



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 06:01 AM GMT

PDB ID : 2ONK
Title : ABC transporter ModBC in complex with its binding protein ModA
Authors : Hollenstein, K.; Frei, D.C.; Locher, K.P.
Deposited on : 2007-01-24
Resolution : 3.10 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>

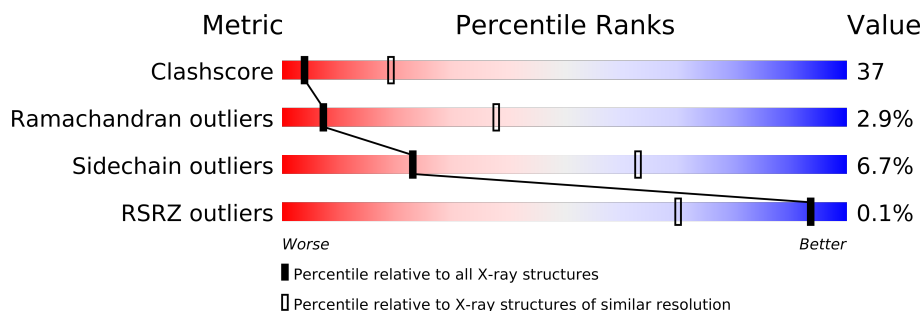
The following versions of software and data (see [references](#)) were used in the production of this report:

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 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	1078 (3.16-3.04)
Ramachandran outliers	78287	1044 (3.16-3.04)
Sidechain outliers	78261	1044 (3.16-3.04)
RSRZ outliers	66119	1008 (3.18-3.02)

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	240	
1	B	240	
1	F	240	
1	G	240	
2	C	284	
2	D	284	
2	H	284	
2	I	284	
3	E	314	
3	J	314	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
6	MG	J	706	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 20218 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 Molybdate/tungstate ABC transporter, ATP-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	240	Total	C	N	O	S	0	0	0
			1902	1212	349	334	7			
1	B	240	Total	C	N	O	S	0	0	0
			1902	1212	349	334	7			
1	F	240	Total	C	N	O	S	0	0	0
			1902	1212	349	334	7			
1	G	240	Total	C	N	O	S	0	0	0
			1902	1212	349	334	7			

- Molecule 2 is a protein called Molybdate/tungstate ABC transporter, permease protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	252	Total	C	N	O	S	0	0	0
			1901	1279	297	320	5			
2	D	252	Total	C	N	O	S	0	0	0
			1901	1279	297	320	5			
2	H	252	Total	C	N	O	S	0	0	0
			1901	1279	297	320	5			
2	I	252	Total	C	N	O	S	0	0	0
			1901	1279	297	320	5			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-22	MET	-	CLONING ARTIFACT	UNP O30143
C	-21	GLY	-	CLONING ARTIFACT	UNP O30143
C	-20	HIS	-	EXPRESSION TAG	UNP O30143
C	-19	HIS	-	EXPRESSION TAG	UNP O30143
C	-18	HIS	-	EXPRESSION TAG	UNP O30143
C	-17	HIS	-	EXPRESSION TAG	UNP O30143
C	-16	HIS	-	EXPRESSION TAG	UNP O30143
C	-15	HIS	-	EXPRESSION TAG	UNP O30143

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-14	HIS	-	EXPRESSION TAG	UNP O30143
C	-13	HIS	-	EXPRESSION TAG	UNP O30143
C	-12	HIS	-	EXPRESSION TAG	UNP O30143
C	-11	HIS	-	EXPRESSION TAG	UNP O30143
C	-10	SER	-	CLONING ARTIFACT	UNP O30143
C	-9	SER	-	CLONING ARTIFACT	UNP O30143
C	-8	GLY	-	CLONING ARTIFACT	UNP O30143
C	-7	GLU	-	CLONING ARTIFACT	UNP O30143
C	-6	ASN	-	CLONING ARTIFACT	UNP O30143
C	-5	LEU	-	CLONING ARTIFACT	UNP O30143
C	-4	TYR	-	CLONING ARTIFACT	UNP O30143
C	-3	PHE	-	CLONING ARTIFACT	UNP O30143
C	-2	GLN	-	CLONING ARTIFACT	UNP O30143
C	-1	GLY	-	CLONING ARTIFACT	UNP O30143
C	0	HIS	-	CLONING ARTIFACT	UNP O30143
D	-22	MET	-	CLONING ARTIFACT	UNP O30143
D	-21	GLY	-	CLONING ARTIFACT	UNP O30143
D	-20	HIS	-	EXPRESSION TAG	UNP O30143
D	-19	HIS	-	EXPRESSION TAG	UNP O30143
D	-18	HIS	-	EXPRESSION TAG	UNP O30143
D	-17	HIS	-	EXPRESSION TAG	UNP O30143
D	-16	HIS	-	EXPRESSION TAG	UNP O30143
D	-15	HIS	-	EXPRESSION TAG	UNP O30143
D	-14	HIS	-	EXPRESSION TAG	UNP O30143
D	-13	HIS	-	EXPRESSION TAG	UNP O30143
D	-12	HIS	-	EXPRESSION TAG	UNP O30143
D	-11	HIS	-	EXPRESSION TAG	UNP O30143
D	-10	SER	-	CLONING ARTIFACT	UNP O30143
D	-9	SER	-	CLONING ARTIFACT	UNP O30143
D	-8	GLY	-	CLONING ARTIFACT	UNP O30143
D	-7	GLU	-	CLONING ARTIFACT	UNP O30143
D	-6	ASN	-	CLONING ARTIFACT	UNP O30143
D	-5	LEU	-	CLONING ARTIFACT	UNP O30143
D	-4	TYR	-	CLONING ARTIFACT	UNP O30143
D	-3	PHE	-	CLONING ARTIFACT	UNP O30143
D	-2	GLN	-	CLONING ARTIFACT	UNP O30143
D	-1	GLY	-	CLONING ARTIFACT	UNP O30143
D	0	HIS	-	CLONING ARTIFACT	UNP O30143
H	-22	MET	-	CLONING ARTIFACT	UNP O30143
H	-21	GLY	-	CLONING ARTIFACT	UNP O30143
H	-20	HIS	-	EXPRESSION TAG	UNP O30143
H	-19	HIS	-	EXPRESSION TAG	UNP O30143

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-18	HIS	-	EXPRESSION TAG	UNP O30143
H	-17	HIS	-	EXPRESSION TAG	UNP O30143
H	-16	HIS	-	EXPRESSION TAG	UNP O30143
H	-15	HIS	-	EXPRESSION TAG	UNP O30143
H	-14	HIS	-	EXPRESSION TAG	UNP O30143
H	-13	HIS	-	EXPRESSION TAG	UNP O30143
H	-12	HIS	-	EXPRESSION TAG	UNP O30143
H	-11	HIS	-	EXPRESSION TAG	UNP O30143
H	-10	SER	-	CLONING ARTIFACT	UNP O30143
H	-9	SER	-	CLONING ARTIFACT	UNP O30143
H	-8	GLY	-	CLONING ARTIFACT	UNP O30143
H	-7	GLU	-	CLONING ARTIFACT	UNP O30143
H	-6	ASN	-	CLONING ARTIFACT	UNP O30143
H	-5	LEU	-	CLONING ARTIFACT	UNP O30143
H	-4	TYR	-	CLONING ARTIFACT	UNP O30143
H	-3	PHE	-	CLONING ARTIFACT	UNP O30143
H	-2	GLN	-	CLONING ARTIFACT	UNP O30143
H	-1	GLY	-	CLONING ARTIFACT	UNP O30143
H	0	HIS	-	CLONING ARTIFACT	UNP O30143
I	-22	MET	-	CLONING ARTIFACT	UNP O30143
I	-21	GLY	-	CLONING ARTIFACT	UNP O30143
I	-20	HIS	-	EXPRESSION TAG	UNP O30143
I	-19	HIS	-	EXPRESSION TAG	UNP O30143
I	-18	HIS	-	EXPRESSION TAG	UNP O30143
I	-17	HIS	-	EXPRESSION TAG	UNP O30143
I	-16	HIS	-	EXPRESSION TAG	UNP O30143
I	-15	HIS	-	EXPRESSION TAG	UNP O30143
I	-14	HIS	-	EXPRESSION TAG	UNP O30143
I	-13	HIS	-	EXPRESSION TAG	UNP O30143
I	-12	HIS	-	EXPRESSION TAG	UNP O30143
I	-11	HIS	-	EXPRESSION TAG	UNP O30143
I	-10	SER	-	CLONING ARTIFACT	UNP O30143
I	-9	SER	-	CLONING ARTIFACT	UNP O30143
I	-8	GLY	-	CLONING ARTIFACT	UNP O30143
I	-7	GLU	-	CLONING ARTIFACT	UNP O30143
I	-6	ASN	-	CLONING ARTIFACT	UNP O30143
I	-5	LEU	-	CLONING ARTIFACT	UNP O30143
I	-4	TYR	-	CLONING ARTIFACT	UNP O30143
I	-3	PHE	-	CLONING ARTIFACT	UNP O30143
I	-2	GLN	-	CLONING ARTIFACT	UNP O30143
I	-1	GLY	-	CLONING ARTIFACT	UNP O30143
I	0	HIS	-	CLONING ARTIFACT	UNP O30143

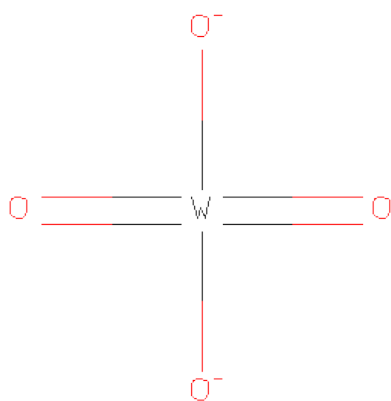
- Molecule 3 is a protein called Molybdate/tungstate binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	311	Total	C	N	O	S	0	0	0
			2489	1590	414	474	11			
3	J	310	Total	C	N	O	S	0	0	0
			2481	1585	415	469	12			

There are 6 discrepancies between the modelled and reference sequences:

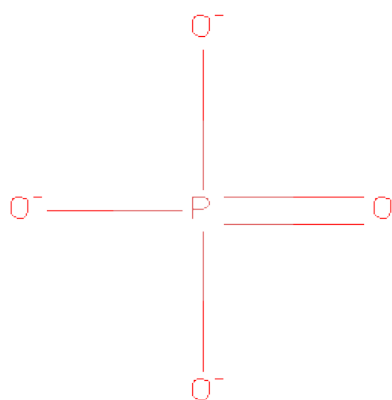
Chain	Residue	Modelled	Actual	Comment	Reference
E	29	GLY	-	CLONING ARTIFACT	UNP O30142
E	30	HIS	-	CLONING ARTIFACT	UNP O30142
E	31	MET	-	CLONING ARTIFACT	UNP O30142
J	29	GLY	-	CLONING ARTIFACT	UNP O30142
J	30	HIS	-	CLONING ARTIFACT	UNP O30142
J	31	MET	-	CLONING ARTIFACT	UNP O30142

- Molecule 4 is TUNGSTATE(VI)ION (three-letter code: WO4) (formula: O₄W).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	E	1	Total	O	W	0	0
			5	4	1		
4	J	1	Total	O	W	0	0
			5	4	1		

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			5	4	1		
5	B	1	Total	O	P	0	0
			5	4	1		
5	F	1	Total	O	P	0	0
			5	4	1		
5	G	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

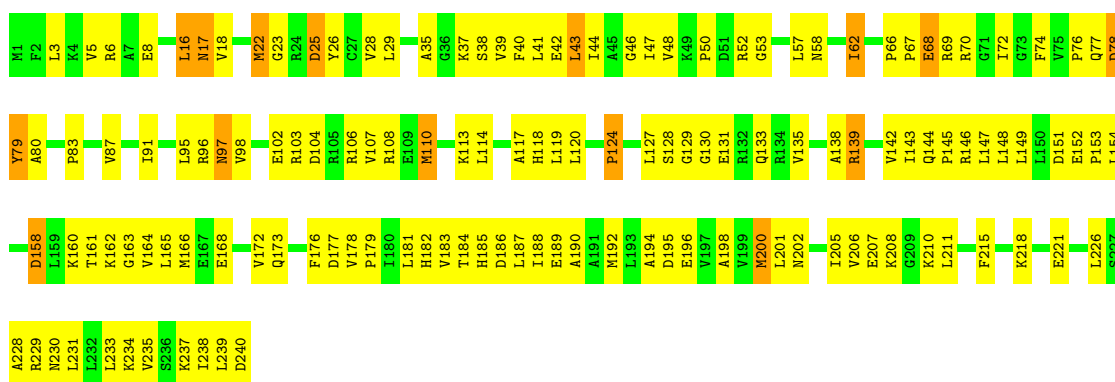
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	G	1	Total	Mg	0	0
			1	1		
6	J	1	Total	Mg	0	0
			1	1		
6	E	1	Total	Mg	0	0
			1	1		
6	B	1	Total	Mg	0	0
			1	1		
6	A	1	Total	Mg	0	0
			1	1		
6	F	1	Total	Mg	0	0
			1	1		

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.

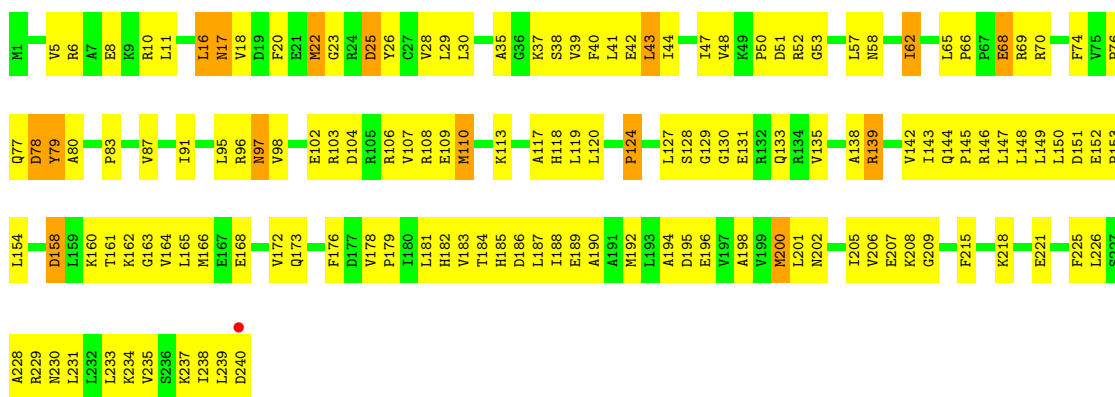
- Molecule 1: Molybdate/tungstate ABC transporter, ATP-binding protein

Chain A:



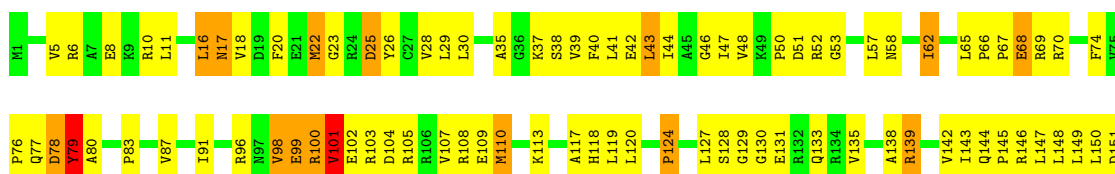
- Molecule 1: Molybdate/tungstate ABC transporter, ATP-binding protein

Chain B:



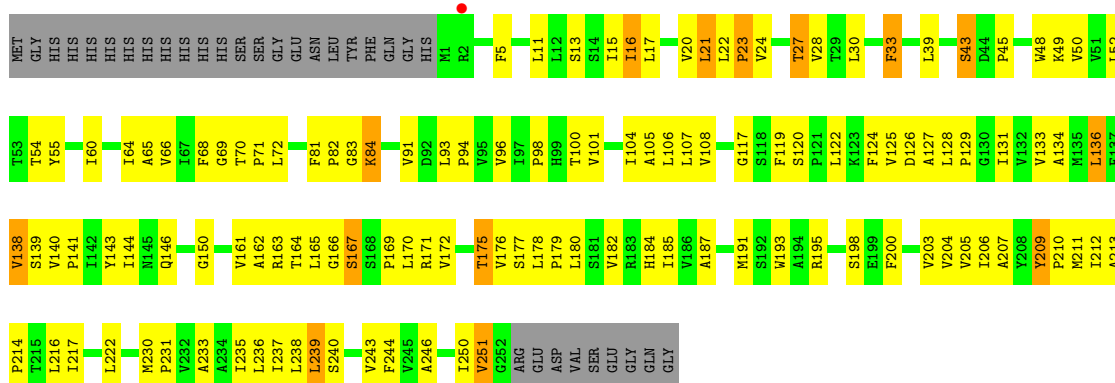
- Molecule 1: Molybdate/tungstate ABC transporter, ATP-binding protein

Chain F:



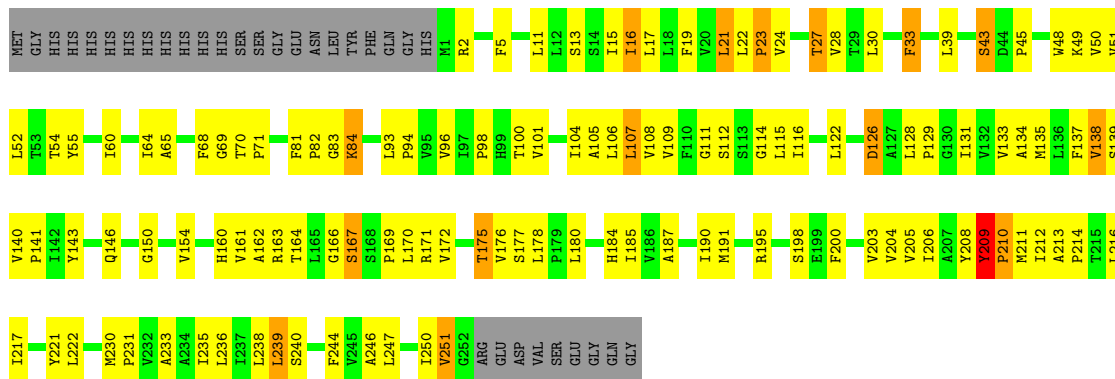
- Molecule 2: Molybdate/tungstate ABC transporter, permease protein

Chain H:



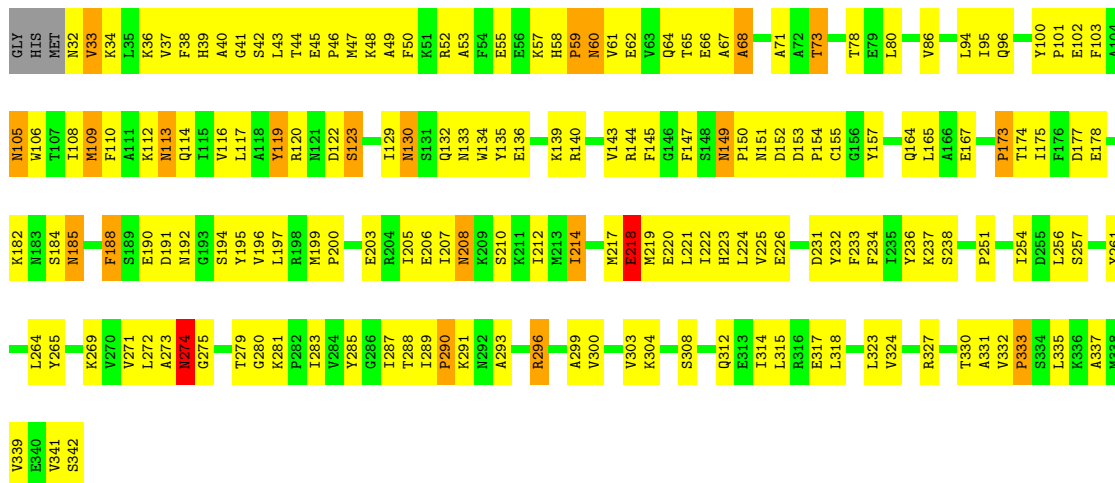
- Molecule 2: Molybdate/tungstate ABC transporter, permease protein

Chain I:



- Molecule 3: Molybdate/tungstate binding protein

Chain E:



- Molecule 3: Molybdate/tungstate binding protein

Chain J:

K336	G29	Q96	E178	S257
A337	H30			
M33B	M31	Y100	K182	A261
VAL	M32	P101		A262
GLU	V33	E102	N185	E263
VAL	K34			L264
SER	L35	N105	F188	Y265
	K36	W106	S189	
	V37	T107	E190	K289
	F38	I108	D191	V270
	H39	M109		V271
	A40	F110	S194	L272
	G41	A111	Y195	A273
	S42	K112	V196	K274
	L43	M113	L197	G275
	T44	Q114	R198	
	E45	I115	M199	T279
	P46	V116	P200	Q280
	M47	L117	S201	K281
	K48	A118	S202	P282
	A49	Y119	E203	I283
	F50		R204	V284
	K51	D122	I205	Y285
	R52	S123	E206	G286
	A53		I207	I287
	F54	I129	N208	T288
	E55	M130	K209	I289
	E56	S131	S210	P290
	K57	Q132	K211	K291
	H58	N133	I212	N292
	P59	W134	M213	A293
	N60	Y135	I214	
	V61	E136		K296
	E62		M217	
	V63	K139	E218	A299
	Q64	R140	N219	V300
	T65		E220	
	E66	V143	L221	V303
	A67	R144	I222	K304
	A68	F145	H223	
		G146	L224	S308
	A71	F147	V225	
	A72	G148	E226	Q312
	T73	N149		E313
	I74	P150	E229	I314
	K76	M151	L230	L315
		D152	D231	R316
		D153	Y232	E317
		P154	F233	
		C155	F234	L323
	L80	G156	I235	
	G81	Y157	Y236	R327
	R82		K237	A328
		L165	S238	D329
	D85			T330
	V86			A331
	I87		P251	V332
	A88	P173		P333
		T174		S334
	T93	I175	T254	
	L94	F176	D255	
	I95	D177	L256	

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	93.03Å 171.20Å 158.47Å 90.00° 98.79° 90.00°	Depositor
Resolution (Å)	30.00 – 3.10 29.69 – 3.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.00-3.10) 100.0 (29.69-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 3.11Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.256 , 0.283 0.254 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	92.1	Xtriage
Anisotropy	0.095	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 58.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 88712 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	20218	wwPDB-VP
Average B, all atoms (Å ²)	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: WO4, PO4, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.43	0/1930	0.75	1/2596 (0.0%)
1	B	0.41	0/1930	0.74	2/2596 (0.1%)
1	F	0.44	0/1930	0.76	2/2596 (0.1%)
1	G	0.42	0/1930	0.74	2/2596 (0.1%)
2	C	0.45	0/1945	0.66	1/2662 (0.0%)
2	D	0.48	0/1945	0.71	1/2662 (0.0%)
2	H	0.42	0/1945	0.65	1/2662 (0.0%)
2	I	0.46	0/1945	0.70	1/2662 (0.0%)
3	E	0.44	0/2540	0.68	0/3435
3	J	0.43	0/2533	0.68	0/3425
All	All	0.44	0/20573	0.71	11/27892 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	D	0	1
2	I	0	1
All	All	0	2

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	78	ASP	CB-CG-OD1	5.80	123.52	118.30
1	F	78	ASP	CB-CG-OD1	5.77	123.49	118.30
1	A	78	ASP	CB-CG-OD1	5.76	123.48	118.30
2	D	210	PRO	N-CA-C	-5.66	97.39	112.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	210	PRO	N-CA-C	-5.63	97.46	112.10
1	G	78	ASP	CB-CG-OD1	5.63	123.36	118.30
2	H	210	PRO	N-CA-C	-5.34	98.21	112.10
2	C	210	PRO	N-CA-C	-5.33	98.25	112.10
1	F	78	ASP	CB-CG-OD2	-5.16	113.66	118.30
1	B	78	ASP	CB-CG-OD2	-5.07	113.74	118.30
1	G	78	ASP	CB-CG-OD2	-5.05	113.75	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	209	TYR	Sidechain
2	I	209	TYR	Sidechain

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	1902	0	2002	175	1
1	B	1902	0	2002	158	0
1	F	1902	0	2002	184	1
1	G	1902	0	2002	182	0
2	C	1901	0	2044	161	0
2	D	1901	0	2044	152	0
2	H	1901	0	2044	165	0
2	I	1901	0	2044	161	0
3	E	2489	0	2487	196	0
3	J	2481	0	2477	197	0
4	E	5	0	0	2	0
4	J	5	0	0	1	0
5	A	5	0	0	1	0
5	B	5	0	0	1	0
5	F	5	0	0	1	0
5	G	5	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	E	1	0	0	0	0
6	F	1	0	0	0	0
6	G	1	0	0	0	0
6	J	1	0	0	0	0
All	All	20218	0	21148	1547	1

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 37.

All (1547) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:G:166:MET:HE1	1:G:189:GLU:HA	1.20	1.17
1:B:187:LEU:HB3	1:B:229:ARG:NH1	1.62	1.15
1:A:187:LEU:HB3	1:A:229:ARG:NH1	1.62	1.15
1:B:166:MET:HE1	1:B:189:GLU:HA	1.21	1.14
1:G:187:LEU:HB3	1:G:229:ARG:NH1	1.62	1.14
1:F:166:MET:HE1	1:F:189:GLU:HA	1.20	1.13
2:C:212:ILE:HG22	2:C:214:PRO:HD2	1.27	1.12
1:F:187:LEU:HB3	1:F:229:ARG:NH1	1.62	1.12
1:A:166:MET:HE1	1:A:189:GLU:HA	1.22	1.10
2:D:212:ILE:HG22	2:D:214:PRO:HD2	1.34	1.10
2:I:212:ILE:HG22	2:I:214:PRO:HD2	1.32	1.09
1:F:98:VAL:HG12	1:F:99:GLU:H	1.03	1.09
1:G:37:LYS:HB3	1:G:183:VAL:HG11	1.35	1.08
2:H:212:ILE:HG22	2:H:214:PRO:HD2	1.28	1.08
1:A:37:LYS:HB3	1:A:183:VAL:HG11	1.37	1.05
1:F:37:LYS:HB3	1:F:183:VAL:HG11	1.37	1.05
1:F:80:ALA:HB3	2:H:161:VAL:HG21	1.39	1.04
3:E:185:ASN:ND2	3:E:206:GLU:H	1.55	1.04
3:E:185:ASN:HD22	3:E:185:ASN:H	1.05	1.04
1:F:66:PRO:CB	2:I:2:ARG:HH22	1.69	1.03
3:J:185:ASN:HD22	3:J:185:ASN:H	1.06	1.02
2:H:203:VAL:HG11	2:H:212:ILE:HD12	1.39	1.00
2:I:209:TYR:O	2:I:211:MET:N	1.94	1.00
3:E:129:ILE:HA	3:E:133:ASN:HD21	1.26	0.99
2:D:209:TYR:O	2:D:211:MET:N	1.95	0.99
3:J:129:ILE:HA	3:J:133:ASN:HD21	1.27	0.99
1:B:37:LYS:HB3	1:B:183:VAL:HG11	1.42	0.98
3:J:32:ASN:HA	3:J:60:ASN:O	1.62	0.98
1:F:66:PRO:HB3	2:I:2:ARG:HH12	1.25	0.97

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:187:LEU:HB3	1:B:229:ARG:HH12	1.24	0.97
2:D:28:VAL:HG11	2:D:238:LEU:HD21	1.44	0.96
3:E:185:ASN:HD21	3:E:206:GLU:H	1.03	0.96
1:B:184:THR:HG22	1:B:185:HIS:H	1.31	0.95
1:F:187:LEU:HB3	1:F:229:ARG:HH12	1.24	0.95
1:G:83:PRO:HA	1:G:124:PRO:HG3	1.47	0.94
1:F:130:GLY:HA2	1:F:133:GLN:NE2	1.83	0.94
1:A:130:GLY:HA2	1:A:133:GLN:NE2	1.80	0.94
1:G:187:LEU:HB3	1:G:229:ARG:HH12	1.24	0.93
1:G:130:GLY:HA2	1:G:133:GLN:NE2	1.83	0.93
1:A:184:THR:HG22	1:A:185:HIS:H	1.33	0.93
1:F:184:THR:HG22	1:F:185:HIS:H	1.31	0.92
1:B:130:GLY:HA2	1:B:133:GLN:NE2	1.83	0.92
3:J:33:VAL:O	3:J:61:VAL:HG13	1.69	0.92
3:J:185:ASN:HD21	3:J:206:GLU:H	1.14	0.92
1:A:187:LEU:HB3	1:A:229:ARG:HH12	1.23	0.91
2:H:212:ILE:HG22	2:H:214:PRO:CD	2.00	0.91
1:G:184:THR:HG22	1:G:185:HIS:H	1.32	0.91
1:F:98:VAL:HG12	1:F:99:GLU:N	1.85	0.90
3:E:130:ASN:HD22	3:E:132:GLN:H	1.13	0.90
1:A:83:PRO:HA	1:A:124:PRO:HG3	1.51	0.90
3:J:185:ASN:ND2	3:J:206:GLU:H	1.70	0.89
1:F:66:PRO:HB3	2:I:2:ARG:NH1	1.87	0.89
1:B:161:THR:O	1:B:164:VAL:HG22	1.73	0.89
2:H:81:PHE:HB2	2:H:82:PRO:HD2	1.54	0.89
2:C:101:VAL:HG22	2:D:217:ILE:HD12	1.55	0.88
2:C:203:VAL:HG11	2:C:212:ILE:HD12	1.53	0.88
1:G:161:THR:O	1:G:164:VAL:HG22	1.73	0.88
1:A:161:THR:O	1:A:164:VAL:HG22	1.73	0.88
1:F:161:THR:O	1:F:164:VAL:HG22	1.74	0.88
2:I:81:PHE:HB2	2:I:82:PRO:HD2	1.56	0.88
3:E:324:VAL:HB	3:J:263:GLU:HG3	1.55	0.87
3:E:208:ASN:HD22	3:E:208:ASN:C	1.77	0.87
3:J:208:ASN:HD22	3:J:208:ASN:C	1.78	0.87
3:J:130:ASN:ND2	3:J:133:ASN:OD1	2.07	0.87
2:D:81:PHE:HB2	2:D:82:PRO:HD2	1.55	0.86
1:F:238:ILE:HD12	1:G:192:MET:HE2	1.58	0.86
1:F:131:GLU:O	1:F:135:VAL:HG23	1.76	0.86
1:A:235:VAL:HG22	1:B:192:MET:HE3	1.56	0.85
2:H:240:SER:HB3	2:I:96:VAL:HG12	1.59	0.85
2:C:212:ILE:HG22	2:C:214:PRO:CD	2.05	0.85
1:F:66:PRO:CG	2:I:2:ARG:HH22	1.90	0.85

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:80:ALA:HB3	2:C:161:VAL:HG21	1.59	0.85
2:C:81:PHE:HB2	2:C:82:PRO:HD2	1.56	0.85
1:A:130:GLY:HA2	1:A:133:GLN:HE21	1.39	0.85
1:A:66:PRO:HB2	1:A:68:GLU:HG2	1.58	0.85
1:A:131:GLU:O	1:A:135:VAL:HG23	1.77	0.84
2:C:28:VAL:HG11	2:C:238:LEU:HD21	1.56	0.84
1:F:130:GLY:HA2	1:F:133:GLN:HE21	1.41	0.84
1:B:130:GLY:HA2	1:B:133:GLN:HE21	1.41	0.84
2:C:134:ALA:HB2	2:C:206:ILE:HD12	1.60	0.84
1:G:131:GLU:O	1:G:135:VAL:HG23	1.77	0.84
2:H:28:VAL:HG11	2:H:238:LEU:HD21	1.60	0.84
2:H:209:TYR:O	2:H:211:MET:N	2.11	0.84
2:C:209:TYR:HE1	3:E:214:ILE:HG12	1.42	0.84
1:F:166:MET:CE	1:F:189:GLU:HA	2.08	0.83
2:H:134:ALA:HB2	2:H:206:ILE:HD12	1.59	0.83
2:H:212:ILE:CG2	2:H:214:PRO:HD2	2.08	0.83
1:A:47:ILE:HD13	2:C:160:HIS:HB3	1.60	0.83
1:B:131:GLU:O	1:B:135:VAL:HG23	1.78	0.83
3:J:208:ASN:ND2	3:J:210:SER:H	1.76	0.83
1:G:66:PRO:HB2	1:G:68:GLU:HG2	1.59	0.83
3:J:45:GLU:HB2	3:J:46:PRO:HD3	1.61	0.83
3:E:130:ASN:ND2	3:E:132:GLN:H	1.76	0.82
3:E:208:ASN:ND2	3:E:210:SER:H	1.77	0.82
3:E:45:GLU:HB2	3:E:46:PRO:HD3	1.60	0.82
2:H:203:VAL:HG11	2:H:212:ILE:CD1	2.09	0.82
3:E:185:ASN:H	3:E:185:ASN:ND2	1.78	0.81
3:E:208:ASN:HD21	3:E:210:SER:HB2	1.45	0.81
3:J:208:ASN:HD21	3:J:210:SER:HB2	1.45	0.81
3:E:149:ASN:ND2	3:E:151:ASN:N	2.29	0.81
2:C:209:TYR:O	2:C:211:MET:N	2.12	0.81
3:J:149:ASN:ND2	3:J:151:ASN:N	2.28	0.81
1:G:166:MET:CE	1:G:189:GLU:HA	2.08	0.81
1:F:83:PRO:HA	1:F:124:PRO:HG3	1.62	0.80
2:H:211:MET:CE	2:H:216:LEU:HD12	2.10	0.80
3:J:185:ASN:H	3:J:185:ASN:ND2	1.79	0.80
1:G:130:GLY:HA2	1:G:133:GLN:HE21	1.42	0.80
1:A:192:MET:HE3	1:B:235:VAL:HG22	1.63	0.80
2:I:212:ILE:CG2	2:I:214:PRO:HD2	2.12	0.79
3:E:165:LEU:HB3	3:E:254:ILE:HG22	1.64	0.79
1:G:68:GLU:CB	2:I:166:GLY:HA2	2.13	0.79
2:D:212:ILE:CG2	2:D:214:PRO:HD2	2.12	0.79
1:F:66:PRO:CB	2:I:2:ARG:NH2	2.45	0.79

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:G:83:PRO:HA	1:G:124:PRO:CG	2.11	0.79
1:A:163:GLY:HA3	1:B:231:LEU:HD13	1.63	0.79
1:F:98:VAL:CG1	1:F:99:GLU:H	1.88	0.78
1:F:98:VAL:CG1	1:F:102:GLU:HB3	2.13	0.78
1:F:184:THR:HG22	1:F:185:HIS:N	1.99	0.77
1:B:166:MET:CE	1:B:189:GLU:HA	2.09	0.77
3:E:149:ASN:HD21	3:E:151:ASN:HB2	1.50	0.77
1:B:47:ILE:HD13	2:D:160:HIS:HB3	1.65	0.77
1:A:166:MET:CE	1:A:189:GLU:HA	2.10	0.77
2:I:213:ALA:HB1	2:I:236:LEU:HD11	1.67	0.77
2:H:96:VAL:HG12	2:I:240:SER:HB3	1.67	0.76
1:F:66:PRO:HD2	1:F:69:ARG:HB2	1.66	0.76
1:F:187:LEU:HD13	1:F:229:ARG:CZ	2.15	0.76
1:F:229:ARG:HD2	1:G:239:LEU:HD13	1.66	0.76
2:D:217:ILE:HD11	2:D:236:LEU:HD12	1.68	0.76
1:G:29:LEU:HD21	1:G:183:VAL:HG22	1.68	0.76
3:J:149:ASN:HD21	3:J:151:ASN:HB2	1.50	0.76
1:B:83:PRO:HA	1:B:124:PRO:HG3	1.66	0.76
1:F:66:PRO:HB2	1:F:68:GLU:HG2	1.68	0.76
1:B:66:PRO:HD2	1:B:69:ARG:HB2	1.68	0.76
3:J:149:ASN:ND2	3:J:151:ASN:H	1.84	0.76
1:G:187:LEU:HD13	1:G:229:ARG:CZ	2.16	0.76
1:B:187:LEU:HD13	1:B:229:ARG:CZ	2.15	0.75
2:H:96:VAL:CG1	2:I:240:SER:HB3	2.16	0.75
3:E:149:ASN:ND2	3:E:151:ASN:H	1.85	0.75
1:A:187:LEU:HD13	1:A:229:ARG:CZ	2.15	0.75
2:H:240:SER:HB3	2:I:96:VAL:CG1	2.17	0.75
3:J:149:ASN:C	3:J:149:ASN:HD22	1.90	0.75
1:F:129:GLY:O	1:F:133:GLN:HG3	1.86	0.75
1:G:129:GLY:O	1:G:133:GLN:HG3	1.87	0.75
1:B:184:THR:HG22	1:B:185:HIS:N	2.00	0.75
1:G:184:THR:HG22	1:G:185:HIS:N	2.01	0.75
1:A:129:GLY:O	1:A:133:GLN:HG3	1.87	0.74
2:C:212:ILE:CG2	2:C:214:PRO:HD2	2.12	0.74
1:A:37:LYS:HB3	1:A:183:VAL:CG1	2.17	0.74
2:C:96:VAL:CG1	2:D:240:SER:HB3	2.17	0.74
3:E:185:ASN:HD21	3:E:206:GLU:N	1.82	0.74
1:F:238:ILE:HD12	1:G:192:MET:CE	2.16	0.74
3:E:324:VAL:HB	3:J:263:GLU:CG	2.18	0.74
3:J:102:GLU:O	3:J:291:LYS:HD3	1.87	0.74
1:A:184:THR:HG22	1:A:185:HIS:N	2.01	0.74
2:C:203:VAL:HG11	2:C:212:ILE:CD1	2.18	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:I:28:VAL:HG11	2:I:238:LEU:HD21	1.70	0.73
3:J:35:LEU:HD12	3:J:85:ASP:OD2	1.87	0.73
2:D:213:ALA:HB1	2:D:236:LEU:HD11	1.69	0.73
1:F:68:GLU:HA	2:H:166:GLY:HA2	1.70	0.73
2:I:128:LEU:HB3	2:I:129:PRO:HD3	1.70	0.73
1:A:187:LEU:HD22	1:A:229:ARG:NH2	2.03	0.73
3:E:149:ASN:HD22	3:E:149:ASN:C	1.91	0.73
1:G:47:ILE:HD13	2:I:160:HIS:HB3	1.70	0.73
1:B:22:MET:HA	1:B:208:LYS:NZ	2.03	0.73
2:D:128:LEU:HB3	2:D:129:PRO:HD3	1.70	0.73
1:A:66:PRO:HD2	1:A:69:ARG:HB2	1.71	0.73
2:D:222:LEU:HD22	3:E:220:GLU:HG2	1.71	0.73
2:C:5:PHE:CD1	2:D:170:LEU:HD13	2.23	0.73
2:C:217:ILE:HD11	2:C:236:LEU:HD12	1.71	0.73
1:B:187:LEU:HD22	1:B:229:ARG:NH2	2.04	0.72
1:F:187:LEU:HD22	1:F:229:ARG:NH2	2.03	0.72
2:I:217:ILE:HD11	2:I:236:LEU:HD12	1.69	0.72
1:G:37:LYS:HB3	1:G:183:VAL:CG1	2.17	0.72
1:A:47:ILE:CD1	2:C:160:HIS:HB3	2.19	0.72
1:B:129:GLY:O	1:B:133:GLN:HG3	1.88	0.72
1:G:187:LEU:HD22	1:G:229:ARG:NH2	2.03	0.72
1:F:168:GLU:O	1:F:172:VAL:HG23	1.90	0.72
1:F:37:LYS:HB3	1:F:183:VAL:CG1	2.18	0.72
1:A:29:LEU:HD21	1:A:183:VAL:HG22	1.72	0.72
1:A:66:PRO:HG2	2:D:2:ARG:HH22	1.55	0.72
1:A:231:LEU:HD13	1:B:163:GLY:HA3	1.71	0.72
1:A:83:PRO:HA	1:A:124:PRO:CG	2.19	0.72
1:G:168:GLU:O	1:G:172:VAL:HG23	1.91	0.71
3:J:190:GLU:HB2	3:J:195:TYR:CE1	2.25	0.71
2:H:211:MET:HE3	2:H:216:LEU:HD12	1.70	0.71
1:A:168:GLU:O	1:A:172:VAL:HG23	1.89	0.71
1:G:35:ALA:O	1:G:200:MET:HE2	1.90	0.71
2:I:150:GLY:HA2	2:I:184:HIS:CD2	2.25	0.71
3:J:130:ASN:ND2	3:J:132:GLN:H	1.88	0.71
1:F:29:LEU:HD21	1:F:183:VAL:HG22	1.73	0.71
3:J:31:MET:HB2	3:J:60:ASN:ND2	2.06	0.71
2:H:217:ILE:HD11	2:H:236:LEU:HD12	1.71	0.71
2:C:209:TYR:CE1	3:E:214:ILE:HG12	2.25	0.70
2:D:150:GLY:HA2	2:D:184:HIS:CD2	2.27	0.70
2:D:135:MET:HE1	2:D:212:ILE:HD13	1.72	0.70
3:J:130:ASN:HD22	3:J:130:ASN:C	1.93	0.70
1:F:66:PRO:CG	2:I:2:ARG:NH2	2.55	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:66:PRO:HB2	2:I:2:ARG:HH22	1.55	0.70
3:E:190:GLU:HB2	3:E:195:TYR:CE1	2.26	0.70
2:H:131:ILE:HG23	2:H:212:ILE:HD11	1.74	0.70
2:H:213:ALA:HB1	2:H:236:LEU:HD11	1.74	0.70
1:F:66:PRO:CB	2:I:2:ARG:HH12	2.00	0.70
3:J:31:MET:HB2	3:J:60:ASN:HD21	1.56	0.70
3:J:329:ASP:N	3:J:329:ASP:OD1	2.15	0.70
2:H:150:GLY:HA2	2:H:184:HIS:CD2	2.27	0.69
1:B:168:GLU:O	1:B:172:VAL:HG23	1.90	0.69
2:D:107:LEU:HD23	2:D:111:GLY:HA3	1.73	0.69
3:E:32:ASN:HA	3:E:60:ASN:O	1.91	0.69
2:C:163:ARG:NH1	2:C:169:PRO:HG3	2.07	0.69
3:E:185:ASN:HD22	3:E:185:ASN:N	1.87	0.69
3:E:185:ASN:ND2	3:E:206:GLU:N	2.37	0.69
3:E:33:VAL:O	3:E:61:VAL:HG13	1.91	0.69
1:G:28:VAL:HG22	1:G:182:HIS:HB3	1.75	0.69
3:E:308:SER:O	3:E:312:GLN:HG3	1.93	0.69
1:F:192:MET:HE1	1:G:238:ILE:HD12	1.74	0.69
2:C:150:GLY:HA2	2:C:184:HIS:CD2	2.28	0.69
3:J:76:LYS:HG2	3:J:80:LEU:HD12	1.75	0.69
2:I:135:MET:HE3	2:I:212:ILE:HD13	1.75	0.68
1:A:80:ALA:C	1:A:139:ARG:HH22	1.96	0.68
1:B:28:VAL:HG22	1:B:182:HIS:HB3	1.76	0.68
2:I:163:ARG:NH1	2:I:169:PRO:HG3	2.08	0.68
2:D:163:ARG:NH1	2:D:169:PRO:HG3	2.08	0.68
1:B:95:LEU:HD11	1:B:142:VAL:HG11	1.75	0.68
1:B:29:LEU:HD21	1:B:183:VAL:HG22	1.75	0.68
3:J:165:LEU:HB3	3:J:254:ILE:HG22	1.75	0.68
3:E:196:VAL:HA	3:E:269:LYS:O	1.93	0.68
3:E:102:GLU:O	3:E:291:LYS:HD3	1.93	0.68
1:F:74:PHE:HB3	2:H:164:THR:HG21	1.76	0.68
2:C:211:MET:CE	2:C:216:LEU:HD12	2.24	0.68
1:F:66:PRO:HG2	2:I:2:ARG:NH2	2.10	0.67
2:H:68:PHE:HB3	2:I:16:ILE:CG1	2.24	0.67
2:I:107:LEU:HD23	2:I:111:GLY:HA3	1.75	0.67
1:A:95:LEU:HD11	1:A:142:VAL:HG11	1.75	0.67
2:C:213:ALA:HB3	2:C:214:PRO:HD3	1.76	0.67
1:A:74:PHE:HB3	2:C:164:THR:HG21	1.76	0.67
1:A:66:PRO:CG	2:D:2:ARG:HH12	2.07	0.67
3:J:308:SER:O	3:J:312:GLN:HG3	1.94	0.67
2:H:163:ARG:NH1	2:H:169:PRO:HG3	2.08	0.67
1:G:57:LEU:CB	1:G:62:ILE:HD11	2.24	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:66:PRO:HG2	2:I:2:ARG:HH22	1.60	0.67
2:C:96:VAL:HG12	2:D:240:SER:HB3	1.75	0.67
3:J:196:VAL:HA	3:J:269:LYS:O	1.95	0.67
2:D:134:ALA:O	2:D:138:VAL:HG23	1.95	0.67
2:C:68:PHE:HB3	2:D:16:ILE:CG1	2.24	0.67
1:A:47:ILE:HD13	2:C:160:HIS:CB	2.25	0.67
1:F:22:MET:HA	1:F:208:LYS:NZ	2.09	0.67
2:H:68:PHE:HB3	2:I:16:ILE:HG13	1.76	0.67
2:D:134:ALA:HB2	2:D:206:ILE:HD12	1.77	0.67
1:A:163:GLY:HA3	1:B:231:LEU:CD1	2.24	0.66
2:H:101:VAL:HG22	2:I:217:ILE:HD12	1.76	0.66
3:E:208:ASN:HD22	3:E:210:SER:H	1.41	0.66
2:C:134:ALA:O	2:C:138:VAL:HG23	1.95	0.66
1:A:35:ALA:O	1:A:200:MET:HE2	1.95	0.66
1:A:194:ALA:HB1	1:A:196:GLU:O	1.96	0.66
2:H:209:TYR:HE1	3:J:214:ILE:HG12	1.60	0.66
3:J:149:ASN:C	3:J:149:ASN:ND2	2.49	0.66
1:F:104:ASP:O	1:F:108:ARG:HG3	1.95	0.66
1:B:80:ALA:C	1:B:139:ARG:HH22	2.00	0.66
1:G:66:PRO:HD2	1:G:69:ARG:HB2	1.77	0.65
1:B:47:ILE:CD1	2:D:160:HIS:HB3	2.25	0.65
2:H:200:PHE:CE1	2:H:204:VAL:HG11	2.31	0.65
3:J:129:ILE:HA	3:J:133:ASN:ND2	2.09	0.65
3:J:130:ASN:HD22	3:J:132:GLN:H	1.43	0.65
1:G:61:ASP:OD1	1:G:62:ILE:N	2.30	0.65
2:I:126:ASP:O	2:I:210:PRO:HG3	1.96	0.65
1:G:194:ALA:HB1	1:G:196:GLU:O	1.96	0.65
3:J:130:ASN:ND2	3:J:133:ASN:H	1.94	0.65
1:G:28:VAL:HB	1:G:194:ALA:HB2	1.79	0.65
1:G:57:LEU:N	1:G:62:ILE:HD11	2.12	0.65
3:J:55:GLU:OE2	3:J:62:GLU:HA	1.97	0.65
2:I:134:ALA:O	2:I:138:VAL:HG23	1.96	0.65
2:H:134:ALA:O	2:H:138:VAL:HG23	1.96	0.65
2:I:122:LEU:HD11	2:I:129:PRO:HG2	1.78	0.65
2:C:68:PHE:HB3	2:D:16:ILE:HG13	1.78	0.65
2:D:122:LEU:HD11	2:D:129:PRO:HG2	1.78	0.65
3:J:208:ASN:ND2	3:J:208:ASN:C	2.50	0.65
1:F:28:VAL:HG22	1:F:182:HIS:HB3	1.79	0.65
1:F:158:ASP:OD2	1:F:160:LYS:HB3	1.97	0.65
3:J:208:ASN:HD22	3:J:210:SER:H	1.41	0.65
1:B:194:ALA:HB1	1:B:196:GLU:O	1.97	0.65
2:D:187:ALA:O	2:D:191:MET:HG3	1.97	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:187:ALA:O	2:C:191:MET:HG3	1.97	0.64
1:F:35:ALA:O	1:F:200:MET:HE2	1.97	0.64
2:H:105:ALA:HA	2:I:27:THR:HG21	1.79	0.64
2:H:72:LEU:HD23	2:H:144:ILE:HD13	1.79	0.64
1:B:95:LEU:HD11	1:B:142:VAL:CG1	2.26	0.64
2:C:240:SER:HB3	2:D:96:VAL:HG12	1.79	0.64
2:C:23:PRO:O	2:C:27:THR:HG23	1.97	0.64
3:E:129:ILE:HA	3:E:133:ASN:ND2	2.07	0.64
1:G:158:ASP:OD2	1:G:160:LYS:HB3	1.97	0.64
3:J:208:ASN:ND2	3:J:210:SER:N	2.46	0.64
2:I:134:ALA:HB2	2:I:206:ILE:HD12	1.78	0.64
1:B:158:ASP:OD2	1:B:160:LYS:HB3	1.97	0.64
3:E:205:ILE:CG2	3:E:207:ILE:HD11	2.27	0.64
2:D:209:TYR:HE1	3:E:65:THR:O	1.80	0.64
3:E:55:GLU:OE2	3:E:62:GLU:HA	1.97	0.64
1:A:158:ASP:OD2	1:A:160:LYS:HB3	1.97	0.64
3:J:273:ALA:C	3:J:275:GLY:H	2.02	0.64
1:B:37:LYS:HB3	1:B:183:VAL:CG1	2.23	0.63
2:H:187:ALA:O	2:H:191:MET:HG3	1.99	0.63
2:C:200:PHE:CE1	2:C:204:VAL:HG11	2.33	0.63
3:E:135:TYR:O	3:E:139:LYS:HG3	1.98	0.63
3:E:327:ARG:HD3	3:E:342:SER:OG	1.97	0.63
1:F:145:PRO:HB2	1:F:147:LEU:O	1.99	0.63
3:J:135:TYR:O	3:J:139:LYS:HG3	1.98	0.63
1:G:80:ALA:HB3	2:I:161:VAL:HG21	1.79	0.63
1:F:28:VAL:HB	1:F:194:ALA:HB2	1.81	0.63
1:A:145:PRO:HB2	1:A:147:LEU:O	1.98	0.63
2:C:211:MET:HE3	2:C:216:LEU:HD12	1.78	0.63
2:H:100:THR:HG21	2:I:217:ILE:HB	1.81	0.63
3:E:150:PRO:HD2	3:E:199:MET:HE1	1.80	0.63
3:E:149:ASN:C	3:E:149:ASN:ND2	2.51	0.63
1:F:194:ALA:HB1	1:F:196:GLU:O	1.99	0.63
1:B:229:ARG:O	1:B:233:LEU:HG	1.98	0.63
1:A:229:ARG:O	1:A:233:LEU:HG	1.99	0.63
3:E:296:ARG:O	3:E:299:ALA:HB3	1.98	0.63
1:G:145:PRO:HB2	1:G:147:LEU:O	1.99	0.63
1:F:229:ARG:O	1:F:233:LEU:HG	1.98	0.63
3:J:333:PRO:O	3:J:336:LYS:HG2	1.98	0.63
3:J:119:TYR:HB3	3:J:232:TYR:CD1	2.34	0.63
2:C:217:ILE:HD12	2:D:101:VAL:HG22	1.80	0.62
1:F:74:PHE:H	2:H:164:THR:HG21	1.64	0.62
1:F:184:THR:HG22	1:F:186:ASP:H	1.64	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:240:SER:HB3	2:D:96:VAL:CG1	2.29	0.62
2:H:23:PRO:O	2:H:27:THR:HG23	1.98	0.62
1:G:229:ARG:O	1:G:233:LEU:HG	1.99	0.62
1:B:66:PRO:HB2	1:B:68:GLU:HG2	1.81	0.62
1:G:80:ALA:C	1:G:139:ARG:HH22	2.03	0.62
1:A:28:VAL:HB	1:A:194:ALA:HB2	1.80	0.62
1:F:80:ALA:C	1:F:139:ARG:HH22	2.02	0.62
2:H:16:ILE:CG1	2:I:68:PHE:HB3	2.29	0.62
2:D:28:VAL:CG1	2:D:238:LEU:HD21	2.23	0.62
3:E:208:ASN:ND2	3:E:210:SER:N	2.46	0.62
1:A:28:VAL:HG22	1:A:182:HIS:HB3	1.81	0.62
2:D:200:PHE:CE1	2:D:204:VAL:HG11	2.35	0.62
3:J:221:LEU:O	3:J:225:VAL:HG23	1.99	0.62
2:H:128:LEU:HB2	2:H:129:PRO:HD3	1.82	0.62
1:B:187:LEU:HD11	1:B:228:ALA:HB3	1.80	0.62
1:G:187:LEU:HD11	1:G:228:ALA:HB3	1.82	0.62
2:D:138:VAL:HG11	2:D:195:ARG:NH2	2.15	0.62
1:A:187:LEU:HD11	1:A:228:ALA:HB3	1.81	0.62
1:G:68:GLU:HB3	2:I:166:GLY:HA2	1.81	0.62
2:C:16:ILE:CG1	2:D:68:PHE:HB3	2.30	0.62
2:C:16:ILE:H	2:C:16:ILE:HD12	1.65	0.62
2:I:187:ALA:O	2:I:191:MET:HG3	1.99	0.62
3:E:273:ALA:C	3:E:275:GLY:H	2.02	0.62
1:G:83:PRO:HG2	2:I:180:LEU:HD21	1.80	0.62
1:A:184:THR:HG22	1:A:186:ASP:H	1.65	0.62
1:F:163:GLY:HA3	1:G:231:LEU:HD13	1.82	0.62
2:H:138:VAL:HG11	2:H:195:ARG:NH2	2.14	0.62
2:H:246:ALA:O	2:H:250:ILE:HG13	2.00	0.62
2:H:27:THR:HG21	2:I:105:ALA:HA	1.81	0.61
1:B:145:PRO:HB2	1:B:147:LEU:O	1.99	0.61
2:D:230:MET:HB2	2:D:231:PRO:HD3	1.81	0.61
2:I:200:PHE:CE1	2:I:204:VAL:HG11	2.35	0.61
2:D:23:PRO:O	2:D:27:THR:HG23	1.99	0.61
2:C:230:MET:HB2	2:C:231:PRO:HD3	1.82	0.61
1:B:118:HIS:CD2	1:B:119:LEU:HG	2.36	0.61
3:J:296:ARG:O	3:J:299:ALA:HB3	2.00	0.61
2:C:104:ILE:HD12	2:D:217:ILE:CG2	2.31	0.61
1:B:184:THR:HG22	1:B:186:ASP:H	1.65	0.61
2:C:138:VAL:HG11	2:C:195:ARG:NH2	2.15	0.61
1:F:83:PRO:HA	1:F:124:PRO:CG	2.29	0.61
1:G:200:MET:HG3	1:G:205:ILE:HG12	1.82	0.61
3:J:300:VAL:HG12	3:J:304:LYS:HE2	1.82	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:246:ALA:O	2:D:250:ILE:HG13	2.01	0.61
3:J:206:GLU:O	3:J:207:ILE:HD13	2.01	0.61
2:D:16:ILE:H	2:D:16:ILE:HD12	1.64	0.61
3:E:221:LEU:O	3:E:225:VAL:HG23	1.99	0.61
2:C:246:ALA:O	2:C:250:ILE:HG13	2.01	0.61
1:B:200:MET:HG3	1:B:205:ILE:HG12	1.83	0.61
1:A:138:ALA:O	1:A:142:VAL:HG23	2.01	0.61
1:F:118:HIS:CD2	1:F:119:LEU:HG	2.36	0.61
1:A:118:HIS:CD2	1:A:119:LEU:HG	2.36	0.61
2:I:230:MET:HB2	2:I:231:PRO:HD3	1.83	0.61
1:F:184:THR:CG2	1:F:185:HIS:H	2.10	0.61
2:I:161:VAL:O	2:I:164:THR:HB	2.01	0.61
1:G:166:MET:HE1	1:G:189:GLU:CA	2.14	0.60
1:F:5:VAL:HG21	1:F:44:ILE:CD1	2.31	0.60
1:A:200:MET:HG3	1:A:205:ILE:HG12	1.83	0.60
2:C:128:LEU:HB2	2:C:129:PRO:HD3	1.82	0.60
1:G:138:ALA:O	1:G:142:VAL:HG23	2.01	0.60
1:G:29:LEU:HD22	1:G:181:LEU:HD11	1.82	0.60
3:J:185:ASN:HD21	3:J:206:GLU:N	1.94	0.60
2:I:138:VAL:HG11	2:I:195:ARG:NH2	2.16	0.60
2:I:246:ALA:O	2:I:250:ILE:HG13	2.01	0.60
1:B:10:ARG:N	1:B:51:ASP:OD2	2.33	0.60
3:J:105:ASN:HD22	3:J:105:ASN:C	2.05	0.60
3:J:153:ASP:OD1	3:J:154:PRO:HD2	2.00	0.60
3:E:130:ASN:ND2	3:E:133:ASN:OD1	2.35	0.60
3:E:300:VAL:HG12	3:E:304:LYS:HE2	1.83	0.60
3:J:108:ILE:HA	3:J:327:ARG:O	2.02	0.60
3:J:117:LEU:HD13	3:J:234:PHE:CE1	2.35	0.60
1:B:138:ALA:O	1:B:142:VAL:HG23	2.02	0.60
2:C:213:ALA:HB1	2:C:236:LEU:HD11	1.83	0.60
2:I:23:PRO:O	2:I:27:THR:HG23	2.01	0.60
2:H:16:ILE:H	2:H:16:ILE:HD12	1.66	0.60
3:E:217:MET:HE2	3:E:219:MET:HB2	1.83	0.60
1:F:138:ALA:O	1:F:142:VAL:HG23	2.02	0.60
1:F:41:LEU:HD22	1:F:149:LEU:HD22	1.84	0.60
3:J:185:ASN:HD22	3:J:185:ASN:N	1.88	0.60
3:E:67:ALA:HB1	3:E:217:MET:CE	2.32	0.60
1:G:184:THR:HG22	1:G:186:ASP:H	1.65	0.60
1:G:95:LEU:HD11	1:G:142:VAL:HG11	1.84	0.60
2:D:65:ALA:O	2:D:69:GLY:N	2.30	0.60
3:J:150:PRO:HD2	3:J:199:MET:HE1	1.83	0.60
3:J:149:ASN:HD21	3:J:151:ASN:N	1.98	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:161:VAL:O	2:D:164:THR:HB	2.02	0.60
3:E:330:THR:HG22	3:E:331:ALA:O	2.02	0.60
1:B:187:LEU:HB3	1:B:229:ARG:CZ	2.31	0.59
2:D:81:PHE:HB2	2:D:82:PRO:CD	2.31	0.59
1:B:28:VAL:HB	1:B:194:ALA:HB2	1.84	0.59
3:E:145:PHE:HA	3:E:232:TYR:O	2.02	0.59
1:G:118:HIS:CD2	1:G:119:LEU:HG	2.36	0.59
1:A:187:LEU:HB3	1:A:229:ARG:CZ	2.30	0.59
1:F:66:PRO:HB3	2:I:2:ARG:CZ	2.31	0.59
3:E:149:ASN:HD21	3:E:151:ASN:N	2.00	0.59
1:A:95:LEU:HD11	1:A:142:VAL:CG1	2.32	0.59
2:D:235:ILE:O	2:D:239:LEU:HB2	2.02	0.59
3:J:149:ASN:HD21	3:J:151:ASN:H	1.50	0.59
2:H:222:LEU:HA	3:J:80:LEU:HD21	1.85	0.59
1:B:109:GLU:O	1:B:113:LYS:HG3	2.02	0.59
1:F:187:LEU:HB3	1:F:229:ARG:CZ	2.30	0.59
2:H:161:VAL:O	2:H:164:THR:HB	2.02	0.59
2:C:81:PHE:HB2	2:C:82:PRO:CD	2.32	0.59
1:B:66:PRO:O	1:B:70:ARG:HG3	2.02	0.59
1:G:5:VAL:HG21	1:G:44:ILE:CD1	2.33	0.59
2:C:161:VAL:O	2:C:164:THR:HB	2.03	0.59
1:F:200:MET:HG3	1:F:205:ILE:HG12	1.84	0.59
2:H:65:ALA:O	2:H:69:GLY:N	2.29	0.59
1:B:5:VAL:HG21	1:B:44:ILE:CD1	2.33	0.59
3:E:57:LYS:HG3	3:E:58:HIS:CE1	2.38	0.59
2:C:65:ALA:O	2:C:69:GLY:N	2.31	0.59
3:E:34:LYS:HD3	3:E:64:GLN:OE1	2.03	0.59
1:B:17:ASN:ND2	1:B:17:ASN:O	2.36	0.58
1:F:187:LEU:HD11	1:F:228:ALA:HB3	1.84	0.58
3:E:105:ASN:HD22	3:E:105:ASN:C	2.06	0.58
1:A:16:LEU:HD23	1:A:18:VAL:HG13	1.85	0.58
1:B:16:LEU:HD23	1:B:18:VAL:HG13	1.85	0.58
1:G:184:THR:CG2	1:G:185:HIS:H	2.11	0.58
2:I:16:ILE:H	2:I:16:ILE:HD12	1.68	0.58
3:J:296:ARG:HB3	3:J:296:ARG:HH11	1.69	0.58
2:I:235:ILE:O	2:I:239:LEU:HB2	2.04	0.58
1:G:187:LEU:HB3	1:G:229:ARG:CZ	2.31	0.58
3:J:57:LYS:HG3	3:J:58:HIS:CE1	2.38	0.58
2:H:235:ILE:O	2:H:239:LEU:HB2	2.03	0.58
1:A:5:VAL:HG21	1:A:44:ILE:CD1	2.32	0.58
1:F:57:LEU:HD23	1:F:146:ARG:HH11	1.67	0.58
2:H:230:MET:HB2	2:H:231:PRO:HD3	1.83	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:G:41:LEU:HD22	1:G:149:LEU:HD22	1.84	0.58
1:F:163:GLY:HA3	1:G:231:LEU:CD1	2.34	0.58
1:F:16:LEU:HD23	1:F:18:VAL:HG13	1.85	0.58
3:E:130:ASN:HD22	3:E:130:ASN:C	2.07	0.58
1:B:110:MET:HE3	1:B:113:LYS:HB2	1.86	0.58
1:A:110:MET:HE3	1:A:113:LYS:HB2	1.85	0.58
1:B:35:ALA:O	1:B:200:MET:HE2	2.04	0.58
1:A:187:LEU:CB	1:A:229:ARG:NH1	2.54	0.58
1:F:74:PHE:H	2:H:164:THR:CG2	2.17	0.58
1:A:184:THR:CG2	1:A:185:HIS:H	2.12	0.58
3:J:71:ALA:HB3	3:J:152:ASP:O	2.03	0.58
2:C:235:ILE:O	2:C:239:LEU:HB2	2.03	0.58
1:G:16:LEU:HD23	1:G:18:VAL:HG13	1.84	0.58
2:C:134:ALA:HB2	2:C:206:ILE:CD1	2.32	0.58
1:G:110:MET:HE3	1:G:113:LYS:HB2	1.86	0.58
2:C:72:LEU:HD23	2:C:144:ILE:HD13	1.85	0.58
1:A:29:LEU:HD22	1:A:181:LEU:HD11	1.85	0.57
1:B:184:THR:CG2	1:B:185:HIS:H	2.11	0.57
3:J:279:THR:O	3:J:281:LYS:HG3	2.04	0.57
1:B:87:VAL:HG13	1:B:135:VAL:HG13	1.85	0.57
2:H:16:ILE:HG13	2:I:68:PHE:HB3	1.84	0.57
3:J:109:MET:HB3	3:J:323:LEU:HD22	1.84	0.57
1:A:41:LEU:HD22	1:A:149:LEU:HD22	1.85	0.57
2:H:91:VAL:O	2:H:141:PRO:HB3	2.04	0.57
3:J:208:ASN:HD21	3:J:210:SER:CB	2.17	0.57
2:C:96:VAL:HG11	2:D:240:SER:HB3	1.85	0.57
2:I:106:LEU:HD13	2:I:133:VAL:HG12	1.84	0.57
3:E:296:ARG:HB3	3:E:296:ARG:HH11	1.69	0.57
3:J:272:LEU:HB2	3:J:274:ASN:ND2	2.19	0.57
1:B:187:LEU:CB	1:B:229:ARG:NH1	2.54	0.57
1:G:215:PHE:CE2	1:G:226:LEU:HB3	2.40	0.57
1:F:105:ARG:O	1:F:109:GLU:HG3	2.03	0.57
1:B:57:LEU:HD23	1:B:146:ARG:HH11	1.70	0.57
3:E:154:PRO:HA	3:E:157:TYR:CE2	2.39	0.57
1:G:187:LEU:CB	1:G:229:ARG:NH1	2.55	0.57
2:H:213:ALA:HB1	2:H:236:LEU:CD1	2.34	0.57
2:C:221:TYR:O	3:E:80:LEU:HD21	2.04	0.57
1:F:103:ARG:O	1:F:107:VAL:HG23	2.04	0.57
2:C:198:SER:HA	2:D:98:PRO:HB3	1.87	0.57
2:I:81:PHE:HB2	2:I:82:PRO:CD	2.32	0.57
2:C:5:PHE:CE1	2:D:170:LEU:HD13	2.38	0.57
2:C:66:VAL:HA	2:C:143:TYR:CE2	2.40	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:E:208:ASN:HD22	3:E:210:SER:N	2.03	0.57
1:F:110:MET:HE3	1:F:113:LYS:HB2	1.86	0.57
3:E:153:ASP:OD1	3:E:154:PRO:HD2	2.05	0.57
2:C:106:LEU:HD13	2:C:133:VAL:HG12	1.86	0.57
2:I:190:ILE:HD13	2:I:247:LEU:HD13	1.86	0.57
3:E:279:THR:O	3:E:281:LYS:HG3	2.05	0.57
2:D:213:ALA:HB1	2:D:236:LEU:CD1	2.35	0.57
3:E:149:ASN:HD21	3:E:151:ASN:H	1.52	0.57
3:J:149:ASN:HD21	3:J:151:ASN:CB	2.18	0.57
1:F:98:VAL:HG11	1:F:102:GLU:HB3	1.87	0.56
1:G:29:LEU:CD2	1:G:183:VAL:HG22	2.35	0.56
3:E:208:ASN:HD21	3:E:210:SER:CB	2.17	0.56
3:E:71:ALA:HB3	3:E:152:ASP:O	2.05	0.56
2:I:213:ALA:O	2:I:217:ILE:HG13	2.05	0.56
3:J:67:ALA:HB1	3:J:217:MET:HE1	1.86	0.56
3:E:188:PHE:CE2	3:E:197:LEU:HB2	2.40	0.56
1:B:215:PHE:CE2	1:B:226:LEU:HB3	2.40	0.56
2:C:131:ILE:HG23	2:C:212:ILE:HD11	1.86	0.56
1:A:57:LEU:HD23	1:A:146:ARG:HH11	1.69	0.56
1:A:215:PHE:CE2	1:A:226:LEU:HB3	2.40	0.56
2:D:213:ALA:O	2:D:217:ILE:HG13	2.04	0.56
1:A:186:ASP:OD2	1:A:188:ILE:HB	2.04	0.56
2:H:104:ILE:O	2:H:108:VAL:HG23	2.06	0.56
3:E:105:ASN:ND2	3:E:106:TRP:HD1	2.02	0.56
3:J:274:ASN:HD22	3:J:274:ASN:H	1.53	0.56
2:C:96:VAL:HG13	2:D:244:PHE:CE1	2.41	0.56
1:F:215:PHE:CE2	1:F:226:LEU:HB3	2.40	0.56
3:E:208:ASN:ND2	3:E:208:ASN:C	2.50	0.56
1:G:57:LEU:H	1:G:62:ILE:HD11	1.71	0.56
3:J:105:ASN:ND2	3:J:106:TRP:HD1	2.02	0.56
3:J:154:PRO:HA	3:J:157:TYR:CE2	2.40	0.56
3:E:274:ASN:H	3:E:274:ASN:HD22	1.52	0.56
2:H:81:PHE:HB2	2:H:82:PRO:CD	2.31	0.56
1:A:163:GLY:CA	1:B:231:LEU:HD13	2.35	0.56
1:G:22:MET:HA	1:G:208:LYS:NZ	2.20	0.56
3:J:208:ASN:HD22	3:J:210:SER:N	2.03	0.56
3:J:145:PHE:HA	3:J:232:TYR:O	2.06	0.56
1:G:25:ASP:HB2	1:G:195:ASP:OD2	2.05	0.56
1:F:233:LEU:HD11	1:G:240:ASP:HB2	1.88	0.56
2:H:50:VAL:HG12	2:H:213:ALA:N	2.20	0.56
2:H:211:MET:HE3	2:H:216:LEU:HA	1.87	0.56
1:B:186:ASP:OD2	1:B:188:ILE:HB	2.06	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:43:LEU:HD21	1:B:50:PRO:HB3	1.88	0.56
2:H:66:VAL:HA	2:H:143:TYR:CE2	2.41	0.56
1:B:25:ASP:HB2	1:B:195:ASP:OD2	2.05	0.56
2:C:204:VAL:HG23	2:C:205:VAL:N	2.21	0.55
1:A:22:MET:HA	1:A:208:LYS:NZ	2.21	0.55
3:E:272:LEU:HB2	3:E:274:ASN:ND2	2.21	0.55
3:J:204:ARG:HE	3:J:204:ARG:HA	1.71	0.55
2:I:106:LEU:HD22	2:I:133:VAL:CG1	2.36	0.55
3:J:332:VAL:O	3:J:336:LYS:HB3	2.07	0.55
2:C:104:ILE:O	2:C:108:VAL:HG23	2.07	0.55
2:D:204:VAL:HG23	2:D:205:VAL:N	2.20	0.55
3:J:43:LEU:HD11	3:J:110:PHE:HZ	1.72	0.55
1:F:186:ASP:OD2	1:F:188:ILE:HB	2.06	0.55
1:B:29:LEU:HB3	1:B:198:ALA:HB3	1.89	0.55
2:C:170:LEU:HD13	2:D:5:PHE:CD1	2.42	0.55
3:E:37:VAL:HG22	3:E:86:VAL:HB	1.89	0.55
2:H:209:TYR:C	2:H:211:MET:N	2.60	0.55
3:J:130:ASN:N	3:J:133:ASN:OD1	2.40	0.55
1:G:186:ASP:OD2	1:G:188:ILE:HB	2.07	0.55
2:H:138:VAL:CG1	2:H:195:ARG:NH2	2.70	0.55
1:G:54:GLU:HB3	1:G:63:THR:OG1	2.07	0.55
2:H:98:PRO:HG2	2:H:101:VAL:HG23	1.89	0.55
1:A:95:LEU:O	1:A:103:ARG:HD3	2.07	0.55
2:I:94:PRO:HB3	2:I:137:PHE:CE2	2.42	0.55
1:F:29:LEU:HD22	1:F:181:LEU:HD11	1.88	0.55
1:G:66:PRO:HB2	1:G:68:GLU:CG	2.32	0.55
3:J:102:GLU:O	3:J:291:LYS:CD	2.55	0.55
3:J:36:LYS:O	3:J:85:ASP:N	2.29	0.55
3:J:190:GLU:HA	3:J:194:SER:O	2.06	0.55
3:J:119:TYR:CD1	3:J:232:TYR:HE1	2.25	0.55
2:D:98:PRO:HG2	2:D:101:VAL:HG23	1.89	0.55
1:A:83:PRO:HG2	2:C:180:LEU:HD21	1.89	0.55
2:C:138:VAL:CG1	2:C:195:ARG:NH2	2.70	0.55
2:H:98:PRO:HG2	2:H:101:VAL:CG2	2.37	0.55
2:C:98:PRO:HG2	2:C:101:VAL:CG2	2.37	0.54
3:E:190:GLU:HA	3:E:194:SER:O	2.06	0.54
2:I:204:VAL:HG23	2:I:205:VAL:N	2.22	0.54
3:J:34:LYS:HD3	3:J:64:GLN:OE1	2.07	0.54
1:A:87:VAL:HG13	1:A:135:VAL:HG13	1.89	0.54
1:F:187:LEU:CB	1:F:229:ARG:NH1	2.54	0.54
2:C:163:ARG:HH12	2:C:169:PRO:HG3	1.73	0.54
1:A:192:MET:HE2	1:B:238:ILE:HD12	1.88	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:22:MET:HG3	1:B:23:GLY:N	2.22	0.54
2:D:106:LEU:HD13	2:D:133:VAL:HG12	1.88	0.54
2:C:33:PHE:HD1	2:C:33:PHE:N	2.05	0.54
2:C:98:PRO:HG2	2:C:101:VAL:HG23	1.88	0.54
2:D:126:ASP:O	2:D:210:PRO:HG3	2.07	0.54
1:F:66:PRO:HB3	2:I:2:ARG:NH2	2.21	0.54
3:E:57:LYS:C	3:E:59:PRO:HD3	2.28	0.54
3:J:119:TYR:N	3:J:119:TYR:CD2	2.76	0.54
1:G:77:GLN:O	1:G:78:ASP:HB2	2.08	0.54
3:E:290:PRO:HG2	3:E:293:ALA:HB2	1.90	0.54
2:D:33:PHE:N	2:D:33:PHE:CD1	2.75	0.54
1:G:143:ILE:O	1:G:143:ILE:HG22	2.08	0.54
2:H:213:ALA:HB3	2:H:214:PRO:HD3	1.90	0.54
3:J:178:GLU:HA	3:J:182:LYS:HD2	1.88	0.54
2:C:209:TYR:C	2:C:211:MET:N	2.60	0.54
1:G:62:ILE:C	1:G:64:PRO:HD2	2.28	0.54
1:B:95:LEU:O	1:B:103:ARG:HD3	2.07	0.54
2:C:16:ILE:HG13	2:D:68:PHE:HB3	1.90	0.54
1:G:95:LEU:O	1:G:103:ARG:HD3	2.07	0.54
3:J:188:PHE:CE2	3:J:197:LEU:HB2	2.42	0.54
3:E:109:MET:HB3	3:E:323:LEU:HD22	1.88	0.54
1:A:143:ILE:O	1:A:143:ILE:HG22	2.08	0.54
3:J:290:PRO:HG2	3:J:293:ALA:HB2	1.89	0.54
1:B:215:PHE:CZ	1:B:229:ARG:NE	2.75	0.54
3:E:130:ASN:N	3:E:133:ASN:OD1	2.39	0.54
1:G:57:LEU:O	1:G:58:ASN:HB2	2.08	0.54
2:D:138:VAL:CG1	2:D:195:ARG:NH2	2.70	0.54
1:F:22:MET:HG3	1:F:23:GLY:N	2.23	0.54
3:J:272:LEU:HB2	3:J:274:ASN:HD21	1.73	0.54
3:J:274:ASN:HD22	3:J:274:ASN:N	2.06	0.54
3:E:274:ASN:N	3:E:274:ASN:HD22	2.04	0.54
2:D:33:PHE:N	2:D:33:PHE:HD1	2.05	0.54
2:I:33:PHE:HD1	2:I:33:PHE:N	2.06	0.54
1:A:215:PHE:CZ	1:A:229:ARG:NE	2.75	0.54
2:D:98:PRO:HG2	2:D:101:VAL:CG2	2.38	0.54
1:F:139:ARG:HD2	2:H:165:LEU:HD11	1.89	0.54
1:B:41:LEU:HD22	1:B:149:LEU:HD22	1.89	0.54
3:E:155:CYS:HB2	3:E:236:TYR:CE2	2.43	0.54
1:B:226:LEU:O	1:B:229:ARG:HG2	2.08	0.54
3:E:332:VAL:HG11	3:E:335:LEU:HD12	1.88	0.54
1:A:187:LEU:HD13	1:A:229:ARG:NE	2.23	0.54
2:H:167:SER:HA	2:H:171:ARG:HD2	1.90	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:221:TYR:CZ	3:E:223:HIS:ND1	2.76	0.54
2:H:33:PHE:N	2:H:33:PHE:HD1	2.06	0.54
2:I:98:PRO:HG2	2:I:101:VAL:CG2	2.39	0.53
1:G:47:ILE:CD1	2:I:160:HIS:HB3	2.36	0.53
2:C:33:PHE:CD1	2:C:33:PHE:N	2.75	0.53
2:I:33:PHE:CD1	2:I:33:PHE:N	2.76	0.53
2:C:140:VAL:N	2:C:141:PRO:HD2	2.23	0.53
1:G:215:PHE:CZ	1:G:229:ARG:NE	2.76	0.53
2:H:131:ILE:CG2	2:H:212:ILE:HD11	2.37	0.53
3:E:178:GLU:HA	3:E:182:LYS:HD2	1.88	0.53
1:B:37:LYS:HD3	5:B:802:PO4:O3	2.08	0.53
3:E:117:LEU:HD13	3:E:234:PHE:CE1	2.43	0.53
3:E:140:ARG:HB2	3:E:143:VAL:HG23	1.90	0.53
1:F:215:PHE:CZ	1:F:229:ARG:NE	2.76	0.53
3:E:58:HIS:N	3:E:59:PRO:HD3	2.24	0.53
3:E:60:ASN:HD22	3:E:60:ASN:H	1.56	0.53
1:A:57:LEU:HB3	1:A:62:ILE:HD12	1.90	0.53
2:I:33:PHE:H	2:I:33:PHE:HD1	1.57	0.53
2:H:33:PHE:N	2:H:33:PHE:CD1	2.76	0.53
3:J:223:HIS:CD2	3:J:224:LEU:N	2.77	0.53
1:F:152:GLU:N	1:F:153:PRO:CD	2.72	0.53
1:F:187:LEU:HD13	1:F:229:ARG:NE	2.22	0.53
2:H:204:VAL:HG23	2:H:205:VAL:N	2.23	0.53
3:J:57:LYS:C	3:J:59:PRO:HD3	2.28	0.53
1:G:22:MET:HG3	1:G:23:GLY:N	2.22	0.53
1:B:77:GLN:O	1:B:78:ASP:HB2	2.08	0.53
1:A:226:LEU:O	1:A:229:ARG:HG2	2.08	0.53
1:F:215:PHE:HE2	1:F:226:LEU:HB3	1.74	0.53
1:A:162:LYS:O	1:A:166:MET:HG3	2.08	0.53
1:G:87:VAL:HG13	1:G:135:VAL:HG13	1.90	0.53
1:G:57:LEU:HB3	1:G:62:ILE:HD11	1.89	0.53
1:B:118:HIS:NE2	1:B:119:LEU:HG	2.24	0.53
1:A:57:LEU:HD21	1:A:146:ARG:HD3	1.89	0.53
3:J:201:SER:O	3:J:204:ARG:N	2.41	0.53
1:A:77:GLN:O	1:A:78:ASP:HB2	2.09	0.53
1:G:162:LYS:O	1:G:166:MET:HG3	2.08	0.53
1:F:29:LEU:HB3	1:F:198:ALA:HB3	1.91	0.53
1:A:103:ARG:O	1:A:107:VAL:HG23	2.08	0.53
1:B:57:LEU:HB3	1:B:62:ILE:HD12	1.89	0.53
3:J:68:ALA:HB3	3:J:73:THR:OG1	2.08	0.53
2:H:162:ALA:O	2:H:167:SER:HB2	2.09	0.53
1:B:143:ILE:HG22	1:B:143:ILE:O	2.08	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:H:106:LEU:HD13	2:H:133:VAL:HG12	1.91	0.53
1:G:187:LEU:HD13	1:G:229:ARG:NE	2.23	0.53
1:F:162:LYS:O	1:F:166:MET:HG3	2.09	0.53
1:F:41:LEU:HD13	1:F:149:LEU:HB3	1.90	0.53
1:G:2:PHE:CZ	1:G:57:LEU:HD11	2.44	0.53
2:I:221:TYR:CZ	3:J:223:HIS:ND1	2.77	0.53
1:F:38:SER:O	1:F:42:GLU:HG3	2.09	0.53
1:F:77:GLN:O	1:F:78:ASP:HB2	2.08	0.53
2:D:104:ILE:O	2:D:108:VAL:HG23	2.09	0.53
2:I:104:ILE:O	2:I:108:VAL:HG23	2.07	0.53
1:A:231:LEU:CD1	1:B:163:GLY:HA3	2.38	0.53
1:G:47:ILE:HG22	1:G:47:ILE:O	2.08	0.53
1:G:95:LEU:HB3	1:G:103:ARG:HG2	1.91	0.53
1:G:16:LEU:CD2	1:G:18:VAL:HG13	2.39	0.53
2:I:143:TYR:OH	2:I:185:ILE:HG23	2.09	0.53
3:E:67:ALA:O	3:E:68:ALA:HB2	2.08	0.53
3:E:218:GLU:OE1	4:E:701:WO4:O4	2.27	0.53
1:B:152:GLU:N	1:B:153:PRO:CD	2.72	0.53
1:F:25:ASP:HB2	1:F:195:ASP:OD2	2.09	0.53
1:G:226:LEU:O	1:G:229:ARG:HG2	2.08	0.53
2:D:108:VAL:HG12	2:D:108:VAL:O	2.08	0.53
1:F:226:LEU:O	1:F:229:ARG:HG2	2.08	0.53
1:A:98:VAL:HB	1:A:103:ARG:HG3	1.91	0.53
2:C:167:SER:HA	2:C:171:ARG:HD2	1.91	0.53
1:A:187:LEU:CD1	1:A:228:ALA:HB3	2.39	0.52
1:G:215:PHE:HE2	1:G:226:LEU:HB3	1.74	0.52
2:H:134:ALA:HB2	2:H:206:ILE:CD1	2.35	0.52
1:G:118:HIS:NE2	1:G:119:LEU:HG	2.23	0.52
1:G:38:SER:O	1:G:42:GLU:HG3	2.09	0.52
1:G:43:LEU:HD21	1:G:50:PRO:HB3	1.91	0.52
3:J:37:VAL:HG22	3:J:86:VAL:HB	1.91	0.52
1:G:5:VAL:HG22	1:G:55:VAL:HG13	1.91	0.52
2:H:217:ILE:HB	2:I:100:THR:HG21	1.90	0.52
2:I:98:PRO:HG2	2:I:101:VAL:HG23	1.90	0.52
3:J:149:ASN:HD22	3:J:151:ASN:N	2.07	0.52
2:I:138:VAL:CG1	2:I:195:ARG:NH2	2.72	0.52
2:D:33:PHE:H	2:D:33:PHE:HD1	1.56	0.52
2:D:72:LEU:HD23	2:D:144:ILE:HD13	1.91	0.52
1:B:187:LEU:CD1	1:B:228:ALA:HB3	2.38	0.52
2:I:108:VAL:O	2:I:114:GLY:HA3	2.09	0.52
1:A:29:LEU:CD2	1:A:183:VAL:HG22	2.39	0.52
2:D:107:LEU:CD2	2:D:111:GLY:HA3	2.40	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:E:119:TYR:N	3:E:119:TYR:CD2	2.76	0.52
2:C:33:PHE:H	2:C:33:PHE:HD1	1.56	0.52
2:C:91:VAL:O	2:C:141:PRO:HB3	2.09	0.52
2:I:162:ALA:O	2:I:167:SER:HB2	2.09	0.52
2:D:162:ALA:O	2:D:167:SER:HB2	2.08	0.52
3:E:130:ASN:ND2	3:E:133:ASN:H	2.07	0.52
1:A:67:PRO:HG2	2:C:163:ARG:HB3	1.92	0.52
3:J:332:VAL:O	3:J:336:LYS:N	2.42	0.52
1:F:118:HIS:NE2	1:F:119:LEU:HG	2.24	0.52
3:J:113:ASN:HB3	3:J:283:ILE:HG21	1.91	0.52
1:A:29:LEU:HB3	1:A:198:ALA:HB3	1.90	0.52
1:F:235:VAL:HG22	1:G:192:MET:HE3	1.92	0.52
1:A:22:MET:HG3	1:A:23:GLY:N	2.23	0.52
3:E:119:TYR:HB3	3:E:232:TYR:CD1	2.45	0.52
2:I:140:VAL:N	2:I:141:PRO:HD2	2.24	0.52
1:G:187:LEU:CD1	1:G:228:ALA:HB3	2.39	0.52
2:C:50:VAL:HG12	2:C:213:ALA:N	2.24	0.52
2:I:131:ILE:HG21	2:I:212:ILE:CD1	2.40	0.52
3:E:149:ASN:HD21	3:E:151:ASN:CB	2.19	0.52
1:A:95:LEU:HB3	1:A:103:ARG:HG2	1.91	0.52
2:D:167:SER:HA	2:D:171:ARG:HD2	1.91	0.52
3:E:149:ASN:HD22	3:E:151:ASN:N	2.06	0.52
1:B:98:VAL:HB	1:B:103:ARG:HG3	1.91	0.52
3:E:68:ALA:HB3	3:E:73:THR:OG1	2.09	0.52
2:H:143:TYR:OH	2:H:185:ILE:HG23	2.09	0.52
2:H:60:ILE:O	2:H:64:ILE:HG13	2.10	0.52
1:F:143:ILE:HG22	1:F:143:ILE:O	2.08	0.52
2:I:65:ALA:O	2:I:69:GLY:N	2.30	0.52
1:F:235:VAL:HG21	1:G:188:ILE:HG23	1.91	0.52
1:A:118:HIS:NE2	1:A:119:LEU:HG	2.25	0.52
1:G:98:VAL:HB	1:G:103:ARG:HG3	1.91	0.52
1:B:16:LEU:CD2	1:B:18:VAL:HG13	2.40	0.52
3:E:188:PHE:CD2	3:E:197:LEU:HB2	2.45	0.52
1:B:143:ILE:HD11	2:D:165:LEU:HD22	1.92	0.52
2:I:222:LEU:HD22	3:J:220:GLU:HG2	1.90	0.52
3:J:140:ARG:HB2	3:J:143:VAL:HG23	1.91	0.52
1:A:215:PHE:HE2	1:A:226:LEU:HB3	1.75	0.52
2:C:28:VAL:CG1	2:C:238:LEU:HD21	2.36	0.52
1:B:47:ILE:CG2	1:B:47:ILE:O	2.57	0.52
1:B:80:ALA:HB3	2:D:161:VAL:HG21	1.92	0.52
1:A:16:LEU:CD2	1:A:18:VAL:HG13	2.40	0.52
3:J:67:ALA:HB1	3:J:217:MET:CE	2.40	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:E:272:LEU:HB2	3:E:274:ASN:HD21	1.73	0.52
1:G:152:GLU:N	1:G:153:PRO:CD	2.73	0.52
2:D:250:ILE:HG22	2:D:250:ILE:O	2.10	0.52
1:G:103:ARG:O	1:G:107:VAL:HG23	2.09	0.52
2:H:140:VAL:N	2:H:141:PRO:HD2	2.25	0.52
1:F:47:ILE:CG2	1:F:47:ILE:O	2.57	0.52
3:J:155:CYS:HB2	3:J:236:TYR:CE2	2.45	0.52
2:C:100:THR:HG21	2:D:217:ILE:HB	1.92	0.51
2:I:131:ILE:HG21	2:I:212:ILE:HD12	1.92	0.51
1:A:66:PRO:HG3	2:D:2:ARG:HH12	1.76	0.51
2:I:150:GLY:HA2	2:I:184:HIS:CG	2.46	0.51
1:F:16:LEU:CD2	1:F:18:VAL:HG13	2.40	0.51
3:J:223:HIS:CD2	3:J:224:LEU:HD23	2.45	0.51
2:C:162:ALA:O	2:C:167:SER:HB2	2.10	0.51
3:E:314:ILE:HG22	3:E:315:LEU:N	2.24	0.51
1:B:215:PHE:HE2	1:B:226:LEU:HB3	1.74	0.51
1:B:162:LYS:O	1:B:166:MET:HG3	2.09	0.51
3:J:58:HIS:N	3:J:59:PRO:HD3	2.24	0.51
1:B:172:VAL:O	1:B:176:PHE:HD1	1.93	0.51
2:I:250:ILE:O	2:I:250:ILE:HG22	2.11	0.51
3:J:199:MET:HB2	3:J:271:VAL:O	2.09	0.51
1:B:187:LEU:HD13	1:B:229:ARG:NE	2.23	0.51
1:F:229:ARG:NH1	1:G:239:LEU:HD13	2.25	0.51
1:A:166:MET:HE1	1:A:189:GLU:CA	2.16	0.51
1:F:98:VAL:HG12	1:F:102:GLU:HB3	1.88	0.51
1:F:57:LEU:HB3	1:F:62:ILE:HD12	1.92	0.51
1:G:62:ILE:HG23	1:G:65:LEU:HD12	1.92	0.51
3:E:45:GLU:HB2	3:E:46:PRO:CD	2.35	0.51
1:B:103:ARG:O	1:B:107:VAL:HG23	2.11	0.51
1:B:95:LEU:HB3	1:B:103:ARG:HG2	1.92	0.51
2:H:163:ARG:HG3	2:H:172:VAL:HG21	1.92	0.51
3:E:108:ILE:HD13	3:E:339:VAL:HG21	1.93	0.51
2:I:167:SER:HA	2:I:171:ARG:HD2	1.90	0.51
1:A:38:SER:O	1:A:42:GLU:HG3	2.10	0.51
1:A:164:VAL:HG23	1:A:165:LEU:N	2.26	0.51
3:J:251:PRO:HD2	3:J:254:ILE:HD11	1.92	0.51
3:J:37:VAL:HG13	3:J:86:VAL:HB	1.92	0.51
3:J:147:PHE:HE2	3:J:212:ILE:HD13	1.75	0.51
1:B:38:SER:O	1:B:42:GLU:HG3	2.10	0.51
1:F:87:VAL:HG13	1:F:135:VAL:HG13	1.92	0.51
3:E:110:PHE:CE2	3:E:287:ILE:HB	2.46	0.51
2:I:60:ILE:O	2:I:64:ILE:HG13	2.10	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:50:VAL:CG1	2:C:213:ALA:N	2.74	0.51
2:H:81:PHE:CB	2:H:82:PRO:HD2	2.36	0.51
2:H:163:ARG:HH12	2:H:169:PRO:HG3	1.74	0.51
1:B:52:ARG:HG2	1:B:53:GLY:N	2.26	0.51
2:H:33:PHE:HD1	2:H:33:PHE:H	1.57	0.51
1:F:43:LEU:HD21	1:F:50:PRO:HB3	1.93	0.51
2:D:143:TYR:OH	2:D:185:ILE:HG23	2.10	0.51
1:B:41:LEU:HD13	1:B:149:LEU:HB3	1.93	0.51
1:A:238:ILE:HD12	1:B:192:MET:HE2	1.93	0.51
2:C:125:VAL:HG13	2:C:206:ILE:O	2.11	0.51
1:A:47:ILE:O	1:A:47:ILE:CG2	2.59	0.51
3:J:106:TRP:CE3	3:J:332:VAL:HG21	2.45	0.51
3:J:52:ARG:HG3	3:J:53:ALA:N	2.26	0.51
1:F:80:ALA:HB3	2:H:161:VAL:CG2	2.25	0.51
3:J:218:GLU:OE1	4:J:702:WO4:O4	2.29	0.51
2:H:50:VAL:CG1	2:H:213:ALA:N	2.73	0.51
3:E:251:PRO:HD2	3:E:254:ILE:HD11	1.92	0.51
3:J:296:ARG:CB	3:J:296:ARG:HH11	2.23	0.51
3:E:67:ALA:HB1	3:E:217:MET:HE1	1.92	0.51
3:J:114:GLN:HG3	3:J:257:SER:HB3	1.93	0.51
3:J:222:ILE:O	3:J:226:GLU:HG3	2.11	0.51
1:G:66:PRO:C	1:G:68:GLU:H	2.15	0.50
3:E:58:HIS:O	3:E:60:ASN:N	2.44	0.50
1:G:110:MET:HG3	1:G:142:VAL:HG22	1.93	0.50
2:C:222:LEU:HD23	3:E:80:LEU:HD11	1.93	0.50
3:E:223:HIS:CD2	3:E:224:LEU:N	2.78	0.50
3:E:223:HIS:CD2	3:E:224:LEU:HD23	2.46	0.50
2:H:45:PRO:O	2:H:49:LYS:HG3	2.11	0.50
2:C:60:ILE:O	2:C:64:ILE:HG13	2.11	0.50
1:B:96:ARG:HH11	1:B:103:ARG:HH12	1.60	0.50
3:E:108:ILE:HA	3:E:327:ARG:O	2.11	0.50
1:F:147:LEU:HD12	1:F:148:LEU:H	1.75	0.50
2:C:17:LEU:O	2:C:21:LEU:HB2	2.11	0.50
1:A:68:GLU:HA	2:C:166:GLY:HA2	1.93	0.50
1:B:83:PRO:HA	1:B:124:PRO:CG	2.38	0.50
2:D:163:ARG:HG3	2:D:172:VAL:HG21	1.93	0.50
3:E:205:ILE:HG22	3:E:207:ILE:HD11	1.92	0.50
3:E:296:ARG:CB	3:E:296:ARG:HH11	2.24	0.50
2:C:16:ILE:N	2:C:16:ILE:HD12	2.27	0.50
1:G:95:LEU:HD11	1:G:142:VAL:CG1	2.40	0.50
2:C:143:TYR:OH	2:C:185:ILE:HG23	2.12	0.50
2:D:140:VAL:N	2:D:141:PRO:HD2	2.26	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:66:PRO:O	1:F:70:ARG:HG3	2.12	0.50
1:A:66:PRO:HG2	2:D:2:ARG:NH2	2.26	0.50
1:F:172:VAL:O	1:F:176:PHE:HD1	1.94	0.50
1:F:110:MET:HG3	1:F:142:VAL:HG22	1.93	0.50
2:D:91:VAL:O	2:D:141:PRO:HB3	2.11	0.50
1:G:147:LEU:HD12	1:G:148:LEU:H	1.76	0.50
2:H:250:ILE:HG22	2:H:250:ILE:O	2.11	0.50
1:A:152:GLU:N	1:A:153:PRO:CD	2.75	0.50
2:H:17:LEU:O	2:H:21:LEU:HB2	2.11	0.50
2:H:217:ILE:HD12	2:I:101:VAL:HG22	1.94	0.50
3:J:58:HIS:O	3:J:60:ASN:N	2.44	0.50
2:H:125:VAL:HB	3:J:229:GLU:HG2	1.94	0.50
2:D:163:ARG:HH11	2:D:163:ARG:HG2	1.77	0.50
1:G:96:ARG:HA	1:G:103:ARG:NH2	2.27	0.50
3:J:67:ALA:O	3:J:68:ALA:HB2	2.11	0.50
3:E:116:VAL:CG1	3:E:237:LYS:HB2	2.41	0.50
3:E:222:ILE:O	3:E:226:GLU:HG3	2.12	0.50
1:F:166:MET:HE1	1:F:189:GLU:CA	2.14	0.50
1:F:57:LEU:HD21	1:F:146:ARG:HD3	1.93	0.50
1:F:29:LEU:CD2	1:F:183:VAL:HG22	2.40	0.50
1:B:29:LEU:HD22	1:B:181:LEU:HD11	1.92	0.50
1:A:147:LEU:HD12	1:A:148:LEU:H	1.77	0.50
2:C:250:ILE:HG22	2:C:250:ILE:O	2.12	0.50
2:I:163:ARG:HG2	2:I:163:ARG:HH11	1.77	0.50
2:I:163:ARG:HG3	2:I:172:VAL:HG21	1.93	0.50
2:H:163:ARG:HG2	2:H:163:ARG:HH11	1.76	0.50
2:C:222:LEU:CD2	3:E:80:LEU:HD11	2.42	0.50
3:J:43:LEU:CD1	3:J:88:ALA:HB1	2.41	0.50
1:G:29:LEU:HB3	1:G:198:ALA:HB3	1.94	0.50
2:H:200:PHE:CE1	2:H:204:VAL:CG1	2.95	0.50
1:F:8:GLU:HA	1:F:16:LEU:O	2.12	0.50
2:D:221:TYR:CZ	3:E:223:HIS:CE1	3.00	0.50
2:I:45:PRO:O	2:I:49:LYS:HG3	2.12	0.50
1:F:187:LEU:CD1	1:F:228:ALA:HB3	2.42	0.49
1:A:74:PHE:CB	2:C:164:THR:HG21	2.42	0.49
1:A:74:PHE:H	2:C:164:THR:HG21	1.76	0.49
2:H:96:VAL:HG12	2:I:240:SER:CB	2.41	0.49
2:D:150:GLY:HA2	2:D:184:HIS:CG	2.47	0.49
1:B:110:MET:HG3	1:B:142:VAL:HG22	1.94	0.49
2:D:16:ILE:N	2:D:16:ILE:HD12	2.26	0.49
2:H:13:SER:HA	2:H:16:ILE:CD1	2.42	0.49
2:D:60:ILE:O	2:D:64:ILE:HG13	2.11	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:11:LEU:O	2:C:15:ILE:HG12	2.11	0.49
2:D:45:PRO:O	2:D:49:LYS:HG3	2.12	0.49
1:B:91:ILE:HA	1:B:139:ARG:HB2	1.94	0.49
2:C:222:LEU:HD23	3:E:80:LEU:CD1	2.42	0.49
1:A:57:LEU:CD2	1:A:146:ARG:HD3	2.42	0.49
3:E:40:ALA:HB1	4:E:701:WO4:O3	2.12	0.49
1:F:239:LEU:HD13	1:G:229:ARG:NH1	2.27	0.49
3:J:314:ILE:HG22	3:J:315:LEU:N	2.27	0.49
1:A:52:ARG:HG2	1:A:53:GLY:N	2.27	0.49
1:G:96:ARG:HH11	1:G:103:ARG:HH12	1.60	0.49
3:J:217:MET:HE2	3:J:219:MET:HB2	1.94	0.49
2:C:45:PRO:O	2:C:49:LYS:HG3	2.12	0.49
1:F:229:ARG:HH11	1:G:239:LEU:HD13	1.77	0.49
1:G:44:ILE:HB	1:G:149:LEU:HD11	1.93	0.49
1:G:5:VAL:HG13	1:G:55:VAL:HG22	1.93	0.49
1:F:68:GLU:OE2	2:I:2:ARG:NH2	2.45	0.49
2:I:213:ALA:HB1	2:I:236:LEU:CD1	2.39	0.49
1:G:172:VAL:O	1:G:176:PHE:HD1	1.95	0.49
2:I:13:SER:HA	2:I:16:ILE:CD1	2.42	0.49
1:B:147:LEU:HD12	1:B:148:LEU:H	1.77	0.49
3:E:52:ARG:HG3	3:E:53:ALA:N	2.26	0.49
2:H:11:LEU:O	2:H:15:ILE:HG12	2.12	0.49
1:F:239:LEU:HD11	1:G:191:ALA:CB	2.42	0.49
3:J:45:GLU:HB2	3:J:46:PRO:CD	2.36	0.49
1:B:164:VAL:HG23	1:B:165:LEU:N	2.27	0.49
1:G:47:ILE:CG2	1:G:47:ILE:O	2.61	0.49
2:H:150:GLY:HA2	2:H:184:HIS:CG	2.47	0.49
2:C:217:ILE:CG2	2:D:104:ILE:HD12	2.43	0.49
2:H:108:VAL:HG12	2:H:108:VAL:O	2.12	0.49
2:D:16:ILE:H	2:D:16:ILE:CD1	2.24	0.49
2:H:23:PRO:HA	2:I:109:VAL:HG21	1.94	0.49
2:C:13:SER:HA	2:C:16:ILE:CD1	2.43	0.49
3:J:296:ARG:O	3:J:300:VAL:HG23	2.12	0.49
3:J:130:ASN:HD21	3:J:133:ASN:H	1.61	0.49
3:J:136:GLU:O	3:J:139:LYS:HB2	2.12	0.49
3:J:35:LEU:HA	3:J:85:ASP:OD2	2.13	0.49
2:D:163:ARG:HH12	2:D:169:PRO:HG3	1.75	0.49
1:A:110:MET:HG3	1:A:142:VAL:HG22	1.95	0.49
1:G:8:GLU:HA	1:G:16:LEU:O	2.12	0.49
3:J:188:PHE:CD2	3:J:197:LEU:HB2	2.47	0.49
3:E:113:ASN:HB2	3:E:285:TYR:HE2	1.78	0.49
2:C:120:SER:C	2:C:122:LEU:H	2.15	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:206:VAL:O	1:B:207:GLU:HG3	2.13	0.49
3:E:136:GLU:O	3:E:139:LYS:HB2	2.13	0.49
2:D:209:TYR:C	2:D:211:MET:N	2.66	0.49
1:B:29:LEU:CD2	1:B:183:VAL:HG22	2.41	0.49
2:C:163:ARG:HH11	2:C:163:ARG:HG2	1.78	0.49
2:C:163:ARG:HG3	2:C:172:VAL:HG21	1.94	0.49
2:H:101:VAL:HG13	2:I:233:ALA:HB1	1.95	0.49
3:E:265:TYR:O	3:E:280:GLY:HA3	2.13	0.49
1:F:74:PHE:HB3	2:H:164:THR:CG2	2.42	0.48
1:G:164:VAL:HG23	1:G:165:LEU:N	2.28	0.48
2:I:163:ARG:HH12	2:I:169:PRO:HG3	1.75	0.48
1:A:96:ARG:HH11	1:A:103:ARG:HH12	1.60	0.48
1:A:96:ARG:HA	1:A:103:ARG:NH2	2.28	0.48
2:D:13:SER:HA	2:D:16:ILE:CD1	2.43	0.48
3:J:200:PRO:O	3:J:273:ALA:HB2	2.13	0.48
3:J:105:ASN:HD21	3:J:106:TRP:HD1	1.61	0.48
1:F:10:ARG:N	1:F:51:ASP:OD2	2.46	0.48
1:F:66:PRO:CB	2:I:2:ARG:NH1	2.67	0.48
2:H:193:TRP:CH2	2:H:243:VAL:HG11	2.48	0.48
3:E:147:PHE:HE2	3:E:212:ILE:HD13	1.77	0.48
3:J:149:ASN:HD22	3:J:152:ASP:H	1.61	0.48
2:C:150:GLY:HA2	2:C:184:HIS:CG	2.48	0.48
2:D:106:LEU:HD22	2:D:133:VAL:CG1	2.43	0.48
2:H:120:SER:C	2:H:122:LEU:H	2.15	0.48
2:I:108:VAL:HG12	2:I:108:VAL:O	2.11	0.48
1:A:66:PRO:CB	2:D:2:ARG:HH12	2.25	0.48
3:E:199:MET:HB2	3:E:271:VAL:O	2.14	0.48
2:H:16:ILE:HD12	2:H:16:ILE:N	2.28	0.48
3:E:273:ALA:C	3:E:275:GLY:N	2.67	0.48
3:E:36:LYS:HG2	3:E:64:GLN:HE21	1.78	0.48
3:E:39:HIS:ND1	3:E:40:ALA:O	2.44	0.48
1:A:102:GLU:O	1:A:106:ARG:HG3	2.14	0.48
3:J:185:ASN:ND2	3:J:206:GLU:N	2.52	0.48
1:A:66:PRO:HB2	1:A:68:GLU:CG	2.35	0.48
2:C:96:VAL:HG12	2:D:240:SER:CB	2.42	0.48
3:J:273:ALA:C	3:J:275:GLY:N	2.66	0.48
1:B:8:GLU:HA	1:B:16:LEU:O	2.13	0.48
3:E:43:LEU:HD11	3:E:110:PHE:HZ	1.78	0.48
1:F:52:ARG:HG2	1:F:53:GLY:N	2.27	0.48
1:A:233:LEU:O	1:A:237:LYS:HG3	2.13	0.48
2:I:131:ILE:HD11	2:I:210:PRO:O	2.13	0.48
1:F:98:VAL:C	1:F:99:GLU:HG2	2.33	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:172:VAL:O	1:A:176:PHE:HD1	1.95	0.48
3:E:113:ASN:HB3	3:E:283:ILE:HG21	1.96	0.48
3:E:256:LEU:HA	3:E:265:TYR:CE2	2.49	0.48
1:A:43:LEU:HD21	1:A:50:PRO:HB3	1.95	0.48
1:G:206:VAL:O	1:G:207:GLU:HG3	2.13	0.48
1:A:206:VAL:O	1:A:207:GLU:HG3	2.12	0.48
2:C:213:ALA:HB1	2:C:236:LEU:CD1	2.44	0.48
1:G:41:LEU:HD13	1:G:149:LEU:HB3	1.94	0.48
1:A:41:LEU:HD13	1:A:149:LEU:HB3	1.94	0.48
1:B:8:GLU:OE1	1:B:52:ARG:HD3	2.14	0.48
2:I:171:ARG:O	2:I:175:THR:OG1	2.32	0.48
2:C:108:VAL:HG12	2:C:108:VAL:O	2.13	0.48
2:I:131:ILE:CG2	2:I:212:ILE:HD12	2.44	0.48
3:E:105:ASN:HD21	3:E:106:TRP:HD1	1.60	0.48
3:J:119:TYR:N	3:J:119:TYR:HD2	2.11	0.48
1:B:215:PHE:HZ	1:B:229:ARG:NE	2.12	0.48
1:A:44:ILE:HB	1:A:149:LEU:HD11	1.96	0.48
1:F:164:VAL:HG23	1:F:165:LEU:N	2.28	0.48
1:B:96:ARG:HA	1:B:103:ARG:NH2	2.27	0.48
2:I:107:LEU:CD2	2:I:111:GLY:HA3	2.43	0.48
2:H:105:ALA:CB	2:I:27:THR:HG21	2.43	0.48
1:A:8:GLU:HA	1:A:16:LEU:O	2.14	0.48
1:F:6:ARG:HA	1:F:18:VAL:O	2.14	0.48
2:I:17:LEU:O	2:I:21:LEU:HB2	2.14	0.48
2:D:131:ILE:HG21	2:D:212:ILE:CD1	2.44	0.48
3:J:178:GLU:OE2	3:J:182:LYS:HE3	2.13	0.48
2:H:96:VAL:HG13	2:I:244:PHE:CE1	2.49	0.48
3:E:78:THR:HG22	3:E:103:PHE:CD2	2.49	0.48
1:B:166:MET:HE1	1:B:189:GLU:CA	2.15	0.48
2:C:164:THR:C	2:C:166:GLY:H	2.16	0.48
1:G:233:LEU:O	1:G:237:LYS:HG3	2.13	0.47
1:F:233:LEU:O	1:F:237:LYS:HG3	2.13	0.47
2:C:101:VAL:HG22	2:D:217:ILE:CD1	2.35	0.47
1:A:68:GLU:OE1	2:C:163:ARG:NH1	2.46	0.47
2:D:164:THR:C	2:D:166:GLY:H	2.17	0.47
2:D:17:LEU:O	2:D:21:LEU:HB2	2.13	0.47
2:H:125:VAL:HG13	2:H:206:ILE:O	2.14	0.47
2:H:96:VAL:HG11	2:I:240:SER:HB3	1.96	0.47
1:F:28:VAL:HG11	1:F:190:ALA:HA	1.97	0.47
3:E:119:TYR:HD2	3:E:119:TYR:N	2.11	0.47
3:E:154:PRO:HA	3:E:157:TYR:CZ	2.50	0.47
1:B:233:LEU:O	1:B:237:LYS:HG3	2.14	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:37:LYS:HD3	5:F:803:PO4:O3	2.14	0.47
2:H:164:THR:C	2:H:166:GLY:H	2.16	0.47
3:E:134:TRP:CG	3:E:135:TYR:N	2.82	0.47
1:F:231:LEU:O	1:F:235:VAL:HG23	2.14	0.47
3:E:102:GLU:O	3:E:291:LYS:CD	2.62	0.47
1:A:28:VAL:HG11	1:A:190:ALA:HA	1.96	0.47
1:B:6:ARG:HA	1:B:18:VAL:O	2.14	0.47
2:D:11:LEU:O	2:D:15:ILE:HG12	2.14	0.47
3:J:256:LEU:HA	3:J:265:TYR:CE2	2.49	0.47
2:I:48:TRP:O	2:I:52:LEU:HG	2.15	0.47
1:G:215:PHE:HZ	1:G:229:ARG:NE	2.13	0.47
1:G:231:LEU:O	1:G:235:VAL:HG23	2.15	0.47
1:A:215:PHE:HZ	1:A:229:ARG:NE	2.12	0.47
1:A:68:GLU:H	1:A:68:GLU:HG2	1.54	0.47
2:H:128:LEU:N	2:H:129:PRO:CD	2.77	0.47
3:E:178:GLU:OE2	3:E:182:LYS:HE3	2.14	0.47
3:J:134:TRP:CG	3:J:135:TYR:N	2.83	0.47
1:G:66:PRO:O	1:G:68:GLU:N	2.48	0.47
3:J:174:THR:O	3:J:177:ASP:N	2.48	0.47
1:G:102:GLU:O	1:G:106:ARG:HG3	2.15	0.47
2:C:200:PHE:CE1	2:C:204:VAL:CG1	2.97	0.47
1:F:74:PHE:CB	2:H:164:THR:HG21	2.43	0.47
2:I:83:GLY:O	2:I:84:LYS:C	2.53	0.47
2:C:81:PHE:CB	2:C:82:PRO:HD2	2.37	0.47
1:B:231:LEU:O	1:B:235:VAL:HG23	2.15	0.47
1:A:192:MET:CE	1:B:235:VAL:HG22	2.40	0.47
3:J:119:TYR:CD1	3:J:232:TYR:CE1	3.03	0.47
3:J:94:LEU:HD11	3:J:154:PRO:HG3	1.96	0.47
1:G:6:ARG:HA	1:G:18:VAL:O	2.15	0.47
3:J:204:ARG:HA	3:J:204:ARG:NE	2.29	0.47
2:H:136:LEU:HD23	2:I:19:PHE:CZ	2.50	0.47
1:B:102:GLU:O	1:B:106:ARG:HG3	2.14	0.47
2:H:93:LEU:N	2:H:94:PRO:HD2	2.29	0.47
2:I:11:LEU:O	2:I:15:ILE:HG12	2.13	0.47
1:F:206:VAL:O	1:F:207:GLU:HG3	2.14	0.47
3:J:47:MET:HA	3:J:50:PHE:HD2	1.79	0.47
2:D:131:ILE:CG2	2:D:212:ILE:HD12	2.45	0.47
2:H:217:ILE:CD1	2:H:236:LEU:HD12	2.44	0.47
1:A:66:PRO:HB3	2:D:2:ARG:HH12	1.78	0.47
2:H:104:ILE:HD12	2:I:217:ILE:CG2	2.45	0.47
3:J:223:HIS:HD2	3:J:224:LEU:HD23	1.80	0.47
2:C:171:ARG:O	2:C:175:THR:OG1	2.33	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:160:LYS:CA	1:B:228:ALA:HB2	2.45	0.47
1:F:91:ILE:HA	1:F:139:ARG:HB2	1.97	0.47
3:J:300:VAL:CG1	3:J:304:LYS:HE2	2.45	0.47
1:A:6:ARG:HA	1:A:18:VAL:O	2.15	0.47
2:H:83:GLY:O	2:H:84:LYS:C	2.53	0.47
1:G:63:THR:N	1:G:64:PRO:HD2	2.30	0.47
1:G:74:PHE:HB3	2:I:164:THR:HG21	1.96	0.47
1:G:91:ILE:HA	1:G:139:ARG:HB2	1.97	0.47
3:E:300:VAL:CG1	3:E:304:LYS:HE2	2.45	0.47
3:J:154:PRO:HA	3:J:157:TYR:CZ	2.50	0.47
3:E:47:MET:HA	3:E:50:PHE:HD2	1.80	0.47
2:H:48:TRP:O	2:H:52:LEU:HG	2.15	0.47
1:F:229:ARG:CD	1:G:239:LEU:HD13	2.43	0.46
3:E:296:ARG:O	3:E:300:VAL:HG23	2.15	0.46
3:E:140:ARG:HB2	3:E:143:VAL:CG2	2.45	0.46
2:D:93:LEU:N	2:D:94:PRO:HD2	2.30	0.46
1:F:239:LEU:O	1:F:240:ASP:C	2.53	0.46
2:D:131:ILE:HD11	2:D:210:PRO:O	2.16	0.46
1:A:29:LEU:CB	1:A:198:ALA:HB3	2.45	0.46
2:C:83:GLY:O	2:C:84:LYS:C	2.53	0.46
1:G:57:LEU:HD21	1:G:146:ARG:HB3	1.98	0.46
2:I:164:THR:C	2:I:166:GLY:H	2.17	0.46
1:G:68:GLU:CA	2:I:166:GLY:HA2	2.46	0.46
1:G:3:LEU:HD22	1:G:147:LEU:HD21	1.98	0.46
3:J:112:LYS:HA	3:J:283:ILE:O	2.14	0.46
2:H:126:ASP:HA	2:H:207:ALA:HB1	1.97	0.46
2:C:98:PRO:HB3	2:D:198:SER:HA	1.96	0.46
1:F:83:PRO:HG2	2:H:180:LEU:HD21	1.98	0.46
1:G:28:VAL:HG11	1:G:190:ALA:HA	1.98	0.46
2:C:93:LEU:N	2:C:94:PRO:HD2	2.29	0.46
2:I:93:LEU:N	2:I:94:PRO:HD2	2.30	0.46
2:D:171:ARG:O	2:D:175:THR:OG1	2.32	0.46
2:C:126:ASP:HA	2:C:207:ALA:HB1	1.96	0.46
2:C:222:LEU:HA	3:E:80:LEU:HD21	1.97	0.46
2:I:162:ALA:HB2	2:I:176:VAL:HG21	1.97	0.46
1:B:239:LEU:O	1:B:240:ASP:C	2.54	0.46
1:F:215:PHE:O	1:F:218:LYS:HG3	2.15	0.46
3:J:130:ASN:C	3:J:130:ASN:ND2	2.64	0.46
2:D:146:GLN:HG3	2:D:191:MET:SD	2.55	0.46
1:G:3:LEU:HD22	1:G:147:LEU:CD2	2.45	0.46
2:I:109:VAL:O	2:I:116:ILE:HB	2.16	0.46
2:I:93:LEU:CB	2:I:94:PRO:CD	2.94	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:J:265:TYR:O	3:J:280:GLY:HA3	2.15	0.46
1:F:201:LEU:HD13	1:F:221:GLU:HG2	1.97	0.46
1:G:201:LEU:HD13	1:G:221:GLU:HG2	1.97	0.46
1:A:37:LYS:HD3	5:A:801:PO4:O3	2.15	0.46
2:I:209:TYR:C	2:I:211:MET:N	2.65	0.46
2:I:16:ILE:N	2:I:16:ILE:HD12	2.29	0.46
2:H:171:ARG:O	2:H:175:THR:OG1	2.31	0.46
3:J:140:ARG:HB2	3:J:143:VAL:CG2	2.46	0.46
3:J:49:ALA:HA	3:J:52:ARG:NH1	2.31	0.46
2:H:93:LEU:CB	2:H:94:PRO:CD	2.94	0.46
2:D:48:TRP:O	2:D:52:LEU:HG	2.16	0.46
2:D:70:THR:HB	2:D:71:PRO:CD	2.46	0.46
3:E:133:ASN:O	3:E:136:GLU:N	2.48	0.46
2:D:83:GLY:O	2:D:84:LYS:C	2.53	0.46
1:A:91:ILE:HA	1:A:139:ARG:HB2	1.97	0.46
2:H:211:MET:HE2	2:H:216:LEU:HB2	1.98	0.46
2:C:93:LEU:CB	2:C:94:PRO:CD	2.93	0.46
2:D:93:LEU:CB	2:D:94:PRO:CD	2.94	0.46
2:H:211:MET:CE	2:H:216:LEU:CD1	2.89	0.46
2:D:109:VAL:O	2:D:116:ILE:HB	2.16	0.46
3:J:66:GLU:OE2	3:J:82:ARG:NH2	2.49	0.46
2:H:170:LEU:HD13	2:I:5:PHE:CD1	2.50	0.46
1:G:37:LYS:CE	1:G:183:VAL:HG12	2.45	0.46
2:H:198:SER:HA	2:I:98:PRO:HB3	1.98	0.46
3:E:149:ASN:HD22	3:E:152:ASP:H	1.63	0.46
1:B:47:ILE:HD13	2:D:160:HIS:CB	2.41	0.46
2:D:163:ARG:HH12	2:D:169:PRO:CD	2.29	0.46
3:E:94:LEU:HD11	3:E:154:PRO:HG3	1.97	0.46
1:A:239:LEU:O	1:A:240:ASP:C	2.54	0.46
1:A:215:PHE:O	1:A:218:LYS:HG3	2.16	0.45
3:E:184:SER:HA	3:E:206:GLU:O	2.16	0.45
3:E:191:ASP:OD1	3:E:192:ASN:ND2	2.49	0.45
2:C:250:ILE:O	2:C:251:VAL:HG23	2.16	0.45
3:J:256:LEU:HD23	3:J:265:TYR:CG	2.51	0.45
3:E:95:ILE:HD13	3:E:288:THR:CG2	2.46	0.45
2:H:125:VAL:HG21	3:J:229:GLU:CD	2.37	0.45
3:J:35:LEU:HD12	3:J:85:ASP:CG	2.36	0.45
2:H:16:ILE:H	2:H:16:ILE:CD1	2.25	0.45
1:F:151:ASP:C	1:F:153:PRO:HD3	2.36	0.45
2:D:162:ALA:HB2	2:D:176:VAL:HG21	1.98	0.45
1:A:201:LEU:HD13	1:A:221:GLU:HG2	1.97	0.45
2:D:131:ILE:HG21	2:D:212:ILE:HD12	1.98	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:J:58:HIS:C	3:J:60:ASN:H	2.20	0.45
2:H:28:VAL:CG1	2:H:238:LEU:HD21	2.39	0.45
1:G:2:PHE:CE2	1:G:57:LEU:HD11	2.51	0.45
1:G:196:GLU:OE1	1:G:208:LYS:HE2	2.17	0.45
2:D:24:VAL:HG13	2:D:237:ILE:HD13	1.99	0.45
2:C:128:LEU:N	2:C:129:PRO:CD	2.78	0.45
2:I:250:ILE:O	2:I:251:VAL:HG23	2.17	0.45
3:J:113:ASN:HB2	3:J:285:TYR:HE2	1.81	0.45
3:E:49:ALA:HA	3:E:52:ARG:NH1	2.31	0.45
1:B:201:LEU:HD13	1:B:221:GLU:HG2	1.97	0.45
2:I:146:GLN:HG3	2:I:191:MET:SD	2.56	0.45
3:E:330:THR:CG2	3:E:331:ALA:N	2.80	0.45
2:C:48:TRP:O	2:C:52:LEU:HG	2.16	0.45
1:G:215:PHE:O	1:G:218:LYS:HG3	2.16	0.45
2:C:101:VAL:CG2	2:D:217:ILE:HD12	2.37	0.45
1:A:231:LEU:O	1:A:235:VAL:HG23	2.16	0.45
2:H:139:SER:HB3	2:H:195:ARG:HB3	1.99	0.45
1:G:178:VAL:HG12	1:G:179:PRO:O	2.15	0.45
2:H:127:ALA:HB1	2:H:129:PRO:HD2	1.98	0.45
2:H:250:ILE:O	2:H:251:VAL:HG23	2.17	0.45
1:F:37:LYS:CE	1:F:183:VAL:HG12	2.47	0.45
3:E:114:GLN:HG3	3:E:257:SER:HB3	1.98	0.45
3:J:335:LEU:C	3:J:337:ALA:N	2.70	0.45
1:G:37:LYS:HD3	5:G:804:PO4:O3	2.16	0.45
1:F:232:LEU:HD13	1:G:235:VAL:HG11	1.99	0.45
1:B:68:GLU:H	1:B:68:GLU:HG2	1.57	0.45
2:D:222:LEU:HD22	3:E:220:GLU:CG	2.44	0.45
2:I:163:ARG:HH12	2:I:169:PRO:CD	2.29	0.45
2:D:250:ILE:O	2:D:251:VAL:HG23	2.16	0.45
2:C:221:TYR:O	3:E:80:LEU:CD2	2.64	0.45
2:D:190:ILE:HD13	2:D:247:LEU:HD13	1.97	0.45
1:B:215:PHE:O	1:B:218:LYS:HG3	2.17	0.45
1:F:29:LEU:CB	1:F:198:ALA:HB3	2.47	0.45
3:E:190:GLU:CG	3:E:191:ASP:N	2.80	0.45
2:D:200:PHE:CE1	2:D:204:VAL:CG1	2.99	0.45
2:H:124:PHE:CE2	2:H:129:PRO:HB3	2.51	0.45
2:I:70:THR:HB	2:I:71:PRO:CD	2.47	0.45
2:C:139:SER:HB3	2:C:195:ARG:HB3	1.99	0.45
2:D:200:PHE:HZ	2:D:218:TYR:CD2	2.35	0.45
1:B:20:PHE:HB2	1:B:205:ILE:HD12	1.98	0.45
2:C:128:LEU:CB	2:C:129:PRO:HD3	2.46	0.45
3:J:110:PHE:CE2	3:J:287:ILE:HB	2.52	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:G:46:GLY:O	1:G:67:PRO:HD3	2.17	0.45
3:E:261:TYR:HD1	3:E:264:LEU:HD11	1.82	0.45
1:G:29:LEU:CB	1:G:198:ALA:HB3	2.47	0.45
1:G:68:GLU:HG2	1:G:68:GLU:H	1.55	0.45
2:C:124:PHE:CE2	2:C:129:PRO:HB3	2.52	0.45
3:E:41:GLY:O	3:E:219:MET:HG3	2.16	0.45
3:E:96:GLN:HA	3:E:100:TYR:CD1	2.52	0.45
2:D:39:LEU:O	2:D:43:SER:OG	2.35	0.45
1:A:37:LYS:CE	1:A:183:VAL:HG12	2.46	0.44
1:F:149:LEU:O	1:F:150:LEU:HD23	2.17	0.44
3:E:212:ILE:HG22	3:E:214:ILE:HG22	1.99	0.44
2:C:146:GLN:HG3	2:C:191:MET:SD	2.56	0.44
2:H:162:ALA:HB2	2:H:176:VAL:HG21	1.98	0.44
2:C:162:ALA:HB2	2:C:176:VAL:HG21	1.99	0.44
3:J:140:ARG:O	3:J:211:LYS:NZ	2.50	0.44
2:C:70:THR:HB	2:C:71:PRO:CD	2.47	0.44
3:E:174:THR:O	3:E:177:ASP:N	2.49	0.44
2:C:205:VAL:HG23	2:C:205:VAL:O	2.16	0.44
3:J:139:LYS:HE3	3:J:178:GLU:HB3	1.99	0.44
3:J:190:GLU:CG	3:J:191:ASP:N	2.80	0.44
3:E:32:ASN:O	3:E:33:VAL:C	2.56	0.44
1:B:143:ILE:CG2	1:B:143:ILE:O	2.65	0.44
1:B:149:LEU:O	1:B:150:LEU:HD23	2.17	0.44
1:F:128:SER:O	1:F:129:GLY:C	2.56	0.44
2:C:163:ARG:HH12	2:C:169:PRO:CD	2.30	0.44
3:E:60:ASN:ND2	3:E:60:ASN:H	2.14	0.44
2:I:139:SER:HB3	2:I:195:ARG:HB3	1.98	0.44
1:G:143:ILE:O	1:G:143:ILE:CG2	2.65	0.44
1:F:215:PHE:HZ	1:F:229:ARG:NE	2.12	0.44
1:G:239:LEU:O	1:G:240:ASP:C	2.54	0.44
2:H:105:ALA:CA	2:I:27:THR:HG21	2.46	0.44
3:E:106:TRP:CZ3	3:E:108:ILE:HG13	2.52	0.44
3:E:223:HIS:HD2	3:E:224:LEU:HD23	1.81	0.44
3:J:38:PHE:N	3:J:38:PHE:CD1	2.85	0.44
3:E:139:LYS:HE3	3:E:178:GLU:HB3	1.99	0.44
2:D:208:TYR:HE2	2:D:211:MET:HE1	1.82	0.44
1:B:128:SER:O	1:B:129:GLY:C	2.56	0.44
1:B:164:VAL:CG2	1:B:165:LEU:N	2.81	0.44
1:A:164:VAL:CG2	1:A:165:LEU:N	2.80	0.44
1:G:47:ILE:O	1:G:48:VAL:HG23	2.18	0.44
1:B:196:GLU:OE1	1:B:208:LYS:HE2	2.17	0.44
1:A:196:GLU:OE1	1:A:208:LYS:HE2	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:E:332:VAL:HG13	3:E:333:PRO:HD2	1.99	0.44
1:F:96:ARG:HD3	2:H:171:ARG:CZ	2.47	0.44
1:B:151:ASP:C	1:B:153:PRO:HD3	2.36	0.44
1:F:47:ILE:HG22	1:F:47:ILE:O	2.18	0.44
3:E:95:ILE:HD13	3:E:288:THR:HG22	2.00	0.44
1:F:178:VAL:HG12	1:F:179:PRO:O	2.18	0.44
3:E:289:ILE:HD11	3:E:303:VAL:HG21	2.00	0.44
1:A:211:LEU:HD23	1:A:211:LEU:HA	1.79	0.44
2:D:209:TYR:CD2	2:D:209:TYR:O	2.71	0.44
1:G:128:SER:O	1:G:129:GLY:C	2.55	0.44
2:H:5:PHE:CD1	2:I:170:LEU:HD13	2.52	0.44
2:I:208:TYR:HE2	2:I:211:MET:HE1	1.82	0.44
1:A:128:SER:O	1:A:129:GLY:C	2.55	0.44
1:B:47:ILE:HG22	1:B:47:ILE:O	2.18	0.44
2:H:163:ARG:HH12	2:H:169:PRO:CD	2.31	0.44
2:I:200:PHE:CE1	2:I:204:VAL:CG1	2.99	0.44
1:F:47:ILE:O	1:F:48:VAL:HG23	2.17	0.44
1:G:46:GLY:CA	1:G:70:ARG:NH1	2.81	0.44
3:J:100:TYR:HA	3:J:101:PRO:HA	1.77	0.44
1:B:178:VAL:HG12	1:B:179:PRO:O	2.18	0.44
2:H:70:THR:HB	2:H:71:PRO:CD	2.48	0.44
1:F:187:LEU:HD13	1:F:229:ARG:NH1	2.33	0.44
1:F:66:PRO:HB2	1:F:68:GLU:CG	2.44	0.44
3:E:58:HIS:C	3:E:60:ASN:H	2.20	0.44
2:D:23:PRO:O	2:D:24:VAL:C	2.56	0.44
3:J:289:ILE:HD11	3:J:303:VAL:HG21	2.00	0.44
1:A:178:VAL:HG12	1:A:179:PRO:O	2.17	0.44
3:J:261:TYR:HD1	3:J:264:LEU:HD11	1.82	0.44
1:B:234:LYS:O	1:B:238:ILE:HG13	2.18	0.44
3:J:106:TRP:CZ3	3:J:108:ILE:HG13	2.53	0.44
1:A:143:ILE:CG2	1:A:143:ILE:O	2.65	0.44
1:F:143:ILE:CG2	1:F:143:ILE:O	2.66	0.44
3:E:256:LEU:HD23	3:E:265:TYR:CG	2.53	0.44
3:J:96:GLN:HA	3:J:100:TYR:CD1	2.52	0.44
1:G:17:ASN:CG	1:G:17:ASN:O	2.56	0.44
1:G:149:LEU:HD23	1:G:181:LEU:HB3	1.99	0.43
1:F:74:PHE:CE2	1:F:76:PRO:HB3	2.53	0.43
3:E:134:TRP:CD2	3:E:135:TYR:N	2.86	0.43
1:F:234:LYS:O	1:F:238:ILE:HG13	2.18	0.43
1:A:47:ILE:HD13	2:C:160:HIS:CG	2.53	0.43
1:B:230:ASN:O	1:B:234:LYS:HG3	2.18	0.43
1:B:110:MET:HE2	1:B:110:MET:O	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:110:MET:HE2	1:A:114:LEU:HD12	2.00	0.43
2:H:128:LEU:CB	2:H:129:PRO:HD3	2.47	0.43
2:C:127:ALA:HB1	2:C:129:PRO:HD2	1.99	0.43
1:G:151:ASP:C	1:G:153:PRO:HD3	2.38	0.43
2:C:120:SER:C	2:C:122:LEU:N	2.71	0.43
2:H:120:SER:C	2:H:122:LEU:N	2.71	0.43
1:A:25:ASP:HB2	1:A:195:ASP:OD2	2.18	0.43
1:B:149:LEU:HD23	1:B:181:LEU:HB3	1.99	0.43
2:C:209:TYR:HD2	2:C:209:TYR:HA	1.54	0.43
1:G:74:PHE:CE2	1:G:76:PRO:HB3	2.53	0.43
3:J:36:LYS:N	3:J:85:ASP:OD2	2.51	0.43
2:D:139:SER:HB3	2:D:195:ARG:HB3	2.00	0.43
1:A:160:LYS:HA	1:B:228:ALA:HB2	1.99	0.43
1:G:187:LEU:HD13	1:G:229:ARG:NH1	2.34	0.43
2:C:98:PRO:CB	2:D:214:PRO:HG3	2.48	0.43
3:E:130:ASN:ND2	3:E:130:ASN:C	2.71	0.43
1:A:234:LYS:O	1:A:238:ILE:HG13	2.18	0.43
1:A:47:ILE:O	1:A:48:VAL:HG23	2.18	0.43
1:G:57:LEU:CD2	1:G:146:ARG:HD3	2.48	0.43
2:C:128:LEU:HD23	2:C:128:LEU:HA	1.84	0.43
3:E:113:ASN:HD21	3:E:238:SER:CB	2.30	0.43
1:F:100:ARG:O	1:F:101:VAL:C	2.57	0.43
1:F:65:LEU:HA	1:F:66:PRO:HD3	1.76	0.43
1:B:29:LEU:CB	1:B:198:ALA:HB3	2.48	0.43
3:E:60:ASN:N	3:E:60:ASN:HD22	2.17	0.43
1:F:196:GLU:OE1	1:F:208:LYS:HE2	2.19	0.43
2:C:23:PRO:O	2:C:24:VAL:C	2.57	0.43
2:I:205:VAL:O	2:I:205:VAL:HG23	2.18	0.43
1:F:39:VAL:HG23	1:F:40:PHE:N	2.33	0.43
1:A:187:LEU:HD13	1:A:229:ARG:NH1	2.33	0.43
1:B:154:LEU:HD12	1:B:189:GLU:OE1	2.17	0.43
2:C:98:PRO:HB2	2:D:214:PRO:HG3	1.99	0.43
1:G:149:LEU:O	1:G:150:LEU:HD23	2.19	0.43
1:A:29:LEU:HD23	1:A:29:LEU:H	1.83	0.43
2:I:209:TYR:CD2	2:I:209:TYR:O	2.71	0.43
3:J:29:GLY:C	3:J:31:MET:H	2.22	0.43
2:H:244:PHE:CE1	2:I:96:VAL:HG13	2.53	0.43
1:B:28:VAL:HG11	1:B:190:ALA:HA	2.00	0.43
2:C:124:PHE:HA	2:C:129:PRO:HB2	2.01	0.43
1:G:66:PRO:C	1:G:68:GLU:N	2.72	0.43
2:H:146:GLN:HG3	2:H:191:MET:SD	2.58	0.43
3:E:119:TYR:CD1	3:E:232:TYR:HE1	2.37	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:I:51:VAL:HG11	2:I:239:LEU:HD11	2.00	0.43
1:A:231:LEU:HD13	1:B:163:GLY:CA	2.44	0.43
1:G:65:LEU:HA	1:G:66:PRO:HD3	1.80	0.43
1:B:47:ILE:O	1:B:48:VAL:HG23	2.18	0.43
2:H:68:PHE:O	2:I:16:ILE:HD11	2.19	0.43
2:I:190:ILE:CD1	2:I:247:LEU:HD13	2.48	0.43
3:E:335:LEU:C	3:E:337:ALA:H	2.21	0.43
3:E:314:ILE:O	3:E:317:GLU:HB2	2.19	0.43
1:B:30:LEU:HB3	1:B:225:PHE:CE2	2.54	0.43
1:F:154:LEU:HD12	1:F:189:GLU:OE1	2.18	0.43
1:A:72:ILE:HG13	1:A:72:ILE:H	1.61	0.43
1:F:57:LEU:CD2	1:F:146:ARG:HD3	2.48	0.43
3:J:133:ASN:O	3:J:134:TRP:C	2.57	0.43
2:D:81:PHE:CE1	2:D:84:LYS:N	2.87	0.43
1:A:127:LEU:HD13	1:A:135:VAL:HG21	2.00	0.43
1:G:64:PRO:HG2	1:G:65:LEU:H	1.83	0.43
1:G:8:GLU:HB2	1:G:52:ARG:HB2	2.00	0.43
2:H:20:VAL:HG13	2:I:94:PRO:HD3	2.01	0.43
2:I:39:LEU:O	2:I:43:SER:OG	2.36	0.43
2:D:209:TYR:HD1	3:E:66:GLU:OE2	2.02	0.43
1:G:127:LEU:HD13	1:G:135:VAL:HG21	2.01	0.43
1:B:127:LEU:HD13	1:B:135:VAL:HG21	2.01	0.43
1:F:176:PHE:O	1:F:177:ASP:C	2.57	0.43
2:C:128:LEU:O	2:C:129:PRO:C	2.57	0.43
3:J:314:ILE:O	3:J:317:GLU:HB2	2.18	0.43
1:A:80:ALA:O	1:A:139:ARG:NH2	2.45	0.43
2:I:23:PRO:O	2:I:24:VAL:C	2.56	0.43
3:E:199:MET:HA	3:E:200:PRO:HD3	1.74	0.43
2:D:251:VAL:O	2:D:251:VAL:HG12	2.19	0.43
3:J:153:ASP:OD1	3:J:154:PRO:CD	2.67	0.43
2:I:55:TYR:OH	2:I:239:LEU:HD22	2.19	0.43
2:H:239:LEU:O	2:H:239:LEU:HD23	2.18	0.43
1:B:201:LEU:O	1:B:202:ASN:HB2	2.19	0.43
1:G:104:ASP:OD1	1:G:108:ARG:HD2	2.19	0.43
1:F:149:LEU:HD23	1:F:181:LEU:HB3	2.00	0.42
3:J:134:TRP:CD2	3:J:135:TYR:N	2.87	0.42
3:J:212:ILE:HG22	3:J:214:ILE:HG22	2.00	0.42
3:J:149:ASN:ND2	3:J:152:ASP:H	2.17	0.42
1:G:201:LEU:O	1:G:202:ASN:HB2	2.18	0.42
1:A:104:ASP:OD1	1:A:108:ARG:HD2	2.19	0.42
1:F:211:LEU:HA	1:F:211:LEU:HD23	1.80	0.42
2:C:198:SER:CB	2:D:98:PRO:HA	2.49	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:37:LYS:HE2	1:A:183:VAL:HG12	2.01	0.42
2:C:163:ARG:HH12	2:C:169:PRO:CG	2.33	0.42
3:E:46:PRO:HA	3:E:318:LEU:HD12	2.01	0.42
2:I:106:LEU:CD1	2:I:134:ALA:HA	2.49	0.42
2:I:203:VAL:O	2:I:204:VAL:C	2.57	0.42
1:B:17:ASN:CG	1:B:17:ASN:O	2.57	0.42
1:B:39:VAL:HG23	1:B:40:PHE:N	2.34	0.42
2:C:39:LEU:O	2:C:43:SER:OG	2.35	0.42
1:G:97:ASN:ND2	1:G:97:ASN:O	2.49	0.42
1:F:17:ASN:CG	1:F:17:ASN:O	2.58	0.42
2:C:131:ILE:CG2	2:C:212:ILE:HD11	2.49	0.42
2:D:222:LEU:CD2	3:E:220:GLU:HG2	2.44	0.42
2:H:124:PHE:HA	2:H:129:PRO:HB2	2.00	0.42
2:C:251:VAL:O	2:C:251:VAL:HG12	2.19	0.42
2:I:251:VAL:O	2:I:251:VAL:HG12	2.19	0.42
1:B:30:LEU:HB3	1:B:225:PHE:HE2	1.83	0.42
3:J:133:ASN:O	3:J:136:GLU:N	2.48	0.42
1:F:127:LEU:HD13	1:F:135:VAL:HG21	2.01	0.42
3:J:75:ARG:NH2	3:J:151:ASN:O	2.44	0.42
2:C:244:PHE:CE1	2:D:96:VAL:HG13	2.54	0.42
2:D:205:VAL:O	2:D:205:VAL:HG23	2.19	0.42
1:F:110:MET:O	1:F:110:MET:HE2	2.19	0.42
3:E:173:PRO:O	3:E:177:ASP:OD2	2.38	0.42
1:G:39:VAL:HG23	1:G:40:PHE:N	2.34	0.42
1:F:30:LEU:HB3	1:F:225:PHE:HE2	1.85	0.42
2:D:216:LEU:O	2:D:216:LEU:HG	2.20	0.42
1:B:187:LEU:HD13	1:B:229:ARG:NH1	2.33	0.42
1:F:44:ILE:HB	1:F:149:LEU:HD11	2.01	0.42
2:D:50:VAL:HG13	2:D:211:MET:O	2.19	0.42
1:F:20:PHE:HB2	1:F:205:ILE:HD12	2.01	0.42
1:G:109:GLU:O	1:G:113:LYS:HG3	2.19	0.42
1:A:25:ASP:HB2	1:A:26:TYR:H	1.64	0.42
1:A:154:LEU:HD12	1:A:189:GLU:OE1	2.19	0.42
2:C:104:ILE:HD12	2:D:217:ILE:HG22	2.01	0.42
1:F:230:ASN:O	1:F:234:LYS:HG3	2.20	0.42
1:A:3:LEU:HD22	1:A:147:LEU:CD2	2.49	0.42
2:I:221:TYR:CZ	3:J:223:HIS:CE1	3.07	0.42
1:F:188:ILE:HG23	1:G:235:VAL:HG21	2.02	0.42
1:G:65:LEU:HD22	1:G:69:ARG:HB3	2.02	0.42
3:E:165:LEU:CB	3:E:254:ILE:HG22	2.44	0.42
2:D:203:VAL:O	2:D:204:VAL:C	2.58	0.42
2:H:55:TYR:OH	2:H:239:LEU:HD22	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:57:LEU:CB	1:B:62:ILE:HD12	2.50	0.42
2:D:110:PHE:HB3	2:D:124:PHE:CG	2.55	0.42
2:H:39:LEU:O	2:H:43:SER:OG	2.37	0.42
1:B:74:PHE:CE2	1:B:76:PRO:HB3	2.54	0.42
3:J:42:SER:C	3:J:44:THR:H	2.23	0.42
1:G:154:LEU:HD12	1:G:189:GLU:OE1	2.20	0.42
1:B:37:LYS:CE	1:B:183:VAL:HG12	2.50	0.42
1:F:164:VAL:CG2	1:F:165:LEU:N	2.82	0.42
2:I:81:PHE:CE1	2:I:84:LYS:N	2.88	0.42
3:E:45:GLU:O	3:E:48:LYS:HB2	2.20	0.42
1:A:176:PHE:O	1:A:177:ASP:C	2.57	0.42
1:A:151:ASP:C	1:A:153:PRO:HD3	2.39	0.42
2:C:81:PHE:CE1	2:C:84:LYS:N	2.87	0.42
1:B:57:LEU:HD21	1:B:146:ARG:HD3	2.00	0.42
3:J:256:LEU:HA	3:J:265:TYR:CZ	2.55	0.42
3:J:173:PRO:O	3:J:177:ASP:OD2	2.37	0.42
1:F:201:LEU:O	1:F:202:ASN:HB2	2.19	0.42
1:G:211:LEU:HA	1:G:211:LEU:HD23	1.79	0.42
3:E:38:PHE:N	3:E:38:PHE:CD1	2.85	0.42
2:C:104:ILE:CD1	2:D:217:ILE:CG2	2.98	0.42
2:I:208:TYR:CE2	2:I:211:MET:HE1	2.55	0.42
3:E:133:ASN:O	3:E:134:TRP:C	2.57	0.42
2:H:81:PHE:CE1	2:H:84:LYS:N	2.88	0.42
1:G:164:VAL:CG2	1:G:165:LEU:N	2.82	0.42
1:A:68:GLU:OE2	2:D:2:ARG:NH2	2.53	0.42
2:I:50:VAL:HG12	2:I:213:ALA:N	2.35	0.42
2:I:217:ILE:CD1	2:I:236:LEU:HD12	2.43	0.42
2:D:163:ARG:HG2	2:D:163:ARG:NH1	2.35	0.42
1:F:144:GLN:N	1:F:145:PRO:CD	2.83	0.42
2:C:239:LEU:O	2:C:239:LEU:HD23	2.19	0.42
1:G:25:ASP:HB2	1:G:26:TYR:H	1.63	0.42
3:E:116:VAL:HG11	3:E:237:LYS:HB2	2.01	0.42
1:F:99:GLU:O	1:F:100:ARG:C	2.58	0.41
2:H:212:ILE:O	2:H:213:ALA:C	2.58	0.41
2:H:217:ILE:CG2	2:I:104:ILE:HD12	2.49	0.41
1:A:44:ILE:HG22	1:A:72:ILE:HD13	2.01	0.41
1:A:139:ARG:HD2	2:C:165:LEU:HD11	2.02	0.41
1:B:65:LEU:HA	1:B:66:PRO:HD3	1.77	0.41
2:H:251:VAL:O	2:H:251:VAL:HG12	2.20	0.41
3:J:113:ASN:HD21	3:J:238:SER:CB	2.32	0.41
1:A:201:LEU:CD1	1:A:221:GLU:HG2	2.50	0.41
1:A:17:ASN:CG	1:A:17:ASN:O	2.57	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:104:ILE:HD12	2:D:217:ILE:HG21	2.02	0.41
2:H:233:ALA:HB1	2:I:101:VAL:HG13	2.01	0.41
3:J:31:MET:O	3:J:33:VAL:N	2.50	0.41
2:C:211:MET:HE2	2:C:216:LEU:HB2	2.01	0.41
2:D:239:LEU:O	2:D:239:LEU:HD23	2.20	0.41
1:A:57:LEU:CB	1:A:62:ILE:HD12	2.51	0.41
1:G:230:ASN:O	1:G:234:LYS:HG3	2.20	0.41
1:F:29:LEU:HD23	1:F:29:LEU:H	1.86	0.41
1:A:230:ASN:O	1:A:234:LYS:HG3	2.20	0.41
1:G:2:PHE:CE2	1:G:179:PRO:HG3	2.56	0.41
2:D:128:LEU:HB3	2:D:129:PRO:CD	2.46	0.41
2:I:163:ARG:HG2	2:I:163:ARG:NH1	2.35	0.41
2:D:106:LEU:CD1	2:D:134:ALA:HA	2.50	0.41
2:C:93:LEU:HD13	2:D:24:VAL:HG21	2.02	0.41
1:F:109:GLU:O	1:F:113:LYS:HG3	2.20	0.41
1:G:201:LEU:CD1	1:G:221:GLU:HG2	2.50	0.41
1:F:30:LEU:HB3	1:F:225:PHE:CE2	2.56	0.41
2:C:136:LEU:HD23	2:D:19:PHE:CZ	2.55	0.41
3:J:122:ASP:O	3:J:123:SER:C	2.59	0.41
2:D:108:VAL:O	2:D:114:GLY:HA3	2.19	0.41
1:B:29:LEU:H	1:B:29:LEU:HD23	1.84	0.41
2:I:154:VAL:HG22	2:I:180:LEU:HB3	2.02	0.41
1:A:47:ILE:HG22	1:A:47:ILE:O	2.19	0.41
1:A:95:LEU:C	1:A:103:ARG:HD3	2.41	0.41
2:H:124:PHE:CD2	2:H:129:PRO:CB	3.04	0.41
1:G:95:LEU:C	1:G:103:ARG:HD3	2.40	0.41
3:J:93:THR:CG2	3:J:281:LYS:HZ3	2.34	0.41
3:J:114:GLN:HG3	3:J:257:SER:CB	2.50	0.41
2:C:117:GLY:C	2:C:119:PHE:H	2.23	0.41
1:B:104:ASP:OD1	1:B:108:ARG:HD2	2.20	0.41
1:A:233:LEU:HD11	1:B:240:ASP:HB2	2.02	0.41
2:H:50:VAL:CG1	2:H:212:ILE:C	2.89	0.41
1:A:74:PHE:CE2	1:A:76:PRO:HB3	2.56	0.41
2:C:24:VAL:HG13	2:C:237:ILE:HD13	2.03	0.41
2:H:24:VAL:HG13	2:H:237:ILE:HD13	2.02	0.41
2:H:27:THR:HG21	2:I:105:ALA:CB	2.50	0.41
3:J:201:SER:O	3:J:203:GLU:N	2.52	0.41
3:E:164:GLN:O	3:E:167:GLU:HB2	2.20	0.41
1:B:97:ASN:ND2	1:B:97:ASN:O	2.49	0.41
3:J:139:LYS:HE3	3:J:178:GLU:CB	2.51	0.41
1:B:144:GLN:N	1:B:145:PRO:CD	2.84	0.41
2:C:222:LEU:CD2	3:E:80:LEU:CD1	2.99	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:E:78:THR:HA	3:E:103:PHE:CE2	2.54	0.41
2:C:70:THR:O	2:C:71:PRO:C	2.59	0.41
3:E:42:SER:C	3:E:44:THR:H	2.24	0.41
2:H:131:ILE:HG23	2:H:212:ILE:CD1	2.48	0.41
2:H:244:PHE:CD1	2:I:96:VAL:HG13	2.56	0.41
1:B:95:LEU:C	1:B:103:ARG:HD3	2.41	0.41
3:E:94:LEU:CD1	3:E:154:PRO:HG3	2.51	0.41
1:F:46:GLY:O	1:F:67:PRO:HD3	2.21	0.41
2:H:117:GLY:C	2:H:119:PHE:H	2.24	0.41
2:H:204:VAL:HG23	2:H:205:VAL:HG12	2.03	0.41
1:F:163:GLY:CA	1:G:231:LEU:HD13	2.48	0.41
1:G:208:LYS:HG2	1:G:209:GLY:N	2.36	0.41
2:D:163:ARG:HH12	2:D:169:PRO:CG	2.34	0.41
1:B:25:ASP:HB2	1:B:26:TYR:H	1.63	0.41
2:H:20:VAL:CG1	2:I:94:PRO:HD3	2.50	0.41
2:C:31:GLN:HG3	2:C:234:ALA:CB	2.51	0.41
2:H:205:VAL:HG23	2:H:205:VAL:O	2.20	0.41
1:A:149:LEU:HD23	1:A:181:LEU:HB3	2.01	0.41
1:F:44:ILE:O	1:F:70:ARG:NH1	2.52	0.41
1:A:235:VAL:HG22	1:B:192:MET:CE	2.39	0.41
1:A:235:VAL:HG21	1:B:188:ILE:HG23	2.02	0.41
3:J:45:GLU:O	3:J:48:LYS:HB2	2.21	0.41
1:A:3:LEU:HD22	1:A:147:LEU:HD21	2.03	0.41
3:E:296:ARG:CG	3:E:296:ARG:HH11	2.34	0.41
2:H:23:PRO:O	2:H:24:VAL:C	2.57	0.41
3:E:120:ARG:NH1	3:E:225:VAL:O	2.54	0.41
1:G:98:VAL:HG12	1:G:99:GLU:N	2.36	0.41
2:I:239:LEU:HD23	2:I:239:LEU:O	2.21	0.41
3:E:112:LYS:HA	3:E:283:ILE:O	2.21	0.41
1:B:201:LEU:CD1	1:B:221:GLU:HG2	2.50	0.41
3:J:39:HIS:ND1	3:J:40:ALA:O	2.45	0.41
3:J:116:VAL:CG1	3:J:237:LYS:HB2	2.51	0.41
3:E:139:LYS:HE3	3:E:178:GLU:CB	2.51	0.41
1:G:68:GLU:HB2	2:I:166:GLY:HA2	1.99	0.41
3:J:149:ASN:HD21	3:J:151:ASN:CA	2.33	0.41
2:I:28:VAL:CG1	2:I:238:LEU:HD21	2.44	0.41
2:I:128:LEU:HB3	2:I:129:PRO:CD	2.46	0.41
1:B:208:LYS:HG2	1:B:209:GLY:N	2.35	0.41
2:H:163:ARG:HH12	2:H:169:PRO:CG	2.34	0.41
2:H:128:LEU:O	2:H:129:PRO:C	2.59	0.41
3:J:94:LEU:CD1	3:J:154:PRO:HG3	2.51	0.41
3:E:153:ASP:HA	3:E:154:PRO:HD3	1.98	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:201:LEU:O	1:A:202:ASN:HB2	2.20	0.41
2:H:179:PRO:HA	2:H:182:VAL:HG23	2.03	0.41
3:J:230:LEU:HA	3:J:230:LEU:HD23	1.90	0.41
2:C:99:HIS:O	2:C:102:ALA:HB3	2.21	0.41
2:C:203:VAL:O	2:C:204:VAL:C	2.58	0.40
1:A:184:THR:CG2	1:A:185:HIS:N	2.72	0.40
2:H:216:LEU:HG	2:H:216:LEU:O	2.21	0.40
1:A:144:GLN:N	1:A:145:PRO:CD	2.84	0.40
1:G:144:GLN:N	1:G:145:PRO:CD	2.83	0.40
1:F:10:ARG:O	1:F:11:LEU:HD23	2.21	0.40
3:J:174:THR:O	3:J:175:ILE:C	2.59	0.40
1:F:201:LEU:CD1	1:F:221:GLU:HG2	2.50	0.40
3:J:107:THR:O	3:J:328:ALA:HA	2.20	0.40
1:A:39:VAL:HG23	1:A:40:PHE:N	2.35	0.40
3:E:144:ARG:O	3:E:231:ASP:HB2	2.21	0.40
1:A:97:ASN:ND2	1:A:97:ASN:O	2.50	0.40
2:I:81:PHE:CB	2:I:82:PRO:HD2	2.37	0.40
1:G:65:LEU:HD22	1:G:69:ARG:CB	2.51	0.40
2:C:16:ILE:H	2:C:16:ILE:CD1	2.23	0.40
3:J:296:ARG:CG	3:J:296:ARG:HH11	2.34	0.40
1:B:10:ARG:O	1:B:11:LEU:HD23	2.21	0.40
1:F:25:ASP:HB2	1:F:26:TYR:H	1.64	0.40
3:E:100:TYR:HA	3:E:101:PRO:HA	1.77	0.40
1:G:10:ARG:O	1:G:11:LEU:HD23	2.21	0.40
2:D:236:LEU:HD23	2:D:236:LEU:HA	1.89	0.40
2:H:203:VAL:O	2:H:204:VAL:C	2.58	0.40
1:F:62:ILE:HG12	1:F:65:LEU:HD12	2.03	0.40
1:F:68:GLU:H	1:F:68:GLU:HG2	1.55	0.40
1:F:79:TYR:OH	1:F:133:GLN:HG2	2.22	0.40
3:J:147:PHE:CE2	3:J:212:ILE:HD13	2.56	0.40
3:J:190:GLU:HG2	3:J:191:ASP:N	2.36	0.40
2:C:124:PHE:CD2	2:C:129:PRO:CB	3.05	0.40
3:E:52:ARG:CG	3:E:53:ALA:N	2.84	0.40
3:E:122:ASP:O	3:E:123:SER:C	2.59	0.40
2:D:81:PHE:CB	2:D:82:PRO:HD2	2.37	0.40
2:H:193:TRP:CZ3	2:H:244:PHE:CZ	3.10	0.40
1:A:66:PRO:O	1:A:70:ARG:HG3	2.21	0.40
3:E:147:PHE:CE2	3:E:212:ILE:HD13	2.56	0.40
3:J:45:GLU:N	3:J:46:PRO:CD	2.85	0.40
2:H:98:PRO:HB3	2:I:198:SER:HA	2.04	0.40
1:G:176:PHE:O	1:G:177:ASP:C	2.60	0.40
1:G:37:LYS:HE2	1:G:183:VAL:HG12	2.02	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:46:GLY:O	1:A:67:PRO:HD3	2.22	0.40
3:E:45:GLU:N	3:E:46:PRO:CD	2.84	0.40
3:J:273:ALA:O	3:J:275:GLY:N	2.55	0.40
3:J:113:ASN:HD21	3:J:238:SER:HB3	1.86	0.40
2:H:70:THR:O	2:H:71:PRO:C	2.59	0.40
2:I:216:LEU:HG	2:I:216:LEU:O	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:210:LYS:NZ	1:F:174:ARG:O[1_546]	2.14	0.06

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	238/240 (99%)	203 (85%)	31 (13%)	4 (2%)	14	54
1	B	238/240 (99%)	202 (85%)	32 (13%)	4 (2%)	14	54
1	F	238/240 (99%)	202 (85%)	29 (12%)	7 (3%)	7	38
1	G	238/240 (99%)	194 (82%)	40 (17%)	4 (2%)	14	54
2	C	250/284 (88%)	193 (77%)	50 (20%)	7 (3%)	8	39
2	D	250/284 (88%)	192 (77%)	48 (19%)	10 (4%)	5	28
2	H	250/284 (88%)	194 (78%)	49 (20%)	7 (3%)	8	39
2	I	250/284 (88%)	192 (77%)	49 (20%)	9 (4%)	5	31
3	E	309/314 (98%)	254 (82%)	44 (14%)	11 (4%)	5	31
3	J	308/314 (98%)	254 (82%)	43 (14%)	11 (4%)	5	31
All	All	2569/2724 (94%)	2080 (81%)	415 (16%)	74 (3%)	7	38

All (74) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	100	ARG
2	C	84	LYS
2	D	84	LYS
2	D	115	LEU
2	H	84	LYS
2	I	84	LYS
2	I	115	LEU
3	E	59	PRO
3	J	59	PRO
3	J	30	HIS
3	J	123	SER
3	J	202	SER
1	A	79	TYR
1	A	124	PRO
1	B	79	TYR
1	B	124	PRO
1	F	79	TYR
1	F	124	PRO
1	G	79	TYR
1	G	124	PRO
2	C	30	LEU
2	D	30	LEU
2	D	112	SER
2	D	177	SER
2	H	177	SER
2	I	112	SER
2	I	177	SER
3	E	33	VAL
3	E	68	ALA
3	E	123	SER
3	E	333	PRO
3	E	341	VAL
3	J	68	ALA
3	J	218	GLU
1	A	117	ALA
1	B	117	ALA
1	F	117	ALA
1	G	117	ALA
2	C	177	SER
2	C	251	VAL
2	D	251	VAL
2	H	23	PRO
2	H	30	LEU

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Mol	Chain	Res	Type
2	H	251	VAL
2	I	23	PRO
2	I	30	LEU
2	I	251	VAL
3	E	175	ILE
3	E	218	GLU
3	E	274	ASN
3	J	274	ASN
1	A	120	LEU
1	F	101	VAL
1	G	65	LEU
2	C	23	PRO
2	C	54	THR
2	D	23	PRO
2	D	54	THR
2	D	126	ASP
2	H	54	THR
2	I	54	THR
2	I	126	ASP
3	E	173	PRO
3	J	173	PRO
3	J	175	ILE
1	B	120	LEU
1	F	120	LEU
2	C	136	LEU
2	D	136	LEU
2	H	136	LEU
3	J	290	PRO
1	F	98	VAL
3	E	290	PRO
3	J	333	PRO

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	202/202 (100%)	187 (93%)	15 (7%)	20 59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	202/202 (100%)	187 (93%)	15 (7%)	20	59
1	F	202/202 (100%)	186 (92%)	16 (8%)	18	55
1	G	202/202 (100%)	189 (94%)	13 (6%)	25	65
2	C	206/233 (88%)	193 (94%)	13 (6%)	25	66
2	D	206/233 (88%)	193 (94%)	13 (6%)	25	66
2	H	206/233 (88%)	193 (94%)	13 (6%)	25	66
2	I	206/233 (88%)	193 (94%)	13 (6%)	25	66
3	E	273/275 (99%)	256 (94%)	17 (6%)	26	66
3	J	271/275 (98%)	254 (94%)	17 (6%)	25	66
All	All	2176/2290 (95%)	2031 (93%)	145 (7%)	23	63

All (145) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	LEU
1	A	17	ASN
1	A	22	MET
1	A	25	ASP
1	A	43	LEU
1	A	58	ASN
1	A	62	ILE
1	A	68	GLU
1	A	79	TYR
1	A	97	ASN
1	A	110	MET
1	A	139	ARG
1	A	158	ASP
1	A	173	GLN
1	A	200	MET
1	B	16	LEU
1	B	17	ASN
1	B	22	MET
1	B	25	ASP
1	B	43	LEU
1	B	58	ASN
1	B	62	ILE
1	B	68	GLU
1	B	79	TYR
1	B	97	ASN

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Mol	Chain	Res	Type
1	B	110	MET
1	B	139	ARG
1	B	158	ASP
1	B	173	GLN
1	B	200	MET
1	F	16	LEU
1	F	17	ASN
1	F	22	MET
1	F	25	ASP
1	F	43	LEU
1	F	58	ASN
1	F	62	ILE
1	F	68	GLU
1	F	79	TYR
1	F	99	GLU
1	F	101	VAL
1	F	110	MET
1	F	139	ARG
1	F	158	ASP
1	F	173	GLN
1	F	200	MET
1	G	16	LEU
1	G	17	ASN
1	G	22	MET
1	G	25	ASP
1	G	43	LEU
1	G	68	GLU
1	G	79	TYR
1	G	97	ASN
1	G	110	MET
1	G	139	ARG
1	G	158	ASP
1	G	173	GLN
1	G	200	MET
2	C	16	ILE
2	C	21	LEU
2	C	22	LEU
2	C	27	THR
2	C	33	PHE
2	C	43	SER
2	C	107	LEU
2	C	138	VAL

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Mol	Chain	Res	Type
2	C	167	SER
2	C	175	THR
2	C	178	LEU
2	C	209	TYR
2	C	239	LEU
2	D	16	ILE
2	D	21	LEU
2	D	22	LEU
2	D	27	THR
2	D	33	PHE
2	D	43	SER
2	D	107	LEU
2	D	138	VAL
2	D	167	SER
2	D	175	THR
2	D	178	LEU
2	D	209	TYR
2	D	239	LEU
2	H	16	ILE
2	H	21	LEU
2	H	22	LEU
2	H	27	THR
2	H	33	PHE
2	H	43	SER
2	H	107	LEU
2	H	138	VAL
2	H	167	SER
2	H	175	THR
2	H	178	LEU
2	H	209	TYR
2	H	239	LEU
2	I	16	ILE
2	I	21	LEU
2	I	22	LEU
2	I	27	THR
2	I	33	PHE
2	I	43	SER
2	I	107	LEU
2	I	138	VAL
2	I	167	SER
2	I	175	THR
2	I	178	LEU

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Mol	Chain	Res	Type
2	I	209	TYR
2	I	239	LEU
3	E	60	ASN
3	E	73	THR
3	E	105	ASN
3	E	109	MET
3	E	113	ASN
3	E	119	TYR
3	E	130	ASN
3	E	149	ASN
3	E	185	ASN
3	E	188	PHE
3	E	203	GLU
3	E	208	ASN
3	E	214	ILE
3	E	218	GLU
3	E	233	PHE
3	E	274	ASN
3	E	296	ARG
3	J	73	THR
3	J	105	ASN
3	J	109	MET
3	J	113	ASN
3	J	119	TYR
3	J	130	ASN
3	J	149	ASN
3	J	185	ASN
3	J	188	PHE
3	J	208	ASN
3	J	214	ILE
3	J	218	GLU
3	J	233	PHE
3	J	274	ASN
3	J	296	ARG
3	J	329	ASP
3	J	330	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (42) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	ASN
1	A	58	ASN

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Mol	Chain	Res	Type
1	A	133	GLN
1	A	219	ASN
1	B	17	ASN
1	B	58	ASN
1	B	133	GLN
1	B	219	ASN
1	F	17	ASN
1	F	58	ASN
1	F	133	GLN
1	F	219	ASN
1	G	17	ASN
1	G	133	GLN
1	G	219	ASN
2	C	146	GLN
2	C	184	HIS
2	D	146	GLN
2	D	184	HIS
2	H	146	GLN
2	H	184	HIS
2	I	146	GLN
2	I	184	HIS
3	E	60	ASN
3	E	105	ASN
3	E	130	ASN
3	E	149	ASN
3	E	183	ASN
3	E	185	ASN
3	E	192	ASN
3	E	208	ASN
3	E	223	HIS
3	E	274	ASN
3	J	60	ASN
3	J	105	ASN
3	J	130	ASN
3	J	149	ASN
3	J	183	ASN
3	J	185	ASN
3	J	208	ASN
3	J	223	HIS
3	J	274	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 ⓘ

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	PO4	A	801	6	4,4,4	1.80	1 (25%)	6,6,6	0.31	0
5	PO4	B	802	6	4,4,4	1.76	1 (25%)	6,6,6	0.31	0
4	WO4	E	701	3	2,4,4	11.80	2 (100%)	0,6,6	0.00	-
5	PO4	F	803	6	4,4,4	1.82	1 (25%)	6,6,6	0.31	0
5	PO4	G	804	6	4,4,4	1.86	2 (50%)	6,6,6	0.31	0
4	WO4	J	702	3	2,4,4	11.85	2 (100%)	0,6,6	0.00	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PO4	A	801	6	-	0/0/0/0	0/0/0/0
5	PO4	B	802	6	-	0/0/0/0	0/0/0/0
4	WO4	E	701	3	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PO4	F	803	6	-	0/0/0/0	0/0/0/0
5	PO4	G	804	6	-	0/0/0/0	0/0/0/0
4	WO4	J	702	3	-	0/0/0/0	0/0/0/0

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	701	WO4	W-O2	12.37	2.03	1.73
4	J	702	WO4	W-O2	12.37	2.03	1.73
4	J	702	WO4	W-O1	11.31	2.00	1.73
4	E	701	WO4	W-O1	11.21	2.00	1.73
5	G	804	PO4	P-O3	2.24	1.61	1.52
5	G	804	PO4	P-O2	2.11	1.61	1.52
5	A	801	PO4	P-O2	2.10	1.61	1.52
5	F	803	PO4	P-O2	2.02	1.60	1.52
5	B	802	PO4	P-O2	2.01	1.60	1.52

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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	240/240 (100%)	-0.33	0 100 100	32, 73, 148, 178	0
1	B	240/240 (100%)	-0.14	1 (0%) 90 45	60, 115, 183, 200	0
1	F	240/240 (100%)	-0.21	0 100 100	38, 96, 168, 197	0
1	G	240/240 (100%)	-0.01	1 (0%) 90 45	62, 134, 188, 200	0
2	C	252/284 (88%)	-0.40	0 100 100	33, 66, 134, 200	0
2	D	252/284 (88%)	-0.38	0 100 100	39, 76, 146, 200	0
2	H	252/284 (88%)	-0.24	1 (0%) 90 45	40, 93, 175, 199	0
2	I	252/284 (88%)	-0.24	0 100 100	52, 102, 169, 200	0
3	E	311/314 (99%)	-0.33	0 100 100	36, 81, 148, 188	0
3	J	310/314 (98%)	-0.23	0 100 100	32, 87, 156, 198	0
All	All	2589/2724 (95%)	-0.25	3 (0%) 93 70	32, 91, 169, 200	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	240	ASP	2.3
2	H	2	ARG	2.1
1	B	240	ASP	2.1

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 ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
6	MG	J	706	1/1	0.28	4.07	42,42,42,42	0
6	MG	B	702	1/1	0.20	0.37	87,87,87,87	0
6	MG	F	703	1/1	0.23	0.33	89,89,89,89	0
5	PO4	B	802	5/5	0.14	-0.46	84,84,84,84	0
4	WO4	E	701	5/5	0.19	-0.54	49,49,49,49	0
5	PO4	F	803	5/5	0.12	-0.64	60,60,60,60	0
6	MG	E	705	1/1	0.13	-1.02	86,86,86,86	0
6	MG	A	701	1/1	0.13	-1.59	75,75,75,75	0
4	WO4	J	702	5/5	0.20	-1.70	48,48,48,48	0
5	PO4	G	804	5/5	0.09	-1.91	99,99,99,99	0
5	PO4	A	801	5/5	0.09	-1.95	60,60,60,60	0
6	MG	G	704	1/1	0.11	-2.53	83,83,83,83	0

6.5 Other polymers ⓘ

There are no such residues in this entry.