1	G	1477	0	1525	84	0
1	H	1493	0	1554	83	0
2	A	58	0	0	0	0
2	B	55	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	45	0	0	0	0
2	D	46	0	0	0	0
2	E	53	0	0	0	0
2	F	34	0	0	0	0
2	G	36	0	0	0	0
2	H	57	0	0	0	0
All	All	12422	0	12497	665	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 27.

All (665) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:215:LEU:O	1:F:217:LYS:HD3	1.46	1.13
1:D:217:LYS:HZ3	1:D:217:LYS:HB2	1.01	1.11
1:E:207:ASN:HD21	1:E:210:GLU:HB3	1.07	1.11
1:C:138:GLU:HB3	1:C:139:PRO:HD2	1.12	1.10
1:H:19:LEU:HA	1:H:48:ILE:HD11	1.23	1.09
1:A:32:SER:OG	1:A:34:ILE:HD12	1.55	1.07
1:F:182:GLY:HA3	1:F:217:LYS:HE2	1.32	1.06
1:F:185:VAL:HG11	1:F:217:LYS:CA	1.86	1.04
1:A:34:ILE:HD11	1:A:217:LYS:HD2	1.34	1.04
1:F:182:GLY:O	1:F:217:LYS:HG2	1.58	1.04
1:G:168:ASN:HD22	1:G:171:VAL:HG23	1.23	1.01
1:F:185:VAL:HG11	1:F:217:LYS:HA	1.04	1.00
1:G:213:ARG:HA	1:G:216:ILE:HD11	1.43	0.99
1:D:185:VAL:CG1	1:D:217:LYS:HB3	1.95	0.96
1:F:185:VAL:HG21	1:F:217:LYS:C	1.86	0.95
1:D:217:LYS:HZ3	1:D:217:LYS:CB	1.80	0.94
1:D:217:LYS:NZ	1:D:217:LYS:HB2	1.80	0.94
1:C:138:GLU:HB3	1:C:139:PRO:CD	1.96	0.93
1:D:3:ILE:HB	1:D:36:ILE:HG23	1.50	0.93
1:F:182:GLY:HA3	1:F:217:LYS:CE	1.98	0.92
1:A:34:ILE:CD1	1:A:217:LYS:HD2	1.99	0.92
1:F:185:VAL:CG1	1:F:217:LYS:HA	1.99	0.91
1:D:185:VAL:HG11	1:D:217:LYS:HB3	1.53	0.91
1:B:168:ASN:HD22	1:B:171:VAL:HG23	1.30	0.90
1:D:168:ASN:HD22	1:D:171:VAL:HG23	1.33	0.89
1:G:8:LYS:HD3	1:H:68:SER:HA	1.54	0.89
1:E:186:LYS:HA	1:E:189:LEU:HG	1.55	0.88
1:E:207:ASN:ND2	1:E:210:GLU:HB3	1.87	0.88
1:A:216:ILE:HG22	1:A:217:LYS:H	1.39	0.88

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:55:PRO:HA	1:D:84:LYS:HE3	1.53	0.87
1:F:185:VAL:HG21	1:F:217:LYS:HB3	1.57	0.86
1:G:216:ILE:HD12	1:G:217:LYS:H	1.42	0.84
1:G:40:PRO:HG2	1:G:48:ILE:HD13	1.58	0.84
1:B:141:GLU:O	1:B:142:LEU:HB2	1.76	0.84
1:D:217:LYS:NZ	1:D:217:LYS:CB	2.40	0.84
1:E:93:LYS:HG3	1:F:72:HIS:CE1	2.13	0.84
1:C:138:GLU:CB	1:C:139:PRO:HD2	2.05	0.83
1:A:168:ASN:HD22	1:A:171:VAL:HG23	1.39	0.83
1:C:182:GLY:HA3	1:C:217:LYS:O	1.79	0.82
1:D:156:VAL:O	1:D:157:VAL:HG12	1.79	0.81
1:E:71:GLY:H	1:F:59:GLN:HE21	1.27	0.81
1:E:207:ASN:HD21	1:E:210:GLU:CB	1.90	0.80
1:C:59:GLN:HE21	1:D:71:GLY:H	1.29	0.79
1:E:116:VAL:HG11	1:E:127:VAL:HG11	1.65	0.78
1:A:216:ILE:CG2	1:A:217:LYS:H	1.88	0.78
1:F:185:VAL:CG2	1:F:217:LYS:HB3	2.13	0.78
1:H:204:LYS:HG3	1:H:205:ALA:H	1.48	0.78
1:A:115:ILE:HG12	1:A:134:CYS:SG	2.24	0.78
1:F:115:ILE:HG12	1:F:134:CYS:SG	2.24	0.78
1:C:14:ILE:HD13	1:C:41:GLN:OE1	1.84	0.77
1:F:116:VAL:HG11	1:F:127:VAL:HG11	1.64	0.77
1:B:116:VAL:HG11	1:B:127:VAL:HG11	1.67	0.77
1:A:3:ILE:HD11	1:A:217:LYS:O	1.85	0.77
1:H:116:VAL:HG11	1:H:127:VAL:HG11	1.67	0.77
1:A:116:VAL:HG11	1:A:127:VAL:HG11	1.67	0.76
1:G:213:ARG:HA	1:G:216:ILE:CD1	2.14	0.76
1:D:116:VAL:HG11	1:D:127:VAL:HG11	1.67	0.76
1:C:116:VAL:HG11	1:C:127:VAL:HG11	1.67	0.76
1:B:129:ALA:HA	1:B:167:ILE:HD11	1.66	0.75
1:C:139:PRO:HA	1:C:140:PRO:C	2.06	0.75
1:G:162:ARG:O	1:G:166:GLU:HG2	1.87	0.75
1:D:217:LYS:HZ2	1:D:217:LYS:N	1.84	0.75
1:G:116:VAL:HG11	1:G:127:VAL:HG11	1.68	0.74
1:D:174:LEU:HD22	1:D:195:GLY:HA3	1.67	0.74
1:A:186:LYS:HZ2	1:A:186:LYS:HB2	1.52	0.74
1:D:217:LYS:NZ	1:D:217:LYS:CA	2.51	0.74
1:D:206:LYS:HG3	1:D:207:ASN:H	1.53	0.74
1:E:186:LYS:HB3	1:E:218:PHE:C	2.08	0.73
1:G:216:ILE:O	1:G:217:LYS:HB2	1.88	0.73
1:D:3:ILE:N	1:D:3:ILE:HD12	2.04	0.73
1:F:100:ILE:O	1:F:104:ILE:HD13	1.89	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:216:ILE:HG22	1:A:217:LYS:O	1.88	0.72
1:G:168:ASN:ND2	1:G:171:VAL:HG23	2.02	0.72
1:A:186:LYS:HD2	1:A:190:ASP:OD2	1.91	0.71
1:H:100:ILE:O	1:H:104:ILE:HD13	1.91	0.71
1:A:100:ILE:O	1:A:104:ILE:HD13	1.90	0.71
1:C:74:LEU:HD13	1:C:76:GLU:H	1.55	0.71
1:D:100:ILE:O	1:D:104:ILE:HD13	1.90	0.71
1:D:74:LEU:HD13	1:D:76:GLU:H	1.55	0.71
1:C:5:ILE:HD11	1:C:36:ILE:HD11	1.72	0.71
1:F:182:GLY:CA	1:F:217:LYS:HE2	2.18	0.71
1:B:168:ASN:HD22	1:B:171:VAL:CG2	2.03	0.71
1:D:60:HIS:CG	1:D:93:LYS:HD3	2.25	0.71
1:E:122:ASN:HA	1:E:125:LYS:HD3	1.73	0.71
1:G:74:LEU:HD13	1:G:76:GLU:H	1.55	0.71
1:B:100:ILE:O	1:B:104:ILE:HD13	1.91	0.70
1:D:2:VAL:HA	1:D:35:THR:O	1.91	0.70
1:A:74:LEU:HD13	1:A:76:GLU:H	1.55	0.70
1:E:100:ILE:O	1:E:104:ILE:HD13	1.91	0.70
1:A:168:ASN:ND2	1:A:171:VAL:HG23	2.06	0.70
1:H:74:LEU:HD13	1:H:76:GLU:H	1.55	0.70
1:F:215:LEU:O	1:F:216:ILE:HG13	1.91	0.70
1:B:168:ASN:ND2	1:B:171:VAL:HG23	2.07	0.70
1:E:186:LYS:HB3	1:E:218:PHE:CA	2.22	0.70
1:F:215:LEU:C	1:F:217:LYS:N	2.41	0.70
1:D:185:VAL:HG12	1:D:217:LYS:HB3	1.73	0.69
1:B:74:LEU:HD13	1:B:76:GLU:H	1.55	0.69
1:C:207:ASN:OD1	1:C:210:GLU:HB2	1.91	0.69
1:E:74:LEU:HD13	1:E:76:GLU:H	1.55	0.69
1:C:100:ILE:O	1:C:104:ILE:HD13	1.90	0.69
1:G:100:ILE:O	1:G:104:ILE:HD13	1.92	0.69
1:F:196:VAL:HG21	1:F:217:LYS:O	1.93	0.68
1:G:216:ILE:HD12	1:G:217:LYS:N	2.08	0.68
1:F:74:LEU:HD13	1:F:76:GLU:H	1.56	0.68
1:E:181:LYS:NZ	1:E:181:LYS:HB3	2.09	0.68
1:H:157:VAL:O	1:H:161:VAL:HG23	1.93	0.68
1:E:61:ILE:HD12	1:E:86:THR:HG21	1.76	0.68
1:D:14:ILE:HB	1:D:17:ARG:NH1	2.09	0.67
1:G:44:ASP:O	1:G:48:ILE:HD12	1.95	0.67
1:A:79:LYS:HE3	1:A:110:LEU:O	1.95	0.66
1:F:61:ILE:HD12	1:F:86:THR:HG21	1.78	0.66
1:G:174:LEU:HD22	1:G:195:GLY:HA3	1.78	0.66
1:E:73:ILE:HG23	1:E:78:ILE:HD11	1.78	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:185:VAL:HG21	1:F:217:LYS:CB	2.26	0.66
1:F:174:LEU:HD22	1:F:195:GLY:HA3	1.77	0.65
1:H:165:LYS:HG3	1:H:169:LYS:HD3	1.78	0.65
1:G:88:ILE:HB	1:G:95:MET:HE1	1.78	0.65
1:F:34:ILE:HG12	1:F:216:ILE:HG22	1.79	0.65
1:D:3:ILE:HD11	1:D:34:ILE:HG21	1.77	0.65
1:F:73:ILE:HG23	1:F:78:ILE:HD11	1.79	0.65
1:F:104:ILE:O	1:F:108:LYS:HG2	1.98	0.64
1:E:96:LEU:HD23	1:G:96:LEU:HD23	1.80	0.64
1:F:185:VAL:CG2	1:F:217:LYS:C	2.65	0.64
1:G:216:ILE:CD1	1:G:217:LYS:N	2.61	0.64
1:D:3:ILE:HD13	1:D:36:ILE:HD13	1.79	0.64
1:F:121:ILE:HG12	1:F:122:ASN:N	2.10	0.64
1:A:137:VAL:HG12	1:A:139:PRO:CD	2.26	0.64
1:A:61:ILE:HD12	1:A:86:THR:HG21	1.79	0.64
1:A:2:VAL:HB	1:A:195:GLY:HA3	1.79	0.64
1:A:71:GLY:H	1:B:59:GLN:HE21	1.45	0.64
1:B:153:ASN:N	1:B:154:PRO:CD	2.61	0.64
1:G:61:ILE:HD12	1:G:86:THR:HG21	1.77	0.64
1:D:217:LYS:HZ2	1:D:217:LYS:CA	2.09	0.64
1:A:34:ILE:CD1	1:A:217:LYS:CD	2.75	0.64
1:H:61:ILE:HD12	1:H:86:THR:HG21	1.80	0.64
1:A:216:ILE:HG22	1:A:217:LYS:N	2.12	0.63
1:E:186:LYS:CE	1:E:189:LEU:HD11	2.29	0.63
1:F:74:LEU:O	1:F:78:ILE:HD13	1.98	0.63
1:D:79:LYS:HE3	1:D:110:LEU:O	1.99	0.63
1:D:19:LEU:HD12	1:D:47:MET:SD	2.39	0.63
1:E:182:GLY:O	1:E:218:PHE:C	2.37	0.63
1:D:73:ILE:HG23	1:D:78:ILE:HD11	1.81	0.63
1:D:217:LYS:NZ	1:D:217:LYS:N	2.46	0.62
1:A:73:ILE:HG23	1:A:78:ILE:HD11	1.81	0.62
1:B:61:ILE:HD12	1:B:86:THR:HG21	1.80	0.62
1:C:10:TYR:CD2	1:C:204:LYS:HE3	2.34	0.62
1:D:3:ILE:N	1:D:3:ILE:CD1	2.63	0.62
1:A:97:LEU:HD12	1:C:100:ILE:HD13	1.81	0.62
1:G:216:ILE:CD1	1:G:217:LYS:H	2.11	0.62
1:A:137:VAL:HG12	1:A:139:PRO:HD2	1.80	0.62
1:B:73:ILE:HG23	1:B:78:ILE:HD11	1.81	0.62
1:G:40:PRO:CG	1:G:48:ILE:HD13	2.27	0.62
1:C:61:ILE:HD12	1:C:86:THR:HG21	1.80	0.62
1:B:46:ARG:O	1:B:50:GLU:HG3	1.99	0.62
1:A:44:ASP:O	1:A:48:ILE:HD13	2.00	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:73:ILE:HG23	1:H:78:ILE:HD11	1.81	0.62
1:E:71:GLY:H	1:F:59:GLN:NE2	1.95	0.61
1:E:34:ILE:H	1:E:34:ILE:HD13	1.65	0.61
1:G:73:ILE:HG23	1:G:78:ILE:HD11	1.82	0.61
1:E:20:GLU:O	1:E:24:ILE:HG12	2.00	0.61
1:D:61:ILE:HD12	1:D:86:THR:HG21	1.80	0.61
1:C:73:ILE:HG23	1:C:78:ILE:HD11	1.81	0.61
1:G:10:TYR:CE2	1:G:204:LYS:HE3	2.34	0.61
1:D:179:ILE:HD13	1:D:179:ILE:N	2.14	0.61
1:F:119:ASN:ND2	1:H:98:ALA:HB2	2.16	0.61
1:F:157:VAL:O	1:F:161:VAL:HG23	2.00	0.61
1:F:207:ASN:HB3	1:F:210:GLU:HG2	1.82	0.61
1:F:11:ASN:HD22	1:F:14:ILE:HD11	1.66	0.61
1:E:186:LYS:HE3	1:E:189:LEU:HD11	1.83	0.61
1:E:100:ILE:HD13	1:G:97:LEU:HD12	1.81	0.61
1:A:57:TYR:CE2	1:A:84:LYS:HG2	2.34	0.61
1:A:74:LEU:HD13	1:A:76:GLU:N	2.17	0.60
1:E:74:LEU:O	1:E:78:ILE:HD13	2.01	0.60
1:B:2:VAL:HG22	1:B:195:GLY:HA3	1.83	0.60
1:E:155:GLU:CD	1:E:155:GLU:H	2.04	0.60
1:F:182:GLY:CA	1:F:217:LYS:CE	2.77	0.60
1:E:186:LYS:HG3	1:E:190:ASP:OD2	2.02	0.60
1:F:74:LEU:HD13	1:F:76:GLU:N	2.17	0.60
1:E:105:ASN:ND2	1:E:108:LYS:HE3	2.16	0.60
1:B:134:CYS:SG	1:B:172:LYS:HE2	2.41	0.60
1:G:74:LEU:HD13	1:G:76:GLU:N	2.16	0.60
1:H:74:LEU:HD13	1:H:76:GLU:N	2.17	0.60
1:G:20:GLU:O	1:G:24:ILE:HG12	2.02	0.60
1:E:74:LEU:HD13	1:E:76:GLU:N	2.16	0.59
1:B:74:LEU:HD13	1:B:76:GLU:N	2.17	0.59
1:D:74:LEU:HD13	1:D:76:GLU:N	2.17	0.59
1:E:99:ASP:O	1:E:103:VAL:HG23	2.02	0.59
1:C:182:GLY:CA	1:C:217:LYS:O	2.49	0.59
1:C:74:LEU:HD13	1:C:76:GLU:N	2.16	0.59
1:A:32:SER:OG	1:A:34:ILE:CD1	2.41	0.59
1:C:182:GLY:HA3	1:C:217:LYS:C	2.23	0.59
1:D:99:ASP:O	1:D:103:VAL:HG23	2.03	0.59
1:A:174:LEU:HD22	1:A:195:GLY:HA3	1.83	0.59
1:A:20:GLU:O	1:A:24:ILE:HG12	2.03	0.59
1:D:20:GLU:O	1:D:24:ILE:HG12	2.03	0.59
1:D:93:LYS:O	1:D:93:LYS:HG3	2.02	0.59
1:B:20:GLU:O	1:B:24:ILE:HG12	2.03	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:54:ILE:HD12	1:C:54:ILE:O	2.03	0.59
1:F:185:VAL:HG21	1:F:217:LYS:CA	2.33	0.58
1:G:54:ILE:O	1:G:54:ILE:HD12	2.03	0.58
1:A:163:ALA:O	1:A:167:ILE:HD13	2.02	0.58
1:F:54:ILE:O	1:F:54:ILE:HD12	2.03	0.58
1:D:93:LYS:CG	1:D:93:LYS:O	2.51	0.58
1:A:76:GLU:HG3	1:A:110:LEU:HD21	1.85	0.58
1:F:165:LYS:HG2	1:F:169:LYS:HG3	1.85	0.58
1:D:54:ILE:HD12	1:D:54:ILE:O	2.03	0.58
1:F:99:ASP:O	1:F:103:VAL:HG23	2.03	0.58
1:H:20:GLU:O	1:H:24:ILE:HG12	2.03	0.58
1:H:54:ILE:HD12	1:H:54:ILE:O	2.03	0.58
1:E:179:ILE:HG21	1:E:196:VAL:HG11	1.86	0.58
1:A:171:VAL:HG22	1:F:206:LYS:NZ	2.19	0.58
1:C:99:ASP:O	1:C:103:VAL:HG23	2.03	0.58
1:E:54:ILE:HD12	1:E:54:ILE:O	2.03	0.58
1:F:20:GLU:O	1:F:24:ILE:HG12	2.03	0.58
1:B:54:ILE:HD12	1:B:54:ILE:O	2.03	0.58
1:C:167:ILE:HD12	1:C:167:ILE:N	2.19	0.58
1:G:93:LYS:HB2	1:H:70:THR:O	2.04	0.58
1:C:20:GLU:O	1:C:24:ILE:HG12	2.03	0.58
1:H:99:ASP:O	1:H:103:VAL:HG23	2.03	0.58
1:E:158:GLU:HG2	1:E:191:LEU:HB3	1.86	0.58
1:F:88:ILE:HB	1:F:95:MET:HE3	1.85	0.58
1:G:212:ILE:O	1:G:216:ILE:HG13	2.03	0.57
1:H:186:LYS:HD3	1:H:190:ASP:OD2	2.04	0.57
1:E:174:LEU:HD22	1:E:195:GLY:HA3	1.86	0.57
1:A:99:ASP:O	1:A:103:VAL:HG23	2.03	0.57
1:G:8:LYS:HD3	1:H:68:SER:CA	2.32	0.57
1:E:96:LEU:HA	1:G:96:LEU:HA	1.87	0.57
1:E:186:LYS:HB3	1:E:218:PHE:H	1.69	0.57
1:B:205:ALA:O	1:B:206:LYS:HB3	2.04	0.57
1:B:99:ASP:O	1:B:103:VAL:HG23	2.03	0.57
1:A:54:ILE:O	1:A:54:ILE:HD12	2.03	0.57
1:F:119:ASN:HA	1:F:138:GLU:HB3	1.87	0.57
1:E:185:VAL:HG21	1:E:215:LEU:O	2.04	0.57
1:G:99:ASP:O	1:G:103:VAL:HG23	2.05	0.57
1:A:198:LEU:HD21	1:A:215:LEU:HD13	1.87	0.57
1:C:168:ASN:HD22	1:C:171:VAL:HG23	1.70	0.57
1:E:137:VAL:HG12	1:E:139:PRO:HD3	1.86	0.57
1:E:97:LEU:HD12	1:G:100:ILE:CD1	2.35	0.56
1:C:44:ASP:O	1:C:48:ILE:HD13	2.04	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:122:ASN:HA	1:A:125:LYS:HD3	1.88	0.56
1:F:182:GLY:C	1:F:217:LYS:HG2	2.24	0.56
1:F:34:ILE:N	1:F:34:ILE:HD12	2.20	0.56
1:F:126:ALA:HB2	1:H:130:LEU:HD11	1.88	0.56
1:D:7:TYR:CD2	1:D:13:SER:HB2	2.39	0.56
1:D:2:VAL:HG13	1:D:2:VAL:O	2.05	0.56
1:G:207:ASN:HB3	1:G:210:GLU:HB2	1.88	0.56
1:H:198:LEU:HD21	1:H:215:LEU:HD13	1.88	0.56
1:F:139:PRO:HD2	1:F:177:ALA:HB3	1.87	0.56
1:G:59:GLN:HE21	1:H:71:GLY:H	1.53	0.56
1:A:78:ILE:N	1:A:78:ILE:HD13	2.21	0.56
1:B:198:LEU:HD21	1:B:215:LEU:HD13	1.88	0.56
1:E:12:GLU:HG3	1:E:17:ARG:NH2	2.21	0.56
1:D:3:ILE:HD11	1:D:34:ILE:CG2	2.36	0.55
1:G:119:ASN:O	1:G:139:PRO:HG3	2.06	0.55
1:A:186:LYS:NZ	1:A:186:LYS:HB2	2.20	0.55
1:G:26:GLU:O	1:G:30:GLU:HG3	2.06	0.55
1:H:174:LEU:HD22	1:H:195:GLY:HA3	1.89	0.55
1:C:71:GLY:H	1:D:59:GLN:HE21	1.55	0.55
1:B:78:ILE:N	1:B:78:ILE:HD13	2.21	0.55
1:H:179:ILE:HG21	1:H:196:VAL:HG11	1.89	0.55
1:B:137:VAL:HG21	1:B:160:THR:HG21	1.89	0.55
1:F:198:LEU:HD21	1:F:215:LEU:HD13	1.87	0.55
1:A:97:LEU:HD12	1:C:100:ILE:CD1	2.36	0.55
1:D:138:GLU:O	1:D:177:ALA:HB2	2.06	0.55
1:B:205:ALA:O	1:B:206:LYS:CB	2.54	0.55
1:D:137:VAL:HG21	1:D:160:THR:HG21	1.89	0.55
1:H:79:LYS:HE3	1:H:110:LEU:O	2.07	0.55
1:A:34:ILE:HD11	1:A:217:LYS:CD	2.22	0.55
1:C:198:LEU:HD21	1:C:215:LEU:HD13	1.89	0.55
1:H:78:ILE:N	1:H:78:ILE:HD13	2.21	0.55
1:C:78:ILE:HD13	1:C:78:ILE:N	2.21	0.55
1:F:185:VAL:CG1	1:F:217:LYS:CA	2.73	0.55
1:D:55:PRO:HA	1:D:84:LYS:CE	2.31	0.55
1:B:162:ARG:O	1:B:166:GLU:HG3	2.07	0.55
1:D:198:LEU:HD21	1:D:215:LEU:HD13	1.88	0.54
1:B:46:ARG:HB3	1:B:81:CYS:HB3	1.88	0.54
1:B:88:ILE:HB	1:B:95:MET:CE	2.38	0.54
1:E:179:ILE:HG13	1:E:196:VAL:HG13	1.88	0.54
1:E:183:GLU:HA	1:E:218:PHE:CB	2.37	0.54
1:C:209:GLU:O	1:C:213:ARG:HG3	2.08	0.54
1:C:162:ARG:O	1:C:166:GLU:HG2	2.08	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:2:VAL:C	1:B:3:ILE:HD12	2.28	0.54
1:A:3:ILE:CD1	1:A:217:LYS:O	2.54	0.54
1:G:7:TYR:CD2	1:G:13:SER:HB2	2.43	0.54
1:H:204:LYS:HG3	1:H:205:ALA:N	2.21	0.54
1:A:106:LYS:O	1:A:110:LEU:HD12	2.07	0.54
1:D:78:ILE:N	1:D:78:ILE:HD13	2.21	0.54
1:B:11:ASN:HD22	1:B:14:ILE:HD11	1.71	0.54
1:F:137:VAL:HG21	1:F:160:THR:HG21	1.89	0.53
1:H:137:VAL:HG21	1:H:160:THR:HG21	1.90	0.53
1:A:171:VAL:HG22	1:F:206:LYS:HZ3	1.73	0.53
1:G:88:ILE:HB	1:G:95:MET:CE	2.39	0.53
1:F:129:ALA:HB1	1:H:125:LYS:HG3	1.89	0.53
1:H:19:LEU:HA	1:H:48:ILE:CD1	2.17	0.53
1:C:137:VAL:HG21	1:C:160:THR:HG21	1.90	0.53
1:F:89:ASN:HD22	1:F:95:MET:H	1.55	0.53
1:E:46:ARG:O	1:E:50:GLU:HG3	2.08	0.53
1:E:122:ASN:HA	1:E:125:LYS:CD	2.39	0.53
1:E:59:GLN:HE21	1:F:71:GLY:H	1.57	0.53
1:H:105:ASN:ND2	1:H:108:LYS:HE2	2.24	0.53
1:F:137:VAL:HG12	1:F:138:GLU:N	2.24	0.52
1:E:137:VAL:HG21	1:E:160:THR:HG21	1.92	0.52
1:C:3:ILE:HB	1:C:36:ILE:HG13	1.90	0.52
1:H:179:ILE:HD12	1:H:179:ILE:N	2.23	0.52
1:B:216:ILE:O	1:B:217:LYS:HB2	2.09	0.52
1:G:10:TYR:CD2	1:G:204:LYS:HE3	2.44	0.52
1:E:161:VAL:O	1:E:165:LYS:HG2	2.09	0.52
1:C:122:ASN:HA	1:C:125:LYS:HE2	1.90	0.52
1:B:141:GLU:O	1:B:142:LEU:CB	2.51	0.52
1:C:14:ILE:HD12	1:D:77:ALA:HB2	1.92	0.52
1:E:181:LYS:HZ3	1:E:181:LYS:HB3	1.74	0.52
1:C:174:LEU:HD22	1:C:195:GLY:HA3	1.91	0.52
1:A:137:VAL:HG21	1:A:160:THR:HG21	1.90	0.51
1:E:216:ILE:O	1:E:217:LYS:HB2	2.09	0.51
1:F:182:GLY:HA2	1:F:217:LYS:CB	2.40	0.51
1:E:186:LYS:HA	1:E:189:LEU:CG	2.36	0.51
1:G:137:VAL:HG21	1:G:160:THR:HG21	1.92	0.51
1:E:60:HIS:HE1	1:E:95:MET:SD	2.34	0.51
1:B:3:ILE:N	1:B:3:ILE:HD12	2.25	0.51
1:D:34:ILE:HD12	1:D:34:ILE:N	2.26	0.51
1:D:14:ILE:HD13	1:D:41:GLN:OE1	2.10	0.51
1:C:156:VAL:O	1:C:156:VAL:HG12	2.10	0.51
1:E:172:LYS:HB3	1:E:194:GLU:OE1	2.10	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:182:GLY:O	1:F:185:VAL:HB	2.11	0.51
1:E:186:LYS:HB3	1:E:218:PHE:N	2.26	0.51
1:F:46:ARG:O	1:F:50:GLU:HG3	2.11	0.51
1:C:163:ALA:O	1:C:167:ILE:HD13	2.11	0.50
1:A:7:TYR:CD2	1:A:13:SER:HB2	2.45	0.50
1:G:34:ILE:N	1:G:34:ILE:HD12	2.26	0.50
1:C:8:LYS:HD3	1:D:68:SER:HA	1.92	0.50
1:H:165:LYS:HG2	1:H:169:LYS:HE2	1.93	0.50
1:B:89:ASN:H	1:B:95:MET:HE2	1.76	0.50
1:B:157:VAL:O	1:B:161:VAL:HG23	2.10	0.50
1:H:46:ARG:O	1:H:50:GLU:HG3	2.11	0.50
1:E:91:SER:HB3	1:E:138:GLU:OE2	2.11	0.50
1:E:186:LYS:H	1:E:218:PHE:C	2.15	0.50
1:E:100:ILE:CD1	1:G:97:LEU:HD12	2.41	0.50
1:H:200:SER:O	1:H:204:LYS:HG2	2.12	0.50
1:H:134:CYS:SG	1:H:172:LYS:HD2	2.52	0.50
1:C:207:ASN:CG	1:C:210:GLU:HB2	2.32	0.49
1:A:111:GLY:HA3	1:F:17:ARG:HD3	1.94	0.49
1:F:165:LYS:HG2	1:F:169:LYS:HE2	1.93	0.49
1:G:33:GLY:C	1:G:34:ILE:HD12	2.33	0.49
1:F:185:VAL:CB	1:F:217:LYS:HB3	2.42	0.49
1:F:183:GLU:C	1:F:185:VAL:H	2.15	0.49
1:G:71:GLY:H	1:H:59:GLN:HE21	1.61	0.49
1:F:182:GLY:HA3	1:F:217:LYS:HE3	1.92	0.49
1:F:89:ASN:H	1:F:95:MET:HE2	1.77	0.49
1:D:189:LEU:HA	1:D:193:ALA:O	2.11	0.49
1:E:168:ASN:ND2	1:E:171:VAL:HG23	2.26	0.49
1:F:198:LEU:HD21	1:F:215:LEU:CD1	2.43	0.49
1:A:167:ILE:N	1:A:167:ILE:HD12	2.28	0.49
1:E:157:VAL:C	1:E:159:GLY:N	2.63	0.49
1:G:95:MET:CE	1:G:100:ILE:HG22	2.42	0.49
1:F:88:ILE:HB	1:F:95:MET:CE	2.42	0.49
1:D:185:VAL:HG11	1:D:217:LYS:CB	2.35	0.49
1:D:157:VAL:O	1:D:161:VAL:HG23	2.13	0.49
1:D:60:HIS:ND1	1:D:93:LYS:HD3	2.28	0.48
1:F:119:ASN:HD21	1:H:98:ALA:HB2	1.76	0.48
1:F:79:LYS:HE3	1:F:110:LEU:O	2.13	0.48
1:F:185:VAL:CG2	1:F:217:LYS:O	2.61	0.48
1:D:3:ILE:CD1	1:D:34:ILE:CG2	2.91	0.48
1:A:105:ASN:ND2	1:A:108:LYS:HE3	2.29	0.48
1:H:19:LEU:HG	1:H:48:ILE:HD13	1.94	0.48
1:F:165:LYS:O	1:F:169:LYS:HD2	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:121:ILE:HG12	1:H:122:ASN:N	2.25	0.48
1:D:185:VAL:HG13	1:D:196:VAL:HG21	1.96	0.48
1:F:168:ASN:ND2	1:F:171:VAL:HG23	2.28	0.48
1:A:130:LEU:HD11	1:C:126:ALA:HB2	1.95	0.48
1:A:100:ILE:HD13	1:C:97:LEU:HD12	1.96	0.48
1:D:121:ILE:HG12	1:D:122:ASN:N	2.25	0.48
1:B:88:ILE:HB	1:B:95:MET:HE2	1.96	0.48
1:C:154:PRO:O	1:C:155:GLU:HG2	2.14	0.48
1:C:46:ARG:O	1:C:50:GLU:HG3	2.14	0.48
1:D:161:VAL:O	1:D:165:LYS:HD2	2.14	0.48
1:E:47:MET:O	1:E:51:ASN:ND2	2.47	0.48
1:F:19:LEU:O	1:F:19:LEU:HD23	2.13	0.48
1:E:40:PRO:HG2	1:E:48:ILE:CD1	2.44	0.47
1:G:198:LEU:HD21	1:G:215:LEU:HD13	1.94	0.47
1:A:46:ARG:O	1:A:50:GLU:HG3	2.14	0.47
1:H:12:GLU:HB2	1:H:203:VAL:HG12	1.96	0.47
1:D:3:ILE:HD13	1:D:34:ILE:HG22	1.97	0.47
1:G:59:GLN:HB3	1:H:71:GLY:H	1.78	0.47
1:B:167:ILE:HD12	1:B:167:ILE:O	2.15	0.47
1:F:185:VAL:HB	1:F:217:LYS:CB	2.44	0.47
1:H:22:ALA:CB	1:H:48:ILE:HD12	2.44	0.47
1:G:179:ILE:HD12	1:G:184:ASP:HB3	1.97	0.47
1:B:19:LEU:O	1:B:23:LYS:HG2	2.15	0.47
1:H:217:LYS:O	1:H:218:PHE:HB2	2.14	0.47
1:F:185:VAL:O	1:F:188:ALA:N	2.47	0.47
1:E:97:LEU:HD12	1:G:100:ILE:HD13	1.97	0.47
1:A:48:ILE:HD12	1:A:48:ILE:N	2.29	0.47
1:C:42:PHE:HZ	1:C:60:HIS:HB3	1.80	0.47
1:C:48:ILE:HD12	1:C:48:ILE:N	2.29	0.47
1:C:139:PRO:HD3	1:C:177:ALA:HB2	1.95	0.47
1:H:19:LEU:O	1:H:23:LYS:HG2	2.14	0.47
1:D:19:LEU:O	1:D:23:LYS:HG2	2.15	0.47
1:H:42:PHE:HZ	1:H:60:HIS:HB3	1.80	0.47
1:E:137:VAL:HG12	1:E:139:PRO:CD	2.44	0.47
1:B:19:LEU:HD23	1:B:19:LEU:O	2.15	0.47
1:A:19:LEU:HD23	1:A:19:LEU:O	2.15	0.47
1:E:183:GLU:HA	1:E:218:PHE:HB3	1.97	0.47
1:E:122:ASN:O	1:E:125:LYS:HG2	2.14	0.47
1:H:19:LEU:O	1:H:19:LEU:HD23	2.15	0.47
1:A:19:LEU:O	1:A:23:LYS:HG2	2.15	0.47
1:F:185:VAL:O	1:F:186:LYS:C	2.53	0.47
1:A:97:LEU:HD11	1:C:127:VAL:HG22	1.96	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:60:HIS:HE1	1:H:95:MET:SD	2.38	0.47
1:H:168:ASN:ND2	1:H:171:VAL:HG23	2.30	0.47
1:E:27:LYS:O	1:E:31:GLU:HG2	2.15	0.47
1:A:186:LYS:HG3	1:A:187:ALA:N	2.29	0.46
1:E:155:GLU:CD	1:E:155:GLU:N	2.68	0.46
1:A:52:VAL:HG12	1:A:54:ILE:HG13	1.98	0.46
1:A:46:ARG:HG2	2:B:222:HOH:O	2.15	0.46
1:D:206:LYS:HG2	1:D:206:LYS:H	1.43	0.46
1:F:78:ILE:CD1	1:F:78:ILE:N	2.77	0.46
1:G:19:LEU:HD23	1:G:19:LEU:O	2.14	0.46
1:C:19:LEU:O	1:C:23:LYS:HG2	2.14	0.46
1:E:19:LEU:O	1:E:23:LYS:HG2	2.15	0.46
1:A:157:VAL:O	1:A:161:VAL:HG23	2.15	0.46
1:F:185:VAL:HB	1:F:217:LYS:CG	2.46	0.46
1:A:42:PHE:HZ	1:A:60:HIS:HB3	1.80	0.46
1:E:44:ASP:O	1:E:48:ILE:HG12	2.15	0.46
1:G:19:LEU:O	1:G:23:LYS:HG2	2.15	0.46
1:G:46:ARG:O	1:G:50:GLU:HG3	2.16	0.46
1:A:204:LYS:HB3	1:A:204:LYS:HE2	1.79	0.46
1:F:19:LEU:O	1:F:23:LYS:HG2	2.15	0.46
1:B:153:ASN:N	1:B:154:PRO:HD2	2.30	0.46
1:B:42:PHE:HZ	1:B:60:HIS:HB3	1.80	0.46
1:C:19:LEU:HD23	1:C:19:LEU:O	2.15	0.46
1:E:69:HIS:HB2	1:F:9:THR:OG1	2.15	0.46
1:A:12:GLU:HB2	1:A:203:VAL:HG12	1.97	0.46
1:H:30:GLU:HG2	1:H:30:GLU:O	2.15	0.46
1:G:52:VAL:HG12	1:G:54:ILE:HG13	1.98	0.46
1:A:2:VAL:HB	1:A:195:GLY:CA	2.44	0.46
1:F:127:VAL:HG22	1:H:97:LEU:HD11	1.96	0.46
1:F:60:HIS:O	1:F:73:ILE:HG21	2.15	0.46
1:E:19:LEU:HD23	1:E:19:LEU:O	2.16	0.46
1:A:101:GLU:HG3	1:C:123:THR:HG23	1.98	0.46
1:G:6:ASN:HA	1:G:39:ALA:HB3	1.98	0.46
1:D:42:PHE:HZ	1:D:60:HIS:HB3	1.80	0.46
1:A:89:ASN:HD22	1:A:95:MET:H	1.63	0.46
1:D:52:VAL:HG12	1:D:54:ILE:HG13	1.98	0.46
1:F:34:ILE:HG12	1:F:216:ILE:CG2	2.44	0.46
1:D:168:ASN:ND2	1:D:171:VAL:HG23	2.15	0.46
1:F:42:PHE:HZ	1:F:60:HIS:HB3	1.81	0.46
1:H:185:VAL:HG13	1:H:196:VAL:HG21	1.97	0.46
1:G:165:LYS:HE2	1:G:171:VAL:O	2.16	0.46
1:E:42:PHE:HZ	1:E:60:HIS:HB3	1.81	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:19:LEU:HD23	1:D:19:LEU:O	2.15	0.46
1:G:42:PHE:HZ	1:G:60:HIS:HB3	1.81	0.46
1:C:89:ASN:HD22	1:C:95:MET:H	1.63	0.46
1:E:52:VAL:HG12	1:E:54:ILE:HG13	1.97	0.46
1:F:2:VAL:CG2	1:F:2:VAL:O	2.64	0.46
1:B:186:LYS:HE3	1:B:186:LYS:HA	1.97	0.46
1:D:2:VAL:C	1:D:3:ILE:HD12	2.36	0.45
1:E:24:ILE:HD12	1:E:209:GLU:OE1	2.16	0.45
1:D:215:LEU:O	1:D:216:ILE:C	2.54	0.45
1:E:64:ILE:HD13	1:E:72:HIS:HB3	1.98	0.45
1:E:6:ASN:HA	1:E:39:ALA:HB3	1.99	0.45
1:G:182:GLY:CA	1:G:215:LEU:HA	2.46	0.45
1:A:169:LYS:HE3	1:A:169:LYS:HB2	1.76	0.45
1:D:73:ILE:N	1:D:73:ILE:HD12	2.32	0.45
1:D:60:HIS:HE1	1:D:95:MET:SD	2.38	0.45
1:E:216:ILE:O	1:E:217:LYS:CB	2.63	0.45
1:F:176:GLY:HA2	1:F:197:LEU:O	2.16	0.45
1:A:34:ILE:HD13	1:A:217:LYS:CD	2.46	0.45
1:H:73:ILE:N	1:H:73:ILE:HD12	2.32	0.45
1:F:14:ILE:HB	1:F:17:ARG:CZ	2.47	0.45
1:E:54:ILE:C	1:E:54:ILE:HD12	2.37	0.45
1:A:121:ILE:HG12	1:A:122:ASN:N	2.25	0.45
1:D:3:ILE:CD1	1:D:34:ILE:HG22	2.46	0.45
1:A:130:LEU:HD11	1:C:126:ALA:CB	2.46	0.45
1:B:129:ALA:HB1	1:D:125:LYS:HG3	1.98	0.45
1:C:60:HIS:HE1	1:C:95:MET:SD	2.39	0.45
1:C:52:VAL:HG12	1:C:54:ILE:HG13	1.98	0.45
1:F:52:VAL:HG12	1:F:54:ILE:HG13	1.99	0.45
1:D:54:ILE:HD12	1:D:54:ILE:C	2.37	0.45
1:H:52:VAL:HG12	1:H:54:ILE:HG13	1.98	0.45
1:C:24:ILE:HG23	1:C:209:GLU:HB3	1.98	0.45
1:E:7:TYR:CD2	1:E:13:SER:HB3	2.52	0.45
1:A:186:LYS:NZ	1:A:186:LYS:CB	2.80	0.45
1:B:52:VAL:HG12	1:B:54:ILE:HG13	1.98	0.45
1:E:172:LYS:HB3	1:E:194:GLU:CD	2.37	0.45
1:C:59:GLN:NE2	1:D:71:GLY:H	2.06	0.44
1:A:73:ILE:N	1:A:73:ILE:HD12	2.32	0.44
1:C:73:ILE:HD12	1:C:73:ILE:N	2.32	0.44
1:H:54:ILE:HD12	1:H:54:ILE:C	2.38	0.44
1:A:54:ILE:C	1:A:54:ILE:HD12	2.38	0.44
1:G:182:GLY:HA2	1:G:215:LEU:O	2.17	0.44
1:A:70:THR:O	1:B:93:LYS:HB2	2.16	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:185:VAL:HB	1:F:217:LYS:HB3	1.97	0.44
1:D:185:VAL:HG11	1:D:217:LYS:C	2.38	0.44
1:G:54:ILE:HD12	1:G:54:ILE:C	2.37	0.44
1:E:78:ILE:N	1:E:78:ILE:CD1	2.79	0.44
1:H:169:LYS:O	1:H:169:LYS:HG3	2.17	0.44
1:A:60:HIS:O	1:A:73:ILE:HG21	2.17	0.44
1:F:54:ILE:HD12	1:F:54:ILE:C	2.37	0.44
1:E:69:HIS:O	1:F:9:THR:HG23	2.17	0.44
1:D:158:GLU:HG3	1:D:162:ARG:NH2	2.32	0.44
1:A:28:VAL:O	1:A:32:SER:HB3	2.18	0.44
1:D:3:ILE:CB	1:D:36:ILE:HG23	2.34	0.44
1:D:3:ILE:HG22	1:D:5:ILE:HG13	1.98	0.44
1:H:204:LYS:CG	1:H:205:ALA:H	2.23	0.44
1:H:60:HIS:O	1:H:73:ILE:HG21	2.17	0.44
1:G:73:ILE:HD12	1:G:73:ILE:N	2.33	0.44
1:C:60:HIS:O	1:C:73:ILE:HG21	2.17	0.44
1:E:17:ARG:O	1:E:21:ILE:HG13	2.17	0.44
1:F:2:VAL:HG22	1:F:2:VAL:O	2.16	0.44
1:A:6:ASN:HA	1:A:39:ALA:HB3	1.99	0.44
1:G:1:MET:HG2	1:G:2:VAL:HG23	1.98	0.44
1:D:3:ILE:HB	1:D:36:ILE:CG2	2.35	0.44
1:E:73:ILE:N	1:E:73:ILE:HD12	2.32	0.44
1:F:73:ILE:N	1:F:73:ILE:HD12	2.32	0.44
1:B:73:ILE:N	1:B:73:ILE:HD12	2.32	0.44
1:H:89:ASN:HD22	1:H:95:MET:H	1.64	0.44
1:G:60:HIS:O	1:G:73:ILE:HG21	2.16	0.44
1:D:6:ASN:HA	1:D:39:ALA:HB3	1.99	0.44
1:G:95:MET:HE2	1:G:100:ILE:HG22	1.99	0.44
1:E:161:VAL:HG11	1:E:192:GLY:HA3	1.99	0.44
1:F:40:PRO:HG2	1:F:48:ILE:HD12	1.98	0.44
1:D:60:HIS:O	1:D:73:ILE:HG21	2.17	0.44
1:E:161:VAL:HA	1:E:173:VAL:HG21	1.98	0.44
1:E:159:GLY:HA2	1:E:162:ARG:NH1	2.33	0.44
1:F:23:LYS:HG2	1:F:23:LYS:H	1.54	0.44
1:D:156:VAL:O	1:D:156:VAL:HG13	2.17	0.44
1:C:54:ILE:C	1:C:54:ILE:HD12	2.38	0.44
1:A:217:LYS:HD3	1:A:217:LYS:HA	1.11	0.44
1:B:60:HIS:O	1:B:73:ILE:HG21	2.17	0.44
1:F:161:VAL:HA	1:F:173:VAL:HG21	1.99	0.44
1:E:70:THR:OG1	1:F:8:LYS:HG2	2.17	0.44
1:H:6:ASN:HA	1:H:39:ALA:HB3	1.99	0.44
1:F:127:VAL:CG2	1:H:97:LEU:HD11	2.48	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:G:42:PHE:CE2	1:G:73:ILE:HG12	2.53	0.43
1:B:89:ASN:H	1:B:95:MET:CE	2.31	0.43
1:C:6:ASN:HA	1:C:39:ALA:HB3	1.99	0.43
1:B:64:ILE:HD13	1:B:72:HIS:HB3	1.99	0.43
1:C:64:ILE:HD13	1:C:72:HIS:HB3	1.99	0.43
1:F:6:ASN:HA	1:F:39:ALA:HB3	2.00	0.43
1:B:54:ILE:HD12	1:B:54:ILE:C	2.37	0.43
1:A:71:GLY:H	1:B:59:GLN:NE2	2.12	0.43
1:B:185:VAL:HG13	1:B:196:VAL:HG21	2.01	0.43
1:E:74:LEU:CD1	1:E:76:GLU:HB2	2.48	0.43
1:E:60:HIS:O	1:E:73:ILE:HG21	2.18	0.43
1:D:161:VAL:HG11	1:D:192:GLY:HA3	2.00	0.43
1:G:46:ARG:HD2	1:H:43:VAL:O	2.19	0.43
1:H:34:ILE:HD13	1:H:216:ILE:HG22	2.01	0.43
1:G:165:LYS:N	1:G:165:LYS:NZ	2.65	0.43
1:E:121:ILE:HG12	1:E:122:ASN:N	2.27	0.43
1:G:74:LEU:CD1	1:G:76:GLU:HB2	2.49	0.43
1:G:78:ILE:HD13	1:G:78:ILE:N	2.34	0.43
1:G:43:VAL:HB	1:H:81:CYS:SG	2.58	0.43
1:H:28:VAL:HA	1:H:31:GLU:HG2	2.01	0.43
1:A:64:ILE:HD13	1:A:72:HIS:HB3	2.00	0.43
1:F:215:LEU:C	1:F:216:ILE:HG13	2.39	0.43
1:C:74:LEU:CD1	1:C:76:GLU:HB2	2.49	0.43
1:B:74:LEU:CD1	1:B:76:GLU:HB2	2.49	0.43
1:D:64:ILE:HD13	1:D:72:HIS:HB3	2.00	0.43
1:A:27:LYS:O	1:A:31:GLU:CG	2.67	0.43
1:B:6:ASN:HA	1:B:39:ALA:HB3	1.99	0.43
1:F:7:TYR:CD2	1:F:13:SER:HB2	2.53	0.43
1:F:185:VAL:CB	1:F:217:LYS:CB	2.96	0.43
1:A:127:VAL:HA	1:A:130:LEU:HD13	2.01	0.43
1:A:74:LEU:CD1	1:A:76:GLU:HB2	2.49	0.43
1:H:74:LEU:CD1	1:H:76:GLU:HB2	2.49	0.43
1:G:89:ASN:HD22	1:G:95:MET:H	1.65	0.43
1:H:64:ILE:HD13	1:H:72:HIS:HB3	1.99	0.43
1:G:64:ILE:HD13	1:G:72:HIS:HB3	1.99	0.43
1:E:38:VAL:C	1:E:40:PRO:HD3	2.39	0.43
1:H:22:ALA:HB3	1:H:48:ILE:HD12	2.01	0.42
1:E:60:HIS:CD2	1:E:93:LYS:HE2	2.54	0.42
1:A:161:VAL:HG11	1:A:192:GLY:HA3	2.01	0.42
1:F:101:GLU:HG3	1:H:123:THR:HG23	2.01	0.42
1:A:213:ARG:HA	1:A:216:ILE:HG12	2.02	0.42
1:A:60:HIS:HE1	1:A:95:MET:SD	2.42	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:G:38:VAL:HG22	1:G:54:ILE:HD13	2.01	0.42
1:E:93:LYS:HG3	1:F:72:HIS:HE1	1.77	0.42
1:H:127:VAL:HA	1:H:130:LEU:HD13	2.01	0.42
1:H:204:LYS:CG	1:H:205:ALA:N	2.81	0.42
1:C:213:ARG:HA	1:C:216:ILE:HG12	2.01	0.42
1:B:23:LYS:HG2	1:B:23:LYS:H	1.54	0.42
1:A:1:MET:O	1:A:2:VAL:HG23	2.18	0.42
1:D:44:ASP:O	1:D:48:ILE:HG12	2.20	0.42
1:D:216:ILE:C	1:D:217:LYS:NZ	2.72	0.42
1:F:64:ILE:HD13	1:F:72:HIS:HB3	2.00	0.42
1:F:74:LEU:CD1	1:F:76:GLU:HB2	2.50	0.42
1:B:89:ASN:HD22	1:B:95:MET:H	1.66	0.42
1:B:121:ILE:HG12	1:B:122:ASN:N	2.25	0.42
1:H:48:ILE:HA	1:H:48:ILE:HD13	1.92	0.42
1:H:161:VAL:HA	1:H:173:VAL:HG21	2.01	0.42
1:F:165:LYS:CG	1:F:169:LYS:HE2	2.50	0.42
1:E:159:GLY:HA2	1:E:162:ARG:HG2	2.02	0.42
1:G:182:GLY:N	1:G:215:LEU:HA	2.34	0.42
1:G:121:ILE:HG12	1:G:122:ASN:N	2.27	0.42
1:A:216:ILE:HG22	1:A:217:LYS:CA	2.50	0.42
1:A:8:LYS:HD2	1:A:10:TYR:CE1	2.54	0.42
1:E:89:ASN:HD22	1:E:95:MET:H	1.66	0.42
1:A:46:ARG:HB3	1:A:81:CYS:HB3	2.02	0.42
1:C:161:VAL:HA	1:C:173:VAL:HG21	2.01	0.42
1:A:212:ILE:O	1:A:216:ILE:HG12	2.20	0.42
1:D:161:VAL:HA	1:D:173:VAL:HG21	2.01	0.42
1:C:127:VAL:HA	1:C:130:LEU:HD13	2.01	0.42
1:C:121:ILE:HG12	1:C:122:ASN:N	2.24	0.42
1:F:1:MET:C	1:F:2:VAL:HG12	2.40	0.42
1:H:159:GLY:HA2	1:H:162:ARG:NH1	2.35	0.42
1:H:23:LYS:H	1:H:23:LYS:HG2	1.54	0.41
1:B:216:ILE:O	1:B:217:LYS:CB	2.68	0.41
1:D:74:LEU:CD1	1:D:76:GLU:HB2	2.49	0.41
1:E:139:PRO:O	1:E:140:PRO:C	2.59	0.41
1:C:23:LYS:H	1:C:23:LYS:HG2	1.54	0.41
1:E:105:ASN:HA	1:E:108:LYS:HE3	2.02	0.41
1:A:161:VAL:HA	1:A:173:VAL:HG21	2.01	0.41
1:F:185:VAL:CG1	1:F:217:LYS:O	2.68	0.41
1:G:38:VAL:C	1:G:40:PRO:HD3	2.40	0.41
1:D:127:VAL:HA	1:D:130:LEU:HD13	2.01	0.41
1:A:137:VAL:HG12	1:A:139:PRO:HD3	1.99	0.41
1:H:182:GLY:HA3	1:H:214:GLU:O	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:135:ILE:HG23	1:E:135:ILE:O	2.19	0.41
1:D:14:ILE:HB	1:D:17:ARG:HH12	1.82	0.41
1:A:96:LEU:HD23	1:C:96:LEU:HD23	2.02	0.41
1:G:109:ASN:HD22	1:G:109:ASN:N	2.18	0.41
1:B:127:VAL:HA	1:B:130:LEU:HD13	2.01	0.41
1:C:76:GLU:N	1:C:76:GLU:OE1	2.54	0.41
1:D:38:VAL:HG22	1:D:54:ILE:HD13	2.03	0.41
1:C:167:ILE:CD1	1:C:167:ILE:N	2.83	0.41
1:B:161:VAL:HA	1:B:173:VAL:HG21	2.01	0.41
1:A:27:LYS:O	1:A:31:GLU:HG3	2.21	0.41
1:A:96:LEU:HA	1:C:96:LEU:HA	2.03	0.41
1:B:76:GLU:N	1:B:76:GLU:OE1	2.54	0.41
1:E:46:ARG:HB3	1:E:81:CYS:HB3	2.03	0.41
1:D:203:VAL:C	1:D:205:ALA:H	2.24	0.41
1:B:161:VAL:HG11	1:B:192:GLY:HA3	2.02	0.41
1:G:161:VAL:HA	1:G:173:VAL:HG21	2.02	0.41
1:B:38:VAL:HG22	1:B:54:ILE:HD13	2.03	0.41
1:A:23:LYS:HG2	1:A:23:LYS:H	1.54	0.41
1:G:15:GLY:HA3	1:H:80:ASP:OD2	2.21	0.41
1:B:141:GLU:O	1:B:142:LEU:HD23	2.21	0.41
1:E:38:VAL:HG22	1:E:54:ILE:HD13	2.03	0.41
1:H:217:LYS:O	1:H:218:PHE:CB	2.69	0.41
1:H:212:ILE:O	1:H:216:ILE:HG12	2.22	0.41
1:E:183:GLU:HA	1:E:218:PHE:C	2.42	0.40
1:G:127:VAL:HA	1:G:130:LEU:HD13	2.03	0.40
1:G:60:HIS:HB2	1:H:71:GLY:HA3	2.02	0.40
1:G:182:GLY:HA2	1:G:215:LEU:HA	2.02	0.40
1:G:179:ILE:CD1	1:G:184:ASP:HB3	2.51	0.40
1:E:45:LEU:O	1:E:49:VAL:HG23	2.21	0.40
1:B:125:LYS:HG3	1:D:129:ALA:HB1	2.03	0.40
1:D:213:ARG:HA	1:D:216:ILE:HG12	2.03	0.40
1:E:97:LEU:HD12	1:G:100:ILE:HD11	2.02	0.40
1:H:161:VAL:O	1:H:165:LYS:HB2	2.21	0.40
1:C:38:VAL:HG22	1:C:54:ILE:HD13	2.03	0.40
1:F:139:PRO:O	1:F:140:PRO:C	2.59	0.40
1:H:168:ASN:HD21	1:H:170:ASP:HB2	1.85	0.40
1:B:19:LEU:HD12	1:B:47:MET:SD	2.62	0.40
1:C:12:GLU:H	1:C:12:GLU:CD	2.25	0.40
1:E:76:GLU:N	1:E:76:GLU:OE1	2.53	0.40
1:H:165:LYS:CG	1:H:169:LYS:HE2	2.51	0.40
1:C:38:VAL:C	1:C:40:PRO:HD3	2.42	0.40
1:H:38:VAL:HG22	1:H:54:ILE:HD13	2.03	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:11:ASN:HA	1:B:11:ASN:HD22	1.71	0.40
1:E:165:LYS:HA	1:E:165:LYS:HD2	1.85	0.40
1:E:183:GLU:HA	1:E:218:PHE:O	2.22	0.40
1:D:165:LYS:HA	1:D:165:LYS:HZ2	1.87	0.40
1:F:38:VAL:HG22	1:F:54:ILE:HD13	2.03	0.40
1:B:212:ILE:O	1:B:216:ILE:HG12	2.22	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	199/219 (91%)	176 (88%)	20 (10%)	3 (2%)	15	13
1	B	205/219 (94%)	177 (86%)	23 (11%)	5 (2%)	9	6
1	C	200/219 (91%)	173 (86%)	26 (13%)	1 (0%)	38	45
1	D	196/219 (90%)	176 (90%)	17 (9%)	3 (2%)	15	13
1	E	203/219 (93%)	181 (89%)	20 (10%)	2 (1%)	22	23
1	F	197/219 (90%)	173 (88%)	20 (10%)	4 (2%)	11	8
1	G	196/219 (90%)	178 (91%)	16 (8%)	2 (1%)	22	23
1	H	197/219 (90%)	174 (88%)	19 (10%)	4 (2%)	11	8
All	All	1593/1752 (91%)	1408 (88%)	161 (10%)	24 (2%)	15	13

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	216	ILE
1	B	142	LEU
1	D	216	ILE
1	G	205	ALA
1	H	205	ALA
1	H	216	ILE

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Mol	Chain	Res	Type
1	A	205	ALA
1	D	157	VAL
1	D	206	LYS
1	E	217	LYS
1	F	32	SER
1	H	201	GLY
1	F	215	LEU
1	H	31	GLU
1	F	31	GLU
1	B	45	LEU
1	B	154	PRO
1	B	207	ASN
1	C	45	LEU
1	E	216	ILE
1	G	139	PRO
1	B	153	ASN
1	F	216	ILE
1	A	138	GLU

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	165/180 (92%)	151 (92%)	14 (8%)	15	18
1	B	170/180 (94%)	160 (94%)	10 (6%)	28	35
1	C	166/180 (92%)	158 (95%)	8 (5%)	35	46
1	D	162/180 (90%)	146 (90%)	16 (10%)	11	13
1	E	169/180 (94%)	152 (90%)	17 (10%)	11	12
1	F	164/180 (91%)	152 (93%)	12 (7%)	20	24
1	G	161/180 (89%)	151 (94%)	10 (6%)	26	33
1	H	164/180 (91%)	155 (94%)	9 (6%)	30	39
All	All	1321/1440 (92%)	1225 (93%)	96 (7%)	20	24

All (96) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	21	ILE
1	A	78	ILE
1	A	84	LYS
1	A	97	LEU
1	A	121	ILE
1	A	134	CYS
1	A	183	GLU
1	A	186	LYS
1	A	198	LEU
1	A	210	GLU
1	A	213	ARG
1	A	216	ILE
1	A	217	LYS
1	B	21	ILE
1	B	78	ILE
1	B	97	LEU
1	B	108	LYS
1	B	121	ILE
1	B	167	ILE
1	B	186	LYS
1	B	194	GLU
1	B	198	LEU
1	B	210	GLU
1	C	21	ILE
1	C	78	ILE
1	C	97	LEU
1	C	108	LYS
1	C	121	ILE
1	C	198	LEU
1	C	210	GLU
1	C	217	LYS
1	D	3	ILE
1	D	17	ARG
1	D	21	ILE
1	D	78	ILE
1	D	84	LYS
1	D	93	LYS
1	D	97	LEU
1	D	121	ILE
1	D	165	LYS
1	D	169	LYS
1	D	179	ILE

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Mol	Chain	Res	Type
1	D	198	LEU
1	D	207	ASN
1	D	210	GLU
1	D	216	ILE
1	D	217	LYS
1	E	21	ILE
1	E	34	ILE
1	E	48	ILE
1	E	78	ILE
1	E	97	LEU
1	E	121	ILE
1	E	140	PRO
1	E	155	GLU
1	E	172	LYS
1	E	181	LYS
1	E	183	GLU
1	E	186	LYS
1	E	198	LEU
1	E	206	LYS
1	E	207	ASN
1	E	216	ILE
1	E	217	LYS
1	F	1	MET
1	F	21	ILE
1	F	31	GLU
1	F	78	ILE
1	F	97	LEU
1	F	121	ILE
1	F	168	ASN
1	F	169	LYS
1	F	183	GLU
1	F	198	LEU
1	F	216	ILE
1	F	217	LYS
1	G	17	ARG
1	G	21	ILE
1	G	30	GLU
1	G	84	LYS
1	G	97	LEU
1	G	121	ILE
1	G	165	LYS
1	G	167	ILE

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Mol	Chain	Res	Type
1	G	198	LEU
1	G	216	ILE
1	H	21	ILE
1	H	78	ILE
1	H	97	LEU
1	H	109	ASN
1	H	121	ILE
1	H	198	LEU
1	H	210	GLU
1	H	217	LYS
1	H	218	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (67) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	GLN
1	A	89	ASN
1	A	105	ASN
1	A	109	ASN
1	A	119	ASN
1	A	120	ASN
1	A	168	ASN
1	B	11	ASN
1	B	59	GLN
1	B	89	ASN
1	B	105	ASN
1	B	109	ASN
1	B	119	ASN
1	B	120	ASN
1	B	153	ASN
1	B	168	ASN
1	C	11	ASN
1	C	59	GLN
1	C	89	ASN
1	C	105	ASN
1	C	119	ASN
1	C	120	ASN
1	C	168	ASN
1	D	59	GLN
1	D	105	ASN
1	D	109	ASN
1	D	119	ASN

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Mol	Chain	Res	Type
1	D	120	ASN
1	D	168	ASN
1	D	207	ASN
1	E	11	ASN
1	E	59	GLN
1	E	65	ASN
1	E	89	ASN
1	E	105	ASN
1	E	109	ASN
1	E	119	ASN
1	E	120	ASN
1	E	168	ASN
1	E	207	ASN
1	F	11	ASN
1	F	59	GLN
1	F	72	HIS
1	F	89	ASN
1	F	105	ASN
1	F	109	ASN
1	F	119	ASN
1	F	120	ASN
1	F	168	ASN
1	F	207	ASN
1	G	11	ASN
1	G	59	GLN
1	G	65	ASN
1	G	89	ASN
1	G	105	ASN
1	G	109	ASN
1	G	119	ASN
1	G	120	ASN
1	G	168	ASN
1	H	11	ASN
1	H	59	GLN
1	H	89	ASN
1	H	105	ASN
1	H	109	ASN
1	H	119	ASN
1	H	120	ASN
1	H	168	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

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, 95th 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 ²)	Q<0.9
1	A	203/219 (92%)	0.30	4 (1%) 62 72	13, 29, 42, 53	0
1	B	209/219 (95%)	0.41	4 (1%) 64 73	16, 33, 44, 50	0
1	C	204/219 (93%)	0.54	10 (4%) 28 39	17, 32, 50, 57	0
1	D	200/219 (91%)	0.43	7 (3%) 42 52	15, 32, 51, 60	0
1	E	207/219 (94%)	0.57	8 (3%) 37 48	17, 35, 52, 60	0
1	F	201/219 (91%)	0.71	14 (6%) 16 23	21, 37, 55, 61	0
1	G	200/219 (91%)	0.76	19 (9%) 8 14	22, 39, 60, 69	0
1	H	201/219 (91%)	0.38	6 (2%) 48 58	9, 32, 43, 57	0
All	All	1625/1752 (92%)	0.51	72 (4%) 33 43	9, 34, 51, 69	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	217	LYS	11.4
1	F	216	ILE	6.6
1	A	217	LYS	6.3
1	C	217	LYS	5.9
1	F	177	ALA	5.7
1	F	178	GLY	5.7
1	G	177	ALA	5.6
1	F	140	PRO	5.4
1	E	215	LEU	4.7
1	C	187	ALA	4.7
1	G	135	ILE	4.2
1	G	216	ILE	3.8
1	D	178	GLY	3.8
1	B	154	PRO	3.7
1	F	217	LYS	3.7
1	E	218	PHE	3.6

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Mol	Chain	Res	Type	RSRZ
1	E	154	PRO	3.6
1	F	179	ILE	3.4
1	F	198	LEU	3.4
1	F	54	ILE	3.4
1	G	115	ILE	3.4
1	G	173	VAL	3.2
1	C	177	ALA	3.1
1	G	161	VAL	3.1
1	D	187	ALA	3.0
1	G	104	ILE	3.0
1	G	132	PRO	2.9
1	C	216	ILE	2.9
1	A	216	ILE	2.8
1	C	179	ILE	2.7
1	G	1	MET	2.7
1	G	178	GLY	2.7
1	D	216	ILE	2.6
1	H	216	ILE	2.6
1	A	178	GLY	2.6
1	G	134	CYS	2.6
1	H	1	MET	2.6
1	E	120	ASN	2.6
1	G	116	VAL	2.6
1	C	38	VAL	2.6
1	B	216	ILE	2.5
1	G	187	ALA	2.5
1	G	158	GLU	2.4
1	G	180	SER	2.4
1	F	189	LEU	2.4
1	G	19	LEU	2.4
1	A	139	PRO	2.3
1	D	135	ILE	2.3
1	C	173	VAL	2.3
1	C	167	ILE	2.3
1	F	212	ILE	2.3
1	G	160	THR	2.3
1	C	135	ILE	2.2
1	E	140	PRO	2.2
1	D	191	LEU	2.2
1	F	32	SER	2.2
1	H	48	ILE	2.2
1	G	176	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	H	187	ALA	2.1
1	G	215	LEU	2.1
1	B	208	VAL	2.1
1	H	196	VAL	2.1
1	F	104	ILE	2.1
1	F	121	ILE	2.1
1	F	53	ASN	2.1
1	E	216	ILE	2.1
1	H	3	ILE	2.0
1	D	19	LEU	2.0
1	C	205	ALA	2.0
1	E	207	ASN	2.0
1	B	127	VAL	2.0
1	E	156	VAL	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.