



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 12:37 AM UTC

PDB ID : 9JDT / pdb_00009jdt
Title : Crystal structure of reductase NaAD
Authors : Tang, J.; Liuqing, C.
Deposited on : 2024-09-01
Resolution : 3.26 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

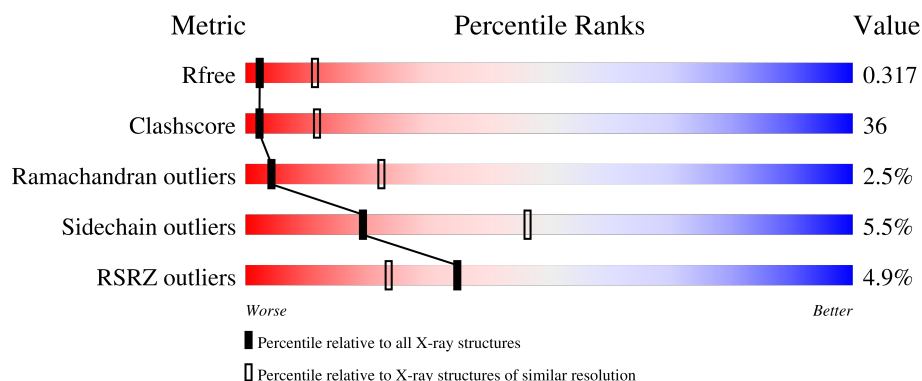
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.26 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1605 (3.30-3.22)
Clashscore	190562	1660 (3.30-3.22)
Ramachandran outliers	187476	1630 (3.30-3.22)
Sidechain outliers	187428	1629 (3.30-3.22)
RSRZ outliers	180081	1605 (3.30-3.22)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	266	3% 36% 53% 7% .
1	B	266	3% 39% 49% 8% .
1	C	266	6% 47% 42% 6% 5%
1	D	266	5% 44% 49% . .
1	E	266	8% 33% 54% 8% . .

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Mol	Chain	Length	Quality of chain
1	F	266	
1	G	266	
1	H	266	
1	I	266	
1	J	266	
1	K	266	
1	L	266	
1	M	266	
1	N	266	
1	O	266	
1	P	266	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 29767 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Short-chain dehydrogenase/reductase SDR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	256	Total	C	N	O	S	0	0	0
			1852	1161	325	352	14			
1	B	257	Total	C	N	O	S	0	0	0
			1860	1167	326	353	14			
1	C	254	Total	C	N	O	S	0	0	0
			1839	1152	323	350	14			
1	D	256	Total	C	N	O	S	0	0	0
			1852	1161	325	352	14			
1	E	255	Total	C	N	O	S	0	0	0
			1847	1158	324	351	14			
1	F	255	Total	C	N	O	S	0	0	0
			1847	1158	324	351	14			
1	G	255	Total	C	N	O	S	0	0	0
			1847	1158	324	351	14			
1	H	256	Total	C	N	O	S	0	0	0
			1852	1161	325	352	14			
1	I	257	Total	C	N	O	S	0	0	0
			1860	1167	326	353	14			
1	J	256	Total	C	N	O	S	0	0	0
			1852	1161	325	352	14			
1	K	256	Total	C	N	O	S	0	0	0
			1852	1161	325	352	14			
1	L	256	Total	C	N	O	S	0	0	0
			1852	1161	325	352	14			
1	M	255	Total	C	N	O	S	0	0	0
			1847	1158	324	351	14			
1	N	256	Total	C	N	O	S	0	0	0
			1852	1161	325	352	14			
1	O	255	Total	C	N	O	S	0	0	0
			1847	1158	324	351	14			
1	P	255	Total	C	N	O	S	0	0	0
			1847	1158	324	351	14			

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A4XEP2
A	2	HIS	-	expression tag	UNP A4XEP2
A	3	HIS	-	expression tag	UNP A4XEP2
A	4	HIS	-	expression tag	UNP A4XEP2
A	5	HIS	-	expression tag	UNP A4XEP2
A	6	HIS	-	expression tag	UNP A4XEP2
A	7	HIS	-	expression tag	UNP A4XEP2
A	148	ALA	GLY	conflict	UNP A4XEP2
A	202	LEU	ILE	conflict	UNP A4XEP2
B	1	MET	-	initiating methionine	UNP A4XEP2
B	2	HIS	-	expression tag	UNP A4XEP2
B	3	HIS	-	expression tag	UNP A4XEP2
B	4	HIS	-	expression tag	UNP A4XEP2
B	5	HIS	-	expression tag	UNP A4XEP2
B	6	HIS	-	expression tag	UNP A4XEP2
B	7	HIS	-	expression tag	UNP A4XEP2
B	148	ALA	GLY	conflict	UNP A4XEP2
B	202	LEU	ILE	conflict	UNP A4XEP2
C	1	MET	-	initiating methionine	UNP A4XEP2
C	2	HIS	-	expression tag	UNP A4XEP2
C	3	HIS	-	expression tag	UNP A4XEP2
C	4	HIS	-	expression tag	UNP A4XEP2
C	5	HIS	-	expression tag	UNP A4XEP2
C	6	HIS	-	expression tag	UNP A4XEP2
C	7	HIS	-	expression tag	UNP A4XEP2
C	148	ALA	GLY	conflict	UNP A4XEP2
C	202	LEU	ILE	conflict	UNP A4XEP2
D	1	MET	-	initiating methionine	UNP A4XEP2
D	2	HIS	-	expression tag	UNP A4XEP2
D	3	HIS	-	expression tag	UNP A4XEP2
D	4	HIS	-	expression tag	UNP A4XEP2
D	5	HIS	-	expression tag	UNP A4XEP2
D	6	HIS	-	expression tag	UNP A4XEP2
D	7	HIS	-	expression tag	UNP A4XEP2
D	148	ALA	GLY	conflict	UNP A4XEP2
D	202	LEU	ILE	conflict	UNP A4XEP2
E	1	MET	-	initiating methionine	UNP A4XEP2
E	2	HIS	-	expression tag	UNP A4XEP2
E	3	HIS	-	expression tag	UNP A4XEP2
E	4	HIS	-	expression tag	UNP A4XEP2
E	5	HIS	-	expression tag	UNP A4XEP2
E	6	HIS	-	expression tag	UNP A4XEP2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	7	HIS	-	expression tag	UNP A4XEP2
E	148	ALA	GLY	conflict	UNP A4XEP2
E	202	LEU	ILE	conflict	UNP A4XEP2
F	1	MET	-	initiating methionine	UNP A4XEP2
F	2	HIS	-	expression tag	UNP A4XEP2
F	3	HIS	-	expression tag	UNP A4XEP2
F	4	HIS	-	expression tag	UNP A4XEP2
F	5	HIS	-	expression tag	UNP A4XEP2
F	6	HIS	-	expression tag	UNP A4XEP2
F	7	HIS	-	expression tag	UNP A4XEP2
F	148	ALA	GLY	conflict	UNP A4XEP2
F	202	LEU	ILE	conflict	UNP A4XEP2
G	1	MET	-	initiating methionine	UNP A4XEP2
G	2	HIS	-	expression tag	UNP A4XEP2
G	3	HIS	-	expression tag	UNP A4XEP2
G	4	HIS	-	expression tag	UNP A4XEP2
G	5	HIS	-	expression tag	UNP A4XEP2
G	6	HIS	-	expression tag	UNP A4XEP2
G	7	HIS	-	expression tag	UNP A4XEP2
G	148	ALA	GLY	conflict	UNP A4XEP2
G	202	LEU	ILE	conflict	UNP A4XEP2
H	1	MET	-	initiating methionine	UNP A4XEP2
H	2	HIS	-	expression tag	UNP A4XEP2
H	3	HIS	-	expression tag	UNP A4XEP2
H	4	HIS	-	expression tag	UNP A4XEP2
H	5	HIS	-	expression tag	UNP A4XEP2
H	6	HIS	-	expression tag	UNP A4XEP2
H	7	HIS	-	expression tag	UNP A4XEP2
H	148	ALA	GLY	conflict	UNP A4XEP2
H	202	LEU	ILE	conflict	UNP A4XEP2
I	1	MET	-	initiating methionine	UNP A4XEP2
I	2	HIS	-	expression tag	UNP A4XEP2
I	3	HIS	-	expression tag	UNP A4XEP2
I	4	HIS	-	expression tag	UNP A4XEP2
I	5	HIS	-	expression tag	UNP A4XEP2
I	6	HIS	-	expression tag	UNP A4XEP2
I	7	HIS	-	expression tag	UNP A4XEP2
I	148	ALA	GLY	conflict	UNP A4XEP2
I	202	LEU	ILE	conflict	UNP A4XEP2
J	1	MET	-	initiating methionine	UNP A4XEP2
J	2	HIS	-	expression tag	UNP A4XEP2
J	3	HIS	-	expression tag	UNP A4XEP2

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Chain	Residue	Modelled	Actual	Comment	Reference
J	4	HIS	-	expression tag	UNP A4XEP2
J	5	HIS	-	expression tag	UNP A4XEP2
J	6	HIS	-	expression tag	UNP A4XEP2
J	7	HIS	-	expression tag	UNP A4XEP2
J	148	ALA	GLY	conflict	UNP A4XEP2
J	202	LEU	ILE	conflict	UNP A4XEP2
K	1	MET	-	initiating methionine	UNP A4XEP2
K	2	HIS	-	expression tag	UNP A4XEP2
K	3	HIS	-	expression tag	UNP A4XEP2
K	4	HIS	-	expression tag	UNP A4XEP2
K	5	HIS	-	expression tag	UNP A4XEP2
K	6	HIS	-	expression tag	UNP A4XEP2
K	7	HIS	-	expression tag	UNP A4XEP2
K	148	ALA	GLY	conflict	UNP A4XEP2
K	202	LEU	ILE	conflict	UNP A4XEP2
L	1	MET	-	initiating methionine	UNP A4XEP2
L	2	HIS	-	expression tag	UNP A4XEP2
L	3	HIS	-	expression tag	UNP A4XEP2
L	4	HIS	-	expression tag	UNP A4XEP2
L	5	HIS	-	expression tag	UNP A4XEP2
L	6	HIS	-	expression tag	UNP A4XEP2
L	7	HIS	-	expression tag	UNP A4XEP2
L	148	ALA	GLY	conflict	UNP A4XEP2
L	202	LEU	ILE	conflict	UNP A4XEP2
M	1	MET	-	initiating methionine	UNP A4XEP2
M	2	HIS	-	expression tag	UNP A4XEP2
M	3	HIS	-	expression tag	UNP A4XEP2
M	4	HIS	-	expression tag	UNP A4XEP2
M	5	HIS	-	expression tag	UNP A4XEP2
M	6	HIS	-	expression tag	UNP A4XEP2
M	7	HIS	-	expression tag	UNP A4XEP2
M	148	ALA	GLY	conflict	UNP A4XEP2
M	202	LEU	ILE	conflict	UNP A4XEP2
N	1	MET	-	initiating methionine	UNP A4XEP2
N	2	HIS	-	expression tag	UNP A4XEP2
N	3	HIS	-	expression tag	UNP A4XEP2
N	4	HIS	-	expression tag	UNP A4XEP2
N	5	HIS	-	expression tag	UNP A4XEP2
N	6	HIS	-	expression tag	UNP A4XEP2
N	7	HIS	-	expression tag	UNP A4XEP2
N	148	ALA	GLY	conflict	UNP A4XEP2
N	202	LEU	ILE	conflict	UNP A4XEP2

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Chain	Residue	Modelled	Actual	Comment	Reference
O	1	MET	-	initiating methionine	UNP A4XEP2
O	2	HIS	-	expression tag	UNP A4XEP2
O	3	HIS	-	expression tag	UNP A4XEP2
O	4	HIS	-	expression tag	UNP A4XEP2
O	5	HIS	-	expression tag	UNP A4XEP2
O	6	HIS	-	expression tag	UNP A4XEP2
O	7	HIS	-	expression tag	UNP A4XEP2
O	148	ALA	GLY	conflict	UNP A4XEP2
O	202	LEU	ILE	conflict	UNP A4XEP2
P	1	MET	-	initiating methionine	UNP A4XEP2
P	2	HIS	-	expression tag	UNP A4XEP2
P	3	HIS	-	expression tag	UNP A4XEP2
P	4	HIS	-	expression tag	UNP A4XEP2
P	5	HIS	-	expression tag	UNP A4XEP2
P	6	HIS	-	expression tag	UNP A4XEP2
P	7	HIS	-	expression tag	UNP A4XEP2
P	148	ALA	GLY	conflict	UNP A4XEP2
P	202	LEU	ILE	conflict	UNP A4XEP2

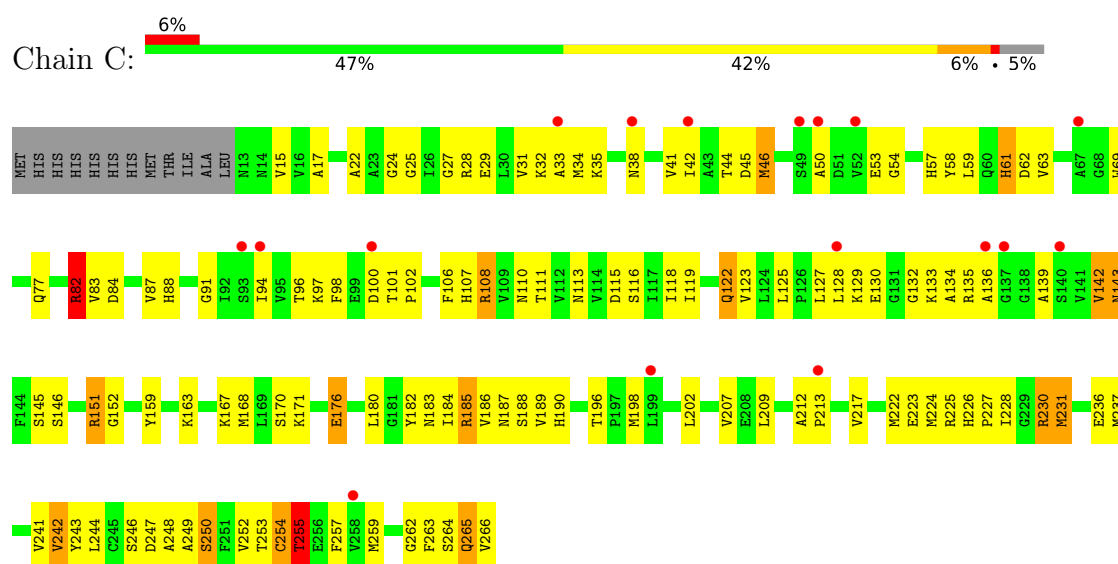
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	13	Total O 13 13	0	0
2	B	11	Total O 11 11	0	0
2	C	7	Total O 7 7	0	0
2	D	8	Total O 8 8	0	0
2	E	13	Total O 13 13	0	0
2	F	4	Total O 4 4	0	0
2	G	9	Total O 9 9	0	0
2	H	7	Total O 7 7	0	0
2	I	11	Total O 11 11	0	0
2	J	12	Total O 12 12	0	0

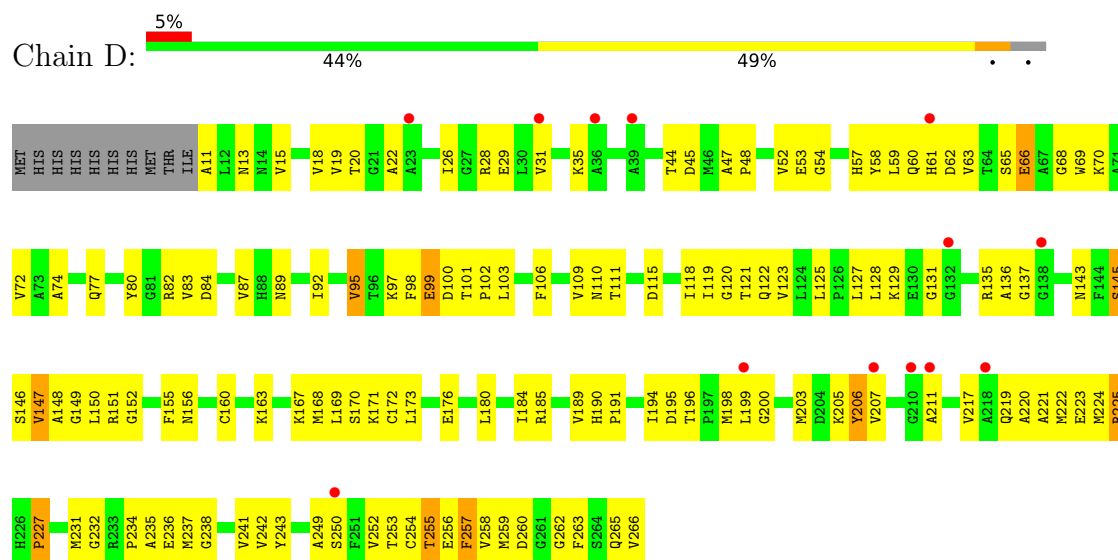
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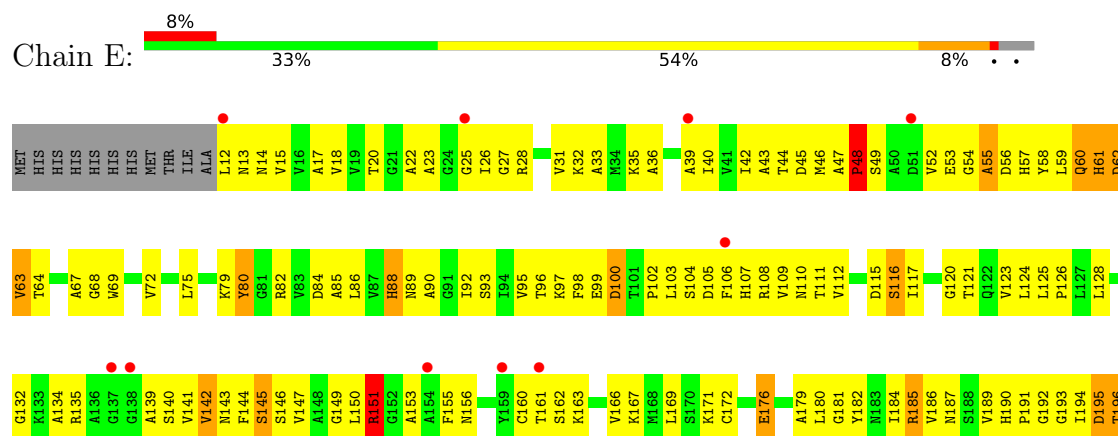
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	K	10	Total 10	O 10	0	0
2	L	7	Total 7	O 7	0	0
2	M	9	Total 9	O 9	0	0
2	N	12	Total 12	O 12	0	0
2	O	14	Total 14	O 14	0	0
2	P	15	Total 15	O 15	0	0

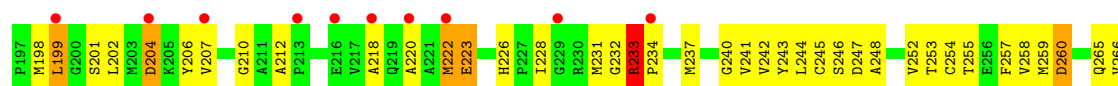


• Molecule 1: Short-chain dehydrogenase/reductase SDR

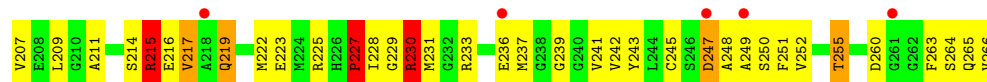
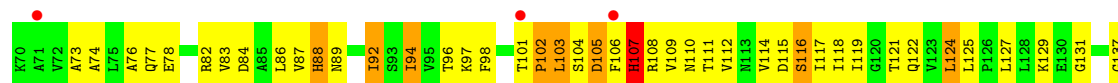


• Molecule 1: Short-chain dehydrogenase/reductase SDR

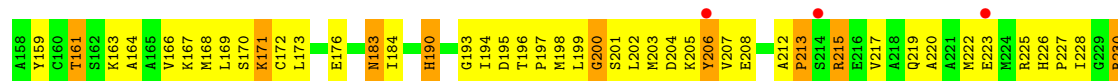
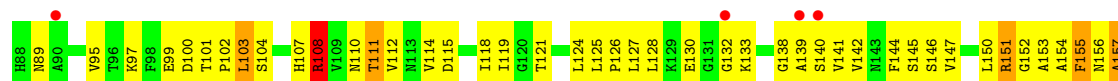
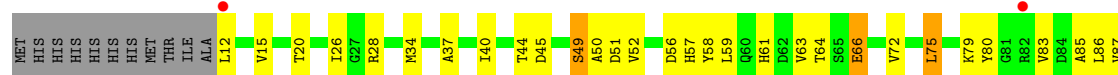
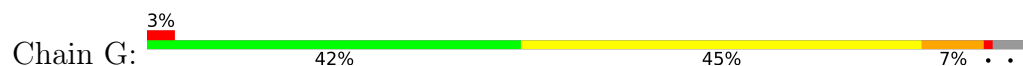




• Molecule 1: Short-chain dehydrogenase/reductase SDR

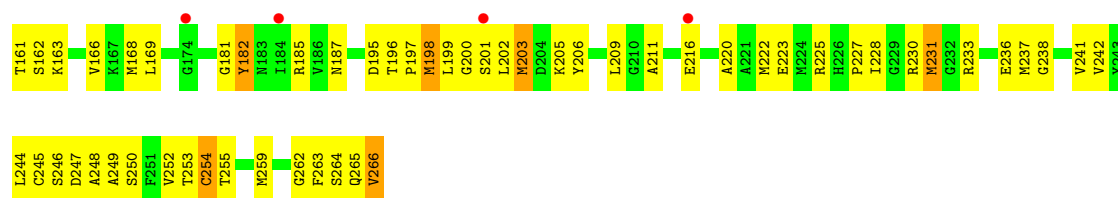


• Molecule 1: Short-chain dehydrogenase/reductase SDR

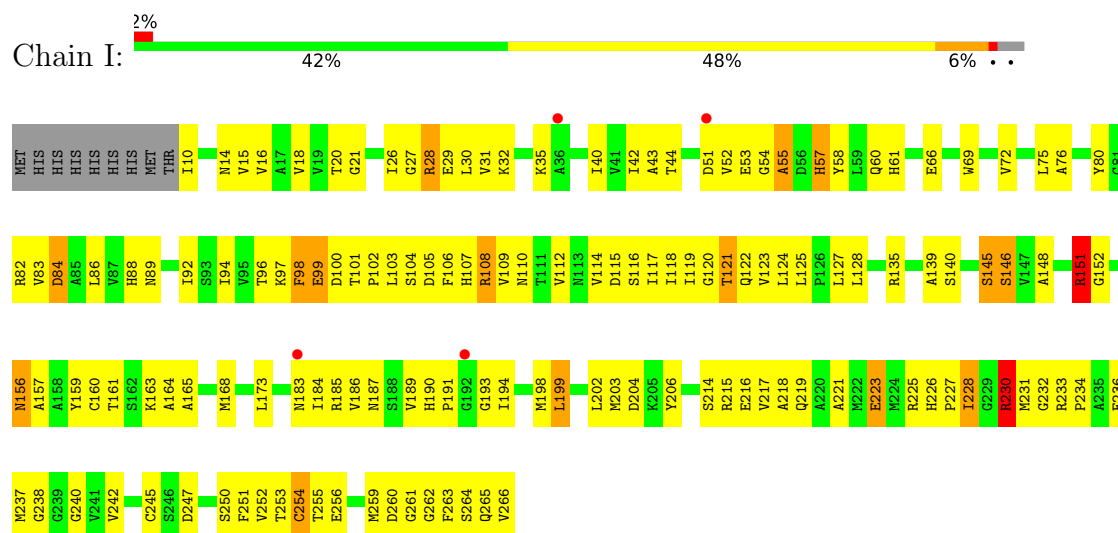


• Molecule 1: Short-chain dehydrogenase/reductase SDR

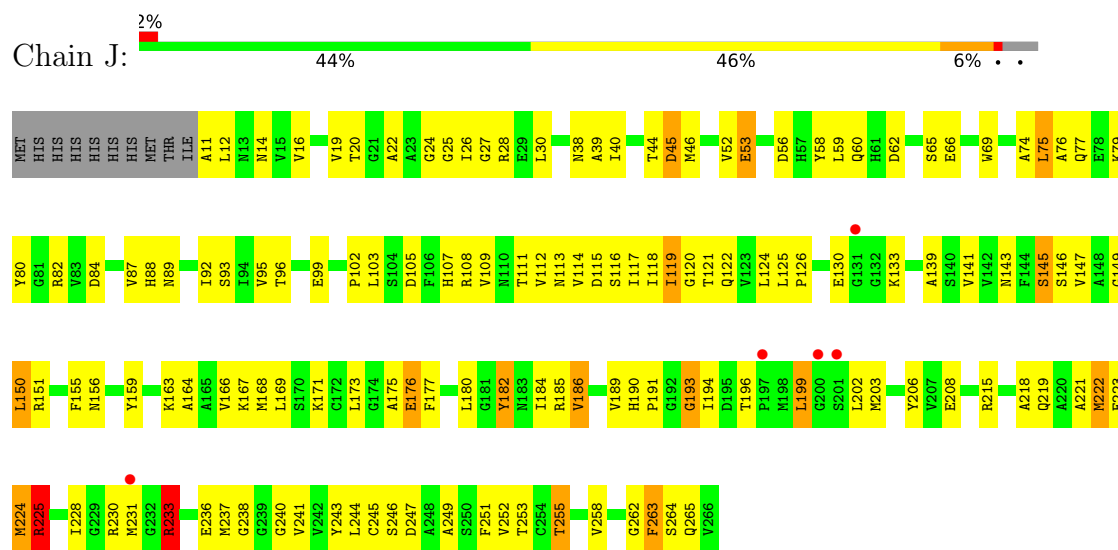




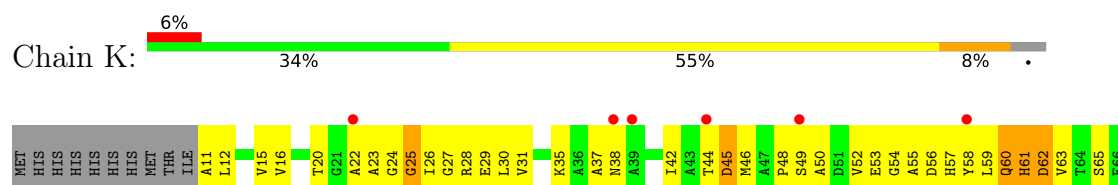
• Molecule 1: Short-chain dehydrogenase/reductase SDR

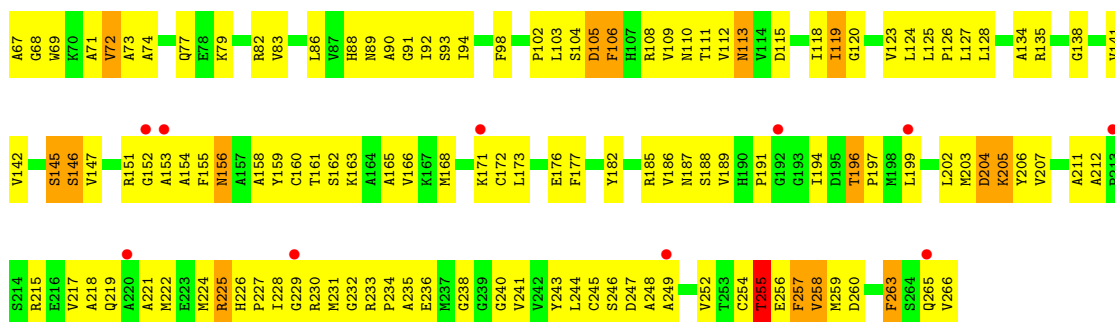


• Molecule 1: Short-chain dehydrogenase/reductase SDR

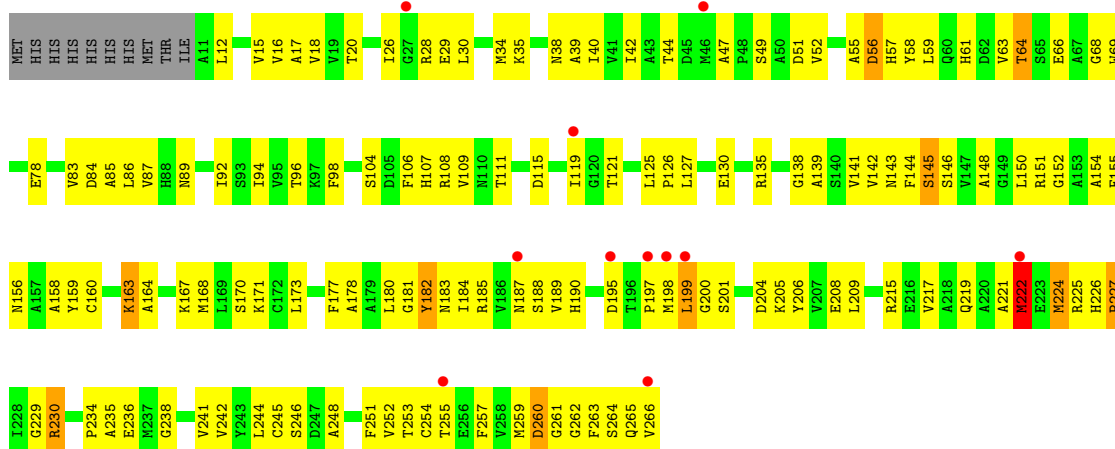
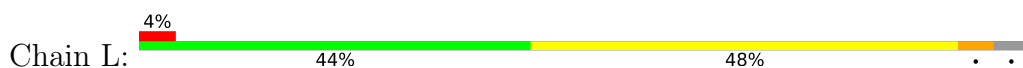


• Molecule 1: Short-chain dehydrogenase/reductase SDR

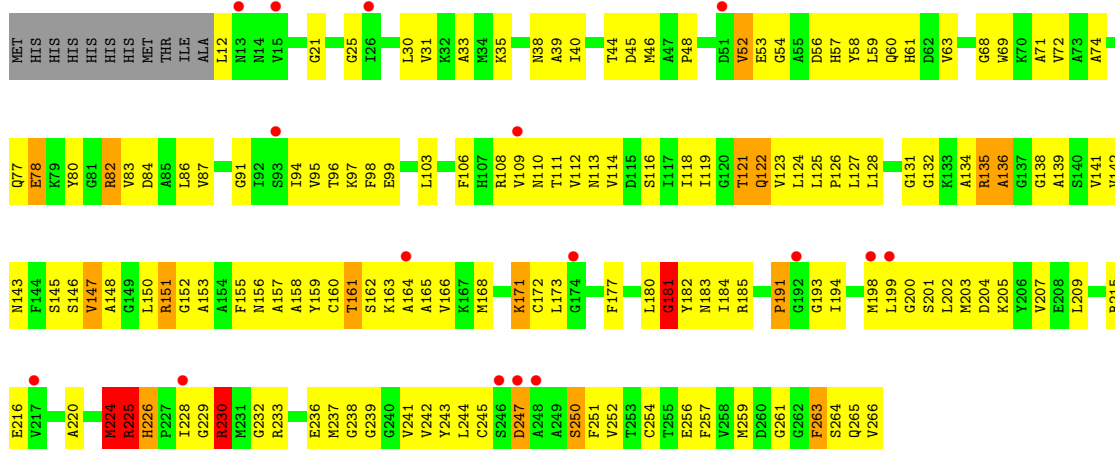




• Molecule 1: Short-chain dehydrogenase/reductase SDR

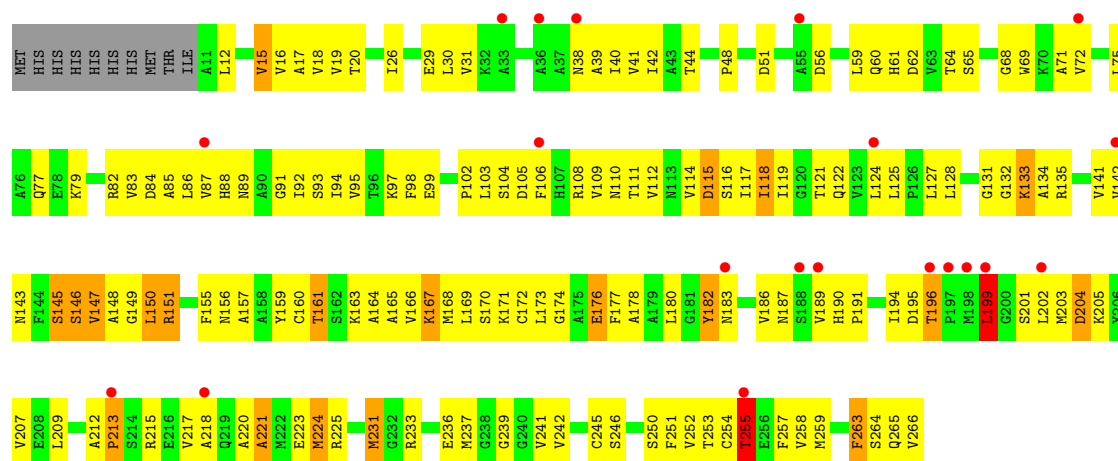


• Molecule 1: Short-chain dehydrogenase/reductase SDR

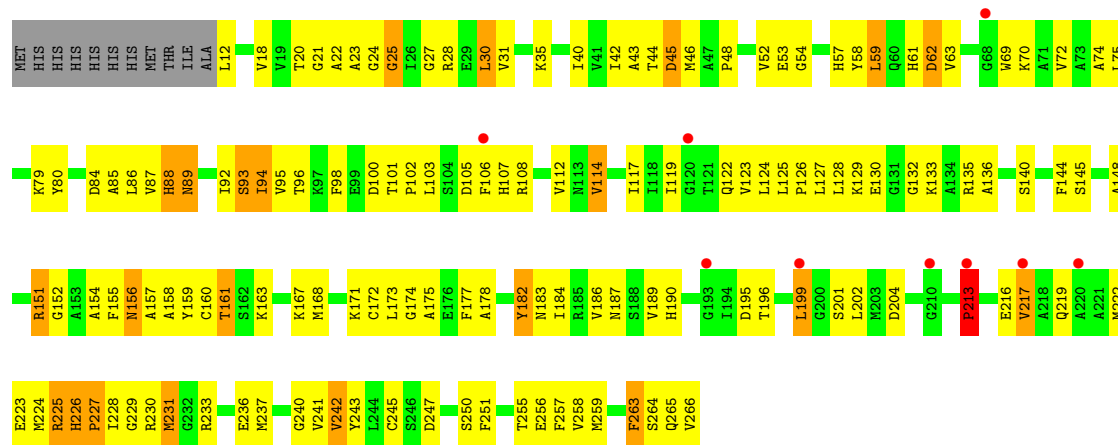


• Molecule 1: Short-chain dehydrogenase/reductase SDR

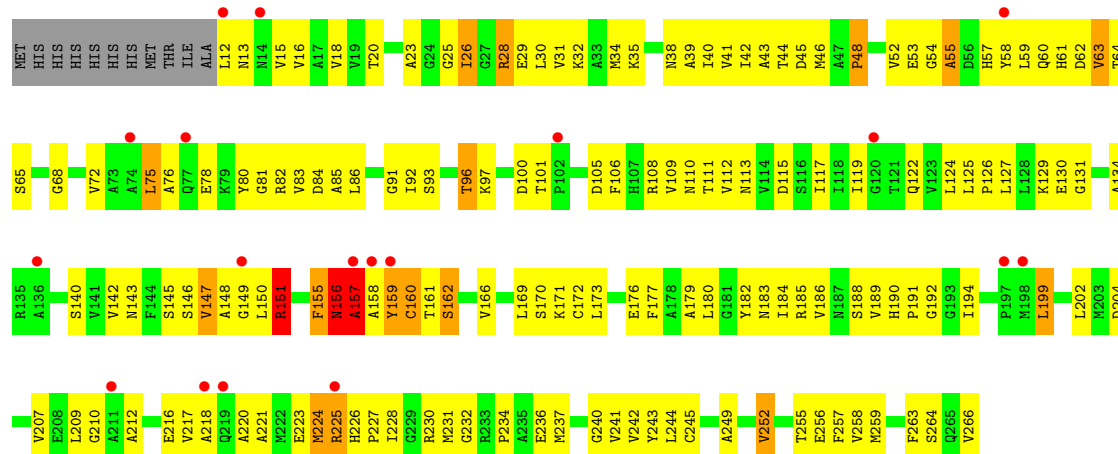




• Molecule 1: Short-chain dehydrogenase/reductase SDR



• Molecule 1: Short-chain dehydrogenase/reductase SDR



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.32Å 121.77Å 276.15Å 90.00° 93.40° 90.00°	Depositor
Resolution (Å)	20.00 – 3.26 20.00 – 3.26	Depositor EDS
% Data completeness (in resolution range)	99.0 (20.00-3.26) 81.0 (20.00-3.26)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.83 (at 3.26Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.260 , 0.300 0.273 , 0.317	Depositor DCC
R_{free} test set	752 reflections (1.37%)	wwPDB-VP
Wilson B-factor (Å ²)	44.8	Xtriage
Anisotropy	0.452	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 66.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	29767	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 59.28 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.8062e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	1.25	7/1881 (0.4%)	1.58	13/2548 (0.5%)
1	B	1.18	5/1889 (0.3%)	1.54	18/2559 (0.7%)
1	C	1.08	0/1868	1.49	18/2530 (0.7%)
1	D	1.11	1/1881 (0.1%)	1.47	9/2548 (0.4%)
1	E	1.26	7/1876 (0.4%)	1.55	17/2541 (0.7%)
1	F	1.22	7/1876 (0.4%)	1.50	11/2541 (0.4%)
1	G	1.19	5/1876 (0.3%)	1.59	21/2541 (0.8%)
1	H	1.18	6/1881 (0.3%)	1.49	9/2548 (0.4%)
1	I	1.13	4/1889 (0.2%)	1.46	11/2559 (0.4%)
1	J	1.19	5/1881 (0.3%)	1.52	9/2548 (0.4%)
1	K	1.19	6/1881 (0.3%)	1.57	17/2548 (0.7%)
1	L	1.11	1/1881 (0.1%)	1.45	14/2548 (0.5%)
1	M	1.11	3/1876 (0.2%)	1.47	13/2541 (0.5%)
1	N	1.14	3/1881 (0.2%)	1.51	17/2548 (0.7%)
1	O	1.20	6/1876 (0.3%)	1.46	12/2541 (0.5%)
1	P	1.26	5/1876 (0.3%)	1.55	19/2541 (0.7%)
All	All	1.18	71/30069 (0.2%)	1.51	228/40730 (0.6%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	4
1	C	0	2
1	D	0	1
1	E	0	3
1	F	0	3
1	G	0	4
1	H	0	2
1	I	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	J	0	4
1	K	0	1
1	L	0	3
1	M	0	8
1	O	0	2
1	P	0	2
All	All	0	44

All (71) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	P	157	ALA	C-O	17.84	1.46	1.24
1	E	176	GLU	CD-OE2	8.76	1.42	1.25
1	E	61	HIS	CG-CD2	-8.73	1.26	1.35
1	J	107	HIS	CG-CD2	-8.35	1.26	1.35
1	I	107	HIS	CD2-NE2	7.72	1.46	1.37
1	H	88	HIS	CE1-NE2	-7.66	1.24	1.32
1	A	226	HIS	CG-CD2	-7.48	1.27	1.35
1	O	107	HIS	CE1-NE2	7.38	1.40	1.32
1	I	230	ARG	NE-CZ	7.10	1.40	1.33
1	N	108	ARG	NE-CZ	7.05	1.40	1.33
1	H	152	GLY	C-O	-7.04	1.14	1.23
1	E	88	HIS	CD2-NE2	-6.95	1.30	1.37
1	H	92	ILE	C-O	-6.94	1.14	1.23
1	E	61	HIS	CE1-NE2	-6.91	1.25	1.32
1	E	55	ALA	C-O	-6.90	1.15	1.23
1	M	250	SER	C-O	6.85	1.32	1.24
1	O	240	GLY	C-O	-6.81	1.16	1.24
1	K	52	VAL	C-O	-6.78	1.16	1.24
1	A	88	HIS	CD2-NE2	-6.71	1.30	1.37
1	A	95	VAL	C-O	-6.61	1.17	1.24
1	H	233	ARG	NE-CZ	6.60	1.40	1.33
1	K	225	ARG	NE-CZ	6.58	1.40	1.33
1	M	226	HIS	CG-CD2	-6.49	1.28	1.35
1	H	99	GLU	CD-OE2	6.42	1.37	1.25
1	P	226	HIS	CE1-NE2	-6.30	1.26	1.32
1	N	29	GLU	CD-OE2	6.19	1.37	1.25
1	O	61	HIS	CD2-NE2	6.16	1.44	1.37
1	H	107	HIS	CE1-NE2	6.16	1.38	1.32
1	A	52	VAL	C-O	-6.07	1.17	1.24
1	A	107	HIS	CD2-NE2	6.07	1.44	1.37
1	E	195	ASP	CG-OD2	6.06	1.36	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	P	226	HIS	CG-CD2	-6.02	1.29	1.35
1	G	99	GLU	CD-OE2	5.99	1.36	1.25
1	B	118	ILE	C-N	5.97	1.41	1.33
1	K	88	HIS	CE1-NE2	5.94	1.38	1.32
1	F	66	GLU	CD-OE2	5.92	1.36	1.25
1	F	88	HIS	CG-CD2	-5.88	1.29	1.35
1	F	53	GLU	CD-OE2	5.84	1.36	1.25
1	O	61	HIS	CG-CD2	-5.74	1.29	1.35
1	F	92	ILE	C-O	5.72	1.29	1.23
1	P	156	ASN	C-O	-5.71	1.16	1.24
1	B	140	SER	C-O	-5.69	1.17	1.24
1	A	107	HIS	CG-CD2	-5.62	1.29	1.35
1	G	66	GLU	CD-OE2	5.62	1.36	1.25
1	J	176	GLU	CD-OE2	5.60	1.35	1.25
1	L	150	LEU	C-O	5.56	1.31	1.24
1	E	142	VAL	C-O	-5.51	1.18	1.24
1	D	66	GLU	CD-OE2	5.45	1.35	1.25
1	I	107	HIS	CG-CD2	-5.42	1.29	1.35
1	F	215	ARG	NE-CZ	5.40	1.39	1.33
1	G	157	ALA	C-O	5.38	1.30	1.24
1	N	176	GLU	CD-OE1	5.35	1.35	1.25
1	K	119	ILE	C-O	-5.34	1.18	1.24
1	F	53	GLU	CD-OE1	5.34	1.35	1.25
1	O	107	HIS	CG-CD2	5.31	1.41	1.35
1	F	185	ARG	NE-CZ	-5.28	1.27	1.33
1	B	195	ASP	CG-OD1	5.22	1.35	1.25
1	B	52	VAL	C-O	-5.17	1.18	1.24
1	I	57	HIS	CE1-NE2	5.16	1.37	1.32
1	B	76	ALA	C-O	-5.15	1.18	1.24
1	M	173	LEU	C-N	5.14	1.41	1.33
1	J	190	HIS	CE1-NE2	-5.13	1.27	1.32
1	K	105	ASP	CG-OD1	5.13	1.35	1.25
1	P	62	ASP	CG-OD2	5.12	1.35	1.25
1	G	190	HIS	CD2-NE2	5.11	1.43	1.37
1	J	186	VAL	C-O	-5.08	1.19	1.24
1	O	226	HIS	CG-CD2	-5.06	1.30	1.35
1	G	49	SER	CA-CB	5.04	1.61	1.53
1	A	193	GLY	C-O	5.03	1.30	1.23
1	K	188	SER	CA-CB	-5.02	1.45	1.53
1	J	93	SER	C-O	-5.01	1.17	1.23

All (228) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	265	GLN	OE1-CD-NE2	-10.14	112.46	122.60
1	C	143	ASN	CB-CA-C	-9.27	99.28	111.42
1	N	255	THR	OG1-CB-CG2	9.25	127.80	109.30
1	N	255	THR	CA-CB-OG1	-9.17	95.84	109.60
1	N	151	ARG	CB-CA-C	8.73	124.65	109.89
1	K	255	THR	OG1-CB-CG2	-8.70	91.90	109.30
1	I	107	HIS	CA-CB-CG	8.65	122.45	113.80
1	F	105	ASP	CA-CB-CG	8.59	121.19	112.60
1	K	60	GLN	OE1-CD-NE2	8.43	131.03	122.60
1	C	151	ARG	CD-NE-CZ	8.23	135.93	124.40
1	O	114	VAL	N-CA-CB	8.23	120.46	111.41
1	G	233	ARG	NE-CZ-NH1	-8.02	113.48	121.50
1	P	78	GLU	CB-CG-CD	8.02	126.24	112.60
1	O	247	ASP	CA-CB-CG	7.99	120.58	112.60
1	B	62	ASP	CA-CB-CG	7.73	120.33	112.60
1	E	253	THR	CA-CB-OG1	-7.65	98.12	109.60
1	G	20	THR	CA-CB-OG1	-7.64	98.14	109.60
1	L	222	MET	N-CA-C	-7.62	103.44	112.89
1	D	255	THR	CA-CB-OG1	-7.61	98.19	109.60
1	B	161	THR	CA-CB-OG1	-7.54	98.28	109.60
1	B	102	PRO	N-CA-CB	7.53	108.28	103.23
1	H	38	ASN	OD1-CG-ND2	-7.43	115.17	122.60
1	G	265	GLN	CG-CD-NE2	-7.37	105.34	116.40
1	F	161	THR	CA-CB-OG1	-7.31	98.63	109.60
1	H	222	MET	CG-SD-CE	7.21	116.77	100.90
1	B	251	PHE	CA-CB-CG	7.20	121.00	113.80
1	M	247	ASP	CA-CB-CG	7.19	119.79	112.60
1	P	156	ASN	CA-CB-CG	7.13	119.73	112.60
1	I	228	ILE	O-C-N	7.13	128.90	121.91
1	H	156	ASN	OD1-CG-ND2	7.11	129.71	122.60
1	K	156	ASN	OD1-CG-ND2	6.96	129.56	122.60
1	K	257	PHE	N-CA-CB	6.90	121.18	110.21
1	C	151	ARG	NE-CZ-NH1	-6.87	114.63	121.50
1	D	225	ARG	NH1-CZ-NH2	-6.86	110.38	119.30
1	I	84	ASP	CA-CB-CG	6.86	119.46	112.60
1	G	51	ASP	CA-CB-CG	6.85	119.45	112.60
1	E	233	ARG	CD-NE-CZ	6.82	133.95	124.40
1	G	161	THR	OG1-CB-CG2	-6.82	95.65	109.30
1	B	176	GLU	CB-CG-CD	6.81	124.18	112.60
1	P	84	ASP	CB-CA-C	6.78	121.54	110.83
1	G	265	GLN	OE1-CD-NE2	6.67	129.27	122.60
1	G	230	ARG	NH1-CZ-NH2	-6.63	110.67	119.30
1	M	143	ASN	CA-CB-CG	-6.60	106.00	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	115	ASP	CA-CB-CG	6.51	119.11	112.60
1	A	72	VAL	N-CA-C	-6.51	103.46	110.23
1	H	130	GLU	CB-CG-CD	6.47	123.59	112.60
1	N	224	MET	CG-SD-CE	6.42	115.02	100.90
1	P	224	MET	CB-CG-SD	6.41	131.94	112.70
1	N	196	THR	OG1-CB-CG2	-6.41	96.48	109.30
1	L	145	SER	O-C-N	6.35	126.23	121.47
1	B	117	ILE	O-C-N	6.34	128.12	121.91
1	H	121	THR	OG1-CB-CG2	-6.33	96.63	109.30
1	J	233	ARG	NH1-CZ-NH2	6.33	127.53	119.30
1	G	20	THR	OG1-CB-CG2	6.32	121.95	109.30
1	K	110	ASN	OD1-CG-ND2	6.27	128.87	122.60
1	G	230	ARG	NE-CZ-NH1	6.27	127.77	121.50
1	G	233	ARG	CA-CB-CG	6.26	126.63	114.10
1	E	62	ASP	CA-CB-CG	6.25	118.85	112.60
1	F	14	ASN	CB-CG-ND2	6.25	125.77	116.40
1	F	247	ASP	CA-CB-CG	6.21	118.81	112.60
1	J	175	ALA	O-C-N	6.18	128.46	122.03
1	P	156	ASN	O-C-N	-6.17	114.38	122.59
1	I	233	ARG	NE-CZ-NH2	6.15	124.73	119.20
1	E	151	ARG	CB-CA-C	6.14	120.13	110.19
1	B	105	ASP	CA-CB-CG	6.11	118.71	112.60
1	E	196	THR	CA-CB-OG1	-6.10	100.45	109.60
1	C	118	ILE	N-CA-C	-6.09	104.80	110.53
1	N	51	ASP	CA-CB-CG	6.06	118.66	112.60
1	C	230	ARG	N-CA-CB	-6.04	101.23	111.31
1	M	224	MET	CG-SD-CE	6.02	114.15	100.90
1	K	45	ASP	CA-CB-CG	6.01	118.61	112.60
1	C	108	ARG	NH1-CZ-NH2	-6.01	111.49	119.30
1	A	57	HIS	CB-CA-C	6.00	122.08	109.79
1	B	56	ASP	CA-CB-CG	5.99	118.59	112.60
1	D	100	ASP	CA-CB-CG	5.93	118.53	112.60
1	K	25	GLY	O-C-N	5.93	127.88	122.19
1	N	161	THR	CA-CB-OG1	-5.92	100.73	109.60
1	B	163	LYS	N-CA-C	-5.90	105.79	112.87
1	H	228	ILE	O-C-N	5.90	127.67	121.89
1	C	151	ARG	NH1-CZ-NH2	5.89	126.96	119.30
1	G	111	THR	CA-CB-OG1	-5.85	100.82	109.60
1	K	60	GLN	CG-CD-NE2	-5.85	107.63	116.40
1	J	247	ASP	CA-CB-CG	5.85	118.45	112.60
1	P	256	GLU	CB-CG-CD	5.84	122.53	112.60
1	A	183	ASN	CA-C-O	-5.84	114.47	120.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	110	ASN	OD1-CG-ND2	5.83	128.43	122.60
1	C	222	MET	CG-SD-CE	5.80	113.67	100.90
1	C	108	ARG	NE-CZ-NH2	5.79	124.42	119.20
1	B	100	ASP	CA-CB-CG	5.77	118.37	112.60
1	L	78	GLU	CG-CD-OE2	5.77	131.68	118.40
1	L	195	ASP	CA-CB-CG	5.77	118.37	112.60
1	E	223	GLU	CG-CD-OE1	5.75	131.63	118.40
1	K	62	ASP	CA-CB-CG	5.75	118.35	112.60
1	B	102	PRO	N-CA-C	-5.75	100.78	110.21
1	E	48	PRO	N-CA-C	5.75	124.31	112.47
1	O	241	VAL	CA-C-O	5.75	124.72	119.20
1	M	171	LYS	CB-CG-CD	5.71	124.43	111.30
1	M	216	GLU	CB-CG-CD	5.70	122.29	112.60
1	N	253	THR	CA-CB-OG1	-5.70	101.05	109.60
1	N	263	PHE	N-CA-CB	5.70	118.27	110.01
1	A	182	TYR	CA-C-N	-5.69	115.44	122.84
1	A	182	TYR	C-N-CA	-5.69	115.44	122.84
1	E	233	ARG	NE-CZ-NH1	-5.68	115.81	121.50
1	C	151	ARG	CA-C-N	5.68	125.50	120.10
1	C	151	ARG	C-N-CA	5.68	125.50	120.10
1	C	255	THR	CA-CB-OG1	-5.67	101.09	109.60
1	B	222	MET	CG-SD-CE	5.67	113.36	100.90
1	P	55	ALA	CA-C-O	-5.65	114.70	120.80
1	E	107	HIS	CA-CB-CG	5.65	119.45	113.80
1	L	181	GLY	O-C-N	5.63	127.79	122.50
1	M	52	VAL	CA-C-O	-5.62	114.45	120.85
1	A	183	ASN	O-C-N	5.61	129.73	123.05
1	M	141	VAL	N-CA-C	-5.60	100.28	109.12
1	G	171	LYS	N-CA-C	-5.59	104.87	110.97
1	M	25	GLY	N-CA-C	-5.59	108.52	114.67
1	B	84	ASP	CB-CA-C	5.59	118.85	110.08
1	A	130	GLU	CG-CD-OE1	-5.58	105.56	118.40
1	B	106	PHE	CA-CB-CG	5.57	119.37	113.80
1	C	122	GLN	OE1-CD-NE2	5.56	128.16	122.60
1	K	219	GLN	OE1-CD-NE2	-5.56	117.04	122.60
1	O	217	VAL	N-CA-C	-5.55	106.39	113.22
1	L	224	MET	N-CA-C	-5.54	106.36	113.01
1	L	215	ARG	NH1-CZ-NH2	5.54	126.50	119.30
1	P	151	ARG	NE-CZ-NH1	-5.54	115.96	121.50
1	P	162	SER	N-CA-C	5.53	118.23	111.82
1	D	227	PRO	N-CA-C	-5.52	106.34	113.57
1	F	227	PRO	N-CA-CB	5.52	109.04	103.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	131	GLY	N-CA-C	-5.52	108.28	114.40
1	P	129	LYS	CB-CA-C	5.49	119.49	110.88
1	D	225	ARG	NE-CZ-NH2	5.48	124.13	119.20
1	P	223	GLU	CB-CA-C	-5.47	101.70	110.79
1	E	14	ASN	OD1-CG-ND2	-5.45	117.15	122.60
1	G	233	ARG	CD-NE-CZ	5.45	132.02	124.40
1	P	252	VAL	N-CA-C	5.44	114.20	106.53
1	P	217	VAL	N-CA-C	-5.43	106.89	111.56
1	N	221	ALA	CA-C-N	5.43	127.50	120.44
1	N	221	ALA	C-N-CA	5.43	127.50	120.44
1	I	98	PHE	CA-CB-CG	5.42	119.22	113.80
1	I	183	ASN	N-CA-C	-5.40	104.39	112.54
1	O	62	ASP	N-CA-CB	5.39	118.44	109.60
1	E	253	THR	OG1-CB-CG2	5.38	120.07	109.30
1	J	208	GLU	CB-CG-CD	5.38	121.74	112.60
1	G	212	ALA	N-CA-C	-5.38	103.26	109.93
1	L	215	ARG	NE-CZ-NH1	-5.37	116.13	121.50
1	J	225	ARG	NE-CZ-NH1	-5.37	116.13	121.50
1	O	106	PHE	CA-CB-CG	5.37	119.17	113.80
1	L	219	GLN	N-CA-C	-5.37	106.67	113.43
1	M	122	GLN	CB-CA-C	-5.36	99.75	110.42
1	P	155	PHE	CA-C-O	-5.36	112.84	120.51
1	I	107	HIS	CB-CA-C	-5.36	102.40	110.92
1	K	247	ASP	CA-CB-CG	5.36	117.96	112.60
1	M	78	GLU	CB-CG-CD	5.35	121.70	112.60
1	G	183	ASN	N-CA-C	-5.35	106.53	112.57
1	L	150	LEU	CA-C-O	5.34	125.68	119.32
1	E	176	GLU	CG-CD-OE1	-5.34	106.12	118.40
1	G	233	ARG	NH1-CZ-NH2	5.34	126.24	119.30
1	O	30	LEU	N-CA-C	-5.34	105.36	111.07
1	P	28	ARG	CD-NE-CZ	5.34	131.87	124.40
1	F	217	VAL	CA-C-O	5.33	123.78	118.98
1	D	13	ASN	OD1-CG-ND2	-5.32	117.28	122.60
1	N	133	LYS	CB-CA-C	5.32	121.01	110.42
1	E	80	TYR	CB-CA-C	5.30	116.00	109.16
1	D	260	ASP	CA-CB-CG	5.30	117.90	112.60
1	I	121	THR	OG1-CB-CG2	-5.28	98.73	109.30
1	N	151	ARG	N-CA-CB	-5.28	101.64	110.57
1	I	223	GLU	N-CA-CB	5.28	118.12	110.26
1	B	98	PHE	CB-CA-C	5.27	119.12	110.95
1	O	213	PRO	N-CA-C	5.27	123.32	112.47
1	A	57	HIS	CB-CG-ND1	5.26	130.59	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	219	GLN	OE1-CD-NE2	-5.26	117.34	122.60
1	K	205	LYS	N-CA-CB	5.25	117.62	110.01
1	A	51	ASP	CA-CB-CG	5.25	117.85	112.60
1	E	222	MET	CG-SD-CE	5.25	112.44	100.90
1	I	247	ASP	CA-CB-CG	5.23	117.83	112.60
1	N	150	LEU	CA-C-O	5.23	125.13	118.54
1	C	176	GLU	CB-CG-CD	5.23	121.49	112.60
1	E	233	ARG	NH1-CZ-NH2	5.23	126.09	119.30
1	G	49	SER	N-CA-CB	5.22	119.31	110.49
1	J	45	ASP	CA-CB-CG	5.21	117.81	112.60
1	C	45	ASP	CB-CA-C	5.20	120.77	110.42
1	D	95	VAL	N-CA-CB	-5.20	104.91	111.46
1	E	260	ASP	CA-CB-CG	5.19	117.79	112.60
1	K	60	GLN	N-CA-CB	5.19	118.11	109.60
1	G	108	ARG	NE-CZ-NH1	-5.19	116.31	121.50
1	F	107	HIS	CA-CB-CG	5.19	118.99	113.80
1	H	151	ARG	CA-C-N	5.18	125.27	120.34
1	H	151	ARG	C-N-CA	5.18	125.27	120.34
1	K	72	VAL	N-CA-C	-5.18	105.79	110.82
1	P	45	ASP	CA-CB-CG	5.18	117.78	112.60
1	M	53	GLU	N-CA-CB	5.17	117.56	109.85
1	P	160	CYS	N-CA-C	-5.16	106.67	113.12
1	F	219	GLN	N-CA-C	-5.15	107.16	112.93
1	A	168	MET	CG-SD-CE	5.14	112.21	100.90
1	E	90	ALA	O-C-N	5.13	129.31	122.95
1	A	96	THR	CA-CB-OG1	-5.13	101.91	109.60
1	J	99	GLU	OE1-CD-OE2	5.12	135.20	122.90
1	J	14	ASN	OD1-CG-ND2	-5.11	117.49	122.60
1	J	44	THR	OG1-CB-CG2	5.11	119.52	109.30
1	N	199	LEU	CA-C-N	5.11	125.65	119.98
1	N	199	LEU	C-N-CA	5.11	125.65	119.98
1	F	153	ALA	N-CA-CB	5.10	119.12	110.49
1	G	50	ALA	N-CA-CB	-5.10	103.16	111.22
1	K	49	SER	CA-C-O	-5.10	115.99	121.45
1	I	230	ARG	CB-CG-CD	5.10	123.03	111.30
1	M	230	ARG	NE-CZ-NH1	-5.09	116.41	121.50
1	O	242	VAL	N-CA-C	-5.09	105.46	111.00
1	O	53	GLU	CB-CG-CD	5.08	121.24	112.60
1	L	163	LYS	CB-CA-C	5.07	118.81	110.95
1	F	45	ASP	CA-CB-CG	5.07	117.67	112.60
1	O	72	VAL	N-CA-C	-5.06	105.45	110.62
1	G	258	VAL	CA-C-O	-5.06	116.00	121.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	90	ALA	O-C-N	5.06	129.13	123.06
1	L	130	GLU	CB-CG-CD	5.06	121.20	112.60
1	A	29	GLU	N-CA-C	5.06	116.79	111.28
1	F	102	PRO	N-CA-C	-5.05	103.02	111.26
1	C	134	ALA	N-CA-C	5.05	118.48	111.71
1	O	45	ASP	CA-CB-CG	5.05	117.65	112.60
1	M	225	ARG	CG-CD-NE	5.05	123.11	112.00
1	C	46	MET	CG-SD-CE	5.05	112.00	100.90
1	H	231	MET	CB-CA-C	-5.04	101.62	109.84
1	L	260	ASP	CA-CB-CG	5.04	117.64	112.60
1	G	206	TYR	CB-CA-C	-5.04	102.38	110.74
1	P	130	GLU	CB-CA-C	-5.04	102.43	110.79
1	P	225	ARG	N-CA-CB	5.04	119.85	111.49
1	A	195	ASP	OD1-CG-OD2	5.03	134.98	122.90
1	K	176	GLU	CB-CG-CD	5.03	121.15	112.60
1	K	111	THR	CA-CB-OG1	-5.02	102.07	109.60
1	B	169	LEU	CD1-CG-CD2	-5.01	99.77	110.80

There are no chirality outliers.

All (44) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	225	ARG	Sidechain
1	B	108	ARG	Sidechain
1	B	11	ALA	Peptide
1	B	230	ARG	Sidechain
1	B	233	ARG	Sidechain
1	C	185	ARG	Sidechain
1	C	82	ARG	Sidechain
1	D	28	ARG	Sidechain
1	E	151	ARG	Sidechain
1	E	185	ARG	Sidechain
1	E	233	ARG	Sidechain
1	F	215	ARG	Sidechain
1	F	230	ARG	Sidechain
1	F	233	ARG	Sidechain
1	G	108	ARG	Sidechain
1	G	215	ARG	Sidechain
1	G	231	MET	Peptide
1	G	233	ARG	Sidechain
1	H	230	ARG	Sidechain
1	H	28	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	I	108	ARG	Sidechain
1	I	151	ARG	Sidechain
1	I	230	ARG	Sidechain
1	I	28	ARG	Sidechain
1	J	156	ASN	Peptide
1	J	185	ARG	Sidechain
1	J	225	ARG	Sidechain
1	J	233	ARG	Sidechain
1	K	225	ARG	Sidechain
1	L	108	ARG	Sidechain
1	L	230	ARG	Sidechain
1	L	28	ARG	Sidechain
1	M	108	ARG	Sidechain
1	M	135	ARG	Sidechain
1	M	151	ARG	Sidechain
1	M	181	GLY	Peptide
1	M	185	ARG	Sidechain
1	M	225	ARG	Sidechain
1	M	230	ARG	Sidechain
1	M	82	ARG	Sidechain
1	O	151	ARG	Sidechain
1	O	225	ARG	Sidechain
1	P	108	ARG	Sidechain
1	P	225	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1852	0	1857	161	0
1	B	1860	0	1868	131	1
1	C	1839	0	1841	124	1
1	D	1852	0	1857	142	0
1	E	1847	0	1852	173	0
1	F	1847	0	1852	169	0
1	G	1847	0	1852	157	0
1	H	1852	0	1857	137	0
1	I	1860	0	1868	170	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	1852	0	1857	108	0
1	K	1852	0	1857	176	0
1	L	1852	0	1857	133	0
1	M	1847	0	1852	152	0
1	N	1852	0	1857	166	0
1	O	1847	0	1852	147	0
1	P	1847	0	1852	163	0
2	A	13	0	0	3	0
2	B	11	0	0	1	0
2	C	7	0	0	6	0
2	D	8	0	0	2	0
2	E	13	0	0	1	0
2	F	4	0	0	2	0
2	G	9	0	0	0	0
2	H	7	0	0	0	0
2	I	11	0	0	2	0
2	J	12	0	0	0	0
2	K	10	0	0	2	0
2	L	7	0	0	6	0
2	M	9	0	0	3	0
2	N	12	0	0	1	0
2	O	14	0	0	0	0
2	P	15	0	0	0	0
All	All	29767	0	29688	2136	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 36.

All (2136) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:157:ALA:O	1:P:160:CYS:N	1.75	1.19
1:A:54:GLY:HA2	2:A:311:HOH:O	1.46	1.13
1:N:165:ALA:HB1	1:P:161:THR:HG23	1.32	1.10
1:A:12:LEU:HB3	1:A:39:ALA:HB2	1.37	1.06
1:P:158:ALA:HA	1:P:161:THR:HB	1.31	1.05
1:K:203:MET:HA	1:K:206:TYR:HD2	1.17	1.03
1:F:168:MET:HE3	1:H:148:ALA:O	1.61	1.01
1:I:226:HIS:HD2	1:I:260:ASP:O	1.42	1.00
1:M:138:GLY:HA3	1:M:183:ASN:O	1.62	0.99
1:I:266:VAL:HG12	1:M:152:GLY:H	1.24	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:265:GLN:O	1:O:151:ARG:HB2	1.62	0.98
1:K:203:MET:HA	1:K:206:TYR:CD2	1.99	0.97
1:F:230:ARG:HG3	1:F:230:ARG:HH11	1.30	0.96
1:F:168:MET:HG3	1:H:161:THR:HG22	1.44	0.96
1:B:118:ILE:HG23	1:C:98:PHE:HE1	1.29	0.96
1:A:227:PRO:HG3	1:A:266:VAL:HG21	1.47	0.95
1:N:155:PHE:HA	1:P:176:GLU:OE2	1.67	0.94
1:A:203:MET:HB3	1:A:218:ALA:HB1	1.47	0.94
1:I:266:VAL:HG23	1:M:151:ARG:HH21	1.33	0.93
1:F:155:PHE:HE2	1:F:211:ALA:HB2	1.33	0.93
1:M:12:LEU:HB3	1:M:39:ALA:HB2	1.48	0.93
1:K:86:LEU:HD22	1:K:124:LEU:HD12	1.49	0.92
1:O:145:SER:HA	1:O:163:LYS:HD2	1.51	0.92
1:M:139:ALA:HB3	1:M:184:ILE:HG12	1.49	0.92
1:C:35:LYS:HG3	1:C:54:GLY:O	1.70	0.91
1:K:91:GLY:HA2	1:K:112:VAL:HG12	1.53	0.91
1:D:189:VAL:HA	1:D:257:PHE:O	1.71	0.90
1:L:187:ASN:OD1	1:L:188:SER:N	2.03	0.90
1:M:132:GLY:HA2	1:M:138:GLY:HA2	1.51	0.90
1:M:99:GLU:OE2	1:O:182:TYR:HE2	1.55	0.90
1:I:226:HIS:CD2	1:I:260:ASP:O	2.25	0.90
1:K:134:ALA:O	1:K:135:ARG:HG3	1.72	0.89
1:G:151:ARG:HH21	1:G:153:ALA:HB2	1.37	0.89
1:C:82:ARG:CG	2:C:302:HOH:O	2.19	0.89
1:B:250:SER:OG	1:H:236:GLU:HG2	1.72	0.88
1:P:156:ASN:O	1:P:157:ALA:O	1.90	0.88
1:F:231:MET:HE2	2:F:301:HOH:O	1.73	0.87
1:I:152:GLY:O	1:M:266:VAL:HB	1.72	0.87
1:K:196:THR:HB	1:K:197:PRO:HD2	1.55	0.87
1:F:112:VAL:O	1:F:116:SER:HB3	1.75	0.87
1:P:157:ALA:O	1:P:160:CYS:HB2	1.75	0.86
1:G:163:LYS:HA	1:G:166:VAL:HB	1.58	0.86
1:E:22:ALA:HA	1:E:27:GLY:HA3	1.58	0.85
1:H:227:PRO:HG2	1:H:262:GLY:HA3	1.59	0.85
1:I:266:VAL:HG12	1:M:152:GLY:N	1.90	0.85
1:O:130:GLU:OE1	1:O:133:LYS:HE3	1.77	0.85
1:M:139:ALA:O	1:M:184:ILE:HA	1.77	0.84
1:E:22:ALA:HA	1:E:27:GLY:CA	2.07	0.84
1:E:187:ASN:HB3	1:E:255:THR:HG22	1.60	0.84
1:N:176:GLU:OE2	1:P:155:PHE:HA	1.77	0.83
1:N:189:VAL:HA	1:N:257:PHE:O	1.78	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:196:THR:HB	1:K:197:PRO:CD	2.08	0.83
1:I:157:ALA:O	1:I:161:THR:HG23	1.76	0.83
1:O:130:GLU:OE1	1:O:133:LYS:CE	2.26	0.83
1:P:156:ASN:O	1:P:157:ALA:C	2.10	0.83
1:B:118:ILE:HG23	1:C:98:PHE:CE1	2.13	0.83
1:C:82:ARG:HG2	2:C:302:HOH:O	1.76	0.83
1:E:63:VAL:HB	1:E:116:SER:HB2	1.60	0.83
1:N:165:ALA:HB1	1:P:161:THR:CG2	2.08	0.83
1:A:173:LEU:HD21	1:D:98:PHE:CD1	2.14	0.82
1:E:82:ARG:NH2	1:E:134:ALA:HB3	1.94	0.82
1:I:10:ILE:HG22	1:I:10:ILE:O	1.78	0.82
1:N:83:VAL:O	1:N:131:GLY:HA3	1.79	0.82
1:L:44:THR:HB	1:L:61:HIS:HB2	1.61	0.82
1:F:231:MET:CE	2:F:301:HOH:O	2.27	0.82
1:B:32:LYS:HE2	1:B:53:GLU:HB3	1.62	0.82
1:L:251:PHE:CD2	1:N:237:MET:HE1	2.15	0.82
1:C:82:ARG:CD	2:C:302:HOH:O	2.27	0.82
1:A:251:PHE:CD1	1:G:228:ILE:HD13	2.14	0.81
1:K:115:ASP:HA	1:K:118:ILE:HD12	1.62	0.81
1:G:86:LEU:HD22	1:G:128:LEU:HD11	1.62	0.81
1:H:253:THR:O	1:H:254:CYS:HB2	1.80	0.81
1:J:194:ILE:HD11	1:J:237:MET:HE3	1.62	0.81
1:L:87:VAL:HA	1:L:142:VAL:O	1.81	0.81
1:B:204:ASP:O	1:B:207:VAL:HB	1.80	0.81
1:P:158:ALA:HA	1:P:161:THR:CB	2.10	0.81
1:N:221:ALA:HB1	1:N:225:ARG:NH2	1.94	0.81
1:E:97:LYS:HB2	1:E:100:ASP:HB2	1.62	0.81
1:N:16:VAL:HB	1:N:84:ASP:H	1.45	0.81
1:C:142:VAL:HG11	1:C:241:VAL:HG13	1.63	0.81
1:A:77:GLN:HA	1:A:81:GLY:HA2	1.63	0.81
1:I:227:PRO:O	1:O:178:ALA:CB	2.28	0.80
1:G:151:ARG:HH21	1:G:153:ALA:CB	1.95	0.80
1:H:125:LEU:HG	1:H:129:LYS:HE3	1.62	0.80
1:F:215:ARG:O	1:F:219:GLN:HB2	1.81	0.79
1:N:91:GLY:HA2	1:N:112:VAL:HG12	1.64	0.79
1:D:171:LYS:HD3	1:E:265:GLN:HB3	1.63	0.79
1:K:259:MET:HA	1:M:252:VAL:HG22	1.62	0.79
1:B:101:THR:HG21	1:B:106:PHE:CD2	2.18	0.79
1:E:112:VAL:O	1:E:116:SER:HB3	1.82	0.79
1:N:236:GLU:HB2	1:N:237:MET:HE2	1.65	0.79
1:I:190:HIS:NE2	1:I:256:GLU:HA	1.97	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:168:MET:HG3	1:H:161:THR:CG2	2.12	0.79
1:F:168:MET:SD	1:H:160:CYS:HB3	2.23	0.79
1:B:106:PHE:CE1	1:B:158:ALA:HA	2.17	0.78
1:E:115:ASP:OD2	1:G:107:HIS:NE2	2.16	0.78
1:F:31:VAL:HG21	1:F:52:VAL:CG1	2.14	0.78
1:C:77:GLN:OE1	1:C:127:LEU:HD21	1.82	0.78
1:P:158:ALA:C	1:P:160:CYS:N	2.36	0.78
1:A:248:ALA:HB1	1:G:239:GLY:HA3	1.66	0.78
1:F:114:VAL:HG11	1:H:106:PHE:CZ	2.19	0.78
1:E:155:PHE:HA	1:G:176:GLU:OE2	1.83	0.77
1:P:157:ALA:O	1:P:160:CYS:CA	2.32	0.77
1:P:106:PHE:CE1	1:P:161:THR:HG21	2.20	0.77
1:L:17:ALA:HA	1:L:85:ALA:O	1.84	0.77
1:O:156:ASN:O	1:O:159:TYR:N	2.18	0.77
1:D:185:ARG:HD3	1:D:250:SER:O	1.84	0.77
1:J:199:LEU:HA	1:J:202:LEU:HD12	1.66	0.77
1:E:180:LEU:HB2	1:E:182:TYR:CE2	2.20	0.76
1:P:145:SER:HB3	1:P:190:HIS:ND1	2.00	0.76
1:I:194:ILE:HD11	1:I:237:MET:HE3	1.66	0.76
1:I:232:GLY:HA2	1:O:251:PHE:CE1	2.21	0.76
1:B:107:HIS:ND1	1:G:208:GLU:OE1	2.19	0.76
1:O:159:TYR:CE1	1:O:163:LYS:HG3	2.21	0.76
1:I:227:PRO:O	1:O:178:ALA:HB3	1.86	0.76
1:L:185:ARG:NH2	1:L:244:LEU:O	2.18	0.76
1:G:12:LEU:HD22	1:G:15:VAL:HG21	1.66	0.76
1:F:155:PHE:CE2	1:F:211:ALA:HB2	2.20	0.76
1:G:194:ILE:O	1:G:196:THR:N	2.19	0.75
1:O:237:MET:O	1:O:259:MET:HE1	1.86	0.75
1:P:192:GLY:O	1:P:194:ILE:HG12	1.86	0.75
1:D:203:MET:SD	1:D:219:GLN:HA	2.26	0.75
1:I:92:ILE:HG23	1:I:112:VAL:HG11	1.69	0.75
1:J:59:LEU:HD11	1:J:75:LEU:HD22	1.68	0.75
1:J:96:THR:O	1:J:155:PHE:HA	1.87	0.75
1:K:168:MET:SD	1:K:168:MET:O	2.44	0.75
1:J:243:TYR:OH	1:P:259:MET:HE3	1.87	0.74
1:P:106:PHE:HE1	1:P:161:THR:HG21	1.51	0.74
1:B:35:LYS:HG3	1:B:54:GLY:O	1.87	0.74
1:K:25:GLY:HA2	1:K:28:ARG:NH2	2.02	0.74
1:N:115:ASP:HA	1:N:118:ILE:HD12	1.68	0.74
1:F:168:MET:CE	1:H:148:ALA:O	2.36	0.74
1:G:49:SER:HA	1:G:58:TYR:CE2	2.22	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:168:MET:SD	1:K:172:CYS:SG	2.86	0.74
1:M:94:ILE:HD12	1:M:109:VAL:HG22	1.69	0.74
1:I:232:GLY:CA	1:O:251:PHE:CE1	2.71	0.73
1:O:167:LYS:HD2	1:O:256:GLU:OE1	1.88	0.73
1:L:29:GLU:OE2	1:L:235:ALA:HB2	1.88	0.73
1:M:68:GLY:O	1:M:71:ALA:HB3	1.88	0.73
1:B:86:LEU:HD22	1:B:124:LEU:HD12	1.69	0.73
1:A:265:GLN:NE2	1:G:256:GLU:HG3	2.03	0.73
1:E:32:LYS:HG2	1:E:53:GLU:HB3	1.69	0.73
1:I:97:LYS:O	1:I:101:THR:N	2.21	0.73
1:O:266:VAL:HG23	1:O:266:VAL:O	1.88	0.73
1:G:45:ASP:O	1:G:61:HIS:N	2.21	0.73
1:C:25:GLY:O	1:C:29:GLU:HG2	1.89	0.73
1:D:238:GLY:O	1:D:242:VAL:HG23	1.89	0.73
1:N:86:LEU:HD13	1:N:124:LEU:HD12	1.70	0.73
1:P:55:ALA:HB1	1:P:57:HIS:O	1.88	0.73
1:L:260:ASP:HB2	1:L:263:PHE:CB	2.18	0.73
1:D:29:GLU:HG3	1:D:234:PRO:HB2	1.69	0.72
1:A:11:ALA:N	2:A:301:HOH:O	2.21	0.72
1:M:151:ARG:HD3	1:M:263:PHE:HE1	1.54	0.72
1:N:149:GLY:O	1:N:150:LEU:HD23	1.90	0.72
1:A:227:PRO:HG3	1:A:266:VAL:CG2	2.17	0.72
1:B:228:ILE:HD12	1:H:253:THR:HG22	1.71	0.72
1:F:13:ASN:OD1	1:F:38:ASN:HB2	1.90	0.72
1:L:26:ILE:HA	1:L:234:PRO:HB3	1.70	0.72
1:N:180:LEU:HB3	1:N:182:TYR:CZ	2.25	0.72
1:I:238:GLY:O	1:I:242:VAL:HG23	1.88	0.72
1:P:252:VAL:HG12	1:P:255:THR:HG21	1.71	0.72
1:K:151:ARG:HB2	1:O:266:VAL:HA	1.72	0.72
1:B:63:VAL:HG21	1:B:90:ALA:HB1	1.71	0.72
1:M:91:GLY:HA2	1:M:112:VAL:HG12	1.72	0.72
1:J:95:VAL:HA	1:J:155:PHE:O	1.90	0.71
1:N:103:LEU:HD22	1:P:119:ILE:HD11	1.69	0.71
1:B:156:ASN:HB3	1:B:160:CYS:SG	2.30	0.71
1:M:180:LEU:O	1:M:182:TYR:N	2.23	0.71
1:N:221:ALA:HB1	1:N:225:ARG:CZ	2.20	0.71
1:P:157:ALA:O	1:P:160:CYS:CB	2.37	0.71
1:H:223:GLU:OE1	1:H:231:MET:HE2	1.89	0.71
1:I:98:PHE:CE2	1:K:173:LEU:HD13	2.25	0.71
1:A:47:ALA:HB3	1:A:58:TYR:OH	1.90	0.71
1:B:238:GLY:O	1:B:242:VAL:HG23	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:148:ALA:O	1:K:168:MET:HE3	1.90	0.71
1:B:107:HIS:HB2	1:G:208:GLU:HG2	1.73	0.71
1:D:95:VAL:HA	1:D:155:PHE:O	1.89	0.71
1:F:115:ASP:CG	1:H:103:LEU:HD11	2.16	0.71
1:I:186:VAL:O	1:I:254:CYS:N	2.19	0.71
1:K:141:VAL:N	1:K:185:ARG:O	2.22	0.70
1:C:145:SER:HG	1:C:146:SER:H	1.35	0.70
1:K:83:VAL:HG23	1:K:127:LEU:HD13	1.73	0.70
1:O:223:GLU:C	1:O:225:ARG:H	1.99	0.70
1:F:247:ASP:C	1:F:249:ALA:H	1.99	0.70
1:O:227:PRO:HG3	1:O:266:VAL:CG2	2.21	0.70
1:P:207:VAL:HA	1:P:212:ALA:O	1.90	0.70
1:I:94:ILE:HD12	1:I:105:ASP:CG	2.16	0.70
1:L:266:VAL:O	1:P:151:ARG:CZ	2.40	0.70
1:D:20:THR:O	1:D:89:ASN:HB3	1.92	0.70
1:G:226:HIS:CE1	1:G:263:PHE:HD2	2.09	0.70
1:M:132:GLY:HA2	1:M:138:GLY:CA	2.21	0.70
1:H:96:THR:HA	1:H:209:LEU:HD11	1.73	0.70
1:I:118:ILE:HD13	1:K:103:LEU:CD1	2.20	0.70
1:E:56:ASP:HB2	1:E:57:HIS:CD2	2.27	0.70
1:I:160:CYS:HB3	1:K:168:MET:SD	2.32	0.70
1:N:75:LEU:HD11	1:N:79:LYS:HE3	1.74	0.70
1:L:222:MET:HA	1:L:225:ARG:HD2	1.72	0.69
1:E:69:TRP:O	1:E:72:VAL:HB	1.92	0.69
1:B:29:GLU:HG3	1:B:234:PRO:HB2	1.73	0.69
1:J:24:GLY:O	1:J:28:ARG:NH1	2.25	0.69
1:E:93:SER:HB3	1:E:198:MET:SD	2.33	0.69
1:J:151:ARG:NH2	1:N:266:VAL:HB	2.07	0.69
1:A:221:ALA:O	1:A:225:ARG:HG3	1.92	0.69
1:E:32:LYS:HE2	1:E:53:GLU:HB3	1.73	0.69
1:F:223:GLU:OE1	1:F:231:MET:HE2	1.92	0.69
1:G:237:MET:HA	1:G:259:MET:CE	2.23	0.69
1:N:122:GLN:NE2	1:P:101:THR:O	2.25	0.69
1:O:155:PHE:C	1:O:157:ALA:H	2.01	0.69
1:A:161:THR:HG22	1:D:169:LEU:HA	1.75	0.69
1:A:192:GLY:O	1:A:194:ILE:HG12	1.93	0.69
1:B:266:VAL:HG23	1:B:266:VAL:O	1.92	0.69
1:G:132:GLY:HA3	1:G:183:ASN:HB3	1.75	0.69
1:G:133:LYS:HB3	1:K:217:VAL:HG11	1.73	0.69
1:I:89:ASN:CG	1:I:89:ASN:O	2.35	0.69
1:O:27:GLY:HA2	1:O:30:LEU:HD12	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:94:ILE:HD11	1:K:108:ARG:HH21	1.58	0.69
1:K:215:ARG:NH2	2:K:301:HOH:O	2.25	0.69
1:C:230:ARG:HH22	1:C:236:GLU:CD	2.01	0.68
1:E:193:GLY:HA3	1:E:222:MET:SD	2.32	0.68
1:K:258:VAL:HG12	1:K:260:ASP:CG	2.18	0.68
1:L:64:THR:HG22	1:L:111:THR:O	1.94	0.68
1:N:65:SER:O	1:N:69:TRP:HD1	1.75	0.68
1:N:114:VAL:HG22	1:N:166:VAL:HG23	1.73	0.68
1:D:66:GLU:HG3	1:D:123:VAL:HG21	1.75	0.68
1:D:145:SER:OG	1:D:146:SER:N	2.27	0.68
1:J:262:GLY:O	1:J:263:PHE:C	2.37	0.68
1:N:111:THR:HA	1:N:115:ASP:CG	2.19	0.68
1:A:67:ALA:HA	1:A:70:LYS:HD2	1.75	0.68
1:D:111:THR:HA	1:D:115:ASP:HB2	1.74	0.68
1:I:96:THR:HG23	1:I:101:THR:OG1	1.93	0.68
1:N:97:LYS:HA	1:N:155:PHE:HD1	1.59	0.68
1:P:83:VAL:HG21	1:P:124:LEU:HD13	1.76	0.68
1:A:191:PRO:HB3	1:A:237:MET:SD	2.34	0.68
1:E:176:GLU:OE2	1:G:157:ALA:HB2	1.93	0.68
1:H:199:LEU:HA	1:H:202:LEU:HG	1.74	0.68
1:H:206:TYR:O	1:H:211:ALA:HB3	1.94	0.68
1:P:92:ILE:HD11	1:P:109:VAL:HG22	1.75	0.68
1:N:103:LEU:HD21	1:P:115:ASP:OD1	1.93	0.68
1:K:142:VAL:HG22	1:K:244:LEU:HD13	1.74	0.67
1:E:146:SER:HA	1:E:191:PRO:HD2	1.77	0.67
1:K:27:GLY:O	1:K:31:VAL:HG23	1.94	0.67
1:A:203:MET:HE2	1:A:222:MET:HE3	1.76	0.67
1:C:213:PRO:HD2	1:C:217:VAL:HG11	1.75	0.67
1:P:158:ALA:O	1:P:159:TYR:C	2.35	0.67
1:F:102:PRO:C	1:F:104:SER:H	2.01	0.67
1:H:227:PRO:HG3	1:H:266:VAL:CG2	2.25	0.67
1:I:118:ILE:CD1	1:K:103:LEU:CD1	2.72	0.67
1:I:227:PRO:O	1:O:178:ALA:HB1	1.94	0.67
1:D:151:ARG:HD3	1:D:263:PHE:CE2	2.30	0.67
1:E:69:TRP:CD2	1:E:120:GLY:HA2	2.29	0.67
1:L:89:ASN:ND2	2:L:302:HOH:O	2.27	0.67
1:N:97:LYS:HE2	1:N:209:LEU:HD23	1.76	0.67
1:E:63:VAL:CB	1:E:116:SER:HB2	2.24	0.67
1:H:151:ARG:HH12	1:H:225:ARG:NE	1.93	0.67
1:A:151:ARG:NE	1:E:266:VAL:C	2.53	0.67
1:B:101:THR:CG2	1:B:106:PHE:HD2	2.08	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:99:GLU:OE2	1:O:182:TYR:CE2	2.45	0.67
1:O:96:THR:HG23	1:O:101:THR:OG1	1.94	0.67
1:P:241:VAL:HA	1:P:244:LEU:HD12	1.76	0.67
1:O:223:GLU:O	1:O:225:ARG:N	2.28	0.67
1:B:150:LEU:HD12	1:B:190:HIS:ND1	2.10	0.67
1:F:96:THR:HG21	1:F:101:THR:HG22	1.74	0.67
1:F:216:GLU:HA	1:F:219:GLN:HB3	1.77	0.67
1:G:26:ILE:HG13	1:G:196:THR:HG21	1.77	0.67
1:L:251:PHE:HD2	1:N:237:MET:HE1	1.60	0.67
1:H:227:PRO:HG3	1:H:266:VAL:HG21	1.77	0.67
1:K:185:ARG:NH1	1:K:244:LEU:O	2.27	0.67
1:L:52:VAL:HB	1:L:55:ALA:HB2	1.77	0.67
1:L:197:PRO:HD2	2:L:306:HOH:O	1.93	0.67
1:L:197:PRO:HG2	2:L:306:HOH:O	1.95	0.67
1:M:135:ARG:O	1:M:136:ALA:C	2.37	0.67
1:L:94:ILE:HG22	1:L:96:THR:HG22	1.77	0.66
1:D:253:THR:HG21	1:E:228:ILE:HD12	1.77	0.66
1:K:125:LEU:HB3	1:K:126:PRO:HD3	1.76	0.66
1:F:102:PRO:C	1:F:104:SER:N	2.53	0.66
1:I:152:GLY:H	1:M:266:VAL:HG12	1.61	0.66
1:P:63:VAL:HG23	1:P:63:VAL:O	1.95	0.66
1:H:153:ALA:HB3	1:H:160:CYS:SG	2.36	0.66
1:N:16:VAL:H	1:N:84:ASP:HB2	1.59	0.66
1:F:145:SER:HB3	1:F:190:HIS:CD2	2.31	0.66
1:F:185:ARG:HD2	1:F:252:VAL:O	1.96	0.66
1:J:146:SER:O	1:J:149:GLY:N	2.29	0.66
1:K:196:THR:CB	1:K:197:PRO:CD	2.74	0.66
1:P:31:VAL:HG11	1:P:52:VAL:HG12	1.78	0.66
1:E:63:VAL:CG2	1:E:116:SER:HB2	2.25	0.66
1:N:160:CYS:HB2	1:P:172:CYS:SG	2.36	0.66
1:A:76:ALA:O	1:A:81:GLY:N	2.29	0.66
1:E:198:MET:HE3	1:E:202:LEU:HD12	1.78	0.66
1:K:196:THR:CB	1:K:197:PRO:HD2	2.26	0.66
1:M:82:ARG:HH21	1:M:131:GLY:HA2	1.61	0.66
1:H:94:ILE:O	1:H:94:ILE:HG22	1.94	0.65
1:A:97:LYS:HE2	1:D:180:LEU:HD21	1.78	0.65
1:C:187:ASN:HB2	1:C:244:LEU:HD13	1.78	0.65
1:K:206:TYR:O	1:K:211:ALA:HB3	1.96	0.65
1:A:136:ALA:O	1:A:183:ASN:ND2	2.28	0.65
1:B:48:PRO:HA	1:B:60:GLN:HB2	1.78	0.65
1:C:151:ARG:HD3	1:C:264:SER:HA	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:92:ILE:HD11	1:J:109:VAL:HA	1.78	0.65
1:K:68:GLY:O	1:K:71:ALA:HB3	1.95	0.65
1:N:160:CYS:CB	1:P:172:CYS:SG	2.84	0.65
1:P:145:SER:CB	1:P:190:HIS:ND1	2.60	0.65
1:H:195:ASP:HA	1:H:199:LEU:HD23	1.79	0.65
1:J:26:ILE:HD11	1:J:194:ILE:HG21	1.76	0.65
1:P:16:VAL:HG11	1:P:80:TYR:CD2	2.31	0.65
1:A:266:VAL:C	1:E:151:ARG:HE	2.03	0.65
1:B:97:LYS:HG3	1:B:209:LEU:HD22	1.79	0.65
1:I:118:ILE:HA	1:K:98:PHE:HZ	1.61	0.65
1:I:190:HIS:NE2	1:I:256:GLU:CA	2.59	0.65
1:J:262:GLY:O	1:J:264:SER:N	2.29	0.65
1:O:85:ALA:HA	1:O:140:SER:O	1.96	0.65
1:P:106:PHE:HE1	1:P:161:THR:CG2	2.10	0.65
1:G:144:PHE:O	1:G:166:VAL:HG11	1.97	0.65
1:F:97:LYS:O	1:F:101:THR:HG23	1.97	0.65
1:I:139:ALA:HB3	1:I:184:ILE:HA	1.79	0.65
1:L:16:VAL:HG22	1:L:40:ILE:HD12	1.79	0.65
1:F:203:MET:HA	1:F:206:TYR:HD2	1.62	0.65
1:K:185:ARG:HD2	1:K:249:ALA:O	1.96	0.65
1:M:74:ALA:HA	1:M:77:GLN:HB3	1.78	0.65
1:M:87:VAL:O	1:M:87:VAL:HG12	1.97	0.65
1:J:230:ARG:NH1	1:J:231:MET:O	2.29	0.65
1:A:151:ARG:CZ	1:E:266:VAL:C	2.70	0.64
1:H:158:ALA:O	1:H:162:SER:N	2.24	0.64
1:M:238:GLY:O	1:M:242:VAL:HG23	1.97	0.64
1:F:20:THR:O	1:F:89:ASN:HB3	1.95	0.64
1:K:232:GLY:HA3	1:M:251:PHE:CG	2.32	0.64
1:O:151:ARG:HD3	1:O:263:PHE:HE1	1.62	0.64
1:E:102:PRO:HD2	1:E:105:ASP:HB2	1.78	0.64
1:F:106:PHE:O	1:F:110:ASN:ND2	2.31	0.64
1:H:196:THR:HB	1:H:197:PRO:CD	2.28	0.64
1:M:145:SER:O	1:M:191:PRO:HD2	1.97	0.64
1:N:99:GLU:HB3	1:P:125:LEU:HD23	1.79	0.64
1:O:69:TRP:HB3	1:O:123:VAL:HG11	1.80	0.64
1:O:94:ILE:HG22	1:O:158:ALA:HB3	1.79	0.64
1:G:79:LYS:HB2	1:G:80:TYR:CE2	2.32	0.64
1:G:237:MET:HA	1:G:259:MET:HE2	1.80	0.64
1:L:106:PHE:CE1	1:L:158:ALA:HA	2.33	0.64
1:O:213:PRO:HB2	1:O:217:VAL:HG21	1.79	0.64
1:P:29:GLU:HG3	1:P:234:PRO:HB2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:185:ARG:CD	1:D:250:SER:O	2.46	0.64
1:E:185:ARG:NH1	1:E:244:LEU:O	2.29	0.64
1:G:12:LEU:CD2	1:G:15:VAL:HG21	2.27	0.64
1:K:229:GLY:O	1:K:230:ARG:HB3	1.98	0.64
1:M:31:VAL:HG11	1:M:52:VAL:HG12	1.79	0.64
1:A:183:ASN:O	1:A:184:ILE:HG13	1.97	0.64
1:K:124:LEU:O	1:K:128:LEU:HG	1.97	0.64
1:M:182:TYR:HB3	1:M:184:ILE:HD12	1.79	0.64
1:K:44:THR:HB	1:K:61:HIS:HB3	1.80	0.64
1:K:142:VAL:HG22	1:K:244:LEU:CD1	2.28	0.64
1:M:162:SER:HA	1:M:165:ALA:HB3	1.79	0.64
1:P:97:LYS:HG3	1:P:209:LEU:HD22	1.79	0.64
1:H:18:VAL:HG22	1:H:42:ILE:HB	1.80	0.64
1:K:11:ALA:N	2:K:302:HOH:O	2.31	0.64
1:K:248:ALA:HB1	1:M:239:GLY:HA3	1.79	0.64
1:A:21:GLY:HA2	1:A:45:ASP:OD2	1.97	0.64
1:C:167:LYS:O	1:C:170:SER:HB2	1.98	0.64
1:I:123:VAL:HG12	1:I:124:LEU:HD23	1.80	0.64
1:K:147:VAL:HG11	1:K:260:ASP:HB2	1.80	0.64
1:G:111:THR:HA	1:G:115:ASP:HB2	1.79	0.64
1:A:161:THR:HG22	1:D:169:LEU:CA	2.27	0.63
1:B:19:VAL:O	1:B:22:ALA:HB2	1.97	0.63
1:G:151:ARG:CZ	1:G:152:GLY:O	2.45	0.63
1:B:147:VAL:HG11	1:B:263:PHE:HB3	1.81	0.63
1:M:125:LEU:HB3	1:M:126:PRO:HD3	1.79	0.63
1:O:125:LEU:O	1:O:129:LYS:HG3	1.97	0.63
1:O:263:PHE:CD1	1:O:263:PHE:C	2.75	0.63
1:C:82:ARG:HD3	2:C:302:HOH:O	1.94	0.63
1:L:58:TYR:C	1:L:59:LEU:HD12	2.23	0.63
1:O:226:HIS:O	1:O:229:GLY:N	2.30	0.63
1:E:246:SER:C	1:E:248:ALA:H	2.06	0.63
1:H:12:LEU:HD21	1:H:242:VAL:HG13	1.78	0.63
1:H:16:VAL:N	1:H:84:ASP:OD2	2.27	0.63
1:N:146:SER:C	1:N:148:ALA:H	2.06	0.63
1:B:101:THR:HG21	1:B:106:PHE:HD2	1.63	0.63
1:B:159:TYR:CZ	1:B:163:LYS:HG3	2.33	0.63
1:C:152:GLY:C	1:H:266:VAL:HG12	2.24	0.63
1:C:265:GLN:HG3	1:F:255:THR:HA	1.79	0.63
1:K:113:ASN:HB2	1:K:162:SER:HB2	1.81	0.63
1:C:145:SER:OG	1:C:146:SER:N	2.31	0.63
1:C:152:GLY:CA	1:H:266:VAL:HG12	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:225:ARG:HD3	1:D:263:PHE:HE1	1.62	0.63
1:G:151:ARG:HD3	1:G:263:PHE:HE1	1.63	0.63
1:M:35:LYS:HG3	1:M:54:GLY:O	1.98	0.63
1:E:187:ASN:CB	1:E:255:THR:HG22	2.29	0.63
1:F:145:SER:O	1:F:191:PRO:HD3	1.99	0.63
1:F:168:MET:CG	1:H:161:THR:HG22	2.25	0.63
1:I:69:TRP:O	1:I:72:VAL:HB	1.98	0.63
1:L:261:GLY:HA2	1:N:251:PHE:O	1.99	0.63
1:M:145:SER:C	1:M:191:PRO:HD2	2.24	0.63
1:B:125:LEU:HD12	1:B:184:ILE:HD13	1.81	0.62
1:D:265:GLN:OE1	1:E:171:LYS:HE2	1.99	0.62
1:E:45:ASP:OD1	1:E:46:MET:N	2.32	0.62
1:J:173:LEU:HD22	1:J:177:PHE:CZ	2.33	0.62
1:K:102:PRO:HG2	1:K:105:ASP:OD2	1.99	0.62
1:G:169:LEU:O	1:G:172:CYS:N	2.33	0.62
1:H:135:ARG:NH2	1:H:245:CYS:O	2.32	0.62
1:K:26:ILE:HD11	1:K:194:ILE:HG21	1.81	0.62
1:M:46:MET:O	1:M:60:GLN:HG3	2.00	0.62
1:M:118:ILE:HG23	1:O:98:PHE:HE1	1.63	0.62
1:B:240:GLY:O	1:B:243:TYR:HB3	1.99	0.62
1:D:156:ASN:HB2	1:D:160:CYS:SG	2.39	0.62
1:I:15:VAL:HG13	1:I:84:ASP:HB2	1.81	0.62
1:I:98:PHE:CE2	1:K:173:LEU:CD1	2.82	0.62
1:O:130:GLU:OE1	1:O:133:LYS:NZ	2.31	0.62
1:O:227:PRO:HG3	1:O:266:VAL:HG22	1.80	0.62
1:F:142:VAL:HG11	1:F:241:VAL:HG22	1.80	0.62
1:I:140:SER:OG	1:I:245:CYS:HA	1.98	0.62
1:J:69:TRP:CD2	1:J:120:GLY:HA2	2.35	0.62
1:E:117:ILE:CD1	1:E:166:VAL:HG13	2.29	0.62
1:A:222:MET:SD	1:A:231:MET:SD	2.97	0.62
1:D:109:VAL:O	1:D:109:VAL:HG12	1.98	0.62
1:K:30:LEU:HD23	1:K:238:GLY:HA2	1.80	0.62
1:I:103:LEU:HD11	1:K:115:ASP:OD1	2.00	0.62
1:D:205:LYS:NZ	2:D:302:HOH:O	2.30	0.62
1:P:42:ILE:HD11	1:P:80:TYR:HE2	1.64	0.62
1:D:146:SER:O	1:D:149:GLY:N	2.29	0.62
1:E:99:GLU:OE2	1:G:125:LEU:HD21	2.00	0.62
1:K:138:GLY:O	1:K:185:ARG:NH2	2.29	0.62
1:N:155:PHE:CA	1:P:176:GLU:OE2	2.44	0.61
1:O:86:LEU:HD22	1:O:128:LEU:HD11	1.82	0.61
1:E:147:VAL:HG22	1:E:192:GLY:HA2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:114:VAL:HG22	1:G:166:VAL:HG23	1.82	0.61
1:G:199:LEU:HD21	1:G:231:MET:HE3	1.82	0.61
1:H:142:VAL:O	1:H:142:VAL:HG12	1.98	0.61
1:P:145:SER:HB3	1:P:190:HIS:CE1	2.35	0.61
1:L:29:GLU:HG3	1:L:234:PRO:HB2	1.82	0.61
1:L:266:VAL:HA	1:P:151:ARG:HB2	1.82	0.61
1:P:236:GLU:C	1:P:237:MET:HE2	2.25	0.61
1:A:266:VAL:O	1:E:151:ARG:NE	2.33	0.61
1:B:93:SER:HA	1:B:159:TYR:CD1	2.35	0.61
1:C:115:ASP:O	1:C:116:SER:C	2.43	0.61
1:C:189:VAL:HG21	1:C:241:VAL:HG22	1.82	0.61
1:K:152:GLY:O	1:O:266:VAL:HG12	1.99	0.61
1:L:44:THR:HB	1:L:61:HIS:CB	2.31	0.61
1:L:87:VAL:HG22	1:L:142:VAL:HB	1.81	0.61
1:N:62:ASP:HB3	1:N:65:SER:HB3	1.81	0.61
1:F:102:PRO:O	1:F:104:SER:N	2.33	0.61
1:L:260:ASP:HB2	1:L:263:PHE:HB3	1.83	0.61
1:N:59:LEU:HD13	1:N:72:VAL:HG13	1.82	0.61
1:P:12:LEU:HD21	1:P:245:CYS:HB2	1.81	0.61
1:B:63:VAL:HG21	1:B:90:ALA:CB	2.29	0.61
1:G:86:LEU:HB3	1:G:141:VAL:HG22	1.81	0.61
1:H:123:VAL:O	1:H:123:VAL:CG1	2.49	0.61
1:K:134:ALA:O	1:K:135:ARG:CG	2.48	0.61
1:A:242:VAL:O	1:A:246:SER:N	2.33	0.61
1:I:29:GLU:HG3	1:I:234:PRO:HB2	1.83	0.61
1:K:187:ASN:ND2	1:K:244:LEU:HD22	2.15	0.61
1:A:135:ARG:NH2	1:A:245:CYS:O	2.34	0.61
1:F:34:MET:HG2	1:F:242:VAL:HG22	1.83	0.61
1:I:199:LEU:HD12	1:I:202:LEU:HD12	1.83	0.61
1:K:55:ALA:O	1:K:56:ASP:C	2.44	0.61
1:L:16:VAL:HA	1:L:40:ILE:HB	1.81	0.61
1:L:242:VAL:O	1:L:246:SER:N	2.32	0.61
1:N:94:ILE:HG22	1:N:95:VAL:N	2.14	0.61
1:N:103:LEU:HD21	1:P:115:ASP:CG	2.26	0.61
1:A:257:PHE:CE1	1:G:257:PHE:CE1	2.89	0.61
1:E:117:ILE:HD11	1:E:166:VAL:HG13	1.83	0.61
1:I:164:ALA:HB2	1:K:168:MET:CB	2.30	0.61
1:J:22:ALA:HA	1:J:27:GLY:HA3	1.83	0.61
1:K:31:VAL:HG11	1:K:53:GLU:O	2.01	0.61
1:K:265:GLN:O	1:O:151:ARG:CB	2.44	0.61
1:D:48:PRO:HA	1:D:60:GLN:CD	2.26	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:45:ASP:O	1:E:60:GLN:HA	2.01	0.60
1:E:146:SER:OG	1:E:147:VAL:N	2.31	0.60
1:F:55:ALA:HB1	1:F:57:HIS:O	2.00	0.60
1:C:91:GLY:HA2	1:C:113:ASN:OD1	2.00	0.60
1:C:145:SER:HG	1:C:190:HIS:CE1	2.18	0.60
1:D:35:LYS:HG3	1:D:54:GLY:O	2.01	0.60
1:I:20:THR:O	1:I:89:ASN:HB3	2.01	0.60
1:B:11:ALA:O	1:B:246:SER:HB2	2.01	0.60
1:D:128:LEU:HB3	1:D:184:ILE:HG21	1.81	0.60
1:E:187:ASN:OD1	1:E:252:VAL:HG12	2.01	0.60
1:M:82:ARG:NH2	1:M:84:ASP:OD1	2.34	0.60
1:K:257:PHE:CE1	1:M:257:PHE:HD2	2.19	0.60
1:M:148:ALA:HB1	1:M:160:CYS:SG	2.41	0.60
1:A:29:GLU:OE1	1:A:32:LYS:HD2	2.01	0.60
1:B:187:ASN:OD1	1:B:255:THR:HG22	2.02	0.60
1:C:111:THR:HA	1:C:115:ASP:OD2	2.01	0.60
1:G:151:ARG:NH2	1:G:152:GLY:O	2.33	0.60
1:I:214:SER:OG	1:I:217:VAL:HG23	2.01	0.60
1:P:158:ALA:C	1:P:160:CYS:H	2.08	0.60
1:B:221:ALA:HA	1:B:224:MET:SD	2.42	0.60
1:C:198:MET:O	1:C:202:LEU:HG	2.01	0.60
1:P:263:PHE:CD1	1:P:263:PHE:C	2.80	0.60
1:D:145:SER:HA	1:D:163:LYS:HD2	1.82	0.60
1:F:20:THR:HG21	1:F:69:TRP:CH2	2.36	0.60
1:G:167:LYS:O	1:G:171:LYS:HE3	2.02	0.60
1:I:164:ALA:CB	1:K:168:MET:HB3	2.31	0.60
1:J:219:GLN:HG2	1:J:223:GLU:OE1	2.02	0.60
1:L:26:ILE:O	1:L:30:LEU:N	2.32	0.60
1:M:163:LYS:O	1:M:166:VAL:HB	2.01	0.60
1:N:223:GLU:HG2	1:N:231:MET:HG3	1.83	0.60
1:O:23:ALA:HA	1:O:28:ARG:HG2	1.84	0.60
1:A:251:PHE:HD1	1:G:228:ILE:HD13	1.67	0.60
1:B:166:VAL:O	1:B:170:SER:OG	2.19	0.60
1:C:87:VAL:HA	1:C:142:VAL:HB	1.82	0.60
1:N:180:LEU:HB2	1:N:182:TYR:CE2	2.37	0.60
1:P:72:VAL:O	1:P:72:VAL:HG12	2.01	0.60
1:P:158:ALA:O	1:P:160:CYS:N	2.35	0.60
1:C:243:TYR:OH	1:F:239:GLY:HA3	2.00	0.60
1:F:31:VAL:HG21	1:F:52:VAL:HG13	1.83	0.60
1:G:226:HIS:HD2	1:G:260:ASP:O	1.85	0.60
1:H:123:VAL:O	1:H:123:VAL:HG12	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:146:SER:HA	1:K:191:PRO:HD2	1.83	0.60
1:P:142:VAL:CG1	1:P:189:VAL:HG23	2.32	0.60
1:F:110:ASN:O	1:F:114:VAL:HB	2.02	0.60
1:N:145:SER:O	1:N:146:SER:HB2	2.02	0.60
1:P:31:VAL:HG13	1:P:41:VAL:HG11	1.84	0.60
1:A:164:ALA:HA	1:A:167:LYS:HB3	1.84	0.59
1:B:164:ALA:O	1:B:165:ALA:C	2.45	0.59
1:I:98:PHE:CD2	1:K:173:LEU:HD22	2.37	0.59
1:K:252:VAL:HG13	1:K:255:THR:HG21	1.82	0.59
1:L:56:ASP:O	1:L:57:HIS:ND1	2.35	0.59
1:M:111:THR:O	1:M:116:SER:HB3	2.02	0.59
1:A:173:LEU:HD11	1:D:98:PHE:CZ	2.37	0.59
1:E:26:ILE:HD11	1:E:194:ILE:HG21	1.83	0.59
1:H:15:VAL:HG22	1:H:135:ARG:HD2	1.84	0.59
1:I:103:LEU:HD11	1:K:115:ASP:CG	2.27	0.59
1:I:152:GLY:N	1:M:266:VAL:HG12	2.17	0.59
1:J:164:ALA:HB2	1:L:168:MET:HE3	1.84	0.59
1:N:20:THR:O	1:N:89:ASN:HB3	2.02	0.59
1:P:169:LEU:O	1:P:170:SER:C	2.43	0.59
1:H:56:ASP:HB2	1:H:57:HIS:CE1	2.37	0.59
1:K:91:GLY:CA	1:K:112:VAL:HG12	2.29	0.59
1:O:129:LYS:HE2	1:O:182:TYR:CG	2.37	0.59
1:O:227:PRO:CG	1:O:266:VAL:HG22	2.32	0.59
1:A:251:PHE:HB2	1:G:236:GLU:OE1	2.03	0.59
1:G:226:HIS:CE1	1:G:263:PHE:CD2	2.90	0.59
1:J:12:LEU:HB3	1:J:39:ALA:HB2	1.82	0.59
1:J:74:ALA:O	1:J:77:GLN:HB3	2.02	0.59
1:A:173:LEU:HD21	1:D:98:PHE:CE1	2.38	0.59
1:A:254:CYS:O	1:G:265:GLN:HG3	2.02	0.59
1:B:221:ALA:O	1:B:224:MET:HE2	2.01	0.59
1:B:237:MET:HA	1:B:259:MET:HE1	1.85	0.59
1:F:96:THR:CG2	1:F:101:THR:HG22	2.31	0.59
1:G:200:GLY:HA2	1:G:215:ARG:NH2	2.18	0.59
1:L:26:ILE:CA	1:L:234:PRO:HB3	2.32	0.59
1:L:185:ARG:HB3	1:L:253:THR:HB	1.83	0.59
1:P:48:PRO:HA	1:P:60:GLN:CD	2.28	0.59
1:E:201:SER:HA	1:E:204:ASP:CG	2.28	0.59
1:E:246:SER:O	1:E:248:ALA:N	2.35	0.59
1:P:143:ASN:HB3	1:P:166:VAL:HG13	1.83	0.59
1:D:15:VAL:HG13	1:D:84:ASP:CB	2.32	0.59
1:E:18:VAL:HG22	1:E:42:ILE:HB	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:30:LEU:HD13	1:J:241:VAL:HG21	1.84	0.59
1:F:44:THR:HB	1:F:61:HIS:HB3	1.85	0.59
1:I:228:ILE:CG2	1:I:261:GLY:HA3	2.32	0.59
1:N:166:VAL:O	1:N:169:LEU:HB3	2.03	0.59
1:N:176:GLU:O	1:N:180:LEU:HG	2.03	0.59
1:H:203:MET:O	1:H:206:TYR:HB2	2.02	0.59
1:E:69:TRP:HZ3	1:E:124:LEU:HD11	1.68	0.59
1:E:145:SER:HA	1:E:163:LYS:HD2	1.85	0.59
1:H:31:VAL:HG13	1:H:41:VAL:HG21	1.85	0.59
1:L:12:LEU:HB3	1:L:39:ALA:HB2	1.84	0.59
1:P:16:VAL:HG22	1:P:40:ILE:CD1	2.33	0.59
1:M:233:ARG:HH21	1:M:236:GLU:CD	2.11	0.58
1:B:162:SER:C	1:B:164:ALA:N	2.59	0.58
1:D:137:GLY:HA3	1:D:250:SER:HB2	1.85	0.58
1:E:112:VAL:O	1:E:116:SER:CB	2.51	0.58
1:H:20:THR:O	1:H:89:ASN:HB3	2.03	0.58
1:H:26:ILE:O	1:H:30:LEU:HG	2.03	0.58
1:K:135:ARG:NH2	1:K:245:CYS:O	2.35	0.58
1:M:56:ASP:O	1:M:57:HIS:CG	2.56	0.58
1:O:216:GLU:HA	1:O:219:GLN:HB3	1.85	0.58
1:F:44:THR:O	1:F:45:ASP:HB2	2.03	0.58
1:F:56:ASP:O	1:F:57:HIS:CG	2.56	0.58
1:H:198:MET:HG2	1:H:198:MET:O	2.01	0.58
1:H:253:THR:O	1:H:254:CYS:CB	2.49	0.58
1:N:48:PRO:HA	1:N:60:GLN:OE1	2.04	0.58
1:F:160:CYS:HB3	1:H:168:MET:SD	2.44	0.58
1:A:118:ILE:HG21	1:D:103:LEU:CD1	2.33	0.58
1:B:101:THR:CG2	1:B:106:PHE:CD2	2.84	0.58
1:B:266:VAL:C	1:F:151:ARG:HE	2.12	0.58
1:H:140:SER:HB3	1:H:245:CYS:HA	1.84	0.58
1:C:241:VAL:O	1:C:244:LEU:N	2.37	0.58
1:F:260:ASP:HB2	1:F:263:PHE:HB3	1.85	0.58
1:H:115:ASP:HA	1:H:118:ILE:HD12	1.85	0.58
1:K:227:PRO:HG3	1:K:266:VAL:HG21	1.85	0.58
1:O:96:THR:O	1:O:155:PHE:O	2.22	0.58
1:P:64:THR:HG22	1:P:111:THR:HG22	1.85	0.58
1:I:92:ILE:HG12	1:I:112:VAL:HB	1.86	0.58
1:L:49:SER:OG	2:L:301:HOH:O	2.17	0.58
1:H:185:ARG:NH2	1:H:246:SER:O	2.37	0.58
1:J:130:GLU:OE1	1:J:133:LYS:NZ	2.36	0.58
1:A:223:GLU:HG2	1:A:231:MET:HG3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:27:GLY:HA2	1:I:30:LEU:HD12	1.86	0.58
1:K:266:VAL:C	1:O:151:ARG:CZ	2.77	0.58
1:O:226:HIS:O	1:O:227:PRO:C	2.46	0.58
1:A:257:PHE:HE1	1:G:257:PHE:CE1	2.22	0.57
1:E:180:LEU:HD12	1:E:182:TYR:HE2	1.69	0.57
1:F:182:TYR:O	1:F:184:ILE:N	2.37	0.57
1:E:13:ASN:HA	2:E:301:HOH:O	2.03	0.57
1:K:86:LEU:CD2	1:K:124:LEU:HD12	2.29	0.57
1:L:66:GLU:HA	1:L:119:ILE:HG21	1.85	0.57
1:P:146:SER:HB3	1:P:148:ALA:HB3	1.86	0.57
1:J:262:GLY:O	1:J:265:GLN:N	2.37	0.57
1:N:44:THR:HB	1:N:61:HIS:HB3	1.86	0.57
1:A:16:VAL:HG21	1:A:80:TYR:HB3	1.86	0.57
1:A:161:THR:CG2	1:D:169:LEU:HA	2.33	0.57
1:C:97:LYS:HD2	1:C:100:ASP:OD2	2.04	0.57
1:E:31:VAL:HG13	1:E:55:ALA:HB2	1.86	0.57
1:E:144:PHE:HA	1:E:189:VAL:HB	1.87	0.57
1:L:260:ASP:OD2	1:L:264:SER:N	2.37	0.57
1:B:32:LYS:HE2	1:B:53:GLU:CB	2.33	0.57
1:F:161:THR:HA	1:H:168:MET:HG3	1.86	0.57
1:I:164:ALA:HB2	1:K:168:MET:HB3	1.86	0.57
1:N:16:VAL:O	1:N:85:ALA:N	2.32	0.57
1:A:132:GLY:HA2	1:A:183:ASN:HB3	1.85	0.57
1:G:203:MET:HA	1:G:206:TYR:HD2	1.68	0.57
1:I:146:SER:H	1:I:190:HIS:HA	1.69	0.57
1:L:236:GLU:O	1:L:259:MET:HE1	2.05	0.57
1:D:253:THR:CG2	1:E:228:ILE:HD12	2.34	0.57
1:H:61:HIS:HE2	1:H:69:TRP:CD1	2.22	0.57
1:J:159:TYR:CE1	1:J:163:LYS:HE2	2.39	0.57
1:K:42:ILE:HG12	1:K:57:HIS:HB2	1.86	0.57
1:K:58:TYR:CD1	1:K:58:TYR:C	2.83	0.57
1:M:48:PRO:HA	1:M:60:GLN:HB2	1.87	0.57
1:F:168:MET:SD	1:F:172:CYS:SG	3.03	0.57
1:K:69:TRP:CD2	1:K:120:GLY:HA2	2.40	0.57
1:A:26:ILE:HD11	1:A:194:ILE:HG21	1.87	0.57
1:B:31:VAL:HG11	1:B:52:VAL:HG12	1.85	0.57
1:B:98:PHE:O	1:B:101:THR:HB	2.05	0.57
1:B:237:MET:HA	1:B:259:MET:CE	2.35	0.57
1:N:59:LEU:HD22	1:N:72:VAL:HA	1.87	0.57
1:N:102:PRO:HB2	1:N:104:SER:OG	2.05	0.57
1:O:219:GLN:O	1:O:222:MET:HB3	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:82:ARG:NH2	1:C:84:ASP:OD1	2.38	0.57
1:H:199:LEU:C	1:H:201:SER:N	2.62	0.57
1:P:44:THR:HG22	1:P:59:LEU:HB2	1.87	0.57
1:A:168:MET:HG2	1:D:160:CYS:C	2.30	0.56
1:G:151:ARG:HD3	1:G:263:PHE:CE1	2.40	0.56
1:G:258:VAL:O	1:G:259:MET:HG3	2.05	0.56
1:H:26:ILE:HG13	1:H:196:THR:HG21	1.86	0.56
1:J:20:THR:OG1	1:J:88:HIS:HA	2.05	0.56
1:C:266:VAL:HB	1:H:151:ARG:NH2	2.20	0.56
1:D:151:ARG:NH2	1:D:152:GLY:O	2.36	0.56
1:G:121:THR:O	1:G:125:LEU:N	2.37	0.56
1:G:220:ALA:HA	1:G:223:GLU:HB2	1.87	0.56
1:K:115:ASP:OD1	1:K:118:ILE:HD12	2.05	0.56
1:L:205:LYS:HA	1:L:208:GLU:HB2	1.86	0.56
1:M:243:TYR:C	1:M:245:CYS:H	2.12	0.56
1:A:247:ASP:C	1:A:249:ALA:H	2.13	0.56
1:B:93:SER:HB3	1:B:202:LEU:HD11	1.87	0.56
1:B:244:LEU:HD11	1:B:257:PHE:CD2	2.40	0.56
1:D:169:LEU:O	1:D:172:CYS:HB2	2.05	0.56
1:D:171:LYS:NZ	1:D:256:GLU:OE1	2.31	0.56
1:E:179:ALA:C	1:E:181:GLY:H	2.12	0.56
1:K:44:THR:HG21	1:K:72:VAL:HG21	1.88	0.56
1:K:145:SER:O	1:K:163:LYS:HD2	2.06	0.56
1:N:19:VAL:HA	1:N:87:VAL:HB	1.87	0.56
1:P:194:ILE:HD13	1:P:232:GLY:HA3	1.85	0.56
1:B:43:ALA:O	1:B:58:TYR:HA	2.04	0.56
1:E:62:ASP:OD2	1:E:64:THR:OG1	2.23	0.56
1:H:111:THR:HA	1:H:115:ASP:HB2	1.86	0.56
1:J:115:ASP:HA	1:J:118:ILE:HD12	1.86	0.56
1:K:147:VAL:CG1	1:K:260:ASP:HB2	2.35	0.56
1:L:86:LEU:HD23	1:L:141:VAL:HG13	1.87	0.56
1:P:44:THR:HB	1:P:61:HIS:HB2	1.87	0.56
1:B:112:VAL:O	1:B:112:VAL:CG1	2.53	0.56
1:F:168:MET:CG	1:H:160:CYS:HB3	2.36	0.56
1:H:86:LEU:HD22	1:H:124:LEU:HD12	1.87	0.56
1:H:196:THR:HB	1:H:197:PRO:HD2	1.87	0.56
1:K:187:ASN:HD22	1:K:244:LEU:HD22	1.69	0.56
1:M:159:TYR:CZ	1:M:163:LYS:HE3	2.40	0.56
1:N:161:THR:HG21	1:P:169:LEU:HB2	1.86	0.56
1:F:145:SER:HB3	1:F:190:HIS:NE2	2.20	0.56
1:F:222:MET:O	1:F:225:ARG:HB2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:28:ARG:O	1:H:32:LYS:HE3	2.05	0.56
1:P:64:THR:CG2	1:P:111:THR:HG22	2.36	0.56
1:P:143:ASN:O	1:P:188:SER:HA	2.06	0.56
1:C:241:VAL:O	1:C:242:VAL:C	2.47	0.56
1:C:248:ALA:C	1:C:250:SER:H	2.13	0.56
1:E:22:ALA:O	1:E:28:ARG:HA	2.05	0.56
1:L:115:ASP:O	1:L:119:ILE:HG13	2.05	0.56
1:G:87:VAL:HG22	1:G:142:VAL:HB	1.87	0.56
1:I:266:VAL:O	1:M:151:ARG:NH2	2.39	0.56
1:M:180:LEU:O	1:M:181:GLY:C	2.49	0.56
1:A:203:MET:O	1:A:204:ASP:C	2.49	0.56
1:C:35:LYS:HG3	1:C:54:GLY:C	2.31	0.56
1:E:20:THR:O	1:E:89:ASN:HB3	2.06	0.56
1:H:71:ALA:O	1:H:74:ALA:HB3	2.05	0.56
1:K:227:PRO:HG3	1:K:266:VAL:CG2	2.36	0.56
1:K:232:GLY:HA3	1:M:251:PHE:CD1	2.41	0.56
1:P:199:LEU:HA	1:P:202:LEU:HD12	1.88	0.56
1:A:12:LEU:HB3	1:A:39:ALA:CB	2.25	0.55
1:C:186:VAL:O	1:C:254:CYS:N	2.38	0.55
1:H:19:VAL:O	1:H:22:ALA:HB2	2.05	0.55
1:I:69:TRP:CD2	1:I:120:GLY:HA2	2.40	0.55
1:I:103:LEU:CD1	1:K:115:ASP:OD1	2.54	0.55
1:I:204:ASP:OD1	1:I:215:ARG:HG3	2.06	0.55
1:J:52:VAL:O	1:J:53:GLU:C	2.48	0.55
1:K:12:LEU:HD22	1:K:15:VAL:HG21	1.88	0.55
1:N:165:ALA:O	1:N:166:VAL:C	2.49	0.55
1:C:231:MET:O	1:F:251:PHE:CE1	2.58	0.55
1:I:225:ARG:O	1:I:227:PRO:HD3	2.06	0.55
1:M:200:GLY:O	1:M:215:ARG:NH2	2.39	0.55
1:N:17:ALA:HA	1:N:85:ALA:HB3	1.88	0.55
1:N:26:ILE:O	1:N:30:LEU:HG	2.07	0.55
1:A:151:ARG:CB	1:E:265:GLN:O	2.55	0.55
1:A:160:CYS:HB2	1:D:172:CYS:SG	2.45	0.55
1:E:17:ALA:O	1:E:18:VAL:HG23	2.06	0.55
1:E:176:GLU:O	1:E:179:ALA:HB3	2.06	0.55
1:F:161:THR:HG21	1:H:169:LEU:HD13	1.87	0.55
1:I:26:ILE:HG22	1:I:30:LEU:HG	1.88	0.55
1:L:61:HIS:CD2	1:L:63:VAL:HA	2.41	0.55
1:N:97:LYS:HA	1:N:155:PHE:CD1	2.40	0.55
1:O:155:PHE:O	1:O:157:ALA:N	2.39	0.55
1:E:144:PHE:CE2	1:E:189:VAL:HG11	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:146:SER:O	1:E:190:HIS:HB3	2.05	0.55
1:F:103:LEU:HG	1:F:107:HIS:NE2	2.22	0.55
1:N:110:ASN:O	1:N:114:VAL:HB	2.06	0.55
1:I:98:PHE:CZ	1:K:173:LEU:HD11	2.41	0.55
1:I:152:GLY:CA	1:M:266:VAL:HG12	2.36	0.55
1:I:250:SER:C	1:I:252:VAL:H	2.14	0.55
1:K:240:GLY:O	1:K:243:TYR:HB3	2.07	0.55
1:O:93:SER:OG	1:O:159:TYR:CD2	2.44	0.55
1:D:152:GLY:C	1:G:266:VAL:HG12	2.31	0.55
1:F:63:VAL:O	1:F:69:TRP:NE1	2.39	0.55
1:I:43:ALA:O	1:I:58:TYR:HA	2.06	0.55
1:M:146:SER:C	1:M:148:ALA:H	2.15	0.55
1:M:236:GLU:O	1:M:259:MET:HE2	2.06	0.55
1:N:16:VAL:HB	1:N:84:ASP:N	2.19	0.55
1:A:168:MET:HG2	1:D:160:CYS:O	2.06	0.55
1:F:170:SER:HA	1:F:186:VAL:CG1	2.36	0.55
1:H:227:PRO:HG2	1:H:262:GLY:CA	2.33	0.55
1:K:119:ILE:O	1:K:123:VAL:HG23	2.06	0.55
1:L:217:VAL:HG12	1:L:217:VAL:O	2.06	0.55
1:N:252:VAL:HG13	1:N:255:THR:HG21	1.88	0.55
1:O:171:LYS:O	1:O:175:ALA:HB2	2.07	0.55
1:A:113:ASN:O	1:A:117:ILE:HD12	2.07	0.55
1:D:265:GLN:OE1	1:E:171:LYS:CE	2.55	0.55
1:I:98:PHE:C	1:I:100:ASP:N	2.63	0.55
1:I:236:GLU:CD	1:O:251:PHE:HB2	2.32	0.55
1:K:89:ASN:CG	1:K:89:ASN:O	2.50	0.55
1:K:203:MET:HE2	1:K:222:MET:HE3	1.89	0.55
1:K:226:HIS:HB3	1:K:228:ILE:HG22	1.89	0.55
1:N:133:LYS:O	1:N:135:ARG:N	2.39	0.55
1:N:180:LEU:CB	1:N:182:TYR:CZ	2.89	0.55
1:P:147:VAL:HG12	1:P:264:SER:HB3	1.89	0.55
1:A:214:SER:HB2	1:A:216:GLU:OE2	2.07	0.55
1:B:115:ASP:HA	1:B:118:ILE:HD12	1.89	0.55
1:G:56:ASP:O	1:G:57:HIS:CD2	2.60	0.55
1:G:222:MET:HG3	1:G:222:MET:O	2.06	0.55
1:J:102:PRO:HD2	1:J:105:ASP:OD2	2.07	0.55
1:M:177:PHE:HB3	1:M:182:TYR:HB2	1.89	0.55
1:N:20:THR:HG21	1:N:69:TRP:CH2	2.42	0.55
1:O:95:VAL:HG23	1:O:202:LEU:HD22	1.89	0.55
1:A:80:TYR:O	1:A:82:ARG:HG2	2.07	0.55
1:F:102:PRO:HD2	1:F:105:ASP:OD2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:117:ILE:O	1:H:118:ILE:C	2.50	0.55
1:N:65:SER:O	1:N:69:TRP:CD1	2.59	0.55
1:E:112:VAL:C	1:E:116:SER:HB3	2.31	0.54
1:K:59:LEU:HD13	1:K:72:VAL:HG13	1.89	0.54
1:N:150:LEU:O	1:N:151:ARG:HB3	2.05	0.54
1:I:18:VAL:HG21	1:I:86:LEU:HD12	1.89	0.54
1:I:118:ILE:CD1	1:K:103:LEU:HD13	2.36	0.54
1:L:260:ASP:HB2	1:L:263:PHE:HB2	1.88	0.54
1:O:124:LEU:HA	1:O:127:LEU:HD12	1.90	0.54
1:P:182:TYR:O	1:P:184:ILE:N	2.39	0.54
1:B:156:ASN:HB3	1:B:160:CYS:HG	1.71	0.54
1:B:168:MET:HA	1:B:171:LYS:HG3	1.90	0.54
1:C:125:LEU:HA	1:C:128:LEU:HB2	1.89	0.54
1:C:97:LYS:HE3	1:C:209:LEU:HD22	1.90	0.54
1:E:140:SER:CB	1:E:245:CYS:HA	2.37	0.54
1:I:160:CYS:HB3	1:K:168:MET:CG	2.38	0.54
1:K:44:THR:HG21	1:K:61:HIS:ND1	2.22	0.54
1:N:173:LEU:HB3	1:N:186:VAL:HG21	1.89	0.54
1:A:176:GLU:HG3	1:A:180:LEU:HD11	1.90	0.54
1:A:176:GLU:OE2	1:D:155:PHE:CD1	2.61	0.54
1:J:82:ARG:NE	1:J:84:ASP:OD2	2.41	0.54
1:M:172:CYS:SG	1:O:152:GLY:HA2	2.48	0.54
1:P:16:VAL:HG22	1:P:40:ILE:HD12	1.89	0.54
1:P:145:SER:OG	1:P:146:SER:N	2.41	0.54
1:E:62:ASP:C	1:E:64:THR:H	2.15	0.54
1:I:10:ILE:N	2:I:305:HOH:O	2.41	0.54
1:I:165:ALA:O	1:I:168:MET:N	2.41	0.54
1:J:164:ALA:O	1:J:167:LYS:HB3	2.08	0.54
1:K:35:LYS:HD3	1:K:54:GLY:O	2.08	0.54
1:M:145:SER:O	1:M:163:LYS:NZ	2.38	0.54
1:N:182:TYR:N	1:N:182:TYR:CD1	2.74	0.54
1:O:195:ASP:HA	1:O:231:MET:SD	2.48	0.54
1:P:131:GLY:HA2	1:P:134:ALA:HB3	1.90	0.54
1:K:145:SER:OG	1:K:146:SER:N	2.25	0.54
1:K:147:VAL:HG11	1:K:263:PHE:HB3	1.89	0.54
1:N:98:PHE:N	1:P:176:GLU:OE1	2.40	0.54
1:G:79:LYS:HB2	1:G:80:TYR:CD2	2.42	0.54
1:J:40:ILE:HA	1:J:56:ASP:OD2	2.08	0.54
1:L:86:LEU:O	1:L:142:VAL:N	2.41	0.54
1:F:31:VAL:HG21	1:F:52:VAL:HG11	1.88	0.54
1:I:156:ASN:OD1	1:I:159:TYR:HB3	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:106:PHE:HZ	1:M:161:THR:OG1	1.90	0.54
1:M:110:ASN:O	1:M:114:VAL:N	2.37	0.54
1:M:243:TYR:O	1:M:245:CYS:N	2.41	0.54
1:N:190:HIS:HB2	1:N:258:VAL:HG13	1.90	0.54
1:P:176:GLU:O	1:P:180:LEU:N	2.41	0.54
1:B:229:GLY:O	1:B:230:ARG:HB3	2.08	0.54
1:C:259:MET:HE3	1:F:243:TYR:OH	2.08	0.54
1:E:44:THR:HB	1:E:61:HIS:CB	2.38	0.54
1:N:142:VAL:HG11	1:N:241:VAL:HG13	1.90	0.54
1:P:91:GLY:HA2	1:P:113:ASN:OD1	2.08	0.54
1:P:124:LEU:HD22	1:P:127:LEU:HD13	1.90	0.54
1:A:182:TYR:CE2	1:D:99:GLU:OE1	2.61	0.53
1:E:110:ASN:O	1:E:111:THR:C	2.51	0.53
1:I:198:MET:O	1:I:202:LEU:HG	2.08	0.53
1:L:248:ALA:HB1	1:N:239:GLY:HA3	1.90	0.53
1:M:30:LEU:O	1:M:33:ALA:N	2.40	0.53
1:N:12:LEU:HB2	1:N:39:ALA:HB2	1.88	0.53
1:N:176:GLU:OE1	1:P:97:LYS:HA	2.07	0.53
1:A:142:VAL:O	1:A:142:VAL:HG12	2.08	0.53
1:C:180:LEU:HD13	1:C:182:TYR:CZ	2.42	0.53
1:E:47:ALA:O	1:E:58:TYR:OH	2.22	0.53
1:H:142:VAL:HG11	1:H:241:VAL:HG13	1.90	0.53
1:L:180:LEU:O	1:L:182:TYR:CD1	2.61	0.53
1:O:89:ASN:HA	1:O:144:PHE:CD1	2.44	0.53
1:O:94:ILE:CG2	1:O:158:ALA:HB3	2.38	0.53
1:P:185:ARG:NE	1:P:249:ALA:O	2.41	0.53
1:B:191:PRO:HB3	1:B:194:ILE:HD11	1.90	0.53
1:C:187:ASN:OD1	1:C:252:VAL:HG12	2.07	0.53
1:D:129:LYS:HG2	1:D:184:ILE:HD11	1.89	0.53
1:D:156:ASN:CB	1:D:160:CYS:SG	2.97	0.53
1:M:118:ILE:HG23	1:O:98:PHE:CE1	2.42	0.53
1:E:139:ALA:HB3	1:E:184:ILE:HG12	1.91	0.53
1:L:15:VAL:HG13	1:L:84:ASP:HB2	1.91	0.53
1:P:96:THR:HA	1:P:209:LEU:HD11	1.90	0.53
1:A:188:SER:O	1:A:257:PHE:N	2.38	0.53
1:B:228:ILE:HD12	1:H:253:THR:CG2	2.36	0.53
1:C:88:HIS:HB2	1:C:143:ASN:HA	1.91	0.53
1:E:63:VAL:HB	1:E:116:SER:CB	2.36	0.53
1:E:64:THR:HG21	1:E:111:THR:HG22	1.91	0.53
1:F:83:VAL:O	1:F:131:GLY:HA3	2.08	0.53
1:H:237:MET:HA	1:H:237:MET:HE2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:115:ASP:O	1:N:118:ILE:N	2.42	0.53
1:N:161:THR:CG2	1:P:169:LEU:HB2	2.39	0.53
1:O:129:LYS:HE2	1:O:182:TYR:CD2	2.43	0.53
1:D:148:ALA:HB1	1:D:160:CYS:HA	1.91	0.53
1:E:246:SER:C	1:E:248:ALA:N	2.67	0.53
1:G:194:ILE:HG22	1:G:196:THR:HG23	1.91	0.53
1:I:118:ILE:O	1:I:122:GLN:HB2	2.09	0.53
1:I:187:ASN:OD1	1:I:253:THR:HA	2.08	0.53
1:I:266:VAL:HG23	1:M:151:ARG:NH2	2.15	0.53
1:J:258:VAL:HG11	1:J:265:GLN:HE21	1.74	0.53
1:O:173:LEU:HB2	1:O:186:VAL:HG11	1.90	0.53
1:O:264:SER:OG	1:O:265:GLN:NE2	2.38	0.53
1:A:176:GLU:C	1:A:178:ALA:H	2.17	0.53
1:E:22:ALA:HA	1:E:27:GLY:C	2.34	0.53
1:F:94:ILE:HD11	1:F:108:ARG:HH21	1.73	0.53
1:F:138:GLY:HA2	1:F:183:ASN:OD1	2.09	0.53
1:F:214:SER:OG	1:F:217:VAL:HG23	2.07	0.53
1:G:222:MET:HG3	1:G:231:MET:SD	2.48	0.53
1:H:151:ARG:HD3	1:H:263:PHE:CE2	2.43	0.53
1:K:12:LEU:HB2	1:K:37:ALA:HB1	1.90	0.53
1:P:25:GLY:O	1:P:234:PRO:HB3	2.08	0.53
1:C:227:PRO:HG3	1:C:266:VAL:HG22	1.90	0.53
1:F:19:VAL:HG22	1:F:87:VAL:HB	1.90	0.53
1:G:164:ALA:O	1:G:167:LYS:HB3	2.08	0.53
1:K:45:ASP:HB3	1:K:58:TYR:OH	2.09	0.53
1:M:30:LEU:HD13	1:M:241:VAL:HG11	1.91	0.53
1:N:172:CYS:SG	1:P:157:ALA:HA	2.48	0.53
1:O:40:ILE:HG21	1:O:80:TYR:CZ	2.44	0.53
1:C:265:GLN:CG	1:F:255:THR:HA	2.39	0.53
1:F:69:TRP:CH2	1:F:88:HIS:CE1	2.97	0.53
1:F:156:ASN:O	1:F:157:ALA:C	2.50	0.53
1:K:147:VAL:CG1	1:K:260:ASP:CB	2.87	0.53
1:M:56:ASP:O	1:M:57:HIS:CD2	2.62	0.53
1:M:109:VAL:O	1:M:113:ASN:ND2	2.42	0.53
1:M:109:VAL:HG21	1:M:158:ALA:HB1	1.91	0.53
1:B:101:THR:HG21	1:B:106:PHE:CE2	2.44	0.53
1:B:190:HIS:HB2	1:B:258:VAL:HA	1.90	0.53
1:B:236:GLU:HB2	1:B:237:MET:HE2	1.91	0.53
1:D:243:TYR:OH	1:E:259:MET:SD	2.66	0.53
1:G:97:LYS:HB2	1:G:100:ASP:HB2	1.91	0.53
1:I:60:GLN:NE2	2:I:303:HOH:O	2.34	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:88:HIS:HB2	1:B:143:ASN:OD1	2.09	0.52
1:G:59:LEU:HD22	1:G:72:VAL:HG22	1.90	0.52
1:G:154:ALA:C	1:G:156:ASN:H	2.17	0.52
1:G:243:TYR:HE2	1:G:252:VAL:HG21	1.74	0.52
1:I:42:ILE:HD13	1:I:75:LEU:HD23	1.91	0.52
1:I:265:GLN:HG3	1:O:255:THR:HA	1.90	0.52
1:J:168:MET:O	1:J:171:LYS:HB2	2.09	0.52
1:K:265:GLN:HG3	1:M:254:CYS:HB2	1.90	0.52
1:O:140:SER:CB	1:O:245:CYS:HA	2.39	0.52
1:B:17:ALA:CB	1:B:85:ALA:HB3	2.39	0.52
1:B:89:ASN:OD1	1:B:144:PHE:CE2	2.62	0.52
1:H:12:LEU:HD11	1:H:242:VAL:HG22	1.90	0.52
1:I:152:GLY:O	1:M:266:VAL:CB	2.53	0.52
1:K:151:ARG:CZ	1:K:263:PHE:CZ	2.93	0.52
1:D:74:ALA:HA	1:D:77:GLN:HB3	1.91	0.52
1:J:203:MET:O	1:J:206:TYR:HB2	2.10	0.52
1:A:26:ILE:O	1:A:30:LEU:HG	2.10	0.52
1:A:176:GLU:CG	1:A:180:LEU:HD11	2.39	0.52
1:D:29:GLU:HB3	1:D:235:ALA:HA	1.90	0.52
1:G:199:LEU:HD21	1:G:231:MET:CE	2.39	0.52
1:I:152:GLY:HA2	1:K:168:MET:HE1	1.91	0.52
1:M:87:VAL:HG21	1:M:241:VAL:HG13	1.92	0.52
1:M:181:GLY:HA2	2:M:305:HOH:O	2.08	0.52
1:P:44:THR:HB	1:P:61:HIS:CB	2.39	0.52
1:G:243:TYR:CE2	1:G:252:VAL:HG21	2.45	0.52
1:J:191:PRO:HB3	1:J:237:MET:SD	2.49	0.52
1:M:132:GLY:CA	1:M:138:GLY:HA2	2.32	0.52
1:M:138:GLY:CA	1:M:183:ASN:O	2.46	0.52
1:A:24:GLY:O	1:A:28:ARG:HG3	2.09	0.52
1:A:225:ARG:O	1:A:263:PHE:CD2	2.63	0.52
1:C:236:GLU:CD	1:F:251:PHE:HB2	2.35	0.52
1:D:82:ARG:NH2	1:D:135:ARG:HG3	2.25	0.52
1:E:67:ALA:O	1:E:68:GLY:C	2.52	0.52
1:F:230:ARG:HG3	1:F:230:ARG:NH1	2.05	0.52
1:F:247:ASP:C	1:F:249:ALA:N	2.59	0.52
1:I:115:ASP:HA	1:I:118:ILE:HD12	1.91	0.52
1:P:20:THR:HA	1:P:44:THR:O	2.10	0.52
1:A:167:LYS:HZ1	1:D:167:LYS:HE3	1.75	0.52
1:C:198:MET:SD	2:C:305:HOH:O	2.58	0.52
1:D:15:VAL:HG13	1:D:84:ASP:HB2	1.92	0.52
1:D:150:LEU:HD21	1:D:256:GLU:OE2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:94:ILE:O	1:F:94:ILE:HG22	2.09	0.52
1:G:101:THR:HG22	1:G:102:PRO:O	2.10	0.52
1:G:146:SER:HA	1:G:190:HIS:HA	1.92	0.52
1:L:83:VAL:HG23	1:L:127:LEU:HB3	1.91	0.52
1:L:187:ASN:HD22	1:L:244:LEU:HD22	1.75	0.52
1:O:23:ALA:HA	1:O:28:ARG:CG	2.39	0.52
1:P:12:LEU:HD12	1:P:34:MET:HG2	1.92	0.52
1:P:23:ALA:HA	1:P:28:ARG:CG	2.39	0.52
1:B:162:SER:O	1:B:165:ALA:N	2.43	0.52
1:C:223:GLU:CG	1:C:231:MET:HG3	2.39	0.52
1:D:31:VAL:HG11	1:D:52:VAL:HG12	1.91	0.52
1:D:257:PHE:HE1	1:D:259:MET:HG3	1.75	0.52
1:J:151:ARG:HD3	1:J:263:PHE:HE1	1.75	0.52
1:L:141:VAL:HG12	1:L:143:ASN:HD21	1.75	0.52
1:N:31:VAL:HG13	1:N:41:VAL:HG11	1.92	0.52
1:N:164:ALA:O	1:N:167:LYS:HB3	2.09	0.52
1:P:125:LEU:N	1:P:126:PRO:HD2	2.25	0.52
1:A:204:ASP:O	1:A:208:GLU:N	2.34	0.52
1:F:180:LEU:C	1:F:182:TYR:H	2.18	0.52
1:I:66:GLU:HA	1:I:119:ILE:HG21	1.92	0.52
1:M:147:VAL:HA	1:M:150:LEU:HB2	1.91	0.52
1:O:93:SER:HA	1:O:159:TYR:HD2	1.75	0.52
1:D:44:THR:HG21	1:D:72:VAL:HG22	1.92	0.52
1:F:25:GLY:HA2	1:F:28:ARG:HH12	1.75	0.52
1:L:254:CYS:C	1:N:265:GLN:HG3	2.35	0.52
1:P:48:PRO:HA	1:P:60:GLN:NE2	2.25	0.52
1:P:61:HIS:ND1	1:P:72:VAL:HG21	2.24	0.52
1:A:243:TYR:OH	1:G:259:MET:HE3	2.10	0.51
1:C:111:THR:O	1:C:115:ASP:HB2	2.10	0.51
1:C:223:GLU:HG2	1:C:231:MET:HG3	1.91	0.51
1:D:266:VAL:C	1:G:151:ARG:NH1	2.68	0.51
1:E:95:VAL:O	1:E:96:THR:HB	2.10	0.51
1:F:145:SER:OG	1:F:190:HIS:CE1	2.63	0.51
1:G:97:LYS:HD3	1:G:100:ASP:OD2	2.10	0.51
1:I:203:MET:SD	1:I:219:GLN:HG3	2.50	0.51
1:J:12:LEU:HD21	1:J:245:CYS:HB2	1.92	0.51
1:L:18:VAL:HG22	1:L:42:ILE:HB	1.91	0.51
1:N:12:LEU:CB	1:N:39:ALA:HB2	2.40	0.51
1:A:19:VAL:O	1:A:44:THR:N	2.41	0.51
1:D:171:LYS:HG2	1:D:254:CYS:O	2.10	0.51
1:F:125:LEU:HG	1:F:129:LYS:HE3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:156:ASN:O	1:F:158:ALA:N	2.42	0.51
1:H:98:PHE:HA	1:H:101:THR:OG1	2.11	0.51
1:B:137:GLY:O	1:B:185:ARG:NE	2.40	0.51
1:E:155:PHE:CA	1:G:176:GLU:OE2	2.56	0.51
1:F:26:ILE:HD13	1:F:237:MET:HG3	1.92	0.51
1:F:87:VAL:HG12	1:F:87:VAL:O	2.10	0.51
1:H:44:THR:HB	1:H:61:HIS:HB3	1.93	0.51
1:L:221:ALA:HA	1:L:224:MET:HB2	1.92	0.51
1:N:86:LEU:HD13	1:N:124:LEU:CD1	2.40	0.51
1:H:115:ASP:O	1:H:116:SER:C	2.52	0.51
1:H:264:SER:OG	1:H:265:GLN:NE2	2.42	0.51
1:J:215:ARG:O	1:J:218:ALA:HB3	2.10	0.51
1:L:156:ASN:HB3	1:L:160:CYS:SG	2.50	0.51
1:A:252:VAL:HG12	1:A:255:THR:HG21	1.93	0.51
1:H:94:ILE:O	1:H:96:THR:HG22	2.10	0.51
1:M:146:SER:C	1:M:148:ALA:N	2.68	0.51
1:M:156:ASN:O	1:M:158:ALA:N	2.43	0.51
1:M:229:GLY:O	1:M:230:ARG:HB3	2.10	0.51
1:P:119:ILE:O	1:P:122:GLN:HB2	2.11	0.51
1:G:130:GLU:HA	1:G:133:LYS:HD2	1.93	0.51
1:I:20:THR:HG22	1:I:44:THR:OG1	2.10	0.51
1:O:27:GLY:O	1:O:31:VAL:HG23	2.10	0.51
1:B:117:ILE:CD1	1:B:166:VAL:HG22	2.40	0.51
1:C:250:SER:HB2	1:F:236:GLU:OE1	2.11	0.51
1:E:33:ALA:HA	1:E:36:ALA:HB3	1.93	0.51
1:I:98:PHE:O	1:I:100:ASP:N	2.44	0.51
1:J:233:ARG:HB2	1:J:236:GLU:HG3	1.92	0.51
1:L:260:ASP:OD2	1:L:265:GLN:HG2	2.11	0.51
1:M:40:ILE:HG21	1:M:80:TYR:CE1	2.45	0.51
1:N:114:VAL:HG11	1:P:106:PHE:CZ	2.46	0.51
1:P:143:ASN:HB2	1:P:170:SER:OG	2.10	0.51
1:B:45:ASP:O	1:B:60:GLN:HA	2.10	0.51
1:C:145:SER:OG	1:C:190:HIS:CE1	2.64	0.51
1:F:94:ILE:HD12	1:F:109:VAL:HG23	1.92	0.51
1:G:104:SER:O	1:G:108:ARG:N	2.44	0.51
1:I:97:LYS:HB2	1:I:100:ASP:HB2	1.92	0.51
1:L:106:PHE:HE1	1:L:158:ALA:HA	1.74	0.51
1:L:139:ALA:HB3	1:L:184:ILE:HG12	1.92	0.51
1:C:227:PRO:HG3	1:C:266:VAL:CG2	2.41	0.51
1:G:237:MET:HA	1:G:259:MET:HE1	1.91	0.51
1:N:125:LEU:HA	1:N:128:LEU:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:15:VAL:HG13	1:D:84:ASP:HB3	1.91	0.51
1:E:149:GLY:O	1:G:168:MET:HE3	2.11	0.51
1:E:153:ALA:HB3	1:E:156:ASN:HB2	1.93	0.51
1:E:218:ALA:C	1:E:220:ALA:H	2.18	0.51
1:E:223:GLU:O	1:E:226:HIS:HB2	2.10	0.51
1:F:62:ASP:OD2	1:F:64:THR:OG1	2.28	0.51
1:F:247:ASP:O	1:F:249:ALA:N	2.43	0.51
1:G:196:THR:C	1:G:198:MET:H	2.19	0.51
1:J:125:LEU:HB3	1:J:126:PRO:HD3	1.92	0.51
1:P:115:ASP:C	1:P:117:ILE:H	2.19	0.51
1:P:125:LEU:N	1:P:126:PRO:CD	2.74	0.51
1:B:26:ILE:HG21	1:B:144:PHE:CZ	2.46	0.50
1:B:107:HIS:CB	1:G:208:GLU:HG2	2.40	0.50
1:G:144:PHE:O	1:G:166:VAL:CG1	2.58	0.50
1:I:118:ILE:HD12	1:K:103:LEU:CD1	2.41	0.50
1:I:251:PHE:HE1	1:O:230:ARG:O	1.94	0.50
1:A:112:VAL:O	1:A:116:SER:OG	2.29	0.50
1:B:26:ILE:HD13	1:B:144:PHE:HE2	1.76	0.50
1:M:60:GLN:OE1	2:M:301:HOH:O	2.18	0.50
1:M:112:VAL:HG12	1:M:112:VAL:O	2.10	0.50
1:P:23:ALA:HA	1:P:28:ARG:HG3	1.93	0.50
1:B:44:THR:OG1	1:B:61:HIS:HB3	2.11	0.50
1:D:137:GLY:HA3	1:D:250:SER:CB	2.42	0.50
1:H:140:SER:CB	1:H:245:CYS:HA	2.41	0.50
1:H:162:SER:O	1:H:166:VAL:HG23	2.11	0.50
1:K:185:ARG:CD	1:K:249:ALA:O	2.60	0.50
1:K:221:ALA:O	1:K:222:MET:C	2.55	0.50
1:P:249:ALA:HA	1:P:252:VAL:HG23	1.94	0.50
1:G:140:SER:OG	1:G:245:CYS:HA	2.11	0.50
1:K:146:SER:OG	1:K:191:PRO:O	2.29	0.50
1:L:185:ARG:HD2	1:L:252:VAL:O	2.11	0.50
1:O:148:ALA:HB1	1:O:160:CYS:SG	2.51	0.50
1:D:35:LYS:HG3	1:D:54:GLY:C	2.36	0.50
1:D:191:PRO:HA	1:D:259:MET:O	2.11	0.50
1:E:98:PHE:HB3	1:G:176:GLU:OE1	2.12	0.50
1:G:145:SER:HB3	1:G:190:HIS:CE1	2.47	0.50
1:G:226:HIS:CD2	1:G:260:ASP:O	2.65	0.50
1:I:118:ILE:HD13	1:K:103:LEU:HD13	1.89	0.50
1:I:225:ARG:HD3	1:I:263:PHE:CZ	2.46	0.50
1:K:25:GLY:HA2	1:K:28:ARG:HH22	1.76	0.50
1:P:180:LEU:C	1:P:182:TYR:H	2.19	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:189:VAL:HG12	1:P:191:PRO:HD3	1.93	0.50
1:A:193:GLY:O	1:G:251:PHE:HZ	1.94	0.50
1:B:71:ALA:O	1:B:74:ALA:HB3	2.12	0.50
1:B:146:SER:O	1:B:149:GLY:N	2.37	0.50
1:D:256:GLU:O	1:D:258:VAL:HG23	2.12	0.50
1:G:226:HIS:HB3	1:G:228:ILE:HG22	1.94	0.50
1:K:92:ILE:HG23	1:K:112:VAL:HG11	1.92	0.50
1:N:18:VAL:HG22	1:N:42:ILE:HD12	1.92	0.50
1:A:19:VAL:HA	1:A:87:VAL:HB	1.94	0.50
1:A:92:ILE:HD11	1:A:109:VAL:HA	1.94	0.50
1:C:142:VAL:HG11	1:C:241:VAL:CG1	2.39	0.50
1:G:12:LEU:HD21	1:G:245:CYS:HB2	1.93	0.50
1:H:187:ASN:OD1	1:H:253:THR:HA	2.11	0.50
1:H:247:ASP:O	1:H:250:SER:HB3	2.11	0.50
1:I:16:VAL:HG21	1:I:80:TYR:HB3	1.94	0.50
1:I:228:ILE:HG21	1:I:261:GLY:HA3	1.92	0.50
1:J:11:ALA:O	1:J:246:SER:HB3	2.12	0.50
1:K:162:SER:O	1:K:166:VAL:N	2.38	0.50
1:N:64:THR:HB	1:N:111:THR:HG22	1.94	0.50
1:O:63:VAL:O	1:O:69:TRP:NE1	2.45	0.50
1:A:112:VAL:O	1:A:116:SER:CB	2.59	0.50
1:A:265:GLN:HE22	1:G:256:GLU:HG3	1.75	0.50
1:D:129:LYS:CG	1:D:184:ILE:HD11	2.42	0.50
1:F:45:ASP:O	1:F:47:ALA:N	2.44	0.50
1:F:171:LYS:HB3	1:H:152:GLY:HA3	1.94	0.50
1:L:94:ILE:CG2	1:L:96:THR:HG22	2.41	0.50
1:O:182:TYR:C	1:O:184:ILE:HG13	2.37	0.50
1:P:81:GLY:O	1:P:127:LEU:HD23	2.12	0.50
1:A:83:VAL:N	1:A:127:LEU:O	2.33	0.50
1:C:17:ALA:O	1:C:41:VAL:HA	2.11	0.50
1:N:26:ILE:HG22	1:N:30:LEU:HD21	1.94	0.50
1:N:203:MET:HB3	1:N:218:ALA:HB1	1.94	0.50
1:A:69:TRP:CZ2	1:A:88:HIS:HE1	2.29	0.49
1:A:240:GLY:O	1:A:244:LEU:HG	2.11	0.49
1:F:140:SER:HB2	1:F:185:ARG:NH2	2.27	0.49
1:G:154:ALA:O	1:G:156:ASN:N	2.45	0.49
1:K:153:ALA:HB3	1:K:156:ASN:HB2	1.94	0.49
1:K:254:CYS:HB2	1:M:265:GLN:HG3	1.92	0.49
1:L:187:ASN:ND2	1:L:244:LEU:HD22	2.27	0.49
1:O:156:ASN:HB3	1:O:159:TYR:HB3	1.93	0.49
1:G:215:ARG:O	1:G:219:GLN:N	2.33	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:121:THR:HG21	1:L:173:LEU:HD13	1.93	0.49
1:O:93:SER:HB3	1:O:202:LEU:HD11	1.94	0.49
1:O:159:TYR:CZ	1:O:163:LYS:HG3	2.45	0.49
1:E:160:CYS:O	1:G:168:MET:HG2	2.12	0.49
1:E:169:LEU:O	1:E:172:CYS:HB2	2.12	0.49
1:F:94:ILE:HD13	1:F:105:ASP:OD1	2.11	0.49
1:H:151:ARG:HD3	1:H:263:PHE:CZ	2.47	0.49
1:I:98:PHE:O	1:I:99:GLU:C	2.54	0.49
1:L:12:LEU:HD11	1:L:245:CYS:HB2	1.93	0.49
1:M:83:VAL:O	1:M:128:LEU:HA	2.12	0.49
1:M:168:MET:O	1:M:172:CYS:SG	2.67	0.49
1:B:266:VAL:O	1:B:266:VAL:CG2	2.58	0.49
1:C:189:VAL:HG22	1:C:257:PHE:HD2	1.78	0.49
1:E:32:LYS:HD3	1:E:53:GLU:OE2	2.12	0.49
1:E:69:TRP:CE2	1:E:120:GLY:HA2	2.47	0.49
1:F:45:ASP:O	1:F:46:MET:C	2.55	0.49
1:F:159:TYR:CE1	1:F:163:LYS:HE2	2.47	0.49
1:J:24:GLY:O	1:J:28:ARG:HG3	2.13	0.49
1:L:180:LEU:O	1:L:182:TYR:CE1	2.65	0.49
1:M:172:CYS:SG	1:O:152:GLY:CA	3.00	0.49
1:O:24:GLY:O	1:O:25:GLY:C	2.55	0.49
1:E:31:VAL:CG1	1:E:55:ALA:HB2	2.41	0.49
1:E:86:LEU:HD22	1:E:128:LEU:HD11	1.93	0.49
1:E:142:VAL:HG13	1:E:189:VAL:CG2	2.43	0.49
1:E:190:HIS:CG	1:E:258:VAL:HG22	2.47	0.49
1:E:237:MET:O	1:E:241:VAL:HG23	2.12	0.49
1:F:34:MET:CG	1:F:242:VAL:HG22	2.42	0.49
1:K:154:ALA:C	1:K:156:ASN:H	2.21	0.49
1:N:174:GLY:HA3	1:N:254:CYS:SG	2.53	0.49
1:P:18:VAL:N	1:P:85:ALA:O	2.34	0.49
1:B:26:ILE:HG21	1:B:144:PHE:CE2	2.47	0.49
1:C:266:VAL:HB	1:H:151:ARG:HH21	1.77	0.49
1:D:70:LYS:HE3	1:D:123:VAL:HG22	1.93	0.49
1:D:125:LEU:HA	1:D:128:LEU:HD12	1.95	0.49
1:E:88:HIS:NE2	1:E:121:THR:OG1	2.46	0.49
1:E:179:ALA:O	1:E:181:GLY:N	2.46	0.49
1:I:240:GLY:HA3	1:I:259:MET:SD	2.52	0.49
1:K:53:GLU:C	1:K:55:ALA:H	2.20	0.49
1:L:26:ILE:HA	1:L:234:PRO:CB	2.41	0.49
1:N:170:SER:HB3	1:N:186:VAL:HG12	1.94	0.49
1:N:225:ARG:NH2	2:N:302:HOH:O	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:146:SER:O	1:P:149:GLY:N	2.46	0.49
1:B:151:ARG:CZ	1:B:263:PHE:HE1	2.26	0.49
1:C:152:GLY:HA3	1:H:266:VAL:HG12	1.93	0.49
1:I:32:LYS:HG2	1:I:53:GLU:HB3	1.95	0.49
1:J:182:TYR:N	1:J:182:TYR:CD1	2.79	0.49
1:L:177:PHE:O	1:L:178:ALA:C	2.55	0.49
1:L:235:ALA:O	1:L:238:GLY:N	2.45	0.49
1:M:87:VAL:HG22	1:M:142:VAL:HB	1.94	0.49
1:M:226:HIS:CD2	1:M:263:PHE:HB2	2.47	0.49
1:O:159:TYR:CE1	1:O:163:LYS:CG	2.92	0.49
1:P:240:GLY:O	1:P:244:LEU:HG	2.13	0.49
1:B:95:VAL:HG23	1:B:202:LEU:HD22	1.95	0.49
1:B:130:GLU:C	1:B:132:GLY:N	2.69	0.49
1:E:199:LEU:HA	1:E:202:LEU:HB2	1.94	0.49
1:F:148:ALA:HB1	1:F:160:CYS:SG	2.53	0.49
1:H:15:VAL:HA	1:H:84:ASP:OD2	2.12	0.49
1:H:216:GLU:O	1:H:220:ALA:N	2.45	0.49
1:M:86:LEU:O	1:M:142:VAL:N	2.40	0.49
1:M:160:CYS:O	1:M:164:ALA:N	2.28	0.49
1:M:194:ILE:HD11	1:M:237:MET:SD	2.52	0.49
1:N:141:VAL:HB	1:N:186:VAL:HG22	1.93	0.49
1:N:241:VAL:O	1:N:245:CYS:SG	2.68	0.49
1:O:144:PHE:O	1:O:163:LYS:NZ	2.44	0.49
1:B:227:PRO:HG3	1:B:266:VAL:HG21	1.94	0.49
1:C:61:HIS:CD2	1:C:62:ASP:O	2.66	0.49
1:E:43:ALA:O	1:E:58:TYR:HA	2.12	0.49
1:E:44:THR:HB	1:E:61:HIS:HB3	1.94	0.49
1:J:12:LEU:O	1:J:39:ALA:HB2	2.13	0.49
1:J:180:LEU:HD21	1:L:155:PHE:CZ	2.48	0.49
1:J:203:MET:HE1	1:J:219:GLN:HG3	1.94	0.49
1:L:145:SER:HB3	1:L:190:HIS:ND1	2.27	0.49
1:N:115:ASP:O	1:N:116:SER:C	2.56	0.49
1:O:18:VAL:HA	1:O:42:ILE:HB	1.95	0.49
1:A:69:TRP:CZ2	1:A:88:HIS:CE1	3.01	0.49
1:A:243:TYR:CZ	1:A:249:ALA:HB2	2.48	0.49
1:B:112:VAL:O	1:B:112:VAL:HG12	2.11	0.49
1:D:185:ARG:CZ	1:D:249:ALA:O	2.61	0.49
1:F:24:GLY:O	1:F:28:ARG:NH1	2.46	0.49
1:F:118:ILE:O	1:F:122:GLN:HB2	2.13	0.49
1:I:151:ARG:HB3	1:M:265:GLN:O	2.13	0.49
1:L:92:ILE:HD11	1:L:109:VAL:HA	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:156:ASN:HB3	1:N:160:CYS:SG	2.53	0.49
1:O:88:HIS:HB3	1:O:117:ILE:HG12	1.95	0.49
1:O:174:GLY:CA	1:O:186:VAL:HB	2.43	0.49
1:B:204:ASP:OD2	1:B:215:ARG:NH1	2.46	0.48
1:C:32:LYS:HE2	1:C:53:GLU:HB3	1.94	0.48
1:F:73:ALA:O	1:F:76:ALA:HB3	2.13	0.48
1:I:97:LYS:O	1:I:100:ASP:C	2.56	0.48
1:I:218:ALA:HA	1:I:221:ALA:HB3	1.95	0.48
1:K:23:ALA:HB2	1:K:50:ALA:HB1	1.95	0.48
1:M:136:ALA:HB3	1:M:247:ASP:OD1	2.14	0.48
1:N:180:LEU:CB	1:N:182:TYR:CE2	2.96	0.48
1:B:162:SER:O	1:B:164:ALA:N	2.45	0.48
1:E:32:LYS:CG	1:E:53:GLU:HB3	2.39	0.48
1:E:176:GLU:HA	1:G:154:ALA:HB1	1.95	0.48
1:E:190:HIS:HB2	1:E:258:VAL:HG22	1.95	0.48
1:E:240:GLY:HA3	1:E:257:PHE:CE2	2.48	0.48
1:F:82:ARG:HH21	1:F:84:ASP:CG	2.22	0.48
1:J:151:ARG:HH21	1:N:266:VAL:HB	1.74	0.48
1:P:43:ALA:HB3	1:P:58:TYR:HD1	1.76	0.48
1:A:77:GLN:O	1:A:81:GLY:N	2.46	0.48
1:G:151:ARG:HH21	1:G:153:ALA:CA	2.26	0.48
1:I:76:ALA:CB	1:I:127:LEU:HD13	2.43	0.48
1:K:171:LYS:NZ	1:K:256:GLU:OE1	2.46	0.48
1:N:202:LEU:O	1:N:205:LYS:HB2	2.13	0.48
1:A:187:ASN:OD1	1:A:252:VAL:O	2.31	0.48
1:B:35:LYS:HA	1:B:39:ALA:HB3	1.95	0.48
1:D:217:VAL:O	1:D:221:ALA:HB2	2.13	0.48
1:L:64:THR:HG22	1:L:111:THR:C	2.37	0.48
1:M:150:LEU:O	1:O:168:MET:HE1	2.14	0.48
1:N:77:GLN:HA	1:N:77:GLN:HE21	1.77	0.48
1:O:69:TRP:CB	1:O:123:VAL:HG11	2.42	0.48
1:A:138:GLY:N	1:A:183:ASN:HD21	2.11	0.48
1:A:140:SER:CB	1:A:245:CYS:HA	2.43	0.48
1:A:176:GLU:HG2	1:A:180:LEU:CD1	2.44	0.48
1:B:12:LEU:HD21	1:B:242:VAL:O	2.14	0.48
1:B:151:ARG:CZ	1:B:263:PHE:CE1	2.96	0.48
1:C:187:ASN:ND2	1:C:244:LEU:HD22	2.29	0.48
1:G:201:SER:O	1:G:204:ASP:HB2	2.12	0.48
1:G:255:THR:OG1	1:G:257:PHE:N	2.45	0.48
1:I:214:SER:C	1:I:216:GLU:H	2.20	0.48
1:L:12:LEU:HD21	1:L:245:CYS:C	2.38	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:62:ASP:HB3	1:N:65:SER:CB	2.44	0.48
1:A:181:GLY:O	1:A:182:TYR:C	2.56	0.48
1:A:196:THR:C	1:A:198:MET:H	2.22	0.48
1:A:199:LEU:HD23	1:A:231:MET:SD	2.54	0.48
1:A:248:ALA:HB1	1:G:239:GLY:CA	2.40	0.48
1:B:176:GLU:OE2	1:C:97:LYS:HA	2.12	0.48
1:D:266:VAL:C	1:G:151:ARG:HD2	2.39	0.48
1:E:186:VAL:O	1:E:254:CYS:N	2.45	0.48
1:G:159:TYR:O	1:G:159:TYR:CD1	2.67	0.48
1:N:146:SER:HA	1:N:190:HIS:HA	1.96	0.48
1:N:187:ASN:OD1	1:N:252:VAL:HG12	2.13	0.48
1:O:69:TRP:CD1	1:O:119:ILE:HG22	2.48	0.48
1:P:145:SER:N	1:P:189:VAL:O	2.46	0.48
1:P:218:ALA:HA	1:P:221:ALA:HB3	1.96	0.48
1:A:221:ALA:HB1	1:A:225:ARG:HE	1.78	0.48
1:B:34:MET:HG2	1:B:242:VAL:HG22	1.95	0.48
1:B:162:SER:C	1:B:164:ALA:H	2.21	0.48
1:C:187:ASN:CB	1:C:244:LEU:HD13	2.44	0.48
1:D:101:THR:HG21	1:D:106:PHE:CD1	2.48	0.48
1:I:118:ILE:HD13	1:K:103:LEU:HD12	1.94	0.48
1:I:232:GLY:N	1:O:251:PHE:CZ	2.82	0.48
1:I:232:GLY:N	1:O:251:PHE:CE1	2.81	0.48
1:K:113:ASN:OD1	1:K:113:ASN:N	2.45	0.48
1:L:148:ALA:HB1	1:L:160:CYS:HA	1.95	0.48
1:N:146:SER:C	1:N:148:ALA:N	2.71	0.48
1:D:143:ASN:ND2	1:D:170:SER:OG	2.45	0.48
1:D:252:VAL:HG22	1:E:259:MET:HG2	1.95	0.48
1:G:44:THR:HG22	1:G:59:LEU:HB2	1.96	0.48
1:I:194:ILE:CD1	1:I:237:MET:HE3	2.42	0.48
1:I:251:PHE:HD1	1:O:228:ILE:HD13	1.78	0.48
1:M:38:ASN:ND2	2:M:303:HOH:O	2.46	0.48
1:M:58:TYR:C	1:M:59:LEU:HD12	2.39	0.48
1:M:123:VAL:HG12	1:M:124:LEU:HD23	1.95	0.48
1:M:159:TYR:OH	1:M:163:LYS:HE3	2.13	0.48
1:P:111:THR:O	1:P:115:ASP:HB2	2.14	0.48
1:A:222:MET:HG3	1:A:223:GLU:HG3	1.95	0.48
1:D:58:TYR:CE1	1:D:59:LEU:O	2.67	0.48
1:D:194:ILE:HD11	1:D:237:MET:HE3	1.96	0.48
1:E:12:LEU:HD12	1:E:242:VAL:HG13	1.96	0.48
1:F:252:VAL:HG13	1:F:255:THR:HG21	1.95	0.48
1:I:88:HIS:CE1	1:I:116:SER:O	2.67	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:214:SER:C	1:I:216:GLU:N	2.69	0.48
1:A:98:PHE:HZ	1:D:121:THR:HB	1.79	0.48
1:B:31:VAL:HG12	1:B:53:GLU:O	2.14	0.48
1:B:150:LEU:HD21	1:B:256:GLU:OE2	2.14	0.48
1:G:103:LEU:O	1:G:107:HIS:N	2.42	0.48
1:K:61:HIS:ND1	1:K:72:VAL:HG21	2.29	0.48
1:K:94:ILE:HD12	1:K:109:VAL:HG22	1.96	0.48
1:M:103:LEU:HD13	1:O:119:ILE:HG12	1.96	0.48
1:A:151:ARG:HB2	1:E:265:GLN:O	2.13	0.47
1:C:115:ASP:O	1:C:119:ILE:HG13	2.14	0.47
1:D:47:ALA:O	1:D:58:TYR:OH	2.30	0.47
1:E:35:LYS:HG3	1:E:54:GLY:HA3	1.96	0.47
1:F:101:THR:O	1:F:102:PRO:C	2.56	0.47
1:F:214:SER:H	1:F:217:VAL:HB	1.79	0.47
1:H:69:TRP:HB3	1:H:123:VAL:HG11	1.94	0.47
1:D:45:ASP:O	1:D:61:HIS:N	2.32	0.47
1:G:213:PRO:HD2	1:G:217:VAL:HG11	1.96	0.47
1:H:138:GLY:HA3	1:H:185:ARG:HE	1.78	0.47
1:H:199:LEU:C	1:H:201:SER:H	2.21	0.47
1:I:86:LEU:HD22	1:I:128:LEU:HD11	1.94	0.47
1:L:12:LEU:HD12	1:L:242:VAL:HG13	1.96	0.47
1:L:266:VAL:C	1:P:151:ARG:NE	2.72	0.47
1:F:13:ASN:O	1:F:14:ASN:HB2	2.15	0.47
1:F:86:LEU:HD22	1:F:124:LEU:HD12	1.96	0.47
1:G:44:THR:HB	1:G:61:HIS:CB	2.43	0.47
1:L:142:VAL:HG11	1:L:241:VAL:HG13	1.97	0.47
1:L:163:LYS:O	1:L:164:ALA:C	2.57	0.47
1:A:109:VAL:O	1:A:110:ASN:C	2.57	0.47
1:A:156:ASN:ND2	1:A:206:TYR:OH	2.47	0.47
1:C:31:VAL:HA	1:C:34:MET:HB2	1.96	0.47
1:F:146:SER:HA	1:F:191:PRO:HD2	1.96	0.47
1:F:161:THR:HG21	1:H:169:LEU:CD1	2.43	0.47
1:I:83:VAL:HG23	1:I:127:LEU:HB3	1.97	0.47
1:J:16:VAL:H	1:J:84:ASP:HB2	1.78	0.47
1:J:20:THR:O	1:J:89:ASN:HB3	2.14	0.47
1:K:142:VAL:CG2	1:K:244:LEU:HD12	2.44	0.47
1:M:160:CYS:HA	1:M:163:LYS:HB2	1.97	0.47
1:B:155:PHE:HA	1:C:176:GLU:OE2	2.15	0.47
1:E:32:LYS:HG2	1:E:53:GLU:CB	2.39	0.47
1:I:18:VAL:CG2	1:I:86:LEU:HD12	2.44	0.47
1:K:161:THR:O	1:K:165:ALA:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:145:SER:OG	1:P:190:HIS:ND1	2.40	0.47
1:B:15:VAL:HG12	1:B:17:ALA:HB2	1.95	0.47
1:B:119:ILE:O	1:B:122:GLN:HB2	2.15	0.47
1:C:22:ALA:HA	1:C:27:GLY:HA3	1.96	0.47
1:F:56:ASP:O	1:F:57:HIS:CD2	2.67	0.47
1:G:95:VAL:HG23	1:G:202:LEU:HD13	1.95	0.47
1:I:223:GLU:OE1	1:I:230:ARG:HA	2.15	0.47
1:A:182:TYR:OH	1:D:99:GLU:OE1	2.27	0.47
1:B:16:VAL:HA	1:B:40:ILE:HB	1.95	0.47
1:B:212:ALA:CB	1:B:218:ALA:HB2	2.44	0.47
1:D:19:VAL:O	1:D:44:THR:N	2.39	0.47
1:D:83:VAL:O	1:D:131:GLY:HA3	2.15	0.47
1:D:206:TYR:HB3	1:D:211:ALA:HB3	1.96	0.47
1:F:170:SER:HA	1:F:186:VAL:HG11	1.97	0.47
1:G:159:TYR:HE1	1:G:163:LYS:HE2	1.78	0.47
1:I:98:PHE:C	1:I:100:ASP:H	2.23	0.47
1:I:145:SER:O	1:I:163:LYS:HD2	2.14	0.47
1:J:62:ASP:O	1:J:65:SER:HB3	2.14	0.47
1:J:155:PHE:HE1	1:L:180:LEU:HD11	1.80	0.47
1:L:125:LEU:HB3	1:L:126:PRO:HD3	1.96	0.47
1:L:151:ARG:HD3	1:L:263:PHE:CE1	2.50	0.47
1:M:171:LYS:HG2	1:M:254:CYS:O	2.15	0.47
1:M:204:ASP:O	1:M:205:LYS:C	2.57	0.47
1:M:225:ARG:HB3	1:M:263:PHE:CE2	2.50	0.47
1:N:204:ASP:OD1	1:N:204:ASP:N	2.46	0.47
1:O:93:SER:HA	1:O:159:TYR:CD2	2.50	0.47
1:O:132:GLY:O	1:O:183:ASN:ND2	2.33	0.47
1:O:182:TYR:N	1:O:182:TYR:CD1	2.82	0.47
1:P:76:ALA:HB1	1:P:83:VAL:HG23	1.95	0.47
1:P:240:GLY:O	1:P:243:TYR:HB3	2.15	0.47
1:A:40:ILE:HG21	1:A:80:TYR:CZ	2.49	0.47
1:A:239:GLY:HA2	1:A:242:VAL:CG2	2.45	0.47
1:B:125:LEU:CD1	1:B:184:ILE:HD13	2.45	0.47
1:C:226:HIS:HB2	1:C:230:ARG:O	2.15	0.47
1:D:150:LEU:HA	1:D:167:LYS:HZ3	1.80	0.47
1:O:93:SER:OG	1:O:159:TYR:CE2	2.59	0.47
1:A:112:VAL:O	1:A:116:SER:HB3	2.15	0.47
1:C:167:LYS:HB2	1:C:190:HIS:HE1	1.79	0.47
1:C:230:ARG:NH2	1:C:236:GLU:OE1	2.48	0.47
1:G:168:MET:O	1:G:171:LYS:HB2	2.15	0.47
1:H:98:PHE:O	1:H:99:GLU:C	2.57	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:137:GLY:HA3	1:H:247:ASP:HB3	1.96	0.47
1:I:102:PRO:HD2	1:I:105:ASP:OD2	2.15	0.47
1:K:199:LEU:HA	1:K:202:LEU:HD12	1.96	0.47
1:L:182:TYR:CD1	1:L:182:TYR:N	2.78	0.47
1:M:164:ALA:HB2	1:O:168:MET:HG2	1.97	0.47
1:N:145:SER:OG	1:N:163:LYS:O	2.27	0.47
1:N:173:LEU:CB	1:N:186:VAL:HG21	2.45	0.47
1:P:119:ILE:O	1:P:122:GLN:N	2.48	0.47
1:C:170:SER:OG	1:C:188:SER:HB3	2.15	0.47
1:C:207:VAL:HG13	1:C:213:PRO:O	2.15	0.47
1:D:176:GLU:O	1:D:180:LEU:HG	2.14	0.47
1:D:266:VAL:C	1:G:151:ARG:HH11	2.22	0.47
1:F:41:VAL:O	1:F:56:ASP:HB2	2.14	0.47
1:F:145:SER:O	1:F:191:PRO:CD	2.61	0.47
1:F:180:LEU:C	1:F:182:TYR:N	2.73	0.47
1:G:40:ILE:HG21	1:G:80:TYR:CZ	2.50	0.47
1:G:57:HIS:CE1	1:G:79:LYS:HE3	2.50	0.47
1:G:85:ALA:HA	1:G:140:SER:O	2.15	0.47
1:G:147:VAL:O	1:G:150:LEU:HB2	2.15	0.47
1:I:125:LEU:HA	1:I:128:LEU:HB2	1.96	0.47
1:K:22:ALA:C	1:K:24:GLY:H	2.23	0.47
1:N:127:LEU:O	1:N:131:GLY:N	2.33	0.47
1:A:131:GLY:HA3	1:A:139:ALA:HB2	1.97	0.46
1:A:168:MET:HE1	1:D:150:LEU:O	2.15	0.46
1:H:225:ARG:HD3	1:H:263:PHE:HE1	1.80	0.46
1:K:12:LEU:HD21	1:K:245:CYS:C	2.40	0.46
1:K:233:ARG:NH2	1:K:236:GLU:OE1	2.48	0.46
1:M:21:GLY:HA2	1:M:45:ASP:OD2	2.15	0.46
1:P:59:LEU:HD22	1:P:72:VAL:HG22	1.96	0.46
1:B:93:SER:HA	1:B:159:TYR:CE1	2.50	0.46
1:C:139:ALA:HB3	1:C:184:ILE:HG12	1.97	0.46
1:F:97:LYS:HE3	1:F:209:LEU:HD22	1.97	0.46
1:F:170:SER:OG	1:F:188:SER:HB3	2.15	0.46
1:F:207:VAL:O	1:F:209:LEU:N	2.48	0.46
1:I:118:ILE:HA	1:K:98:PHE:CZ	2.47	0.46
1:I:152:GLY:HA3	1:K:171:LYS:HB3	1.97	0.46
1:J:66:GLU:HA	1:J:119:ILE:HG21	1.97	0.46
1:J:145:SER:OG	1:J:146:SER:N	2.35	0.46
1:K:61:HIS:C	1:K:61:HIS:CD2	2.93	0.46
1:M:94:ILE:HD12	1:M:109:VAL:CG2	2.44	0.46
1:M:220:ALA:O	1:M:224:MET:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:HIS:C	1:A:61:HIS:CD2	2.93	0.46
1:B:108:ARG:HB2	1:G:208:GLU:HA	1.96	0.46
1:B:241:VAL:O	1:B:242:VAL:C	2.58	0.46
1:B:256:GLU:OE1	2:B:301:HOH:O	2.20	0.46
1:D:26:ILE:HG13	1:D:196:THR:HG21	1.97	0.46
1:D:227:PRO:HG3	1:D:266:VAL:CG2	2.45	0.46
1:F:92:ILE:HG12	1:F:112:VAL:HG11	1.96	0.46
1:G:139:ALA:HB3	1:G:184:ILE:HG12	1.97	0.46
1:H:125:LEU:HG	1:H:129:LYS:CE	2.40	0.46
1:L:35:LYS:O	1:L:38:ASN:N	2.46	0.46
1:C:69:TRP:O	1:C:123:VAL:HG11	2.16	0.46
1:F:115:ASP:O	1:F:118:ILE:N	2.48	0.46
1:H:185:ARG:NH1	1:H:244:LEU:O	2.38	0.46
1:I:168:MET:CG	1:K:160:CYS:HB3	2.45	0.46
1:K:248:ALA:HB1	1:M:239:GLY:CA	2.46	0.46
1:M:35:LYS:HD3	1:M:56:ASP:OD2	2.14	0.46
1:N:194:ILE:HG22	1:N:195:ASP:N	2.30	0.46
1:O:70:LYS:O	1:O:74:ALA:N	2.38	0.46
1:P:97:LYS:HB2	1:P:100:ASP:HB2	1.97	0.46
1:C:152:GLY:O	1:H:266:VAL:HG12	2.15	0.46
1:H:20:THR:OG1	1:H:88:HIS:HA	2.15	0.46
1:H:91:GLY:HA2	1:H:112:VAL:HG12	1.97	0.46
1:I:69:TRP:HE3	1:I:124:LEU:HD11	1.81	0.46
1:J:263:PHE:C	1:J:263:PHE:CD1	2.94	0.46
1:M:12:LEU:CB	1:M:39:ALA:HB2	2.34	0.46
1:F:111:THR:O	1:F:115:ASP:HB2	2.15	0.46
1:I:52:VAL:HB	1:I:55:ALA:HB2	1.98	0.46
1:K:83:VAL:CG2	1:K:127:LEU:HD13	2.44	0.46
1:K:159:TYR:CE1	1:K:163:LYS:HE3	2.51	0.46
1:L:167:LYS:HB2	1:L:190:HIS:HE1	1.81	0.46
1:M:63:VAL:HG23	1:M:116:SER:HB2	1.96	0.46
1:N:115:ASP:HA	1:N:118:ILE:CD1	2.42	0.46
1:O:12:LEU:HD21	1:O:245:CYS:HB2	1.98	0.46
1:O:69:TRP:C	1:O:123:VAL:HG11	2.40	0.46
1:C:44:THR:HG22	1:C:59:LEU:HB2	1.98	0.46
1:D:227:PRO:HG2	1:D:262:GLY:O	2.16	0.46
1:J:112:VAL:O	1:J:112:VAL:HG12	2.16	0.46
1:K:221:ALA:HA	1:K:224:MET:HE2	1.96	0.46
1:K:257:PHE:CE1	1:M:257:PHE:CD2	3.02	0.46
1:L:164:ALA:O	1:L:167:LYS:HB3	2.15	0.46
1:L:251:PHE:CE2	1:N:237:MET:HE1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:31:VAL:HG11	1:O:52:VAL:CG1	2.46	0.46
1:O:84:ASP:OD1	1:O:135:ARG:HG3	2.15	0.46
1:C:132:GLY:HA3	1:C:183:ASN:O	2.16	0.46
1:D:127:LEU:O	1:D:131:GLY:N	2.49	0.46
1:E:92:ILE:HD11	1:E:109:VAL:HA	1.98	0.46
1:F:159:TYR:CZ	1:F:163:LYS:HE3	2.50	0.46
1:F:229:GLY:O	1:F:230:ARG:HB3	2.16	0.46
1:I:104:SER:O	1:I:108:ARG:HB2	2.16	0.46
1:J:20:THR:HG1	1:J:88:HIS:HA	1.80	0.46
1:L:251:PHE:HB2	1:N:236:GLU:CD	2.41	0.46
1:M:198:MET:O	1:M:202:LEU:HG	2.15	0.46
1:P:263:PHE:C	1:P:263:PHE:HD1	2.24	0.46
1:A:265:GLN:HG3	1:G:254:CYS:O	2.15	0.46
1:D:48:PRO:HA	1:D:60:GLN:NE2	2.31	0.46
1:D:180:LEU:HD23	1:D:180:LEU:HA	1.82	0.46
1:E:155:PHE:CD1	1:G:176:GLU:HG3	2.51	0.46
1:F:98:PHE:CZ	1:H:118:ILE:HA	2.50	0.46
1:F:202:LEU:O	1:F:205:LYS:N	2.49	0.46
1:G:83:VAL:HG23	1:G:127:LEU:CB	2.46	0.46
1:M:94:ILE:HG22	1:M:96:THR:HG22	1.97	0.46
1:O:233:ARG:N	1:O:236:GLU:OE2	2.49	0.46
1:P:35:LYS:HG3	1:P:54:GLY:CA	2.46	0.46
1:D:101:THR:HG22	1:D:102:PRO:O	2.16	0.46
1:E:20:THR:HA	1:E:44:THR:OG1	2.16	0.46
1:E:44:THR:HG22	1:E:59:LEU:HB2	1.98	0.46
1:E:64:THR:CG2	1:E:111:THR:HG22	2.46	0.46
1:E:162:SER:O	1:E:166:VAL:HG23	2.15	0.46
1:G:147:VAL:HA	1:G:150:LEU:HD12	1.98	0.46
1:I:44:THR:HB	1:I:61:HIS:HB2	1.97	0.46
1:I:237:MET:HA	1:I:259:MET:HE1	1.97	0.46
1:I:266:VAL:CG1	1:M:152:GLY:N	2.71	0.46
1:J:45:ASP:O	1:J:60:GLN:HA	2.16	0.46
1:M:203:MET:O	1:M:207:VAL:HG23	2.16	0.46
1:N:68:GLY:O	1:N:71:ALA:HB3	2.16	0.46
1:N:93:SER:HA	1:N:159:TYR:CD1	2.51	0.46
1:N:233:ARG:HB2	1:N:236:GLU:HG3	1.98	0.46
1:P:80:TYR:C	1:P:82:ARG:H	2.23	0.46
1:P:173:LEU:O	1:P:177:PHE:N	2.38	0.46
1:A:64:THR:O	1:A:119:ILE:HD12	2.16	0.45
1:A:66:GLU:C	1:A:68:GLY:N	2.74	0.45
1:A:79:LYS:O	1:A:80:TYR:CG	2.69	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:62:ASP:O	1:D:65:SER:HB3	2.16	0.45
1:F:103:LEU:HD12	1:H:118:ILE:HG21	1.96	0.45
1:F:143:ASN:O	1:F:188:SER:HA	2.15	0.45
1:G:227:PRO:HD3	1:G:262:GLY:O	2.15	0.45
1:H:17:ALA:O	1:H:42:ILE:N	2.48	0.45
1:J:88:HIS:CG	1:J:143:ASN:OD1	2.69	0.45
1:J:251:PHE:CE1	1:P:231:MET:C	2.94	0.45
1:K:228:ILE:HG21	1:M:251:PHE:HE1	1.81	0.45
1:M:61:HIS:CE1	1:M:72:VAL:HG21	2.51	0.45
1:M:145:SER:HB2	1:M:166:VAL:CG1	2.46	0.45
1:M:150:LEU:C	1:O:168:MET:HE1	2.41	0.45
1:O:35:LYS:HG3	1:O:54:GLY:O	2.16	0.45
1:C:227:PRO:CG	1:C:266:VAL:HG22	2.46	0.45
1:E:147:VAL:HG11	1:E:260:ASP:HB2	1.98	0.45
1:H:15:VAL:HA	1:H:84:ASP:CG	2.41	0.45
1:I:76:ALA:HB1	1:I:127:LEU:HD13	1.97	0.45
1:I:88:HIS:CE1	1:I:117:ILE:HA	2.51	0.45
1:I:92:ILE:HD11	1:I:109:VAL:HA	1.98	0.45
1:I:110:ASN:O	1:I:114:VAL:HB	2.15	0.45
1:I:232:GLY:CA	1:O:251:PHE:CZ	2.99	0.45
1:N:16:VAL:N	1:N:84:ASP:HB2	2.30	0.45
1:N:201:SER:HA	1:N:215:ARG:CZ	2.46	0.45
1:N:205:LYS:C	1:N:207:VAL:H	2.24	0.45
1:O:227:PRO:HG3	1:O:266:VAL:HG21	1.98	0.45
1:A:125:LEU:N	1:A:126:PRO:HD2	2.31	0.45
1:B:64:THR:HG21	1:B:111:THR:HG22	1.97	0.45
1:G:142:VAL:HG22	1:G:244:LEU:HD13	1.98	0.45
1:H:145:SER:OG	1:H:146:SER:N	2.46	0.45
1:I:237:MET:HE2	1:I:259:MET:HE2	1.98	0.45
1:K:141:VAL:HB	1:K:186:VAL:HG22	1.98	0.45
1:K:189:VAL:HG12	1:K:191:PRO:HD3	1.98	0.45
1:L:201:SER:O	1:L:204:ASP:N	2.40	0.45
1:L:227:PRO:O	1:N:178:ALA:HB1	2.16	0.45
1:N:111:THR:HA	1:N:115:ASP:HB2	1.98	0.45
1:N:133:LYS:C	1:N:135:ARG:H	2.24	0.45
1:N:167:LYS:HE3	1:N:171:LYS:HE3	1.98	0.45
1:P:12:LEU:O	1:P:39:ALA:HB2	2.17	0.45
1:P:157:ALA:O	1:P:161:THR:N	2.49	0.45
1:I:122:GLN:NE2	1:K:98:PHE:O	2.47	0.45
1:I:161:THR:O	1:I:164:ALA:HB3	2.16	0.45
1:J:76:ALA:O	1:J:80:TYR:N	2.36	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:88:HIS:NE2	1:J:141:VAL:HG13	2.31	0.45
1:J:182:TYR:N	1:J:182:TYR:HD1	2.14	0.45
1:K:266:VAL:C	1:O:151:ARG:NH2	2.74	0.45
1:M:112:VAL:O	1:M:112:VAL:CG1	2.64	0.45
1:O:199:LEU:HD21	1:O:222:MET:HE3	1.97	0.45
1:C:244:LEU:HD11	1:C:257:PHE:CD2	2.51	0.45
1:D:129:LYS:HA	1:D:184:ILE:HD11	1.98	0.45
1:F:98:PHE:HZ	1:H:118:ILE:HA	1.81	0.45
1:F:146:SER:O	1:F:190:HIS:ND1	2.47	0.45
1:F:177:PHE:CE2	1:F:186:VAL:CG2	3.00	0.45
1:H:12:LEU:O	1:H:15:VAL:HB	2.16	0.45
1:I:10:ILE:HD11	1:O:242:VAL:HB	1.99	0.45
1:J:241:VAL:O	1:J:244:LEU:N	2.49	0.45
1:K:16:VAL:HG21	1:K:82:ARG:HG3	1.98	0.45
1:L:189:VAL:CG2	1:L:244:LEU:HD12	2.47	0.45
1:M:198:MET:O	1:M:201:SER:OG	2.33	0.45
1:O:195:ASP:CA	1:O:231:MET:SD	3.04	0.45
1:P:97:LYS:O	1:P:101:THR:N	2.50	0.45
1:A:176:GLU:C	1:A:178:ALA:N	2.74	0.45
1:C:237:MET:SD	1:C:259:MET:CE	3.05	0.45
1:D:101:THR:CG2	1:D:106:PHE:HD1	2.29	0.45
1:D:257:PHE:C	1:D:257:PHE:CD1	2.95	0.45
1:E:79:LYS:HB3	1:E:80:TYR:CD2	2.52	0.45
1:E:187:ASN:HB3	1:E:255:THR:CG2	2.39	0.45
1:G:15:VAL:O	1:G:40:ILE:N	2.47	0.45
1:H:22:ALA:HA	1:H:27:GLY:HA3	1.98	0.45
1:H:97:LYS:HG3	1:H:209:LEU:HD13	1.98	0.45
1:I:259:MET:HE3	1:O:243:TYR:OH	2.15	0.45
1:I:266:VAL:C	1:M:151:ARG:CZ	2.90	0.45
1:J:113:ASN:O	1:J:166:VAL:HG22	2.16	0.45
1:L:266:VAL:CA	1:P:151:ARG:HB2	2.46	0.45
1:M:121:THR:O	1:M:122:GLN:C	2.60	0.45
1:N:105:ASP:O	1:N:109:VAL:HG23	2.17	0.45
1:P:18:VAL:CG1	1:P:86:LEU:HD12	2.47	0.45
1:P:35:LYS:HD2	1:P:39:ALA:O	2.16	0.45
1:P:252:VAL:CG1	1:P:255:THR:HG21	2.43	0.45
1:D:29:GLU:CG	1:D:234:PRO:HB2	2.45	0.45
1:E:52:VAL:CG1	1:E:55:ALA:HB3	2.46	0.45
1:F:30:LEU:HD11	1:F:89:ASN:OD1	2.16	0.45
1:F:86:LEU:HD13	1:F:124:LEU:HD12	1.99	0.45
1:G:56:ASP:O	1:G:57:HIS:CG	2.70	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:125:LEU:HB3	1:G:126:PRO:HD3	1.99	0.45
1:G:132:GLY:HA2	1:G:138:GLY:HA2	1.98	0.45
1:G:146:SER:OG	1:G:147:VAL:N	2.50	0.45
1:I:84:ASP:HB3	1:I:135:ARG:HH11	1.81	0.45
1:L:139:ALA:O	1:L:184:ILE:HA	2.17	0.45
1:M:145:SER:HB2	1:M:166:VAL:HG11	1.99	0.45
1:A:135:ARG:NH2	1:A:247:ASP:OD1	2.44	0.45
1:B:201:SER:HA	1:B:204:ASP:OD2	2.17	0.45
1:C:101:THR:HG22	1:C:102:PRO:O	2.16	0.45
1:C:167:LYS:HD3	1:C:190:HIS:CE1	2.52	0.45
1:F:83:VAL:HG23	1:F:127:LEU:HD22	1.98	0.45
1:G:169:LEU:O	1:G:170:SER:C	2.59	0.45
1:G:241:VAL:O	1:G:244:LEU:HB2	2.17	0.45
1:J:194:ILE:HG22	1:J:196:THR:HG23	1.98	0.45
1:K:23:ALA:HB2	1:K:50:ALA:CB	2.47	0.45
1:M:148:ALA:O	1:M:160:CYS:SG	2.74	0.45
1:N:16:VAL:HG11	1:N:83:VAL:HA	1.99	0.45
1:N:173:LEU:HB3	1:N:177:PHE:CE2	2.52	0.45
1:O:187:ASN:OD1	1:O:255:THR:HG22	2.17	0.45
1:P:124:LEU:HD22	1:P:127:LEU:CD1	2.46	0.45
1:P:176:GLU:O	1:P:179:ALA:HB3	2.17	0.45
1:B:115:ASP:O	1:B:119:ILE:HG13	2.17	0.45
1:B:136:ALA:C	1:B:138:GLY:H	2.25	0.45
1:D:11:ALA:N	2:D:304:HOH:O	2.49	0.45
1:D:26:ILE:HG12	1:D:234:PRO:HA	1.98	0.45
1:D:82:ARG:NH2	1:D:84:ASP:OD1	2.49	0.45
1:D:237:MET:O	1:D:241:VAL:HG23	2.17	0.45
1:E:181:GLY:O	1:E:182:TYR:C	2.60	0.45
1:F:66:GLU:HA	1:F:119:ILE:HG21	1.99	0.45
1:J:255:THR:OG1	1:P:258:VAL:HG12	2.17	0.45
1:L:148:ALA:HB2	1:L:159:TYR:CE2	2.52	0.45
1:M:97:LYS:HE3	1:M:209:LEU:CD2	2.47	0.45
1:N:167:LYS:O	1:N:168:MET:C	2.60	0.45
1:P:140:SER:HA	1:P:185:ARG:O	2.17	0.45
1:A:114:VAL:O	1:A:118:ILE:HG13	2.17	0.45
1:C:129:LYS:O	1:C:133:LYS:HG3	2.17	0.45
1:E:123:VAL:HG12	1:E:124:LEU:HD23	1.97	0.45
1:F:40:ILE:HA	1:F:56:ASP:OD2	2.16	0.45
1:F:61:HIS:CE1	1:F:63:VAL:HG12	2.52	0.45
1:H:21:GLY:O	1:H:89:ASN:ND2	2.50	0.45
1:I:252:VAL:CG1	1:I:255:THR:HG21	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:26:ILE:CG1	1:K:234:PRO:HB3	2.45	0.45
1:K:151:ARG:NE	1:O:266:VAL:C	2.75	0.45
1:K:185:ARG:NH1	1:K:249:ALA:O	2.50	0.45
1:L:152:GLY:C	1:P:266:VAL:HB	2.42	0.45
1:M:147:VAL:O	1:M:151:ARG:O	2.35	0.45
1:P:105:ASP:O	1:P:109:VAL:HG23	2.17	0.45
1:A:151:ARG:HB3	1:E:265:GLN:O	2.17	0.44
1:A:185:ARG:HD3	1:A:250:SER:O	2.15	0.44
1:A:222:MET:O	1:A:226:HIS:CE1	2.71	0.44
1:B:18:VAL:HG11	1:B:72:VAL:HG11	1.99	0.44
1:C:227:PRO:HG2	1:C:262:GLY:O	2.17	0.44
1:E:210:GLY:C	1:E:212:ALA:H	2.25	0.44
1:G:12:LEU:HD11	1:G:245:CYS:HB2	2.00	0.44
1:J:26:ILE:HD13	1:J:237:MET:HG3	1.99	0.44
1:J:221:ALA:HA	1:J:224:MET:HE2	1.98	0.44
1:N:217:VAL:HA	1:N:220:ALA:HB3	1.99	0.44
1:P:146:SER:O	1:P:150:LEU:HG	2.17	0.44
1:P:162:SER:O	1:P:166:VAL:HG23	2.16	0.44
1:D:236:GLU:O	1:D:259:MET:HE1	2.16	0.44
1:G:215:ARG:O	1:G:219:GLN:HB2	2.17	0.44
1:H:124:LEU:HD23	1:H:124:LEU:HA	1.78	0.44
1:H:181:GLY:C	1:H:182:TYR:HD1	2.26	0.44
1:I:35:LYS:HG3	1:I:54:GLY:HA3	1.98	0.44
1:J:112:VAL:O	1:J:112:VAL:CG1	2.64	0.44
1:P:16:VAL:HA	1:P:40:ILE:HB	1.98	0.44
1:A:136:ALA:C	1:A:138:GLY:H	2.24	0.44
1:A:196:THR:C	1:A:198:MET:N	2.76	0.44
1:D:61:HIS:CD2	1:D:68:GLY:C	2.96	0.44
1:D:205:LYS:C	1:D:207:VAL:H	2.24	0.44
1:I:15:VAL:HG13	1:I:84:ASP:CB	2.47	0.44
1:L:197:PRO:CG	2:L:306:HOH:O	2.58	0.44
1:M:160:CYS:C	1:M:162:SER:H	2.25	0.44
1:M:193:GLY:O	1:M:232:GLY:N	2.44	0.44
1:A:88:HIS:CG	1:A:117:ILE:HG12	2.53	0.44
1:C:180:LEU:HD13	1:C:182:TYR:CE2	2.51	0.44
1:D:15:VAL:HG22	1:D:135:ARG:NE	2.32	0.44
1:E:48:PRO:HA	1:E:60:GLN:CD	2.43	0.44
1:E:150:LEU:HD23	1:E:167:LYS:HD2	1.99	0.44
1:K:20:THR:O	1:K:89:ASN:HB3	2.17	0.44
1:K:77:GLN:HB2	1:K:127:LEU:HD11	1.99	0.44
1:N:168:MET:HE3	1:P:148:ALA:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:194:ILE:CG2	1:N:195:ASP:N	2.80	0.44
1:N:204:ASP:O	1:N:207:VAL:HB	2.18	0.44
1:O:266:VAL:O	1:O:266:VAL:CG2	2.56	0.44
1:P:76:ALA:HB3	1:P:127:LEU:HD13	1.99	0.44
1:B:140:SER:HB2	1:B:185:ARG:NH2	2.33	0.44
1:E:20:THR:O	1:E:89:ASN:ND2	2.39	0.44
1:F:74:ALA:O	1:F:78:GLU:HB2	2.17	0.44
1:G:167:LYS:HG2	1:G:171:LYS:CE	2.47	0.44
1:I:88:HIS:NE2	1:I:117:ILE:HA	2.32	0.44
1:L:107:HIS:O	1:L:111:THR:N	2.48	0.44
1:P:204:ASP:O	1:P:207:VAL:HB	2.17	0.44
1:A:239:GLY:HA2	1:A:242:VAL:HG23	1.99	0.44
1:D:22:ALA:HB3	1:D:45:ASP:HB2	1.99	0.44
1:D:97:LYS:HD3	1:D:99:GLU:CG	2.48	0.44
1:D:227:PRO:HG3	1:D:266:VAL:HG22	1.99	0.44
1:E:35:LYS:HG3	1:E:54:GLY:C	2.43	0.44
1:E:86:LEU:HD21	1:E:88:HIS:NE2	2.33	0.44
1:E:147:VAL:CG2	1:E:192:GLY:HA2	2.47	0.44
1:F:24:GLY:O	1:F:28:ARG:HG3	2.18	0.44
1:F:168:MET:SD	1:H:160:CYS:CB	3.02	0.44
1:G:163:LYS:O	1:G:167:LYS:N	2.46	0.44
1:K:159:TYR:CZ	1:K:163:LYS:HE3	2.53	0.44
1:N:114:VAL:HG12	1:N:118:ILE:HD11	1.99	0.44
1:P:147:VAL:HA	1:P:150:LEU:HB2	1.99	0.44
1:B:173:LEU:HB2	1:B:186:VAL:HG11	2.00	0.44
1:C:168:MET:HA	1:C:171:LYS:HD2	2.00	0.44
1:E:17:ALA:O	1:E:18:VAL:CG2	2.65	0.44
1:F:227:PRO:O	1:F:229:GLY:N	2.51	0.44
1:G:28:ARG:HD3	1:G:52:VAL:HA	2.00	0.44
1:J:173:LEU:HB2	1:J:186:VAL:HG11	1.99	0.44
1:O:125:LEU:HA	1:O:128:LEU:HD12	1.99	0.44
1:A:141:VAL:HB	1:A:186:VAL:HA	2.00	0.44
1:B:253:THR:O	1:B:255:THR:N	2.51	0.44
1:C:24:GLY:O	1:C:28:ARG:HG3	2.18	0.44
1:C:31:VAL:C	1:C:33:ALA:N	2.76	0.44
1:C:225:ARG:NH2	2:C:303:HOH:O	2.51	0.44
1:D:220:ALA:HA	1:D:223:GLU:HB2	1.98	0.44
1:E:62:ASP:O	1:E:64:THR:N	2.50	0.44
1:F:25:GLY:HA2	1:F:28:ARG:NH1	2.31	0.44
1:G:115:ASP:HA	1:G:118:ILE:HD12	2.00	0.44
1:G:225:ARG:O	1:G:263:PHE:HA	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:44:THR:HB	1:I:61:HIS:CB	2.48	0.44
1:J:169:LEU:C	1:J:171:LYS:N	2.73	0.44
1:K:204:ASP:OD1	1:K:215:ARG:HG3	2.18	0.44
1:N:82:ARG:NH1	1:N:134:ALA:HB3	2.33	0.44
1:P:230:ARG:HG3	1:P:231:MET:O	2.18	0.44
1:B:122:GLN:HG3	1:C:98:PHE:CZ	2.53	0.44
1:C:83:VAL:HG23	1:C:127:LEU:HB3	1.99	0.44
1:C:253:THR:C	1:C:255:THR:N	2.75	0.44
1:D:255:THR:OG1	1:D:256:GLU:N	2.51	0.44
1:D:265:GLN:OE1	1:E:171:LYS:NZ	2.47	0.44
1:F:20:THR:CG2	1:F:69:TRP:CH2	3.00	0.44
1:H:248:ALA:C	1:H:250:SER:H	2.26	0.44
1:K:106:PHE:CE1	1:K:158:ALA:HA	2.53	0.44
1:L:12:LEU:HD23	1:L:12:LEU:HA	1.86	0.44
1:N:94:ILE:CG2	1:N:95:VAL:N	2.79	0.44
1:N:189:VAL:HG12	1:N:191:PRO:HD3	1.99	0.44
1:O:22:ALA:O	1:O:28:ARG:HG2	2.18	0.44
1:A:138:GLY:H	1:A:183:ASN:HD21	1.64	0.43
1:C:17:ALA:HB3	1:C:41:VAL:HG22	1.99	0.43
1:F:170:SER:HA	1:F:186:VAL:HG12	2.00	0.43
1:G:12:LEU:HB2	1:G:37:ALA:HB1	2.00	0.43
1:G:140:SER:CB	1:G:245:CYS:HA	2.48	0.43
1:J:19:VAL:HG22	1:J:87:VAL:HB	2.00	0.43
1:J:76:ALA:O	1:J:79:LYS:N	2.51	0.43
1:A:145:SER:C	1:A:163:LYS:HD2	2.42	0.43
1:B:130:GLU:C	1:B:132:GLY:H	2.25	0.43
1:D:109:VAL:O	1:D:109:VAL:CG1	2.66	0.43
1:E:12:LEU:HD13	1:E:39:ALA:HB2	2.00	0.43
1:E:42:ILE:HG23	1:E:57:HIS:HB2	2.00	0.43
1:F:164:ALA:O	1:F:167:LYS:HB3	2.18	0.43
1:K:204:ASP:OD1	1:K:204:ASP:N	2.51	0.43
1:K:205:LYS:O	1:K:206:TYR:C	2.61	0.43
1:L:26:ILE:HG22	1:L:30:LEU:HG	2.00	0.43
1:L:164:ALA:O	1:L:167:LYS:HE2	2.18	0.43
1:M:153:ALA:H	1:O:172:CYS:HG	1.67	0.43
1:O:59:LEU:HD13	1:O:75:LEU:HD22	1.98	0.43
1:A:249:ALA:HB1	1:A:252:VAL:HB	2.00	0.43
1:C:62:ASP:OD1	1:C:63:VAL:N	2.52	0.43
1:C:237:MET:SD	1:C:259:MET:HE2	2.59	0.43
1:D:185:ARG:NE	1:D:250:SER:O	2.52	0.43
1:D:224:MET:O	1:D:225:ARG:C	2.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:23:ALA:HA	1:E:28:ARG:HG2	2.00	0.43
1:E:88:HIS:N	1:E:142:VAL:O	2.50	0.43
1:I:28:ARG:HD3	1:I:51:ASP:O	2.17	0.43
1:I:54:GLY:O	1:I:55:ALA:C	2.61	0.43
1:J:119:ILE:O	1:J:120:GLY:C	2.60	0.43
1:J:221:ALA:O	1:J:225:ARG:HG3	2.19	0.43
1:K:12:LEU:HD23	1:K:246:SER:HA	2.00	0.43
1:M:118:ILE:O	1:M:122:GLN:HG3	2.18	0.43
1:N:16:VAL:CG1	1:N:83:VAL:HA	2.48	0.43
1:N:26:ILE:HD11	1:N:194:ILE:HG13	2.00	0.43
1:A:120:GLY:C	1:A:122:GLN:H	2.26	0.43
1:B:111:THR:HA	1:B:115:ASP:HB2	2.00	0.43
1:B:125:LEU:O	1:B:129:LYS:HG3	2.18	0.43
1:C:34:MET:HB3	1:C:41:VAL:HG21	1.99	0.43
1:C:265:GLN:CD	1:F:255:THR:HA	2.44	0.43
1:D:57:HIS:NE2	1:D:80:TYR:OH	2.48	0.43
1:E:88:HIS:HB3	1:E:117:ILE:HG12	2.00	0.43
1:F:44:THR:HG21	1:F:61:HIS:ND1	2.32	0.43
1:F:263:PHE:CD1	1:F:263:PHE:C	2.96	0.43
1:H:159:TYR:CE1	1:H:163:LYS:HE2	2.54	0.43
1:I:226:HIS:HB3	1:I:228:ILE:HG22	2.01	0.43
1:J:20:THR:HG21	1:J:69:TRP:CH2	2.53	0.43
1:N:103:LEU:O	1:N:106:PHE:HB3	2.18	0.43
1:O:174:GLY:HA3	1:O:186:VAL:HB	2.00	0.43
1:C:145:SER:CB	1:C:190:HIS:CE1	3.01	0.43
1:C:266:VAL:O	1:H:151:ARG:CZ	2.66	0.43
1:C:266:VAL:O	1:H:151:ARG:NH1	2.51	0.43
1:E:12:LEU:HD23	1:E:12:LEU:HA	1.91	0.43
1:E:233:ARG:HE	1:E:233:ARG:HB2	1.57	0.43
1:G:151:ARG:NE	1:G:152:GLY:O	2.51	0.43
1:H:237:MET:O	1:H:259:MET:HE1	2.18	0.43
1:J:121:THR:O	1:J:125:LEU:N	2.51	0.43
1:J:151:ARG:NE	1:N:266:VAL:C	2.76	0.43
1:K:173:LEU:O	1:K:177:PHE:CG	2.72	0.43
1:M:83:VAL:HG23	1:M:127:LEU:HB3	2.01	0.43
1:M:155:PHE:CD1	1:M:209:LEU:HD13	2.53	0.43
1:M:237:MET:O	1:M:241:VAL:HG23	2.19	0.43
1:N:115:ASP:O	1:N:119:ILE:HG13	2.18	0.43
1:O:125:LEU:N	1:O:126:PRO:CD	2.81	0.43
1:O:151:ARG:HD3	1:O:263:PHE:CE1	2.49	0.43
1:O:189:VAL:HG22	1:O:257:PHE:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:ILE:HG21	1:D:103:LEU:HD12	2.01	0.43
1:E:195:ASP:HB3	1:E:232:GLY:O	2.19	0.43
1:E:240:GLY:HA2	1:E:243:TYR:HB3	2.00	0.43
1:F:37:ALA:O	1:F:38:ASN:HB2	2.18	0.43
1:I:237:MET:HE1	1:I:259:MET:CB	2.48	0.43
1:I:237:MET:HE1	1:I:259:MET:HB3	2.01	0.43
1:L:125:LEU:N	1:L:126:PRO:CD	2.81	0.43
1:N:40:ILE:HG23	1:N:56:ASP:OD2	2.18	0.43
1:A:145:SER:HB3	1:A:190:HIS:CD2	2.53	0.43
1:B:26:ILE:HA	1:B:234:PRO:HB3	2.01	0.43
1:D:195:ASP:OD1	1:D:195:ASP:C	2.61	0.43
1:E:179:ALA:C	1:E:181:GLY:N	2.76	0.43
1:E:180:LEU:HD21	1:G:155:PHE:CZ	2.54	0.43
1:F:27:GLY:O	1:F:31:VAL:HG23	2.18	0.43
1:F:168:MET:HG2	1:H:160:CYS:HB3	2.01	0.43
1:G:64:THR:CG2	1:G:112:VAL:HA	2.48	0.43
1:H:198:MET:O	1:H:202:LEU:N	2.52	0.43
1:J:151:ARG:O	1:J:151:ARG:HG3	2.19	0.43
1:J:164:ALA:HB2	1:L:168:MET:CE	2.46	0.43
1:K:103:LEU:HA	1:K:106:PHE:HB2	2.01	0.43
1:K:231:MET:HE3	1:K:231:MET:HB2	1.86	0.43
1:L:86:LEU:HB3	1:L:141:VAL:HA	2.01	0.43
1:N:86:LEU:HD23	1:N:128:LEU:HD11	2.00	0.43
1:N:88:HIS:HB2	1:N:143:ASN:HA	2.01	0.43
1:N:156:ASN:CB	1:N:160:CYS:SG	3.06	0.43
1:N:194:ILE:CG2	1:N:195:ASP:H	2.32	0.43
1:A:138:GLY:HA2	1:A:183:ASN:ND2	2.34	0.43
1:A:169:LEU:O	1:A:170:SER:C	2.62	0.43
1:A:176:GLU:O	1:A:180:LEU:HD12	2.19	0.43
1:A:183:ASN:C	1:A:184:ILE:HG13	2.44	0.43
1:B:209:LEU:HD23	1:B:209:LEU:HA	1.92	0.43
1:E:140:SER:HB3	1:E:245:CYS:HA	2.00	0.43
1:F:140:SER:CB	1:F:245:CYS:HA	2.49	0.43
1:H:158:ALA:HA	1:H:161:THR:OG1	2.18	0.43
1:I:120:GLY:O	1:I:124:LEU:HG	2.18	0.43
1:J:103:LEU:HD21	1:L:115:ASP:HB3	1.99	0.43
1:J:249:ALA:HB1	1:J:252:VAL:HB	2.00	0.43
1:K:26:ILE:HG12	1:K:234:PRO:HB3	2.00	0.43
1:K:243:TYR:CZ	1:K:249:ALA:HB2	2.53	0.43
1:L:189:VAL:HA	1:L:257:PHE:O	2.19	0.43
1:N:141:VAL:O	1:N:186:VAL:HA	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:92:ILE:CG2	1:O:112:VAL:HG11	2.48	0.43
1:P:143:ASN:ND2	1:P:170:SER:HA	2.33	0.43
1:P:145:SER:CB	1:P:190:HIS:HD1	2.24	0.43
1:A:54:GLY:O	1:A:55:ALA:C	2.61	0.43
1:B:83:VAL:HG11	1:B:124:LEU:HD13	2.01	0.43
1:G:219:GLN:HG2	1:G:223:GLU:OE1	2.19	0.43
1:I:42:ILE:HA	1:I:57:HIS:HB2	2.00	0.43
1:J:113:ASN:O	1:J:166:VAL:CG2	2.66	0.43
1:L:30:LEU:HD11	1:L:144:PHE:CZ	2.54	0.43
1:M:228:ILE:HB	1:M:261:GLY:O	2.18	0.43
1:N:242:VAL:O	1:N:246:SER:N	2.44	0.43
1:O:44:THR:HA	1:O:59:LEU:O	2.18	0.43
1:P:91:GLY:HA2	1:P:112:VAL:HG12	1.99	0.43
1:A:103:LEU:HD11	1:D:118:ILE:HD12	2.00	0.43
1:A:137:GLY:HA3	1:A:247:ASP:CG	2.44	0.43
1:C:135:ARG:NE	1:C:247:ASP:OD1	2.52	0.43
1:D:151:ARG:HD2	1:G:266:VAL:O	2.18	0.43
1:E:12:LEU:HD22	1:E:15:VAL:HG11	2.00	0.43
1:E:25:GLY:HA3	1:E:196:THR:HG22	2.00	0.43
1:E:142:VAL:HG13	1:E:189:VAL:HG23	2.01	0.43
1:E:207:VAL:HA	1:E:212:ALA:HB3	2.01	0.43
1:G:125:LEU:N	1:G:126:PRO:CD	2.82	0.43
1:G:203:MET:HE1	1:G:219:GLN:HA	2.01	0.43
1:G:228:ILE:HG12	1:G:230:ARG:HG2	2.00	0.43
1:H:154:ALA:O	1:H:156:ASN:N	2.49	0.43
1:I:88:HIS:HE1	1:I:120:GLY:HA3	1.83	0.43
1:I:189:VAL:HG12	1:I:191:PRO:HD3	2.00	0.43
1:I:227:PRO:HD2	1:I:263:PHE:N	2.34	0.43
1:L:138:GLY:HA3	1:L:183:ASN:O	2.18	0.43
1:M:145:SER:O	1:M:191:PRO:HG2	2.18	0.43
1:M:171:LYS:HZ1	1:M:256:GLU:HG2	1.83	0.43
1:P:32:LYS:HG2	1:P:53:GLU:O	2.18	0.43
1:D:63:VAL:C	1:D:65:SER:H	2.27	0.42
1:D:194:ILE:CD1	1:D:237:MET:HE3	2.49	0.42
1:F:117:ILE:O	1:F:118:ILE:C	2.62	0.42
1:F:177:PHE:C	1:F:179:ALA:H	2.26	0.42
1:I:264:SER:C	1:I:266:VAL:N	2.76	0.42
1:J:122:GLN:HG3	1:L:98:PHE:CE2	2.54	0.42
1:L:61:HIS:CD2	1:L:68:GLY:HA3	2.54	0.42
1:L:266:VAL:O	1:P:151:ARG:NE	2.52	0.42
1:A:263:PHE:CD1	1:A:263:PHE:C	2.97	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:69:TRP:CE3	1:B:120:GLY:HA2	2.54	0.42
1:C:180:LEU:CD1	1:C:182:TYR:CE2	3.02	0.42
1:D:31:VAL:HG12	1:D:53:GLU:O	2.19	0.42
1:E:180:LEU:HD12	1:E:182:TYR:CE2	2.51	0.42
1:F:177:PHE:C	1:F:179:ALA:N	2.77	0.42
1:K:151:ARG:NH1	1:K:263:PHE:CZ	2.87	0.42
1:L:156:ASN:ND2	1:L:206:TYR:OH	2.47	0.42
1:N:88:HIS:CG	1:N:117:ILE:HG12	2.55	0.42
1:N:157:ALA:HA	1:P:172:CYS:SG	2.60	0.42
1:C:15:VAL:CG2	1:C:135:ARG:NH1	2.83	0.42
1:D:169:LEU:O	1:D:173:LEU:HG	2.19	0.42
1:E:63:VAL:O	1:E:116:SER:HA	2.20	0.42
1:E:117:ILE:HG21	1:E:169:LEU:HD23	2.01	0.42
1:F:102:PRO:HB2	1:F:104:SER:OG	2.18	0.42
1:J:147:VAL:HA	1:J:150:LEU:HB2	2.00	0.42
1:K:53:GLU:O	1:K:55:ALA:N	2.52	0.42
1:K:61:HIS:HE2	1:K:69:TRP:CD1	2.37	0.42
1:K:98:PHE:HE1	1:K:106:PHE:CZ	2.36	0.42
1:K:243:TYR:CD2	1:K:244:LEU:HD23	2.54	0.42
1:M:168:MET:HB3	1:O:161:THR:HG22	2.02	0.42
1:N:111:THR:HA	1:N:115:ASP:CB	2.48	0.42
1:O:20:THR:OG1	1:O:89:ASN:N	2.53	0.42
1:A:176:GLU:CG	1:A:180:LEU:CD1	2.97	0.42
1:D:167:LYS:HB2	1:D:190:HIS:HE1	1.83	0.42
1:D:257:PHE:CE2	1:E:257:PHE:HE1	2.36	0.42
1:E:176:GLU:HA	1:G:154:ALA:CB	2.48	0.42
1:H:158:ALA:O	1:H:159:TYR:C	2.62	0.42
1:I:14:ASN:C	1:I:82:ARG:HH22	2.27	0.42
1:J:139:ALA:O	1:J:184:ILE:HA	2.19	0.42
1:K:45:ASP:HB3	1:K:58:TYR:CZ	2.55	0.42
1:L:135:ARG:HH11	1:L:139:ALA:HA	1.85	0.42
1:L:226:HIS:O	1:L:229:GLY:N	2.49	0.42
1:N:64:THR:O	1:N:119:ILE:HD13	2.19	0.42
1:N:165:ALA:O	1:N:168:MET:N	2.52	0.42
1:O:130:GLU:OE2	1:O:133:LYS:HD2	2.19	0.42
1:O:154:ALA:C	1:O:156:ASN:H	2.27	0.42
1:E:32:LYS:CD	1:E:53:GLU:HB3	2.50	0.42
1:H:199:LEU:HD12	1:H:202:LEU:HB2	2.00	0.42
1:I:190:HIS:NE2	1:I:256:GLU:CB	2.83	0.42
1:L:244:LEU:HD21	1:L:257:PHE:CD1	2.55	0.42
1:N:75:LEU:C	1:N:77:GLN:H	2.28	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:PHE:HD1	1:G:228:ILE:CD1	2.32	0.42
1:D:146:SER:HA	1:D:191:PRO:HD2	2.00	0.42
1:F:19:VAL:HA	1:F:87:VAL:O	2.20	0.42
1:F:41:VAL:HG12	1:F:42:ILE:N	2.35	0.42
1:H:231:MET:HE3	1:H:231:MET:HB2	1.88	0.42
1:L:222:MET:HE2	1:L:222:MET:HB2	1.79	0.42
1:O:102:PRO:HD2	1:O:105:ASP:HB2	2.01	0.42
1:A:31:VAL:HG11	1:A:55:ALA:HB2	2.02	0.42
1:A:185:ARG:HD3	1:A:250:SER:C	2.44	0.42
1:B:226:HIS:HB3	1:B:228:ILE:HG22	2.02	0.42
1:C:151:ARG:NE	1:H:266:VAL:C	2.78	0.42
1:E:82:ARG:NH2	1:E:134:ALA:CB	2.74	0.42
1:E:82:ARG:HH22	1:E:134:ALA:HB3	1.79	0.42
1:E:106:PHE:CG	1:G:118:ILE:HD13	2.55	0.42
1:G:154:ALA:C	1:G:156:ASN:N	2.78	0.42
1:H:142:VAL:O	1:H:142:VAL:CG1	2.66	0.42
1:I:173:LEU:HD21	1:K:98:PHE:CG	2.54	0.42
1:I:227:PRO:HG2	1:I:262:GLY:HA3	2.01	0.42
1:J:151:ARG:CZ	1:N:266:VAL:C	2.93	0.42
1:K:62:ASP:O	1:K:65:SER:N	2.53	0.42
1:K:134:ALA:C	1:K:135:ARG:HG3	2.41	0.42
1:L:20:THR:O	1:L:89:ASN:HB3	2.20	0.42
1:N:59:LEU:HD22	1:N:72:VAL:HG22	2.00	0.42
1:O:119:ILE:O	1:O:123:VAL:HG23	2.19	0.42
1:A:119:ILE:O	1:A:123:VAL:HG23	2.19	0.42
1:B:20:THR:HB	1:B:63:VAL:HG11	2.02	0.42
1:F:227:PRO:C	1:F:229:GLY:N	2.77	0.42
1:H:33:ALA:HB2	1:H:238:GLY:HA3	2.02	0.42
1:I:215:ARG:O	1:I:215:ARG:HG2	2.20	0.42
1:I:263:PHE:CD1	1:I:263:PHE:C	2.98	0.42
1:L:26:ILE:HA	1:L:29:GLU:HB2	2.02	0.42
1:L:187:ASN:HD21	1:L:257:PHE:HB2	1.85	0.42
1:O:154:ALA:O	1:O:156:ASN:N	2.49	0.42
1:A:120:GLY:C	1:A:122:GLN:N	2.77	0.42
1:A:251:PHE:HA	1:G:228:ILE:CD1	2.50	0.42
1:D:118:ILE:O	1:D:122:GLN:N	2.52	0.42
1:E:143:ASN:O	1:E:189:VAL:HB	2.20	0.42
1:F:161:THR:HA	1:H:168:MET:CG	2.48	0.42
1:G:12:LEU:HD13	1:G:34:MET:HE3	2.01	0.42
1:H:137:GLY:O	1:H:247:ASP:HA	2.20	0.42
1:H:199:LEU:O	1:H:200:GLY:C	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:160:CYS:O	1:I:164:ALA:N	2.53	0.42
1:J:111:THR:O	1:J:115:ASP:HB2	2.20	0.42
1:J:176:GLU:HA	1:L:154:ALA:CB	2.49	0.42
1:J:194:ILE:CD1	1:J:237:MET:HE3	2.42	0.42
1:L:252:VAL:HG22	1:N:259:MET:HA	2.02	0.42
1:M:30:LEU:CD1	1:M:87:VAL:HG11	2.49	0.42
1:N:199:LEU:HD12	1:N:202:LEU:HD12	2.01	0.42
1:P:16:VAL:HG22	1:P:40:ILE:HD13	2.01	0.42
1:A:88:HIS:CE1	1:A:117:ILE:HA	2.55	0.42
1:A:91:GLY:HA2	1:A:113:ASN:OD1	2.19	0.42
1:A:182:TYR:HE2	1:D:99:GLU:OE1	2.03	0.42
1:B:98:PHE:CZ	1:C:122:GLN:HG3	2.55	0.42
1:B:159:TYR:OH	1:B:163:LYS:HG3	2.20	0.42
1:C:25:GLY:HA3	1:C:196:THR:HG22	2.02	0.42
1:C:50:ALA:HB3	1:C:58:TYR:OH	2.20	0.42
1:C:247:ASP:O	1:C:250:SER:CB	2.68	0.42
1:H:146:SER:OG	1:H:147:VAL:N	2.53	0.42
1:H:185:ARG:HD2	1:H:252:VAL:O	2.20	0.42
1:J:114:VAL:O	1:J:117:ILE:HB	2.19	0.42
1:L:259:MET:HG2	1:N:252:VAL:HG22	2.02	0.42
1:M:264:SER:O	1:M:265:GLN:C	2.61	0.42
1:O:216:GLU:HA	1:O:219:GLN:CB	2.50	0.42
1:A:145:SER:N	1:A:189:VAL:O	2.52	0.41
1:B:145:SER:HB3	1:B:190:HIS:CD2	2.55	0.41
1:B:176:GLU:CD	1:C:98:PHE:H	2.27	0.41
1:B:260:ASP:C	1:B:262:GLY:H	2.28	0.41
1:C:185:ARG:HB3	1:C:253:THR:HB	2.01	0.41
1:C:246:SER:OG	1:C:248:ALA:HB3	2.20	0.41
1:E:17:ALA:HA	1:E:85:ALA:HB3	2.02	0.41
1:G:200:GLY:HA2	1:G:215:ARG:HH22	1.85	0.41
1:H:137:GLY:O	1:H:185:ARG:NH2	2.51	0.41
1:H:201:SER:O	1:H:205:LYS:HG2	2.20	0.41
1:J:124:LEU:HD23	1:J:124:LEU:HA	1.89	0.41
1:L:242:VAL:O	1:L:245:CYS:N	2.50	0.41
1:M:31:VAL:HG11	1:M:52:VAL:CG1	2.48	0.41
1:M:125:LEU:C	1:M:127:LEU:H	2.28	0.41
1:M:156:ASN:C	1:M:158:ALA:N	2.78	0.41
1:N:102:PRO:HD2	1:N:105:ASP:OD2	2.20	0.41
1:O:43:ALA:HB3	1:O:57:HIS:O	2.19	0.41
1:P:106:PHE:HD1	1:P:158:ALA:HB2	1.84	0.41
1:A:131:GLY:C	1:A:133:LYS:H	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:ALA:HB3	1:A:184:ILE:HG12	2.01	0.41
1:B:45:ASP:HB3	1:B:58:TYR:OH	2.20	0.41
1:C:107:HIS:O	1:C:111:THR:N	2.46	0.41
1:D:225:ARG:HD3	1:D:263:PHE:CE1	2.50	0.41
1:E:17:ALA:C	1:E:18:VAL:HG23	2.45	0.41
1:F:102:PRO:O	1:F:103:LEU:C	2.62	0.41
1:I:20:THR:HG22	1:I:44:THR:HG1	1.85	0.41
1:K:142:VAL:HG13	1:K:189:VAL:HG23	2.02	0.41
1:L:197:PRO:CD	2:L:306:HOH:O	2.57	0.41
1:N:117:ILE:O	1:N:121:THR:CB	2.68	0.41
1:P:189:VAL:HA	1:P:257:PHE:HB3	2.02	0.41
1:D:168:MET:O	1:D:169:LEU:C	2.63	0.41
1:D:257:PHE:CE1	1:D:259:MET:HG3	2.54	0.41
1:E:104:SER:O	1:E:108:ARG:HB2	2.20	0.41
1:E:141:VAL:HB	1:E:186:VAL:HG22	2.03	0.41
1:H:135:ARG:NH2	1:H:138:GLY:O	2.53	0.41
1:L:47:ALA:HB3	1:L:58:TYR:OH	2.19	0.41
1:L:260:ASP:C	1:L:262:GLY:N	2.77	0.41
1:N:202:LEU:HD23	1:N:202:LEU:HA	1.92	0.41
1:N:212:ALA:HB1	1:N:213:PRO:CD	2.50	0.41
1:A:98:PHE:CZ	1:D:121:THR:HB	2.54	0.41
1:J:251:PHE:CZ	1:P:232:GLY:N	2.89	0.41
1:L:63:VAL:HB	1:L:69:TRP:HZ2	1.85	0.41
1:L:205:LYS:O	1:L:209:LEU:HG	2.20	0.41
1:M:134:ALA:O	1:M:135:ARG:HG3	2.20	0.41
1:M:183:ASN:C	1:M:184:ILE:HG13	2.46	0.41
1:N:15:VAL:HA	1:N:84:ASP:OD2	2.20	0.41
1:O:46:MET:CG	1:O:62:ASP:HA	2.50	0.41
1:P:26:ILE:HG22	1:P:30:LEU:HG	2.03	0.41
1:P:96:THR:HG23	1:P:101:THR:OG1	2.20	0.41
1:A:203:MET:HA	1:A:206:TYR:HD2	1.86	0.41
1:C:159:TYR:CZ	1:C:163:LYS:HE3	2.56	0.41
1:C:185:ARG:HG2	1:F:228:ILE:HD12	2.01	0.41
1:D:66:GLU:HG3	1:D:123:VAL:CG2	2.49	0.41
1:F:45:ASP:C	1:F:47:ALA:N	2.75	0.41
1:F:260:ASP:OD2	1:F:264:SER:OG	2.38	0.41
1:H:17:ALA:HA	1:H:85:ALA:O	2.21	0.41
1:I:190:HIS:CD2	1:I:256:GLU:C	2.98	0.41
1:I:236:GLU:HG2	1:O:250:SER:OG	2.20	0.41
1:M:45:ASP:O	1:M:60:GLN:HA	2.19	0.41
1:N:82:ARG:HH12	1:N:134:ALA:HB3	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:21:GLY:O	1:O:27:GLY:HA3	2.20	0.41
1:P:12:LEU:HG	1:P:242:VAL:HG13	2.03	0.41
1:P:220:ALA:O	1:P:224:MET:HE2	2.21	0.41
1:A:83:VAL:HG21	1:A:124:LEU:HD22	2.02	0.41
1:B:20:THR:HG21	1:B:69:TRP:CH2	2.56	0.41
1:B:69:TRP:CE3	1:B:120:GLY:CA	3.04	0.41
1:C:130:GLU:HA	1:C:133:LYS:HB2	2.01	0.41
1:C:171:LYS:HE2	1:F:265:GLN:OE1	2.21	0.41
1:D:92:ILE:HD11	1:D:109:VAL:HA	2.01	0.41
1:H:100:ASP:O	1:H:101:THR:C	2.62	0.41
1:O:75:LEU:HG	1:O:79:LYS:HG3	2.01	0.41
1:O:190:HIS:HB2	1:O:258:VAL:HA	2.01	0.41
1:A:187:ASN:OD1	1:A:253:THR:HA	2.20	0.41
1:B:32:LYS:CE	1:B:53:GLU:HB3	2.42	0.41
1:E:84:ASP:HB3	1:E:135:ARG:HH11	1.85	0.41
1:E:132:GLY:HA2	1:E:139:ALA:N	2.35	0.41
1:F:265:GLN:O	1:F:266:VAL:CG1	2.69	0.41
1:J:243:TYR:CE1	1:P:240:GLY:N	2.89	0.41
1:K:207:VAL:HA	1:K:212:ALA:O	2.21	0.41
1:M:119:ILE:HG13	1:O:103:LEU:HD13	2.02	0.41
1:N:212:ALA:HB1	1:N:213:PRO:HD2	2.02	0.41
1:P:13:ASN:C	1:P:15:VAL:H	2.28	0.41
1:P:18:VAL:HG21	1:P:124:LEU:CD1	2.51	0.41
1:A:79:LYS:C	1:A:80:TYR:CG	2.98	0.41
1:B:221:ALA:HA	1:B:224:MET:CE	2.50	0.41
1:C:159:TYR:CE1	1:C:163:LYS:HE3	2.56	0.41
1:D:18:VAL:O	1:D:87:VAL:N	2.53	0.41
1:E:72:VAL:HG12	1:E:124:LEU:HD21	2.03	0.41
1:F:103:LEU:O	1:F:107:HIS:NE2	2.54	0.41
1:F:231:MET:HE3	1:F:231:MET:HB2	1.93	0.41
1:F:265:GLN:O	1:F:266:VAL:HG13	2.21	0.41
1:G:12:LEU:HD21	1:G:245:CYS:CB	2.50	0.41
1:I:185:ARG:HD3	1:I:250:SER:O	2.21	0.41
1:I:203:MET:HA	1:I:206:TYR:HD2	1.86	0.41
1:J:96:THR:C	1:J:155:PHE:HA	2.46	0.41
1:K:67:ALA:O	1:K:68:GLY:C	2.63	0.41
1:L:170:SER:O	1:L:171:LYS:C	2.64	0.41
1:N:147:VAL:HG21	1:N:263:PHE:HD2	1.85	0.41
1:N:155:PHE:CD1	1:P:176:GLU:OE2	2.73	0.41
1:O:45:ASP:HB3	1:O:58:TYR:OH	2.21	0.41
1:A:13:ASN:HB2	2:A:304:HOH:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:LEU:HB3	1:A:186:VAL:HG21	2.01	0.41
1:B:31:VAL:HG13	1:B:41:VAL:HG11	2.03	0.41
1:B:117:ILE:O	1:B:121:THR:OG1	2.33	0.41
1:B:251:PHE:CG	1:B:251:PHE:O	2.74	0.41
1:C:151:ARG:HE	1:H:266:VAL:C	2.29	0.41
1:D:66:GLU:HA	1:D:69:TRP:HB2	2.02	0.41
1:E:35:LYS:HG3	1:E:54:GLY:CA	2.51	0.41
1:E:69:TRP:HZ3	1:E:124:LEU:CD1	2.31	0.41
1:E:69:TRP:CE2	1:E:120:GLY:CA	3.04	0.41
1:E:210:GLY:C	1:E:212:ALA:N	2.78	0.41
1:F:73:ALA:O	1:F:77:GLN:N	2.43	0.41
1:F:179:ALA:C	1:F:181:GLY:H	2.28	0.41
1:F:186:VAL:C	1:F:187:ASN:CG	2.89	0.41
1:G:233:ARG:N	1:G:236:GLU:OE2	2.54	0.41
1:G:260:ASP:CG	1:G:263:PHE:H	2.29	0.41
1:I:21:GLY:O	1:I:27:GLY:HA3	2.20	0.41
1:J:167:LYS:O	1:J:171:LYS:HG3	2.21	0.41
1:J:265:GLN:OE1	1:P:171:LYS:NZ	2.49	0.41
1:K:74:ALA:HA	1:K:77:GLN:HB3	2.03	0.41
1:K:142:VAL:CG2	1:K:244:LEU:CD1	2.97	0.41
1:L:139:ALA:HB3	1:L:184:ILE:HG23	2.02	0.41
1:M:243:TYR:C	1:M:245:CYS:N	2.75	0.41
1:N:132:GLY:HA3	1:N:183:ASN:O	2.21	0.41
1:N:143:ASN:OD1	1:N:143:ASN:N	2.54	0.41
1:N:170:SER:O	1:N:173:LEU:N	2.54	0.41
1:O:87:VAL:HG12	1:O:89:ASN:HB2	2.03	0.41
1:O:125:LEU:HG	1:O:129:LYS:HE3	2.03	0.41
1:O:227:PRO:HD2	1:O:263:PHE:HA	2.03	0.41
1:A:111:THR:HA	1:A:115:ASP:HB2	2.02	0.41
1:A:157:ALA:HA	1:D:172:CYS:HB3	2.03	0.41
1:C:94:ILE:HG22	1:C:96:THR:HG22	2.03	0.41
1:F:216:GLU:HA	1:F:219:GLN:CB	2.47	0.41
1:G:193:GLY:CA	1:G:199:LEU:HD13	2.50	0.41
1:H:154:ALA:C	1:H:156:ASN:H	2.29	0.41
1:I:35:LYS:HG3	1:I:54:GLY:CA	2.51	0.41
1:J:240:GLY:O	1:J:244:LEU:HG	2.20	0.41
1:L:12:LEU:HD12	1:L:242:VAL:HG22	2.02	0.41
1:M:151:ARG:HD3	1:M:263:PHE:CE1	2.44	0.41
1:N:111:THR:O	1:N:115:ASP:HB2	2.21	0.41
1:O:108:ARG:O	1:O:112:VAL:HG23	2.20	0.41
1:P:72:VAL:O	1:P:72:VAL:CG1	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:GLY:HA3	1:A:254:CYS:SG	2.61	0.40
1:B:230:ARG:HH22	1:B:236:GLU:CD	2.29	0.40
1:B:237:MET:CA	1:B:259:MET:HE1	2.50	0.40
1:G:194:ILE:HG23	1:G:232:GLY:O	2.21	0.40
1:H:22:ALA:HA	1:H:27:GLY:CA	2.51	0.40
1:I:189:VAL:O	1:I:191:PRO:HD3	2.21	0.40
1:J:166:VAL:O	1:J:167:LYS:C	2.64	0.40
1:K:30:LEU:HD21	1:K:241:VAL:HG21	2.03	0.40
1:L:199:LEU:O	1:L:200:GLY:C	2.64	0.40
1:M:61:HIS:HE1	1:M:69:TRP:CZ3	2.40	0.40
1:M:95:VAL:O	1:M:96:THR:HB	2.20	0.40
1:O:155:PHE:C	1:O:157:ALA:N	2.66	0.40
1:O:156:ASN:O	1:O:157:ALA:C	2.65	0.40
1:O:159:TYR:O	1:O:160:CYS:C	2.64	0.40
1:O:177:PHE:CD2	1:O:184:ILE:HB	2.56	0.40
1:O:201:SER:HA	1:O:204:ASP:CG	2.46	0.40
1:P:42:ILE:CD1	1:P:75:LEU:HD23	2.51	0.40
1:A:96:THR:HG23	1:A:101:THR:OG1	2.21	0.40
1:A:157:ALA:O	1:A:161:THR:HG23	2.21	0.40
1:A:173:LEU:CD2	1:D:98:PHE:CD1	2.96	0.40
1:C:132:GLY:O	1:C:183:ASN:HB3	2.21	0.40
1:F:23:ALA:HB2	1:F:50:ALA:HB3	2.03	0.40
1:F:229:GLY:O	1:F:230:ARG:CB	2.68	0.40
1:G:169:LEU:HG	1:G:173:LEU:HG	2.04	0.40
1:I:10:ILE:CD1	1:O:242:VAL:HB	2.51	0.40
1:J:155:PHE:CE1	1:L:180:LEU:HD11	2.56	0.40
1:K:63:VAL:HG11	1:K:90:ALA:HB3	2.03	0.40
1:K:73:ALA:HB2	1:K:124:LEU:HD23	2.04	0.40
1:L:34:MET:O	1:L:39:ALA:HB3	2.20	0.40
1:L:188:SER:O	1:L:257:PHE:HB3	2.21	0.40
1:O:135:ARG:O	1:O:136:ALA:C	2.63	0.40
1:A:22:ALA:CB	1:A:43:ALA:HB1	2.51	0.40
1:B:224:MET:HE3	1:B:224:MET:HB2	2.00	0.40
1:C:106:PHE:O	1:C:110:ASN:ND2	2.55	0.40
1:C:228:ILE:HG23	1:C:230:ARG:HG2	2.04	0.40
1:D:69:TRP:CD2	1:D:120:GLY:HA2	2.56	0.40
1:E:161:THR:HG21	1:G:169:LEU:HB2	2.02	0.40
1:G:193:GLY:HA3	1:G:199:LEU:HD13	2.02	0.40
1:G:205:LYS:O	1:G:206:TYR:C	2.65	0.40
1:H:96:THR:CA	1:H:209:LEU:HD11	2.48	0.40
1:H:135:ARG:CZ	1:H:138:GLY:O	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:203:MET:HA	1:I:206:TYR:CD2	2.56	0.40
1:J:219:GLN:HA	1:J:222:MET:HB3	2.04	0.40
1:J:253:THR:HG22	1:P:228:ILE:HD12	2.02	0.40
1:J:265:GLN:HG3	1:P:255:THR:HA	2.04	0.40
1:K:48:PRO:HA	1:K:60:GLN:HB2	2.02	0.40
1:K:57:HIS:NE2	1:K:79:LYS:HE3	2.36	0.40
1:P:65:SER:OG	1:P:68:GLY:N	2.42	0.40
1:C:42:ILE:HG23	1:C:57:HIS:O	2.21	0.40
1:E:176:GLU:O	1:E:180:LEU:HG	2.21	0.40
1:F:73:ALA:HA	1:F:76:ALA:HB3	2.03	0.40
1:F:137:GLY:HA3	1:F:250:SER:HB3	2.03	0.40
1:G:26:ILE:HG13	1:G:196:THR:CG2	2.50	0.40
1:G:59:LEU:HD11	1:G:75:LEU:HD22	2.02	0.40
1:I:28:ARG:O	1:I:31:VAL:N	2.55	0.40
1:I:40:ILE:HG21	1:I:80:TYR:CE1	2.56	0.40
1:J:58:TYR:C	1:J:59:LEU:HD12	2.46	0.40
1:J:108:ARG:HA	1:J:111:THR:HB	2.03	0.40
1:J:193:GLY:O	1:J:231:MET:HB3	2.20	0.40
1:M:98:PHE:O	1:O:122:GLN:NE2	2.54	0.40
1:M:171:LYS:NZ	1:M:256:GLU:HG2	2.37	0.40
1:M:194:ILE:HA	1:M:232:GLY:O	2.21	0.40
1:B:17:ALA:HB2	1:B:85:ALA:HB3	2.02	0.40
1:C:212:ALA:HB1	1:C:217:VAL:CG1	2.51	0.40
1:D:83:VAL:HG23	1:D:127:LEU:HB3	2.04	0.40
1:E:48:PRO:HB2	1:E:49:SER:H	1.67	0.40
1:E:156:ASN:HD21	1:E:206:TYR:HE1	1.70	0.40
1:E:160:CYS:C	1:G:168:MET:HG2	2.47	0.40
1:F:20:THR:HG21	1:F:69:TRP:CZ2	2.56	0.40
1:G:86:LEU:CD1	1:G:124:LEU:HD13	2.52	0.40
1:H:146:SER:OG	1:H:148:ALA:N	2.50	0.40
1:I:88:HIS:CG	1:I:117:ILE:HG12	2.56	0.40
1:J:125:LEU:N	1:J:126:PRO:CD	2.84	0.40
1:K:163:LYS:HA	1:K:166:VAL:HB	2.03	0.40
1:P:109:VAL:HG12	1:P:113:ASN:HD22	1.86	0.40
1:P:143:ASN:HD21	1:P:186:VAL:CG1	2.34	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	Interatomic distance (Å)	Clash overlap (Å)
1:B:130:GLU:OE1	1:C:136:ALA:CB[1_455]	1.92	0.28

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	254/266 (96%)	203 (80%)	45 (18%)	6 (2%)	4	23
1	B	255/266 (96%)	213 (84%)	39 (15%)	3 (1%)	10	36
1	C	252/266 (95%)	214 (85%)	33 (13%)	5 (2%)	6	26
1	D	254/266 (96%)	213 (84%)	35 (14%)	6 (2%)	4	23
1	E	253/266 (95%)	215 (85%)	31 (12%)	7 (3%)	4	20
1	F	253/266 (95%)	207 (82%)	36 (14%)	10 (4%)	2	14
1	G	253/266 (95%)	224 (88%)	22 (9%)	7 (3%)	4	20
1	H	254/266 (96%)	216 (85%)	33 (13%)	5 (2%)	6	26
1	I	255/266 (96%)	223 (88%)	27 (11%)	5 (2%)	6	26
1	J	254/266 (96%)	225 (89%)	20 (8%)	9 (4%)	3	17
1	K	254/266 (96%)	212 (84%)	35 (14%)	7 (3%)	4	20
1	L	254/266 (96%)	214 (84%)	37 (15%)	3 (1%)	10	36
1	M	253/266 (95%)	206 (81%)	40 (16%)	7 (3%)	4	20
1	N	254/266 (96%)	214 (84%)	34 (13%)	6 (2%)	4	23
1	O	253/266 (95%)	214 (85%)	33 (13%)	6 (2%)	4	23
1	P	253/266 (95%)	207 (82%)	38 (15%)	8 (3%)	3	18
All	All	4058/4256 (95%)	3420 (84%)	538 (13%)	100 (2%)	4	22

All (100) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	63	VAL
1	F	38	ASN
1	F	45	ASP
1	F	157	ALA
1	G	195	ASP
1	H	118	ILE

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Mol	Chain	Res	Type
1	I	145	SER
1	I	146	SER
1	J	38	ASN
1	J	263	PHE
1	K	145	SER
1	K	218	ALA
1	N	213	PRO
1	P	156	ASN
1	P	157	ALA
1	P	183	ASN
1	A	38	ASN
1	E	247	ASP
1	F	103	LEU
1	F	116	SER
1	F	230	ARG
1	F	248	ALA
1	G	213	PRO
1	H	53	GLU
1	H	254	CYS
1	I	99	GLU
1	J	193	GLY
1	K	38	ASN
1	K	146	SER
1	K	196	THR
1	L	51	ASP
1	M	78	GLU
1	M	181	GLY
1	N	38	ASN
1	N	147	VAL
1	O	25	GLY
1	O	224	MET
1	A	55	ALA
1	A	67	ALA
1	A	145	SER
1	B	254	CYS
1	B	256	GLU
1	C	254	CYS
1	C	263	PHE
1	D	136	ALA
1	D	200	GLY
1	E	48	PRO
1	E	100	ASP

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Mol	Chain	Res	Type
1	F	14	ASN
1	F	227	PRO
1	G	89	ASN
1	G	197	PRO
1	H	249	ALA
1	L	146	SER
1	M	136	ALA
1	M	244	LEU
1	N	145	SER
1	N	146	SER
1	O	213	PRO
1	P	38	ASN
1	A	70	LYS
1	A	197	PRO
1	C	38	ASN
1	D	145	SER
1	D	232	GLY
1	E	60	GLN
1	F	46	MET
1	G	200	GLY
1	I	55	ALA
1	J	53	GLU
1	J	145	SER
1	M	157	ALA
1	O	48	PRO
1	O	156	ASN
1	P	159	TYR
1	P	210	GLY
1	C	249	ALA
1	E	145	SER
1	J	238	GLY
1	K	235	ALA
1	L	198	MET
1	N	167	LYS
1	O	88	HIS
1	C	242	VAL
1	D	206	TYR
1	G	155	PHE
1	J	116	SER
1	K	263	PHE
1	M	263	PHE
1	H	94	ILE

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Mol	Chain	Res	Type
1	J	25	GLY
1	J	119	ILE
1	B	63	VAL
1	P	48	PRO
1	D	147	VAL
1	M	147	VAL
1	P	63	VAL
1	E	234	PRO
1	G	119	ILE
1	I	193	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	188/198 (95%)	175 (93%)	13 (7%)	14	41
1	B	189/198 (96%)	175 (93%)	14 (7%)	13	38
1	C	187/198 (94%)	178 (95%)	9 (5%)	23	50
1	D	188/198 (95%)	180 (96%)	8 (4%)	26	52
1	E	188/198 (95%)	179 (95%)	9 (5%)	23	50
1	F	188/198 (95%)	177 (94%)	11 (6%)	18	45
1	G	188/198 (95%)	178 (95%)	10 (5%)	20	48
1	H	188/198 (95%)	180 (96%)	8 (4%)	26	52
1	I	189/198 (96%)	181 (96%)	8 (4%)	26	53
1	J	188/198 (95%)	178 (95%)	10 (5%)	20	48
1	K	188/198 (95%)	176 (94%)	12 (6%)	16	42
1	L	188/198 (95%)	179 (95%)	9 (5%)	23	50
1	M	188/198 (95%)	181 (96%)	7 (4%)	30	55
1	N	188/198 (95%)	176 (94%)	12 (6%)	16	42
1	O	188/198 (95%)	175 (93%)	13 (7%)	14	41
1	P	188/198 (95%)	177 (94%)	11 (6%)	18	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	3009/3168 (95%)	2845 (94%)	164 (6%)	19	46

All (164) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	MET
1	A	65	SER
1	A	94	ILE
1	A	105	ASP
1	A	147	VAL
1	A	173	LEU
1	A	196	THR
1	A	204	ASP
1	A	213	PRO
1	A	222	MET
1	A	233	ARG
1	A	255	THR
1	A	266	VAL
1	B	10	ILE
1	B	13	ASN
1	B	35	LYS
1	B	44	THR
1	B	46	MET
1	B	99	GLU
1	B	106	PHE
1	B	123	VAL
1	B	150	LEU
1	B	170	SER
1	B	182	TYR
1	B	224	MET
1	B	246	SER
1	B	255	THR
1	C	46	MET
1	C	61	HIS
1	C	82	ARG
1	C	108	ARG
1	C	142	VAL
1	C	224	MET
1	C	231	MET
1	C	250	SER
1	C	255	THR
1	D	99	GLU

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Mol	Chain	Res	Type
1	D	119	ILE
1	D	147	VAL
1	D	198	MET
1	D	199	LEU
1	D	222	MET
1	D	231	MET
1	D	257	PHE
1	E	40	ILE
1	E	75	LEU
1	E	103	LEU
1	E	116	SER
1	E	125	LEU
1	E	126	PRO
1	E	199	LEU
1	E	204	ASP
1	E	231	MET
1	F	94	ILE
1	F	107	HIS
1	F	121	THR
1	F	124	LEU
1	F	144	PHE
1	F	161	THR
1	F	180	LEU
1	F	198	MET
1	F	204	ASP
1	F	230	ARG
1	F	255	THR
1	G	63	VAL
1	G	66	GLU
1	G	75	LEU
1	G	103	LEU
1	G	110	ASN
1	G	151	ARG
1	G	161	THR
1	G	207	VAL
1	G	247	ASP
1	G	258	VAL
1	H	38	ASN
1	H	57	HIS
1	H	63	VAL
1	H	182	TYR
1	H	198	MET

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Mol	Chain	Res	Type
1	H	203	MET
1	H	255	THR
1	H	266	VAL
1	I	106	PHE
1	I	121	THR
1	I	151	ARG
1	I	156	ASN
1	I	199	LEU
1	I	230	ARG
1	I	231	MET
1	I	254	CYS
1	J	46	MET
1	J	75	LEU
1	J	150	LEU
1	J	182	TYR
1	J	189	VAL
1	J	199	LEU
1	J	222	MET
1	J	224	MET
1	J	228	ILE
1	J	255	THR
1	K	29	GLU
1	K	46	MET
1	K	61	HIS
1	K	93	SER
1	K	104	SER
1	K	106	PHE
1	K	113	ASN
1	K	155	PHE
1	K	182	TYR
1	K	204	ASP
1	K	255	THR
1	K	258	VAL
1	L	56	ASP
1	L	64	THR
1	L	104	SER
1	L	182	TYR
1	L	199	LEU
1	L	222	MET
1	L	227	PRO
1	L	230	ARG
1	L	255	THR

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Mol	Chain	Res	Type
1	M	44	THR
1	M	121	THR
1	M	161	THR
1	M	191	PRO
1	M	199	LEU
1	M	224	MET
1	M	250	SER
1	N	15	VAL
1	N	92	ILE
1	N	118	ILE
1	N	182	TYR
1	N	196	THR
1	N	199	LEU
1	N	204	ASP
1	N	224	MET
1	N	231	MET
1	N	250	SER
1	N	255	THR
1	N	264	SER
1	O	59	LEU
1	O	89	ASN
1	O	93	SER
1	O	94	ILE
1	O	100	ASP
1	O	114	VAL
1	O	161	THR
1	O	182	TYR
1	O	196	THR
1	O	199	LEU
1	O	227	PRO
1	O	231	MET
1	O	263	PHE
1	P	26	ILE
1	P	46	MET
1	P	75	LEU
1	P	93	SER
1	P	96	THR
1	P	110	ASN
1	P	147	VAL
1	P	151	ARG
1	P	199	LEU
1	P	216	GLU

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Mol	Chain	Res	Type
1	P	227	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (55) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	88	HIS
1	A	183	ASN
1	A	190	HIS
1	A	226	HIS
1	A	265	GLN
1	B	89	ASN
1	B	110	ASN
1	B	156	ASN
1	C	38	ASN
1	C	89	ASN
1	C	190	HIS
1	D	13	ASN
1	D	38	ASN
1	D	61	HIS
1	D	88	HIS
1	D	110	ASN
1	D	143	ASN
1	D	219	GLN
1	E	77	GLN
1	E	110	ASN
1	E	183	ASN
1	F	38	ASN
1	F	110	ASN
1	F	156	ASN
1	G	14	ASN
1	G	57	HIS
1	G	226	HIS
1	H	88	HIS
1	H	89	ASN
1	H	143	ASN
1	H	265	GLN
1	I	14	ASN
1	I	88	HIS
1	I	89	ASN
1	I	226	HIS
1	J	61	HIS
1	J	156	ASN

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Mol	Chain	Res	Type
1	K	219	GLN
1	L	88	HIS
1	L	89	ASN
1	L	143	ASN
1	M	14	ASN
1	M	38	ASN
1	M	57	HIS
1	M	61	HIS
1	M	113	ASN
1	M	265	GLN
1	N	57	HIS
1	N	77	GLN
1	O	89	ASN
1	P	57	HIS
1	P	77	GLN
1	P	110	ASN
1	P	143	ASN
1	P	265	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

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	256/266 (96%)	0.47	8 (3%) 51 34	4, 25, 62, 107	0
1	B	257/266 (96%)	0.43	9 (3%) 47 31	0, 25, 63, 128	0
1	C	254/266 (95%)	0.58	17 (6%) 24 16	4, 36, 90, 163	0
1	D	256/266 (96%)	0.64	13 (5%) 33 22	9, 37, 84, 130	0
1	E	255/266 (95%)	0.66	20 (7%) 19 14	1, 33, 94, 150	0
1	F	255/266 (95%)	0.65	16 (6%) 26 18	8, 32, 66, 89	0
1	G	255/266 (95%)	0.43	9 (3%) 47 31	0, 33, 76, 106	0
1	H	256/266 (96%)	0.53	9 (3%) 47 31	6, 33, 73, 119	0
1	I	257/266 (96%)	0.40	4 (1%) 70 52	5, 31, 61, 96	0
1	J	256/266 (96%)	0.38	5 (1%) 65 46	5, 26, 56, 95	0
1	K	256/266 (96%)	0.57	16 (6%) 26 18	4, 31, 71, 126	0
1	L	256/266 (96%)	0.48	11 (4%) 40 26	8, 33, 66, 123	0
1	M	255/266 (95%)	0.64	16 (6%) 26 18	10, 39, 82, 138	0
1	N	256/266 (96%)	0.64	20 (7%) 19 14	6, 36, 87, 159	0
1	O	255/266 (95%)	0.41	9 (3%) 47 31	7, 26, 57, 85	0
1	P	255/266 (95%)	0.60	18 (7%) 22 16	9, 31, 79, 117	0
All	All	4090/4256 (96%)	0.53	200 (4%) 35 23	0, 31, 74, 163	0

All (200) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	140	SER	5.4
1	A	120	GLY	5.3
1	M	13	ASN	4.6
1	N	213	PRO	4.4
1	E	51	ASP	4.3

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Mol	Chain	Res	Type	RSRZ
1	F	261	GLY	4.2
1	M	192	GLY	4.2
1	F	101	THR	4.1
1	D	250	SER	3.9
1	P	159	TYR	3.9
1	C	50	ALA	3.9
1	F	193	GLY	3.8
1	P	136	ALA	3.8
1	L	197	PRO	3.8
1	K	39	ALA	3.7
1	A	229	GLY	3.7
1	H	137	GLY	3.6
1	N	197	PRO	3.6
1	I	51	ASP	3.6
1	C	137	GLY	3.6
1	D	31	VAL	3.6
1	K	44	THR	3.6
1	B	130	GLU	3.5
1	A	157	ALA	3.5
1	B	197	PRO	3.5
1	H	216	GLU	3.5
1	E	222	MET	3.5
1	P	219	GLN	3.4
1	C	33	ALA	3.4
1	P	211	ALA	3.4
1	B	192	GLY	3.3
1	J	197	PRO	3.3
1	E	159	TYR	3.2
1	P	74	ALA	3.2
1	G	140	SER	3.2
1	F	249	ALA	3.2
1	G	132	GLY	3.2
1	E	106	PHE	3.2
1	N	124	LEU	3.1
1	N	218	ALA	3.1
1	D	210	GLY	3.1
1	P	198	MET	3.1
1	G	12	LEU	3.1
1	O	68	GLY	3.1
1	C	199	LEU	3.1
1	F	247	ASP	3.1
1	O	106	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	L	266	VAL	3.0
1	F	203	MET	3.0
1	E	204	ASP	3.0
1	H	201	SER	3.0
1	H	134	ALA	3.0
1	G	223	GLU	3.0
1	H	45	ASP	3.0
1	K	192	GLY	3.0
1	K	199	LEU	2.9
1	D	39	ALA	2.9
1	K	58	TYR	2.9
1	E	161	THR	2.9
1	E	218	ALA	2.9
1	K	152	GLY	2.8
1	M	199	LEU	2.8
1	J	201	SER	2.8
1	M	246	SER	2.8
1	O	213	PRO	2.8
1	O	217	VAL	2.8
1	G	90	ALA	2.8
1	I	36	ALA	2.8
1	O	199	LEU	2.8
1	J	200	GLY	2.8
1	L	187	ASN	2.7
1	K	153	ALA	2.7
1	F	106	PHE	2.7
1	B	136	ALA	2.7
1	K	22	ALA	2.7
1	M	164	ALA	2.7
1	E	207	VAL	2.7
1	N	188	SER	2.7
1	A	33	ALA	2.7
1	M	248	ALA	2.7
1	P	157	ALA	2.7
1	E	234	PRO	2.6
1	E	137	GLY	2.6
1	K	229	GLY	2.6
1	N	33	ALA	2.6
1	N	36	ALA	2.6
1	D	199	LEU	2.6
1	B	220	ALA	2.6
1	C	213	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	136	ALA	2.6
1	N	255	THR	2.6
1	C	93	SER	2.6
1	M	93	SER	2.6
1	E	25	GLY	2.6
1	K	38	ASN	2.6
1	K	249	ALA	2.6
1	E	213	PRO	2.5
1	F	199	LEU	2.5
1	L	255	THR	2.5
1	I	192	GLY	2.5
1	K	220	ALA	2.5
1	N	198	MET	2.5
1	P	77	GLN	2.5
1	F	162	SER	2.5
1	N	196	THR	2.5
1	F	218	ALA	2.4
1	C	94	ILE	2.4
1	M	174	GLY	2.4
1	O	210	GLY	2.4
1	M	228	ILE	2.4
1	K	49	SER	2.4
1	E	12	LEU	2.4
1	G	206	TYR	2.4
1	J	231	MET	2.4
1	M	198	MET	2.4
1	P	149	GLY	2.4
1	G	139	ALA	2.4
1	L	119	ILE	2.4
1	P	197	PRO	2.4
1	C	38	ASN	2.3
1	N	106	PHE	2.3
1	D	207	VAL	2.3
1	F	71	ALA	2.3
1	L	222	MET	2.3
1	C	100	ASP	2.3
1	A	28	ARG	2.3
1	G	82	ARG	2.3
1	E	138	GLY	2.3
1	P	58	TYR	2.3
1	F	183	ASN	2.3
1	N	38	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	N	183	ASN	2.3
1	C	258	VAL	2.3
1	E	229	GLY	2.3
1	E	220	ALA	2.3
1	O	220	ALA	2.3
1	B	175	ALA	2.3
1	C	67	ALA	2.3
1	D	138	GLY	2.3
1	E	39	ALA	2.3
1	D	132	GLY	2.2
1	L	27	GLY	2.2
1	N	55	ALA	2.2
1	C	128	LEU	2.2
1	P	225	ARG	2.2
1	M	217	VAL	2.2
1	L	195	ASP	2.2
1	O	120	GLY	2.2
1	C	49	SER	2.2
1	F	141	VAL	2.2
1	N	72	VAL	2.2
1	P	14	ASN	2.2
1	D	211	ALA	2.2
1	H	174	GLY	2.2
1	D	61	HIS	2.2
1	C	52	VAL	2.2
1	M	15	VAL	2.2
1	H	184	ILE	2.2
1	N	199	LEU	2.2
1	E	154	ALA	2.2
1	M	51	ASP	2.2
1	A	151	ARG	2.2
1	D	36	ALA	2.2
1	D	218	ALA	2.2
1	P	158	ALA	2.2
1	N	87	VAL	2.1
1	C	42	ILE	2.1
1	E	216	GLU	2.1
1	B	229	GLY	2.1
1	A	217	VAL	2.1
1	P	12	LEU	2.1
1	H	71	ALA	2.1
1	B	193	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	156	ASN	2.1
1	B	38	ASN	2.1
1	I	183	ASN	2.1
1	M	26	ILE	2.1
1	O	193	GLY	2.1
1	M	109	VAL	2.1
1	M	247	ASP	2.1
1	F	198	MET	2.1
1	L	46	MET	2.1
1	P	102	PRO	2.1
1	G	214	SER	2.1
1	N	142	VAL	2.1
1	N	202	LEU	2.1
1	P	218	ALA	2.1
1	P	120	GLY	2.1
1	F	48	PRO	2.1
1	E	199	LEU	2.0
1	D	23	ALA	2.0
1	K	265	GLN	2.0
1	K	213	PRO	2.0
1	K	171	LYS	2.0
1	H	112	VAL	2.0
1	L	199	LEU	2.0
1	L	198	MET	2.0
1	J	131	GLY	2.0
1	F	236	GLU	2.0
1	N	189	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.