



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:12 PM GMT

PDB ID : 4BI5  
Title : CRYSTAL STRUCTURE OF A DOUBLE MUTANT (C202A AND C222D) OF TRIOSEPHOSPHATE ISOMERASE FROM GIARDIA LAMBLIA.  
Authors : Torres-Larios, A.; Enriquez-Flores, S.; Reyes-Vivas, H.; Oria-Hernandez, J.; Hernandez-Alcantara, G.  
Deposited on : 2013-04-09  
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

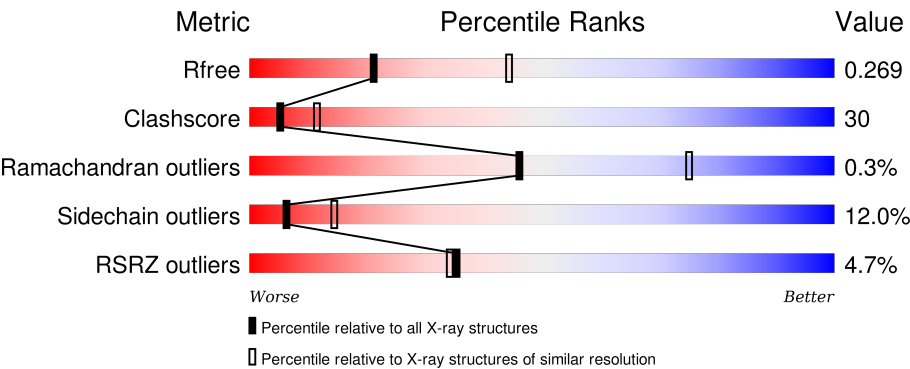
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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 <sub>free</sub>	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	255	<div><div>4%</div><div><div></div><div>56%</div><div>37%</div><div>7%</div></div></div>
1	B	255	<div><div>3%</div><div><div></div><div>62%</div><div>33%</div><div>.</div></div></div>
1	C	255	<div><div>3%</div><div><div></div><div>54%</div><div>40%</div><div>5%</div></div></div>
1	D	255	<div><div>2%</div><div><div></div><div>56%</div><div>36%</div><div>8%</div></div></div>
1	E	255	<div><div>4%</div><div><div></div><div>52%</div><div>41%</div><div>6%</div></div></div>

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Mol	Chain	Length	Quality of chain
1	F	255	
1	G	255	
1	H	255	
1	I	255	
1	J	255	
1	K	255	
1	L	255	
1	M	255	
1	N	255	
1	O	255	
1	P	255	
1	Q	255	
1	R	255	
1	S	255	
1	T	255	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 38560 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 TRIOSEPHOSPHATE ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	B	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	C	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	D	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	E	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	F	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	G	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	H	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	I	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	J	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	K	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	L	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	M	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	N	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	O	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	P	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	254	Total 1928	C 1212	N 341	O 364	S 11	0	0	0
1	R	254	Total 1928	C 1212	N 341	O 364	S 11	0	0	0
1	S	254	Total 1928	C 1212	N 341	O 364	S 11	0	0	0
1	T	254	Total 1928	C 1212	N 341	O 364	S 11	0	0	0

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
A	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
B	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
B	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
C	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
C	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
D	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
D	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
E	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
E	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
F	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
F	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
G	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
G	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
H	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
H	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
I	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
I	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
J	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
J	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
K	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
K	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
L	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
L	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
M	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
M	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
N	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
N	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
O	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
O	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
P	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186

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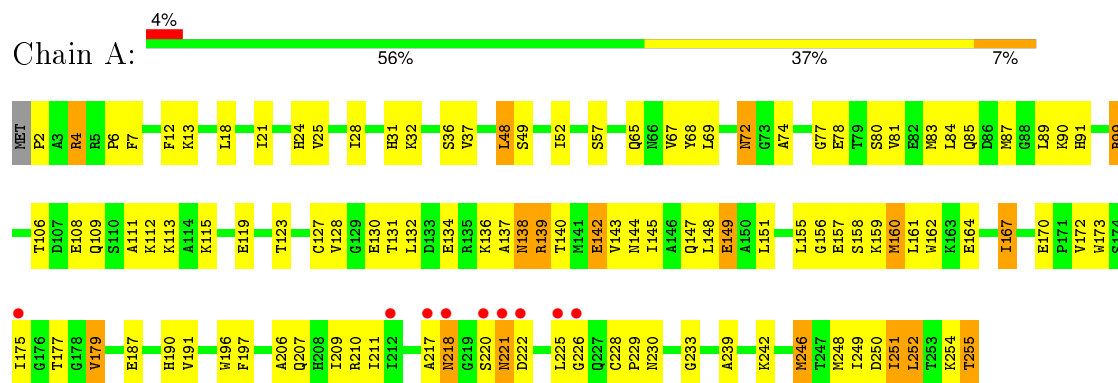
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Chain	Residue	Modelled	Actual	Comment	Reference
P	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
Q	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
Q	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
R	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
R	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
S	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
S	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
T	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
T	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186

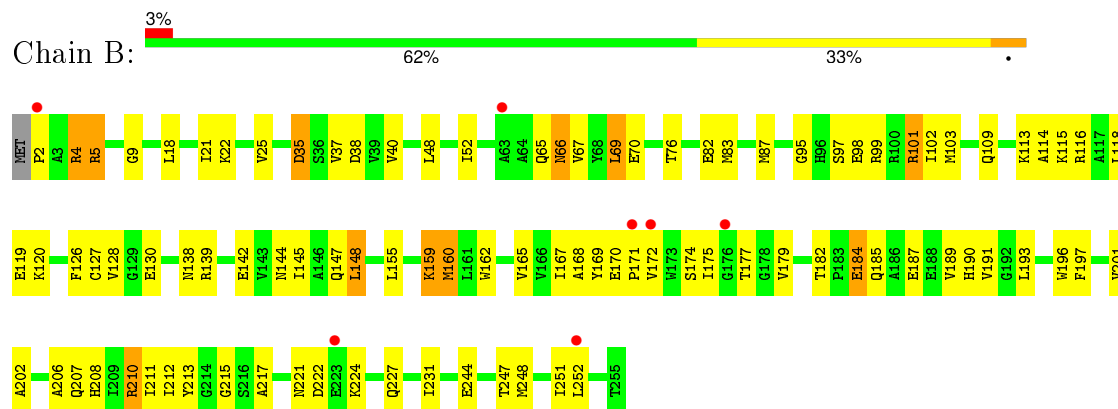
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

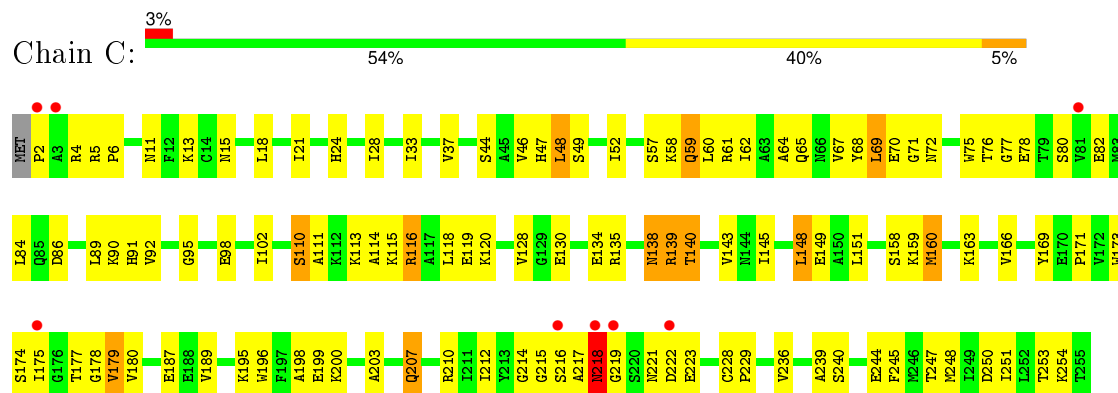
#### • Molecule 1: TRIOSEPHOSPHATE ISOMERASE



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Chain D:

Category	Count
MET	2
P2	1
A3	56
R4	1
R5	1
P6	1
F7	1
I8	1
G9	1
K13	1
L18	1
K22	1
S23	1
H24	1
I28	1
K32	1
I33	1
P34	1
D35	1
S36	1
V37	1
D38	1
V39	1
V40	1
S44	1
L48	1
I52	1
N55	1
T56	1
S57	1
K58	1
Q59	1
L60	1
R61	1
I62	1
V67	1
Y68	1
L69	1
W75	1
T76	1
G77	1
E78	1
V81	1
E82	1
M83	1
L84	1
Q85	1
R86	1

Chain E:

4% 52% 41% 6%

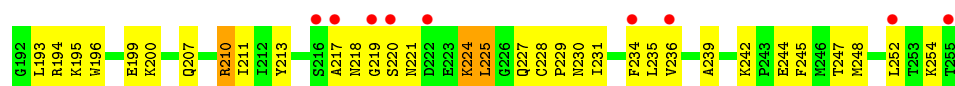
Chain F:

Item	Category
V179	Yellow
V180	Yellow
A181	Yellow
F182	Yellow
F183	Yellow
E184	Yellow
Q185	Yellow
V186	Yellow
F187	Yellow
A188	Yellow
E189	Yellow
F200	Yellow
V201	Yellow
A202	Yellow
A206	Yellow
Q207	Yellow
I208	Yellow
I209	Yellow
R210	Yellow
I211	Yellow
I212	Yellow
Y213	Yellow
G214	Yellow
G215	Yellow
N218	Yellow
G219	Yellow
S220	Yellow
N221	Yellow
D222	Yellow
G228	Yellow
P229	Yellow
L235	Yellow
V236	Yellow
A239	Yellow
S240	Yellow
E244	Yellow
F245	Yellow
M248	Yellow
T255	Yellow
H91	Yellow
G95	Yellow
B98	Yellow
R99	Yellow
I102	Yellow
M103	Yellow
E108	Yellow
Q109	Yellow
S110	Yellow
V111	Yellow
K112	Yellow
K113	Yellow
R116	Yellow
A117	Yellow
L118	Yellow
R119	Yellow
K120	Yellow
T123	Yellow
C127	Yellow
V128	Yellow
L132	Yellow
D133	Yellow
E134	Yellow
R135	Yellow
K136	Yellow
A137	Yellow
M138	Yellow
R139	Yellow
V143	Yellow
M144	Yellow
I145	Yellow
L148	Yellow
L151	Yellow
L155	Yellow
K159	Yellow
M160	Yellow
L161	Yellow
W162	Yellow
P171	Yellow
W172	Yellow
S173	Yellow
I175	Yellow
G176	Yellow
T177	Yellow
C178	Yellow
PET	Red
F2	Red
A3	Red
R4	Red
R5	Red
G9	Red
F12	Red
K13	Red
C14	Red
R15	Red
G16	Red
S17	Red
L18	Red
I21	Red
K22	Red
S23	Red
V25	Red
I28	Red
V40	Red
S44	Red
H47	Red
L48	Red
I52	Red
K58	Red
R61	Red
I62	Red
A63	Red
G64	Red
O65	Red
G66	Red
V67	Red
V68	Red
L69	Red
E70	Red
A74	Red
W75	Red
L76	Red
G77	Red
E78	Red
I79	Red
S80	Red
V81	Red
E82	Red
R83	Red
M87	Red
V90	Red

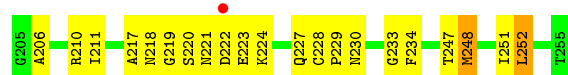
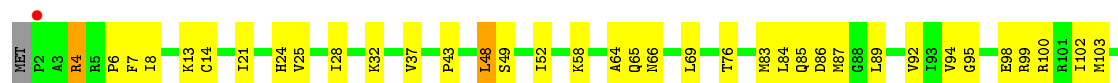
Chain G:

Category	Percentage
MET	
P2	4%
A3	
R4	
R5	
P6	
F7	
I8	
G9	
G10	
N11	
F12	
S17	
L18	
L14	
I21	
K22	
S23	
H24	
V25	
I28	
S36	
V37	
D38	
V39	
V40	
I41	
L60	
R61	
I62	
A63	
A64	
Q65	
N66	
V67	
Y68	
L69	
E70	
G71	
N72	
G73	
A74	
W75	
T76	
G77	
S80	
V81	
E82	
M83	
M87	
K90	
H91	
W92	

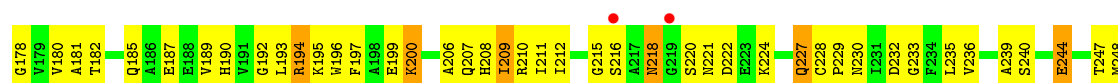
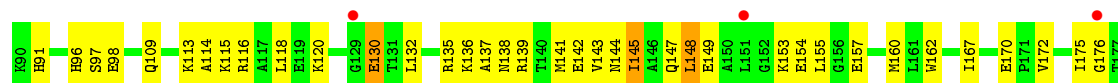




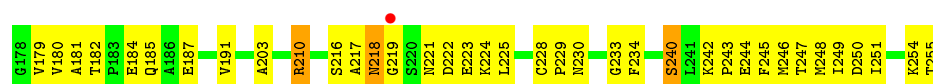
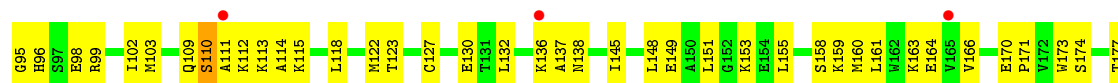
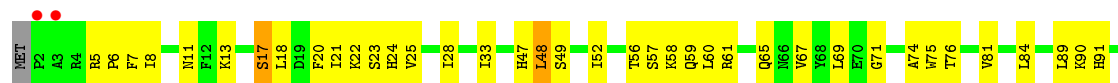
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE



• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

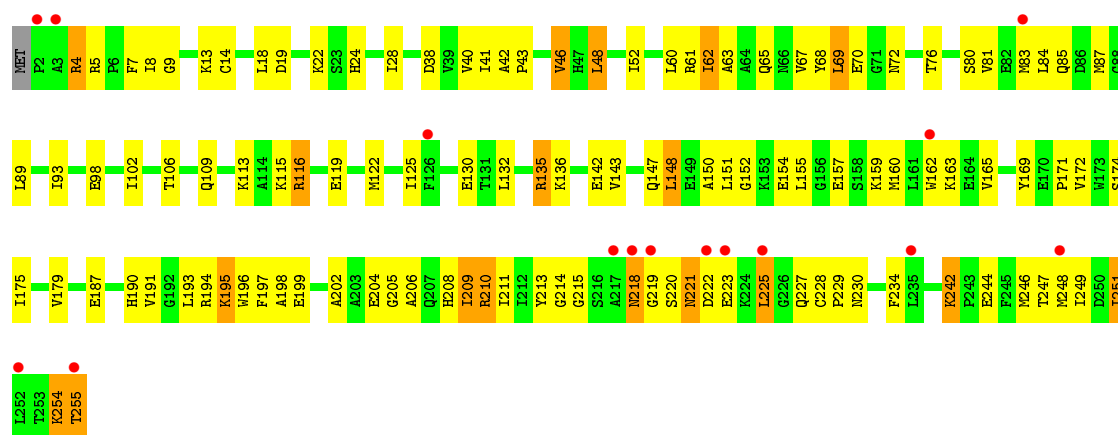


• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

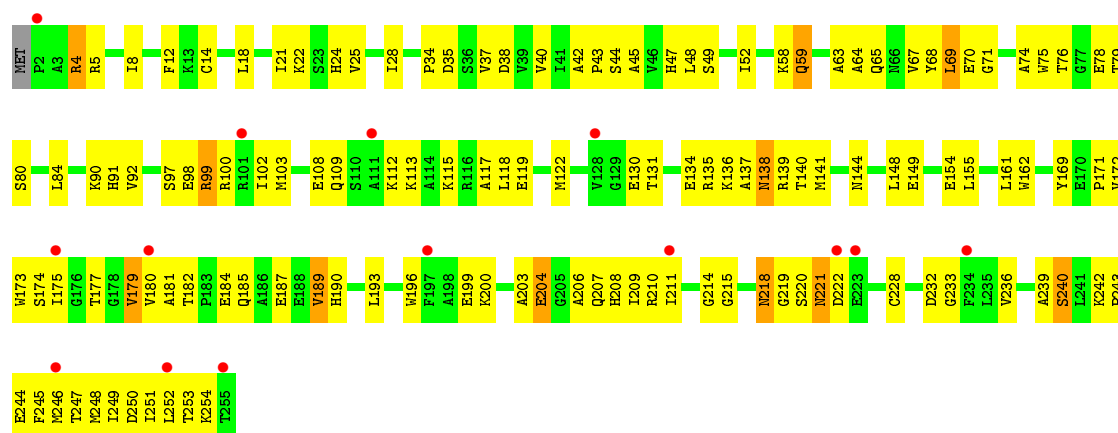


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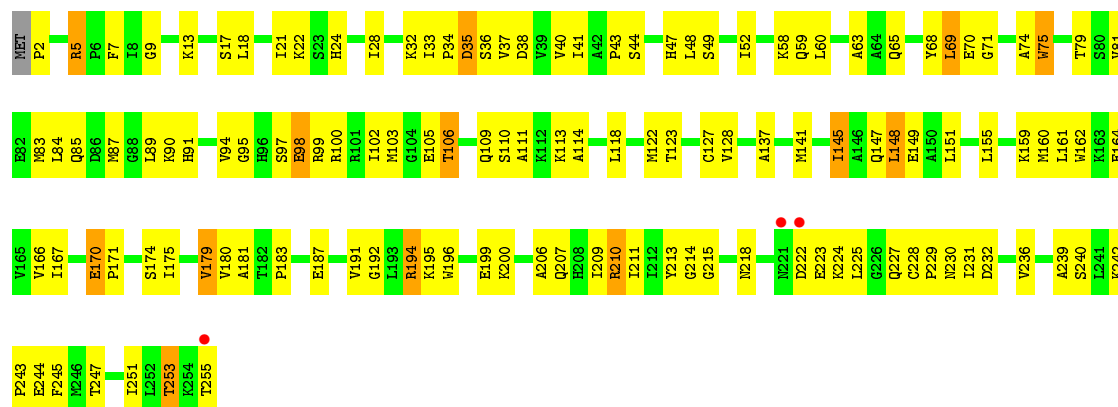




• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

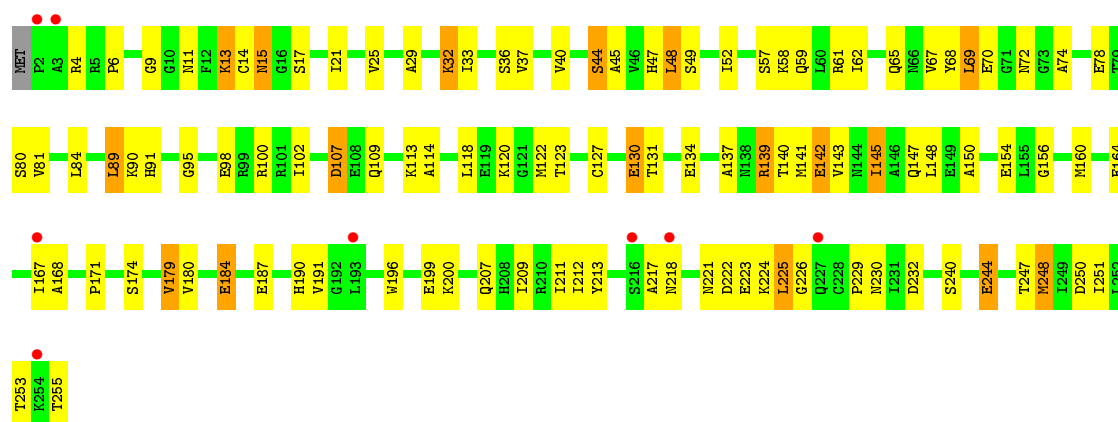


• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

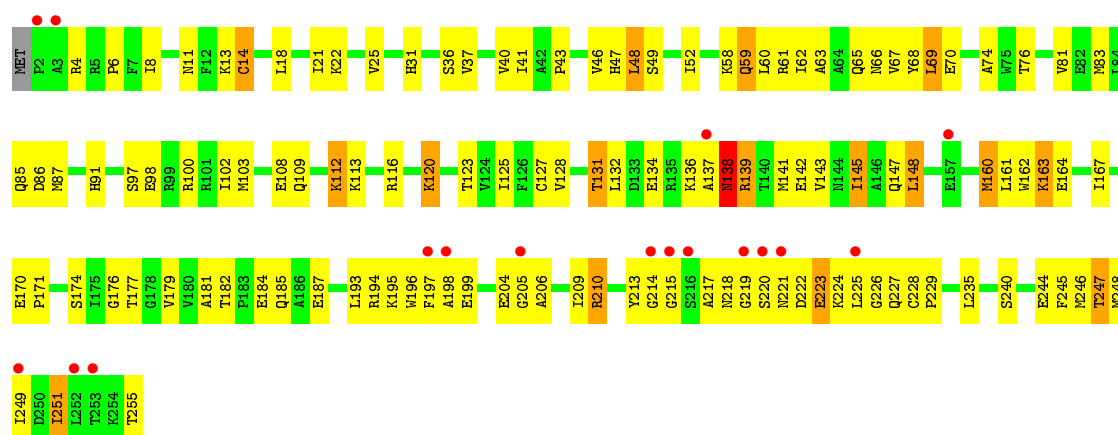


• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

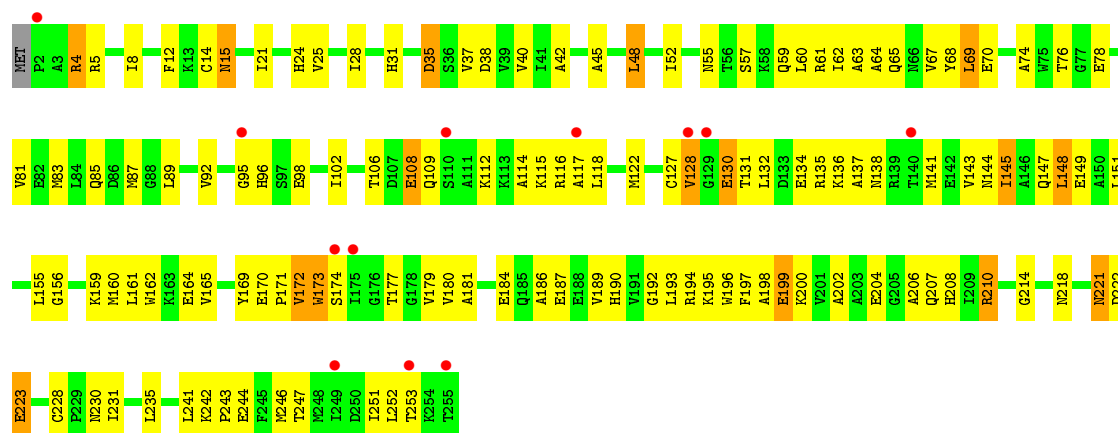




• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

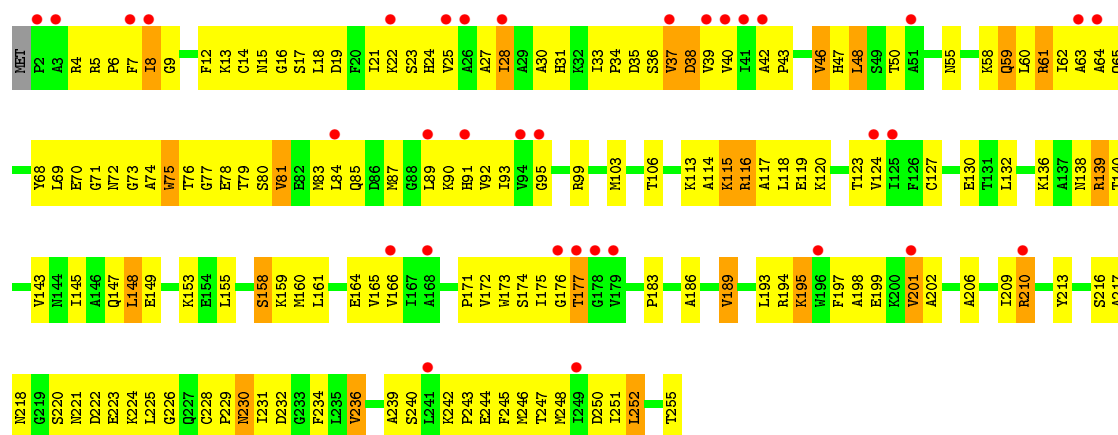


• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

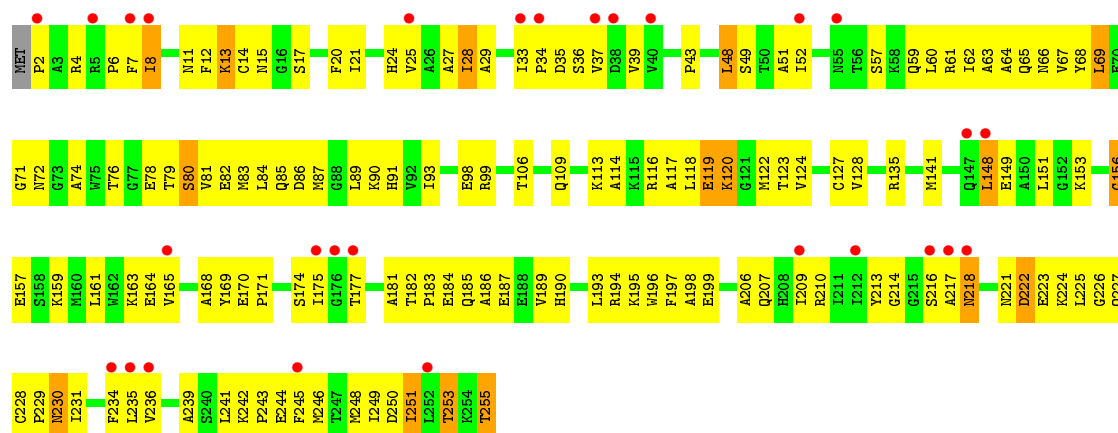
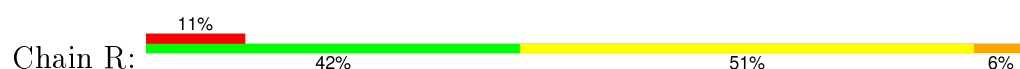


• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

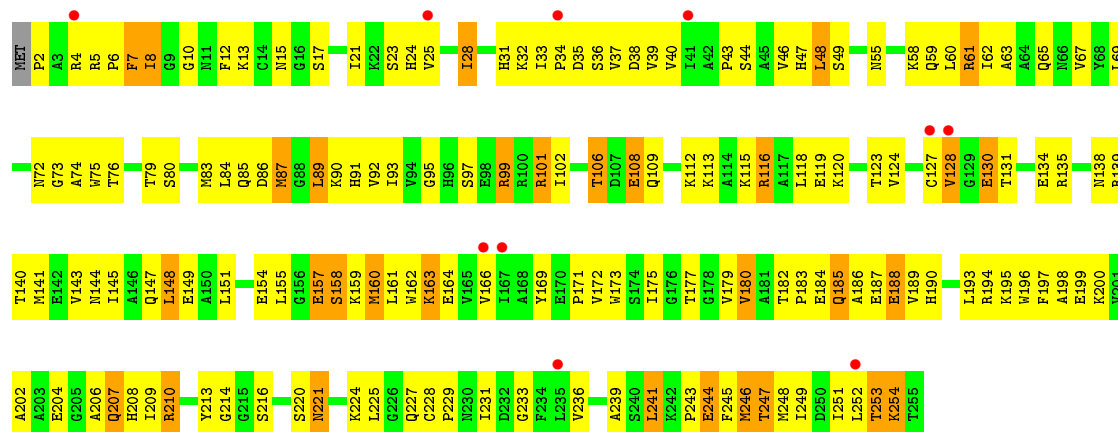




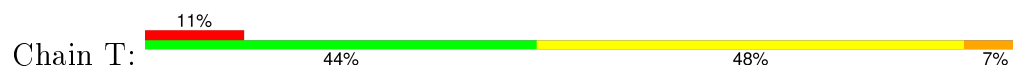
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

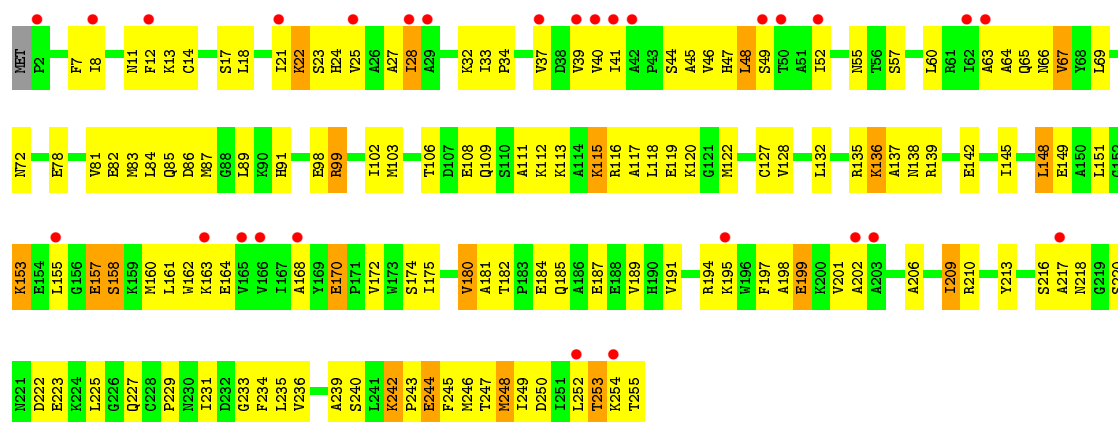


• Molecule 1: TRIOSEPHOSPHATE ISOMERASE



• Molecule 1: TRIOSEPHOSPHATE ISOMERASE





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.22Å 131.57Å 132.55Å 115.73° 89.81° 90.24°	Depositor
Resolution (Å)	78.87 – 2.70 78.88 – 2.70	Depositor EDS
% Data completeness (in resolution range)	82.0 (78.87-2.70) 65.6 (78.88-2.70)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.46 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.239 , 0.272 0.236 , 0.269	Depositor DCC
$R_{free}$ test set	8804 reflections (6.43%)	DCC
Wilson B-factor (Å <sup>2</sup> )	50.3	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.418 for h,-k,-l 0.197 for -h,-l,-k 0.197 for -h,l,k	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	0 of 144197 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	38560	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.64% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.48	0/1960	0.49	0/2644
1	B	0.58	2/1960 (0.1%)	0.50	0/2644
1	C	0.55	0/1960	0.53	0/2644
1	D	0.40	0/1960	0.48	0/2644
1	E	0.63	0/1960	0.53	0/2644
1	F	0.49	1/1960 (0.1%)	0.52	0/2644
1	G	0.62	2/1960 (0.1%)	0.52	0/2644
1	H	0.58	0/1960	0.52	0/2644
1	I	0.37	0/1960	0.50	0/2644
1	J	0.44	0/1960	0.49	0/2644
1	K	0.34	0/1960	0.51	0/2644
1	L	0.55	0/1960	0.56	0/2644
1	M	0.34	0/1960	0.47	0/2644
1	N	0.27	0/1960	0.46	0/2644
1	O	0.30	0/1960	0.50	0/2644
1	P	0.28	0/1960	0.49	0/2644
1	Q	0.33	0/1960	0.49	0/2644
1	R	0.37	0/1960	0.50	0/2644
1	S	0.32	0/1960	0.50	0/2644
1	T	0.28	0/1960	0.50	0/2644
All	All	0.44	5/39200 (0.0%)	0.50	0/52880

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	14	CYS	CB-SG	-5.68	1.72	1.81
1	B	169	TYR	CE2-CZ	-5.38	1.31	1.38
1	G	68	TYR	CD2-CE2	-5.31	1.31	1.39
1	G	68	TYR	CE1-CZ	-5.25	1.31	1.38
1	B	169	TYR	CD2-CE2	-5.00	1.31	1.39

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1928	0	1949	111	0
1	B	1928	0	1949	82	0
1	C	1928	0	1949	95	0
1	D	1928	0	1949	103	0
1	E	1928	0	1949	136	0
1	F	1928	0	1949	93	0
1	G	1928	0	1949	98	0
1	H	1928	0	1949	80	0
1	I	1928	0	1949	137	0
1	J	1928	0	1949	104	0
1	K	1928	0	1949	113	0
1	L	1928	0	1949	141	0
1	M	1928	0	1949	104	0
1	N	1928	0	1949	110	0
1	O	1928	0	1949	141	0
1	P	1928	0	1949	127	0
1	Q	1928	0	1949	195	0
1	R	1928	0	1949	184	0
1	S	1928	0	1949	184	0
1	T	1928	0	1949	130	0
All	All	38560	0	38980	2346	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 30.

All (2346) 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:C:76:THR:CG2	1:D:98:GLU:OE1	1.67	1.42
1:T:115:LYS:HG2	1:T:155:LEU:CD2	1.47	1.41
1:B:66:ASN:HD22	1:B:67:VAL:N	1.25	1.31
1:L:177:THR:HG22	1:L:179:VAL:CG2	1.60	1.30

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:66:ASN:ND2	1:B:67:VAL:H	1.30	1.27
1:L:200:LYS:O	1:L:200:LYS:HD2	1.39	1.19
1:Q:183:PRO:HB3	1:Q:225:LEU:HD23	1.25	1.17
1:P:210:ARG:HG3	1:P:210:ARG:HH11	1.03	1.15
1:N:14:CYS:C	1:N:15:ASN:HD22	1.51	1.14
1:O:58:LYS:HG3	1:O:59:GLN:NE2	1.65	1.12
1:P:14:CYS:C	1:P:15:ASN:HD22	1.52	1.12
1:L:177:THR:HG22	1:L:179:VAL:HG23	1.13	1.12
1:C:217:ALA:O	1:C:218:ASN:HB3	1.46	1.12
1:T:115:LYS:CG	1:T:155:LEU:CD2	2.28	1.11
1:C:178:GLY:HA2	1:R:175:ILE:HD13	1.30	1.10
1:T:115:LYS:HG2	1:T:155:LEU:HD23	1.27	1.10
1:O:58:LYS:HE2	1:O:59:GLN:OE1	1.52	1.10
1:T:115:LYS:CG	1:T:155:LEU:HD23	1.79	1.09
1:E:251:ILE:HA	1:E:254:LYS:HE3	1.32	1.09
1:E:171:PRO:HG2	1:E:215:GLY:HA3	1.16	1.08
1:L:177:THR:CG2	1:L:179:VAL:HG23	1.82	1.08
1:S:210:ARG:HG2	1:S:210:ARG:HH11	0.92	1.08
1:B:66:ASN:ND2	1:B:67:VAL:N	1.91	1.07
1:Q:183:PRO:CB	1:Q:225:LEU:HD23	1.83	1.07
1:G:213:TYR:HB3	1:G:234:PHE:CD1	1.89	1.07
1:E:171:PRO:CG	1:E:215:GLY:HA3	1.85	1.07
1:I:84:LEU:HD22	1:I:89:LEU:HD12	1.31	1.07
1:F:171:PRO:O	1:F:175:ILE:HD13	1.53	1.06
1:E:175:ILE:HA	1:I:176:GLY:HA3	1.33	1.06
1:E:217:ALA:HB3	1:I:178:GLY:CA	1.86	1.06
1:E:217:ALA:HB3	1:I:178:GLY:HA2	1.36	1.06
1:O:226:GLY:HA3	1:O:255:THR:HG21	1.36	1.06
1:Q:61:ARG:HH22	1:Q:90:LYS:HG2	1.19	1.06
1:O:58:LYS:HG3	1:O:59:GLN:CD	1.77	1.05
1:Q:210:ARG:HD3	1:Q:210:ARG:H	1.20	1.05
1:R:225:LEU:HB3	1:R:234:PHE:CE1	1.93	1.04
1:H:218:ASN:O	1:H:222:ASP:HB2	1.58	1.02
1:L:171:PRO:HG2	1:L:174:SER:OG	1.60	1.02
1:Q:197:PHE:O	1:Q:201:VAL:HB	1.58	1.02
1:C:175:ILE:O	1:R:175:ILE:HG21	1.60	1.01
1:T:115:LYS:HG2	1:T:155:LEU:HD21	1.39	1.01
1:O:218:ASN:HD22	1:O:220:SER:H	1.08	1.01
1:Q:75:TRP:CD1	1:R:14:CYS:SG	2.52	1.01
1:L:218:ASN:N	1:L:221:ASN:HD21	1.57	1.01
1:S:158:SER:HB2	1:S:161:LEU:HD23	1.42	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:59:GLN:NE2	1:O:59:GLN:H	1.56	1.01
1:R:225:LEU:HB3	1:R:234:PHE:HE1	1.23	1.00
1:R:195:LYS:O	1:R:199:GLU:HB2	1.62	1.00
1:S:221:ASN:CB	1:S:224:LYS:HE2	1.92	1.00
1:L:177:THR:CG2	1:L:179:VAL:CG2	2.39	0.99
1:C:76:THR:HG23	1:D:98:GLU:CD	1.83	0.98
1:M:2:PRO:HG2	1:M:207:GLN:HB3	1.45	0.98
1:S:6:PRO:HG2	1:S:37:VAL:HA	1.46	0.98
1:P:173:TRP:O	1:P:177:THR:HG21	1.62	0.98
1:B:102:ILE:HG12	1:O:179:VAL:HG22	1.46	0.98
1:L:218:ASN:H	1:L:221:ASN:ND2	1.62	0.98
1:M:191:VAL:HG22	1:M:230:ASN:OD1	1.64	0.97
1:N:226:GLY:C	1:N:255:THR:HG21	1.83	0.97
1:A:172:VAL:HA	1:A:175:ILE:CD1	1.95	0.97
1:O:171:PRO:HD2	1:O:214:GLY:O	1.63	0.96
1:S:210:ARG:HG2	1:S:210:ARG:NH1	1.72	0.96
1:R:251:ILE:O	1:R:255:THR:HB	1.66	0.96
1:K:159:LYS:O	1:K:160:MET:HG2	1.64	0.95
1:S:7:PHE:HE2	1:S:166:VAL:HG21	1.31	0.95
1:C:76:THR:HG23	1:D:98:GLU:OE1	0.77	0.95
1:H:160:MET:O	1:H:163:LYS:HG3	1.65	0.95
1:O:58:LYS:CG	1:O:59:GLN:NE2	2.30	0.94
1:E:190:HIS:HE2	1:E:213:TYR:HB2	1.28	0.94
1:Q:61:ARG:NH2	1:Q:90:LYS:HG2	1.83	0.94
1:G:97:SER:HB3	1:G:170:GLU:OE1	1.66	0.94
1:M:94:VAL:HG11	1:M:114:ALA:HB2	1.49	0.94
1:O:58:LYS:CG	1:O:59:GLN:HE22	1.80	0.94
1:G:236:VAL:CG1	1:G:239:ALA:HB3	1.98	0.93
1:G:69:LEU:HD12	1:G:70:GLU:HG2	1.50	0.93
1:R:228:CYS:CB	1:R:231:ILE:HG13	1.99	0.92
1:G:195:LYS:O	1:G:199:GLU:HG3	1.69	0.92
1:E:169:TYR:CE1	1:E:189:VAL:HG11	2.04	0.92
1:Q:7:PHE:HD1	1:Q:38:ASP:HB2	1.34	0.91
1:Q:89:LEU:HD12	1:Q:90:LYS:H	1.35	0.91
1:S:61:ARG:HG3	1:S:61:ARG:HH11	1.33	0.91
1:T:109:GLN:O	1:T:113:LYS:HG3	1.71	0.91
1:E:171:PRO:HD2	1:E:215:GLY:CA	1.99	0.91
1:E:190:HIS:NE2	1:E:213:TYR:HB2	1.85	0.90
1:H:126:PHE:CZ	1:H:151:LEU:HD11	2.06	0.90
1:E:171:PRO:HD2	1:E:215:GLY:HA2	1.52	0.90
1:L:221:ASN:HD22	1:L:222:ASP:N	1.69	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:210:ARG:HG3	1:P:210:ARG:NH1	1.82	0.89
1:D:4:ARG:HD3	1:D:207:GLN:O	1.72	0.89
1:K:172:VAL:HA	1:K:175:ILE:HD12	1.55	0.89
1:E:4:ARG:HD3	1:E:207:GLN:O	1.72	0.89
1:I:194:ARG:CG	1:I:194:ARG:HH11	1.86	0.89
1:S:210:ARG:HH11	1:S:210:ARG:CG	1.84	0.88
1:J:11:ASN:ND2	1:J:13:LYS:HG3	1.88	0.88
1:T:115:LYS:CD	1:T:155:LEU:HD23	2.04	0.87
1:Q:89:LEU:HD12	1:Q:90:LYS:N	1.89	0.87
1:M:99:ARG:HA	1:M:103:MET:HB2	1.54	0.87
1:Q:7:PHE:CD1	1:Q:38:ASP:HB2	2.09	0.87
1:E:135:ARG:HA	1:E:140:THR:HG22	1.54	0.87
1:R:66:ASN:OD1	1:R:67:VAL:N	2.07	0.87
1:O:218:ASN:ND2	1:O:220:SER:H	1.73	0.86
1:B:224:LYS:O	1:B:227:GLN:HG3	1.74	0.86
1:B:69:LEU:HD23	1:B:70:GLU:HG2	1.58	0.86
1:O:58:LYS:HG2	1:O:59:GLN:HE22	1.39	0.86
1:I:4:ARG:HG2	1:I:4:ARG:HH11	1.41	0.85
1:B:97:SER:HB3	1:B:170:GLU:OE1	1.76	0.85
1:O:59:GLN:HE21	1:O:59:GLN:H	1.19	0.85
1:Q:79:THR:HG21	1:Q:84:LEU:HD21	1.59	0.85
1:P:131:THR:HA	1:P:172:VAL:CG1	2.06	0.85
1:H:217:ALA:HB1	1:H:248:MET:HE1	1.58	0.85
1:G:236:VAL:HG11	1:G:239:ALA:HB3	1.57	0.85
1:R:183:PRO:HG2	1:R:224:LYS:HD3	1.59	0.85
1:K:165:VAL:O	1:K:209:ILE:HD11	1.76	0.85
1:E:130:GLU:OE2	1:E:135:ARG:HB2	1.76	0.84
1:O:171:PRO:HG3	1:O:215:GLY:HA3	1.57	0.84
1:P:131:THR:HA	1:P:172:VAL:HG11	1.59	0.84
1:R:228:CYS:HB2	1:R:231:ILE:HG13	1.58	0.84
1:H:84:LEU:HD22	1:H:89:LEU:HD12	1.59	0.83
1:O:213:TYR:CZ	1:O:215:GLY:HA3	2.13	0.83
1:S:130:GLU:OE2	1:S:140:THR:HG23	1.77	0.83
1:T:155:LEU:HD22	1:T:161:LEU:HD12	1.59	0.83
1:C:69:LEU:HD23	1:C:70:GLU:HG2	1.58	0.83
1:Q:195:LYS:O	1:Q:199:GLU:HB2	1.78	0.83
1:T:115:LYS:HD3	1:T:155:LEU:CD2	2.09	0.83
1:Q:61:ARG:HH22	1:Q:90:LYS:CG	1.92	0.83
1:L:69:LEU:HD23	1:L:70:GLU:HG2	1.61	0.83
1:A:218:ASN:C	1:A:218:ASN:HD22	1.81	0.83
1:G:213:TYR:HB3	1:G:234:PHE:CE1	2.11	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:17:SER:O	1:T:21:ILE:HG12	1.78	0.83
1:F:218:ASN:HB2	1:F:220:SER:OG	1.78	0.83
1:C:175:ILE:O	1:R:175:ILE:CG2	2.26	0.82
1:O:171:PRO:HG3	1:O:215:GLY:CA	2.08	0.82
1:S:157:GLU:OE1	1:S:157:GLU:HA	1.78	0.82
1:N:14:CYS:C	1:N:15:ASN:ND2	2.30	0.82
1:F:171:PRO:HB3	1:F:173:TRP:NE1	1.93	0.82
1:Q:234:PHE:CD2	1:Q:248:MET:CE	2.61	0.82
1:A:172:VAL:HG13	1:A:175:ILE:HD12	1.59	0.82
1:E:218:ASN:OD1	1:E:219:GLY:N	2.13	0.82
1:S:8:ILE:HD11	1:S:245:PHE:CE1	2.15	0.82
1:D:218:ASN:HD22	1:D:219:GLY:N	1.77	0.82
1:Q:197:PHE:CD2	1:Q:206:ALA:HA	2.14	0.82
1:R:4:ARG:HD3	1:R:207:GLN:O	1.79	0.82
1:R:246:MET:HA	1:R:249:ILE:HD12	1.60	0.82
1:I:194:ARG:HG2	1:I:194:ARG:HH11	1.45	0.81
1:E:219:GLY:O	1:E:220:SER:HB3	1.79	0.81
1:S:183:PRO:HD2	1:S:184:GLU:OE1	1.81	0.81
1:K:218:ASN:HD22	1:K:219:GLY:N	1.78	0.81
1:P:173:TRP:O	1:P:177:THR:CG2	2.29	0.81
1:S:7:PHE:CE2	1:S:166:VAL:HG21	2.15	0.81
1:R:2:PRO:HB3	1:R:207:GLN:HG2	1.62	0.81
1:R:63:ALA:HB2	1:R:91:HIS:HB2	1.60	0.81
1:N:15:ASN:N	1:N:15:ASN:HD22	1.78	0.80
1:J:242:LYS:HB3	1:J:244:GLU:OE1	1.80	0.80
1:A:217:ALA:HB1	1:A:248:MET:HE3	1.62	0.80
1:Q:183:PRO:CB	1:Q:225:LEU:CD2	2.58	0.80
1:I:13:LYS:HG3	1:J:76:THR:CG2	2.11	0.80
1:K:223:GLU:HG3	1:K:254:LYS:HZ1	1.45	0.80
1:H:187:GLU:O	1:H:191:VAL:HG23	1.81	0.80
1:J:222:ASP:HA	1:J:225:LEU:HB2	1.63	0.80
1:N:226:GLY:CA	1:N:255:THR:HG21	2.12	0.80
1:E:247:THR:O	1:E:251:ILE:HD13	1.81	0.80
1:T:115:LYS:HG2	1:T:155:LEU:CG	2.11	0.80
1:T:83:MET:O	1:T:86:ASP:HB3	1.82	0.80
1:P:108:GLU:O	1:P:112:LYS:HG3	1.82	0.80
1:O:226:GLY:CA	1:O:255:THR:HG21	2.12	0.79
1:T:115:LYS:CD	1:T:155:LEU:CD2	2.59	0.79
1:R:69:LEU:H	1:R:69:LEU:HD23	1.45	0.79
1:O:59:GLN:N	1:O:59:GLN:NE2	2.30	0.79
1:N:191:VAL:HG22	1:N:230:ASN:HD22	1.46	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:132:LEU:O	1:P:136:LYS:HG3	1.83	0.79
1:N:6:PRO:HB2	1:N:37:VAL:HG13	1.64	0.79
1:M:228:CYS:HB2	1:M:231:ILE:HD12	1.63	0.78
1:S:221:ASN:HB2	1:S:224:LYS:HE2	1.65	0.78
1:K:159:LYS:O	1:K:160:MET:CG	2.30	0.78
1:I:11:ASN:HD21	1:J:76:THR:HG21	1.47	0.78
1:I:109:GLN:O	1:I:113:LYS:HG3	1.82	0.78
1:P:5:ARG:O	1:P:210:ARG:HD3	1.82	0.78
1:H:160:MET:O	1:H:163:LYS:CG	2.31	0.78
1:Q:5:ARG:HH12	1:Q:36:SER:HA	1.48	0.78
1:L:108:GLU:O	1:L:112:LYS:HG3	1.83	0.78
1:J:240:SER:HA	1:J:245:PHE:HB2	1.65	0.78
1:R:225:LEU:HA	1:R:228:CYS:SG	2.23	0.78
1:G:69:LEU:CD1	1:G:70:GLU:HG2	2.13	0.78
1:G:225:LEU:HB3	1:G:234:PHE:HZ	1.48	0.78
1:M:225:LEU:O	1:M:231:ILE:HD12	1.83	0.78
1:S:177:THR:HG22	1:S:179:VAL:HG22	1.65	0.78
1:L:204:GLU:CD	1:L:204:GLU:H	1.86	0.78
1:S:61:ARG:HG3	1:S:61:ARG:NH1	1.96	0.78
1:R:217:ALA:O	1:R:218:ASN:C	2.22	0.78
1:O:61:ARG:HE	1:O:62:ILE:H	1.32	0.77
1:P:96:HIS:HD2	1:P:98:GLU:H	1.32	0.77
1:O:58:LYS:CE	1:O:59:GLN:OE1	2.30	0.77
1:H:160:MET:O	1:H:163:LYS:CD	2.32	0.77
1:A:48:LEU:O	1:A:52:ILE:HG13	1.85	0.77
1:R:14:CYS:O	1:R:14:CYS:SG	2.43	0.77
1:K:171:PRO:HG3	1:K:213:TYR:CE1	2.19	0.77
1:R:225:LEU:CB	1:R:234:PHE:CE1	2.65	0.77
1:L:171:PRO:HD2	1:L:214:GLY:O	1.85	0.77
1:F:4:ARG:HD3	1:F:207:GLN:O	1.83	0.77
1:E:45:ALA:HA	1:E:48:LEU:CD2	2.15	0.77
1:B:48:LEU:O	1:B:52:ILE:HG13	1.85	0.77
1:E:217:ALA:HB3	1:I:178:GLY:HA3	1.66	0.77
1:H:160:MET:O	1:H:163:LYS:HD3	1.84	0.77
1:K:195:LYS:HG2	1:K:196:TRP:N	1.99	0.77
1:E:210:ARG:HA	1:E:232:ASP:OD2	1.85	0.77
1:K:171:PRO:HG3	1:K:213:TYR:HE1	1.50	0.77
1:Q:7:PHE:CE2	1:Q:210:ARG:HG3	2.20	0.76
1:A:172:VAL:HA	1:A:175:ILE:HD11	1.66	0.76
1:H:126:PHE:CD1	1:H:151:LEU:HD21	2.20	0.76
1:I:4:ARG:CG	1:I:4:ARG:HH11	1.97	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:248:MET:O	1:Q:251:ILE:HG22	1.86	0.76
1:N:223:GLU:HA	1:N:223:GLU:OE1	1.84	0.76
1:D:52:ILE:HD11	1:D:89:LEU:HD21	1.67	0.76
1:O:171:PRO:CG	1:O:215:GLY:HA2	2.15	0.76
1:I:11:ASN:HD21	1:J:76:THR:CG2	1.98	0.76
1:Q:85:GLN:HE22	1:Q:120:LYS:HB3	1.48	0.76
1:N:45:ALA:HA	1:N:48:LEU:HD22	1.68	0.76
1:Q:201:VAL:HG12	1:Q:202:ALA:N	2.01	0.76
1:J:98:GLU:O	1:J:102:ILE:HB	1.86	0.76
1:E:132:LEU:O	1:E:136:LYS:HG3	1.86	0.76
1:N:226:GLY:O	1:N:255:THR:HG21	1.86	0.76
1:I:247:THR:O	1:I:251:ILE:HD13	1.86	0.75
1:L:171:PRO:CG	1:L:174:SER:OG	2.33	0.75
1:O:76:THR:HG23	1:P:65:GLN:HB3	1.67	0.75
1:J:182:THR:HG22	1:J:184:GLU:OE1	1.85	0.75
1:N:191:VAL:HG22	1:N:230:ASN:ND2	2.02	0.75
1:R:225:LEU:C	1:R:234:PHE:HZ	1.89	0.75
1:R:250:ASP:HA	1:R:253:THR:CG2	2.16	0.75
1:J:177:THR:HG22	1:J:179:VAL:H	1.52	0.75
1:G:224:LYS:O	1:G:227:GLN:HG3	1.85	0.75
1:L:109:GLN:O	1:L:113:LYS:HG3	1.86	0.75
1:K:218:ASN:O	1:K:222:ASP:HB2	1.87	0.75
1:I:13:LYS:HG3	1:J:76:THR:HG22	1.68	0.75
1:M:2:PRO:HG2	1:M:207:GLN:CB	2.16	0.75
1:R:52:ILE:HD13	1:R:62:ILE:HD12	1.67	0.75
1:C:217:ALA:O	1:C:218:ASN:CB	2.31	0.74
1:T:236:VAL:HG13	1:T:239:ALA:HB3	1.69	0.74
1:A:67:VAL:O	1:A:113:LYS:HD3	1.87	0.74
1:L:219:GLY:H	1:L:222:ASP:CG	1.91	0.74
1:S:7:PHE:HD1	1:S:8:ILE:N	1.85	0.74
1:B:189:VAL:O	1:B:193:LEU:HG	1.86	0.74
1:M:187:GLU:O	1:M:191:VAL:HG23	1.87	0.74
1:B:213:TYR:CZ	1:B:215:GLY:HA3	2.22	0.74
1:R:106:THR:OG1	1:R:109:GLN:HG3	1.87	0.74
1:P:15:ASN:HD22	1:P:15:ASN:N	1.85	0.74
1:F:98:GLU:O	1:F:102:ILE:HB	1.86	0.74
1:J:69:LEU:HD23	1:J:69:LEU:H	1.51	0.74
1:L:98:GLU:HA	1:L:102:ILE:HD12	1.69	0.74
1:C:21:ILE:HG13	1:C:47:HIS:HB3	1.70	0.74
1:A:206:ALA:O	1:A:209:ILE:HG22	1.86	0.74
1:H:198:ALA:HA	1:H:202:ALA:O	1.88	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:177:THR:CG2	1:P:179:VAL:HG22	2.18	0.74
1:J:24:HIS:O	1:J:28:ILE:HG13	1.87	0.74
1:N:69:LEU:HB3	1:N:113:LYS:HG2	1.70	0.74
1:O:69:LEU:HD23	1:O:70:GLU:HG2	1.70	0.73
1:N:139:ARG:HB3	1:N:139:ARG:HH11	1.52	0.73
1:Q:123:THR:HA	1:Q:164:GLU:HG3	1.68	0.73
1:C:76:THR:HG22	1:D:13:LYS:HD3	1.69	0.73
1:F:175:ILE:HD12	1:F:175:ILE:N	2.02	0.73
1:Q:210:ARG:CD	1:Q:210:ARG:H	2.00	0.73
1:N:217:ALA:HB1	1:N:248:MET:HE1	1.70	0.73
1:R:15:ASN:HD21	1:R:241:LEU:HD11	1.50	0.73
1:O:58:LYS:HG3	1:O:59:GLN:OE1	1.88	0.73
1:R:190:HIS:CE1	1:R:231:ILE:HD13	2.24	0.73
1:N:226:GLY:O	1:N:255:THR:CG2	2.36	0.73
1:S:130:GLU:OE2	1:S:135:ARG:NH2	2.21	0.73
1:I:11:ASN:ND2	1:J:76:THR:HG21	2.03	0.73
1:N:248:MET:O	1:N:251:ILE:HG22	1.89	0.73
1:N:90:LYS:HE3	1:N:91:HIS:CE1	2.24	0.73
1:Q:62:ILE:O	1:Q:89:LEU:CD1	2.37	0.73
1:O:220:SER:O	1:O:221:ASN:HB3	1.88	0.73
1:J:217:ALA:O	1:J:248:MET:HE1	1.89	0.73
1:M:95:GLY:O	1:M:127:CYS:HB2	1.87	0.73
1:Q:4:ARG:HD2	1:Q:232:ASP:OD2	1.87	0.73
1:D:158:SER:OG	1:D:160:MET:HE2	1.89	0.73
1:D:218:ASN:ND2	1:D:220:SER:H	1.86	0.73
1:M:98:GLU:O	1:M:102:ILE:HB	1.88	0.73
1:H:115:LYS:HE2	1:H:119:GLU:OE2	1.88	0.73
1:P:170:GLU:OE2	1:P:235:LEU:HD23	1.89	0.72
1:L:141:MET:HE3	1:L:141:MET:HA	1.71	0.72
1:R:228:CYS:HB2	1:R:231:ILE:CG1	2.19	0.72
1:I:194:ARG:CG	1:I:194:ARG:NH1	2.47	0.72
1:O:143:VAL:O	1:O:147:GLN:HG3	1.88	0.72
1:S:221:ASN:HB3	1:S:224:LYS:HE2	1.69	0.72
1:I:69:LEU:HD23	1:I:70:GLU:HG2	1.71	0.72
1:E:251:ILE:HA	1:E:254:LYS:CE	2.16	0.72
1:H:126:PHE:CE1	1:H:151:LEU:HD21	2.24	0.72
1:P:40:VAL:CG1	1:P:63:ALA:HB2	2.19	0.72
1:C:67:VAL:O	1:C:113:LYS:HD3	1.89	0.72
1:R:175:ILE:O	1:R:175:ILE:HG13	1.88	0.72
1:M:2:PRO:CG	1:M:207:GLN:HB3	2.17	0.72
1:D:247:THR:O	1:D:251:ILE:HD13	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:175:ILE:HG23	1:R:177:THR:OG1	1.90	0.72
1:F:171:PRO:HB3	1:F:173:TRP:HE1	1.54	0.72
1:S:130:GLU:O	1:S:172:VAL:HB	1.90	0.72
1:I:195:LYS:NZ	1:I:199:GLU:OE2	2.23	0.72
1:T:98:GLU:HA	1:T:102:ILE:HD12	1.69	0.72
1:Q:210:ARG:N	1:Q:210:ARG:HD3	2.01	0.72
1:P:195:LYS:HG3	1:P:199:GLU:OE1	1.89	0.72
1:O:145:ILE:HG23	1:O:196:TRP:CD1	2.25	0.72
1:Q:61:ARG:HH11	1:Q:61:ARG:HG3	1.52	0.72
1:B:69:LEU:CD2	1:B:70:GLU:HG2	2.20	0.72
1:E:171:PRO:CD	1:E:215:GLY:CA	2.67	0.71
1:T:63:ALA:HB2	1:T:91:HIS:HB2	1.70	0.71
1:T:85:GLN:HE22	1:T:120:LYS:HB3	1.55	0.71
1:S:97:SER:O	1:S:101:ARG:HB2	1.90	0.71
1:T:242:LYS:HB2	1:T:243:PRO:HD2	1.72	0.71
1:T:195:LYS:O	1:T:199:GLU:HB2	1.90	0.71
1:T:46:VAL:HG23	1:T:47:HIS:CD2	2.25	0.71
1:O:48:LEU:O	1:O:52:ILE:HG13	1.90	0.71
1:Q:183:PRO:HG3	1:Q:225:LEU:CD2	2.21	0.71
1:G:213:TYR:HD2	1:G:234:PHE:CD1	2.09	0.71
1:J:24:HIS:NE2	1:J:240:SER:O	2.21	0.71
1:R:217:ALA:O	1:R:218:ASN:O	2.08	0.71
1:F:24:HIS:O	1:F:28:ILE:HG13	1.91	0.71
1:S:160:MET:H	1:S:160:MET:HE3	1.56	0.71
1:N:68:TYR:HB2	1:N:78:GLU:HB3	1.73	0.71
1:B:213:TYR:CE2	1:B:215:GLY:HA3	2.25	0.71
1:Q:230:ASN:N	1:Q:230:ASN:HD22	1.88	0.71
1:B:217:ALA:HB1	1:B:222:ASP:OD1	1.90	0.71
1:A:137:ALA:O	1:A:138:ASN:HB3	1.90	0.71
1:G:213:TYR:CD2	1:G:234:PHE:CE1	2.79	0.70
1:P:177:THR:HG23	1:P:179:VAL:HG22	1.72	0.70
1:S:130:GLU:HG2	1:S:144:ASN:HD21	1.55	0.70
1:C:90:LYS:HD3	1:C:91:HIS:CE1	2.26	0.70
1:D:244:GLU:O	1:D:248:MET:HG3	1.91	0.70
1:L:242:LYS:HB3	1:L:243:PRO:HD2	1.72	0.70
1:T:115:LYS:CG	1:T:155:LEU:HD21	2.07	0.70
1:S:155:LEU:HG	1:S:161:LEU:HD11	1.71	0.70
1:A:172:VAL:HA	1:A:175:ILE:CG1	2.20	0.70
1:L:200:LYS:CD	1:L:200:LYS:O	2.30	0.70
1:Q:228:CYS:HB3	1:Q:231:ILE:HG13	1.73	0.70
1:C:98:GLU:O	1:C:102:ILE:HB	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:145:ILE:HG12	1:I:196:TRP:CD1	2.26	0.70
1:C:69:LEU:H	1:C:69:LEU:HD22	1.54	0.70
1:R:206:ALA:O	1:R:209:ILE:HG22	1.92	0.70
1:C:115:LYS:O	1:C:119:GLU:HG3	1.90	0.70
1:L:218:ASN:H	1:L:221:ASN:HD21	0.80	0.70
1:I:194:ARG:NH2	1:I:232:ASP:OD2	2.24	0.70
1:R:69:LEU:H	1:R:69:LEU:CD2	2.05	0.70
1:C:218:ASN:OD1	1:C:219:GLY:N	2.23	0.70
1:Q:234:PHE:CE2	1:Q:248:MET:CE	2.75	0.70
1:P:170:GLU:HG2	1:P:214:GLY:HA3	1.73	0.70
1:A:132:LEU:O	1:A:136:LYS:HG3	1.92	0.70
1:F:13:LYS:H	1:F:65:GLN:NE2	1.90	0.70
1:Q:46:VAL:HG23	1:Q:47:HIS:CD2	2.26	0.70
1:S:92:VAL:CG1	1:S:124:VAL:HG22	2.22	0.70
1:Q:171:PRO:HB2	1:Q:174:SER:OG	1.92	0.69
1:M:5:ARG:HH11	1:M:5:ARG:HG2	1.54	0.69
1:O:182:THR:H	1:O:185:GLN:HE21	1.37	0.69
1:Q:183:PRO:HA	1:Q:225:LEU:CD2	2.22	0.69
1:O:197:PHE:CD2	1:O:206:ALA:HA	2.27	0.69
1:M:5:ARG:HH11	1:M:5:ARG:CG	2.05	0.69
1:E:171:PRO:CG	1:E:215:GLY:CA	2.68	0.69
1:Q:197:PHE:HD2	1:Q:206:ALA:HA	1.54	0.69
1:Q:234:PHE:CE2	1:Q:248:MET:HE3	2.26	0.69
1:A:217:ALA:CB	1:A:248:MET:HE3	2.23	0.69
1:I:72:ASN:ND2	1:I:80:SER:OG	2.25	0.69
1:I:187:GLU:OE1	1:I:228:CYS:HB3	1.91	0.69
1:D:130:GLU:OE2	1:D:135:ARG:HB2	1.92	0.69
1:Q:7:PHE:CE2	1:Q:210:ARG:NH1	2.61	0.69
1:G:225:LEU:HB3	1:G:234:PHE:CZ	2.26	0.69
1:F:171:PRO:O	1:F:175:ILE:CD1	2.34	0.69
1:H:100:ARG:NH2	1:H:126:PHE:CZ	2.60	0.69
1:Q:17:SER:O	1:Q:21:ILE:HG12	1.92	0.69
1:I:37:VAL:HG21	1:I:253:THR:OG1	1.93	0.69
1:Q:115:LYS:HE2	1:Q:119:GLU:OE2	1.92	0.69
1:Q:183:PRO:CG	1:Q:225:LEU:HD23	2.22	0.69
1:I:194:ARG:HG3	1:I:194:ARG:NH1	2.07	0.69
1:G:18:LEU:O	1:G:22:LYS:HG3	1.92	0.69
1:B:222:ASP:OD2	1:B:248:MET:HE3	1.93	0.69
1:H:220:SER:O	1:H:221:ASN:HB3	1.90	0.69
1:T:115:LYS:HD3	1:T:155:LEU:HD23	1.71	0.69
1:Q:62:ILE:O	1:Q:89:LEU:HD13	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:63:ALA:HA	1:Q:89:LEU:HD21	1.75	0.69
1:M:187:GLU:OE1	1:M:228:CYS:HB3	1.92	0.69
1:P:98:GLU:HA	1:P:102:ILE:HD12	1.74	0.69
1:A:158:SER:HB3	1:A:161:LEU:HG	1.73	0.69
1:F:182:THR:OG1	1:F:185:GLN:HB2	1.93	0.69
1:K:143:VAL:O	1:K:147:GLN:HG3	1.93	0.69
1:C:218:ASN:OD1	1:C:218:ASN:C	2.29	0.69
1:R:48:LEU:O	1:R:52:ILE:HG12	1.92	0.69
1:A:187:GLU:O	1:A:191:VAL:HG23	1.92	0.69
1:I:4:ARG:HD2	1:I:208:HIS:C	2.14	0.68
1:S:172:VAL:HA	1:S:175:ILE:HG12	1.75	0.68
1:N:134:GLU:O	1:N:139:ARG:HB2	1.92	0.68
1:S:197:PHE:CE2	1:S:209:ILE:HD13	2.27	0.68
1:Q:61:ARG:NH1	1:Q:61:ARG:HG3	2.08	0.68
1:J:216:SER:O	1:J:221:ASN:ND2	2.26	0.68
1:C:77:GLY:HA3	1:D:99:ARG:HH11	1.59	0.68
1:G:69:LEU:HD12	1:G:69:LEU:C	2.13	0.68
1:E:195:LYS:O	1:E:199:GLU:HG2	1.93	0.68
1:A:130:GLU:OE2	1:A:140:THR:HG23	1.94	0.68
1:F:69:LEU:HD23	1:F:70:GLU:HG2	1.74	0.68
1:E:98:GLU:OE2	1:F:74:ALA:HB1	1.93	0.68
1:S:63:ALA:HB2	1:S:91:HIS:HB2	1.75	0.68
1:S:118:LEU:HD13	1:S:161:LEU:HD12	1.74	0.68
1:A:145:ILE:O	1:A:149:GLU:HB2	1.93	0.68
1:L:43:PRO:HD2	1:L:48:LEU:CD1	2.23	0.68
1:K:187:GLU:OE1	1:K:228:CYS:HB3	1.93	0.68
1:H:48:LEU:O	1:H:52:ILE:HG13	1.92	0.68
1:O:198:ALA:HB2	1:O:206:ALA:CB	2.24	0.68
1:R:17:SER:O	1:R:21:ILE:HG12	1.93	0.68
1:I:83:MET:O	1:I:87:MET:HG3	1.94	0.68
1:L:177:THR:HG22	1:L:179:VAL:HG21	1.72	0.68
1:K:171:PRO:CG	1:K:213:TYR:CE1	2.77	0.68
1:K:106:THR:OG1	1:K:109:GLN:HG3	1.94	0.68
1:M:109:GLN:O	1:M:113:LYS:HG3	1.94	0.68
1:S:109:GLN:O	1:S:113:LYS:HG3	1.94	0.68
1:K:247:THR:O	1:K:251:ILE:HD13	1.94	0.68
1:J:111:ALA:HB1	1:J:151:LEU:HA	1.76	0.68
1:S:177:THR:CG2	1:S:179:VAL:HG22	2.24	0.68
1:A:134:GLU:HG2	1:A:143:VAL:HG21	1.76	0.68
1:K:41:ILE:HG23	1:K:60:LEU:HD11	1.76	0.68
1:R:29:ALA:HA	1:R:57:SER:OG	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:84:LEU:HD22	1:I:89:LEU:CD1	2.15	0.67
1:A:218:ASN:ND2	1:A:218:ASN:C	2.48	0.67
1:R:230:ASN:N	1:R:230:ASN:HD22	1.92	0.67
1:I:218:ASN:O	1:I:222:ASP:HB2	1.93	0.67
1:C:130:GLU:OE2	1:C:140:THR:HB	1.94	0.67
1:F:177:THR:O	1:F:177:THR:HG22	1.93	0.67
1:R:156:GLY:O	1:R:159:LYS:HG3	1.94	0.67
1:Q:197:PHE:O	1:Q:201:VAL:CB	2.39	0.67
1:O:221:ASN:HA	1:O:224:LYS:NZ	2.09	0.67
1:A:172:VAL:HA	1:A:175:ILE:HG13	1.74	0.67
1:K:159:LYS:O	1:K:160:MET:CB	2.41	0.67
1:T:69:LEU:HB3	1:T:113:LYS:HG2	1.76	0.67
1:I:4:ARG:HB2	1:I:4:ARG:CZ	2.25	0.67
1:R:194:ARG:HH11	1:R:209:ILE:HG23	1.60	0.67
1:O:171:PRO:CG	1:O:215:GLY:CA	2.73	0.67
1:K:227:GLN:O	1:K:228:CYS:C	2.33	0.67
1:D:109:GLN:O	1:D:113:LYS:HG3	1.95	0.67
1:A:24:HIS:O	1:A:28:ILE:HG13	1.95	0.67
1:K:81:VAL:HG13	1:K:122:MET:SD	2.33	0.67
1:R:194:ARG:HH11	1:R:209:ILE:CG2	2.06	0.67
1:S:65:GLN:O	1:S:93:ILE:HB	1.95	0.67
1:A:218:ASN:HD21	1:A:221:ASN:H	1.43	0.67
1:R:8:ILE:HG22	1:R:39:VAL:HA	1.75	0.67
1:S:171:PRO:HA	1:S:173:TRP:HE1	1.59	0.67
1:M:195:LYS:O	1:M:199:GLU:HG3	1.95	0.67
1:G:130:GLU:OE2	1:G:135:ARG:HB2	1.95	0.67
1:P:210:ARG:CG	1:P:210:ARG:HH11	1.95	0.67
1:C:11:ASN:ND2	1:C:13:LYS:HG2	2.09	0.67
1:R:34:PRO:HB2	1:R:36:SER:OG	1.94	0.67
1:O:18:LEU:O	1:O:22:LYS:HG3	1.94	0.67
1:R:226:GLY:N	1:R:234:PHE:HZ	1.92	0.67
1:R:71:GLY:CA	1:R:116:ARG:NH2	2.58	0.67
1:G:69:LEU:HD12	1:G:70:GLU:CG	2.25	0.67
1:N:187:GLU:OE2	1:N:229:PRO:HG2	1.95	0.67
1:I:218:ASN:HD21	1:I:220:SER:HB3	1.59	0.67
1:N:190:HIS:CE1	1:N:211:ILE:HG22	2.29	0.67
1:Q:183:PRO:CA	1:Q:225:LEU:CD2	2.73	0.66
1:R:12:PHE:O	1:R:13:LYS:HB2	1.95	0.66
1:Q:172:VAL:O	1:Q:175:ILE:HG22	1.95	0.66
1:B:182:THR:OG1	1:B:185:GLN:HG3	1.96	0.66
1:E:115:LYS:HG2	1:E:155:LEU:HD23	1.75	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:7:PHE:CD2	1:Q:210:ARG:HG3	2.30	0.66
1:Q:177:THR:CG2	1:Q:177:THR:O	2.43	0.66
1:R:114:ALA:O	1:R:118:LEU:HD13	1.95	0.66
1:R:118:LEU:HD23	1:R:161:LEU:HB3	1.76	0.66
1:G:72:ASN:HA	1:H:14:CYS:O	1.95	0.66
1:H:21:ILE:O	1:H:25:VAL:HG23	1.94	0.66
1:H:218:ASN:OD1	1:H:219:GLY:N	2.29	0.66
1:S:67:VAL:O	1:S:113:LYS:HD3	1.94	0.66
1:T:213:TYR:HB2	1:T:231:ILE:HD13	1.76	0.66
1:H:155:LEU:HD12	1:H:162:TRP:NE1	2.10	0.66
1:L:97:SER:OG	1:L:175:ILE:CD1	2.43	0.66
1:R:227:GLN:HA	1:R:227:GLN:HE21	1.59	0.66
1:N:145:ILE:HG23	1:N:196:TRP:CD1	2.30	0.66
1:L:118:LEU:HD13	1:L:161:LEU:O	1.96	0.66
1:N:4:ARG:HD3	1:N:207:GLN:O	1.95	0.66
1:Q:13:LYS:HD3	1:R:74:ALA:HA	1.78	0.66
1:O:223:GLU:O	1:O:227:GLN:HG3	1.95	0.66
1:H:126:PHE:CG	1:H:151:LEU:HD21	2.30	0.66
1:K:4:ARG:HG2	1:K:208:HIS:HA	1.78	0.66
1:L:90:LYS:HE3	1:L:91:HIS:CE1	2.31	0.66
1:Q:225:LEU:O	1:Q:228:CYS:HB2	1.95	0.66
1:R:109:GLN:O	1:R:113:LYS:HG3	1.96	0.66
1:A:138:ASN:O	1:A:138:ASN:ND2	2.29	0.66
1:D:108:GLU:O	1:D:112:LYS:HG3	1.95	0.66
1:P:128:VAL:HG12	1:P:147:GLN:HB2	1.76	0.66
1:A:137:ALA:O	1:A:138:ASN:CB	2.41	0.66
1:M:170:GLU:HB2	1:M:175:ILE:HD11	1.78	0.66
1:K:218:ASN:ND2	1:K:219:GLY:N	2.43	0.66
1:P:98:GLU:O	1:P:102:ILE:HB	1.95	0.66
1:B:18:LEU:O	1:B:22:LYS:HG3	1.96	0.66
1:I:244:GLU:O	1:I:248:MET:HG3	1.94	0.66
1:G:64:ALA:O	1:G:93:ILE:HG23	1.96	0.65
1:F:116:ARG:O	1:F:120:LYS:HG3	1.96	0.65
1:I:74:ALA:HB1	1:J:98:GLU:OE2	1.96	0.65
1:K:132:LEU:O	1:K:136:LYS:HG3	1.97	0.65
1:G:9:GLY:HA2	1:G:40:VAL:O	1.96	0.65
1:Q:165:VAL:O	1:Q:210:ARG:NE	2.28	0.65
1:L:220:SER:OG	1:L:221:ASN:N	2.28	0.65
1:T:236:VAL:CG1	1:T:239:ALA:HB3	2.26	0.65
1:A:160:MET:H	1:A:160:MET:HE3	1.61	0.65
1:L:177:THR:CG2	1:L:179:VAL:HG21	2.24	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:69:LEU:H	1:T:69:LEU:HD23	1.62	0.65
1:R:68:TYR:CD1	1:R:78:GLU:HG3	2.31	0.65
1:N:67:VAL:O	1:N:113:LYS:HD3	1.97	0.65
1:K:109:GLN:O	1:K:113:LYS:HG3	1.97	0.65
1:R:71:GLY:HA2	1:R:116:ARG:NH2	2.12	0.65
1:H:221:ASN:ND2	1:H:221:ASN:O	2.30	0.65
1:S:115:LYS:O	1:S:119:GLU:HG3	1.97	0.65
1:L:130:GLU:O	1:L:172:VAL:HB	1.97	0.65
1:A:84:LEU:HD22	1:A:89:LEU:HD12	1.76	0.65
1:G:17:SER:O	1:G:21:ILE:HG12	1.97	0.65
1:L:40:VAL:CG1	1:L:63:ALA:HB2	2.27	0.65
1:I:4:ARG:HD2	1:I:208:HIS:CA	2.27	0.65
1:I:83:MET:HG2	1:J:47:HIS:CE1	2.32	0.65
1:N:209:ILE:HG23	1:N:211:ILE:HD11	1.79	0.65
1:L:155:LEU:HD12	1:L:162:TRP:CE2	2.32	0.65
1:D:171:PRO:HD2	1:D:214:GLY:O	1.97	0.65
1:L:138:ASN:O	1:L:138:ASN:ND2	2.30	0.65
1:P:14:CYS:O	1:P:15:ASN:ND2	2.30	0.65
1:P:48:LEU:O	1:P:52:ILE:HG13	1.96	0.65
1:O:137:ALA:O	1:O:138:ASN:HB2	1.96	0.65
1:T:206:ALA:O	1:T:209:ILE:HG22	1.97	0.65
1:A:139:ARG:NH1	1:A:142:GLU:OE2	2.30	0.64
1:T:25:VAL:HA	1:T:28:ILE:HG13	1.78	0.64
1:E:155:LEU:HD12	1:E:162:TRP:CE2	2.32	0.64
1:L:134:GLU:O	1:L:139:ARG:N	2.30	0.64
1:S:239:ALA:O	1:S:245:PHE:HB2	1.97	0.64
1:A:217:ALA:HB1	1:A:248:MET:CE	2.27	0.64
1:H:99:ARG:HA	1:H:103:MET:HB2	1.80	0.64
1:Q:158:SER:HB2	1:Q:161:LEU:HD12	1.79	0.64
1:Q:143:VAL:O	1:Q:147:GLN:HG3	1.98	0.64
1:N:14:CYS:O	1:N:15:ASN:ND2	2.30	0.64
1:M:242:LYS:HB3	1:M:243:PRO:HD2	1.79	0.64
1:P:148:LEU:HB3	1:P:196:TRP:CH2	2.33	0.64
1:I:233:GLY:HA2	1:I:252:LEU:CD1	2.28	0.64
1:J:137:ALA:O	1:J:138:ASN:CB	2.43	0.64
1:L:4:ARG:HD2	1:L:207:GLN:O	1.98	0.64
1:M:13:LYS:H	1:M:65:GLN:NE2	1.96	0.64
1:Q:198:ALA:HB2	1:Q:206:ALA:CB	2.27	0.64
1:Q:132:LEU:HG	1:Q:136:LYS:HE2	1.80	0.64
1:L:251:ILE:HD13	1:L:254:LYS:NZ	2.13	0.63
1:F:145:ILE:HG23	1:F:196:TRP:NE1	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:6:PRO:HB2	1:H:37:VAL:HG13	1.80	0.63
1:Q:239:ALA:O	1:Q:245:PHE:HB2	1.98	0.63
1:L:222:ASP:OD2	1:L:248:MET:HE3	1.98	0.63
1:S:39:VAL:HG12	1:S:60:LEU:HD12	1.79	0.63
1:L:137:ALA:O	1:L:138:ASN:HB3	1.98	0.63
1:Q:244:GLU:O	1:Q:247:THR:HB	1.98	0.63
1:G:65:GLN:O	1:G:93:ILE:HG12	1.98	0.63
1:P:148:LEU:HB3	1:P:196:TRP:CZ3	2.34	0.63
1:S:43:PRO:HG2	1:S:48:LEU:HD12	1.81	0.63
1:S:131:THR:OG1	1:S:134:GLU:HG3	1.98	0.63
1:D:155:LEU:HD12	1:D:162:TRP:NE1	2.14	0.63
1:S:8:ILE:HD11	1:S:245:PHE:CZ	2.33	0.63
1:K:194:ARG:HD3	1:K:206:ALA:O	1.98	0.63
1:B:244:GLU:O	1:B:248:MET:HG3	1.99	0.63
1:L:48:LEU:O	1:L:52:ILE:HG13	1.98	0.63
1:P:69:LEU:HD23	1:P:70:GLU:HG2	1.80	0.63
1:N:137:ALA:HB3	1:N:139:ARG:HG3	1.80	0.63
1:T:98:GLU:O	1:T:102:ILE:HB	1.99	0.63
1:H:220:SER:O	1:H:221:ASN:CB	2.46	0.63
1:S:173:TRP:CD1	1:S:173:TRP:N	2.56	0.63
1:M:171:PRO:HG2	1:M:174:SER:HB2	1.80	0.63
1:T:34:PRO:HG2	1:T:253:THR:OG1	1.98	0.63
1:J:127:CYS:HB3	1:J:170:GLU:OE2	1.98	0.63
1:B:175:ILE:O	1:O:176:GLY:N	2.32	0.63
1:L:182:THR:OG1	1:L:185:GLN:HG3	1.99	0.63
1:G:67:VAL:O	1:G:113:LYS:HD3	1.99	0.63
1:D:18:LEU:O	1:D:22:LYS:HG3	1.98	0.63
1:L:222:ASP:OD2	1:L:248:MET:CE	2.46	0.62
1:D:57:SER:HB3	1:D:60:LEU:HB3	1.81	0.62
1:L:67:VAL:O	1:L:113:LYS:HD3	1.99	0.62
1:M:106:THR:OG1	1:M:109:GLN:HG3	1.99	0.62
1:P:149:GLU:OE1	1:P:200:LYS:HE3	1.98	0.62
1:O:109:GLN:O	1:O:113:LYS:HG3	1.99	0.62
1:N:171:PRO:HB2	1:N:174:SER:OG	1.98	0.62
1:E:97:SER:HB3	1:E:170:GLU:OE1	1.99	0.62
1:E:190:HIS:CE1	1:E:213:TYR:HB2	2.32	0.62
1:Q:183:PRO:CG	1:Q:225:LEU:CD2	2.77	0.62
1:F:175:ILE:H	1:F:175:ILE:HD12	1.61	0.62
1:I:141:MET:O	1:I:145:ILE:HB	1.99	0.62
1:K:204:GLU:HG2	1:K:205:GLY:N	2.14	0.62
1:R:174:SER:O	1:R:175:ILE:CG2	2.48	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:213:TYR:CE1	1:O:215:GLY:HA3	2.35	0.62
1:Q:222:ASP:OD1	1:Q:223:GLU:N	2.33	0.62
1:N:139:ARG:HH12	1:N:143:VAL:HG22	1.63	0.62
1:F:109:GLN:O	1:F:113:LYS:HG3	1.99	0.62
1:Q:8:ILE:CG2	1:Q:39:VAL:HG22	2.30	0.62
1:E:197:PHE:O	1:E:201:VAL:N	2.33	0.62
1:N:48:LEU:O	1:N:52:ILE:HG13	1.98	0.62
1:D:159:LYS:C	1:D:161:LEU:H	2.03	0.62
1:Q:15:ASN:OD1	1:R:72:ASN:HB3	1.99	0.62
1:T:172:VAL:HA	1:T:175:ILE:HD12	1.80	0.62
1:E:222:ASP:O	1:E:226:GLY:N	2.27	0.62
1:G:213:TYR:HD2	1:G:234:PHE:CE1	2.18	0.62
1:L:218:ASN:HB2	1:L:221:ASN:OD1	1.99	0.62
1:G:9:GLY:O	1:G:235:LEU:HA	2.00	0.62
1:O:83:MET:O	1:O:87:MET:HG3	1.99	0.62
1:R:228:CYS:CB	1:R:231:ILE:CG1	2.77	0.62
1:O:197:PHE:HD2	1:O:206:ALA:HA	1.64	0.62
1:A:139:ARG:NH1	1:A:142:GLU:OE1	2.33	0.62
1:A:144:ASN:O	1:A:148:LEU:HB2	2.00	0.62
1:E:174:SER:O	1:I:176:GLY:HA3	2.00	0.62
1:S:6:PRO:CD	1:S:36:SER:O	2.48	0.61
1:G:69:LEU:O	1:G:116:ARG:HD2	2.00	0.61
1:M:118:LEU:HB3	1:M:161:LEU:HD22	1.82	0.61
1:M:40:VAL:CG1	1:M:63:ALA:HB2	2.29	0.61
1:I:5:ARG:NH2	1:I:35:ASP:O	2.33	0.61
1:S:79:THR:HG21	1:S:84:LEU:HD21	1.82	0.61
1:R:71:GLY:HA2	1:R:116:ARG:HH21	1.65	0.61
1:G:109:GLN:O	1:G:113:LYS:HG3	2.00	0.61
1:L:64:ALA:HB3	1:L:92:VAL:HG23	1.80	0.61
1:G:218:ASN:O	1:G:220:SER:N	2.33	0.61
1:C:178:GLY:CA	1:R:175:ILE:HD13	2.21	0.61
1:E:175:ILE:HA	1:I:176:GLY:CA	2.20	0.61
1:E:171:PRO:CD	1:E:215:GLY:HA3	2.30	0.61
1:O:171:PRO:CD	1:O:214:GLY:O	2.46	0.61
1:G:21:ILE:O	1:G:25:VAL:HG23	2.01	0.61
1:K:98:GLU:O	1:K:102:ILE:HB	2.00	0.61
1:S:246:MET:O	1:S:249:ILE:HB	2.00	0.61
1:J:95:GLY:HA2	1:J:110:SER:OG	2.00	0.61
1:G:213:TYR:CD2	1:G:234:PHE:CD1	2.88	0.61
1:M:228:CYS:HB2	1:M:231:ILE:CD1	2.30	0.61
1:A:145:ILE:HG23	1:A:196:TRP:CD1	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:95:GLY:O	1:P:127:CYS:HB2	2.00	0.61
1:N:109:GLN:O	1:N:113:LYS:HG3	2.00	0.61
1:M:111:ALA:HB1	1:M:151:LEU:HA	1.81	0.61
1:A:31:HIS:NE2	1:A:250:ASP:OD1	2.31	0.61
1:Q:9:GLY:HA2	1:Q:40:VAL:HG13	1.83	0.61
1:R:225:LEU:CB	1:R:234:PHE:HE1	2.03	0.61
1:R:251:ILE:N	1:R:251:ILE:HD13	2.15	0.61
1:O:98:GLU:OE2	1:P:74:ALA:HB1	2.01	0.61
1:A:177:THR:OG1	1:A:179:VAL:HG13	2.00	0.61
1:C:240:SER:HA	1:C:245:PHE:HB2	1.82	0.61
1:Q:89:LEU:CD1	1:Q:91:HIS:H	2.13	0.61
1:Q:197:PHE:CE1	1:Q:209:ILE:HD13	2.35	0.61
1:H:197:PHE:O	1:H:201:VAL:HB	2.00	0.61
1:J:132:LEU:HD22	1:J:177:THR:HG21	1.83	0.61
1:R:15:ASN:OD1	1:R:15:ASN:N	2.34	0.61
1:R:60:LEU:O	1:R:61:ARG:HD2	2.00	0.61
1:R:61:ARG:HH22	1:R:90:LYS:HD3	1.64	0.61
1:C:72:ASN:ND2	1:C:80:SER:OG	2.33	0.61
1:P:14:CYS:C	1:P:15:ASN:ND2	2.38	0.61
1:S:95:GLY:O	1:S:127:CYS:HB2	1.99	0.61
1:R:174:SER:C	1:R:175:ILE:HG22	2.21	0.61
1:Q:243:PRO:HA	1:Q:246:MET:CE	2.31	0.61
1:E:195:LYS:O	1:E:199:GLU:CG	2.49	0.61
1:R:156:GLY:O	1:R:159:LYS:CG	2.49	0.61
1:J:48:LEU:O	1:J:52:ILE:HG13	2.01	0.61
1:A:123:THR:HA	1:A:164:GLU:HG3	1.81	0.61
1:A:21:ILE:O	1:A:25:VAL:HG23	2.01	0.61
1:E:191:VAL:HG22	1:E:230:ASN:ND2	2.16	0.60
1:F:175:ILE:H	1:F:175:ILE:CD1	2.14	0.60
1:Q:166:VAL:HG22	1:Q:210:ARG:CZ	2.31	0.60
1:N:143:VAL:O	1:N:147:GLN:HG3	2.01	0.60
1:S:83:MET:O	1:S:87:MET:HG3	2.01	0.60
1:C:195:LYS:O	1:C:199:GLU:HG3	2.01	0.60
1:C:6:PRO:HB2	1:C:37:VAL:HG13	1.83	0.60
1:D:194:ARG:HD3	1:D:206:ALA:O	2.01	0.60
1:B:4:ARG:HG2	1:B:208:HIS:O	2.02	0.60
1:H:109:GLN:O	1:H:113:LYS:HG3	2.01	0.60
1:G:213:TYR:CD2	1:G:234:PHE:HE1	2.18	0.60
1:B:98:GLU:O	1:B:102:ILE:HB	2.00	0.60
1:I:4:ARG:NH1	1:I:232:ASP:OD1	2.34	0.60
1:K:251:ILE:O	1:K:255:THR:HB	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:92:VAL:HG12	1:S:124:VAL:HG22	1.84	0.60
1:E:98:GLU:HB2	1:F:76:THR:HG22	1.83	0.60
1:P:148:LEU:HG	1:P:196:TRP:CZ3	2.36	0.60
1:T:185:GLN:O	1:T:189:VAL:HG23	2.01	0.60
1:K:155:LEU:HD12	1:K:162:TRP:CE2	2.37	0.60
1:P:195:LYS:O	1:P:199:GLU:HB2	2.02	0.60
1:D:81:VAL:O	1:D:85:GLN:HG3	2.02	0.60
1:O:160:MET:O	1:O:163:LYS:HB2	2.00	0.60
1:R:157:GLU:OE1	1:R:157:GLU:HA	2.01	0.60
1:D:8:ILE:HB	1:D:252:LEU:HD22	1.83	0.60
1:C:76:THR:N	1:D:98:GLU:OE1	2.33	0.60
1:I:4:ARG:HD2	1:I:208:HIS:HA	1.83	0.60
1:I:4:ARG:CB	1:I:4:ARG:NH1	2.64	0.60
1:Q:201:VAL:HG12	1:Q:202:ALA:H	1.65	0.60
1:A:218:ASN:ND2	1:A:220:SER:N	2.50	0.60
1:J:130:GLU:OE2	1:J:173:TRP:CD1	2.54	0.60
1:R:225:LEU:HB3	1:R:234:PHE:CZ	2.35	0.60
1:S:7:PHE:O	1:S:233:GLY:HA3	2.00	0.60
1:R:183:PRO:HB2	1:R:224:LYS:HE2	1.84	0.60
1:D:218:ASN:C	1:D:218:ASN:HD22	2.05	0.60
1:T:243:PRO:HA	1:T:246:MET:CE	2.32	0.60
1:N:4:ARG:HE	1:N:232:ASP:CG	2.05	0.60
1:O:164:GLU:OE1	1:O:164:GLU:HA	2.02	0.60
1:T:11:ASN:ND2	1:T:13:LYS:HG3	2.16	0.60
1:L:236:VAL:HG11	1:L:239:ALA:HB3	1.82	0.60
1:J:123:THR:HG23	1:J:164:GLU:O	2.02	0.60
1:B:155:LEU:HD12	1:B:162:TRP:NE1	2.16	0.60
1:Q:92:VAL:HG12	1:Q:124:VAL:HG22	1.84	0.60
1:T:157:GLU:OE1	1:T:157:GLU:HA	2.00	0.60
1:J:244:GLU:N	1:J:244:GLU:OE1	2.28	0.60
1:R:227:GLN:HA	1:R:227:GLN:NE2	2.15	0.60
1:T:250:ASP:O	1:T:253:THR:HB	2.02	0.60
1:K:151:LEU:O	1:K:155:LEU:HG	2.01	0.60
1:A:83:MET:O	1:A:87:MET:HG3	2.02	0.60
1:F:174:SER:HB2	1:F:179:VAL:HG12	1.82	0.59
1:G:97:SER:CB	1:G:170:GLU:OE1	2.45	0.59
1:K:197:PHE:CD1	1:K:206:ALA:HA	2.37	0.59
1:I:98:GLU:OE1	1:J:76:THR:HG23	2.02	0.59
1:N:199:GLU:C	1:N:200:LYS:HD2	2.22	0.59
1:S:21:ILE:O	1:S:25:VAL:HG23	2.02	0.59
1:C:111:ALA:HB1	1:C:151:LEU:HA	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:203:ALA:HB3	1:L:204:GLU:OE2	2.03	0.59
1:O:137:ALA:O	1:O:138:ASN:CB	2.49	0.59
1:Q:7:PHE:CE1	1:Q:38:ASP:CG	2.76	0.59
1:I:11:ASN:ND2	1:J:76:THR:CG2	2.63	0.59
1:O:162:TRP:CH2	1:O:196:TRP:HH2	2.21	0.59
1:R:82:GLU:H	1:R:82:GLU:CD	2.06	0.59
1:E:171:PRO:HB2	1:E:174:SER:OG	2.01	0.59
1:H:162:TRP:CE3	1:H:197:PHE:HE2	2.20	0.59
1:E:219:GLY:O	1:E:220:SER:CB	2.50	0.59
1:J:21:ILE:O	1:J:25:VAL:HG23	2.01	0.59
1:Q:69:LEU:O	1:Q:116:ARG:HD2	2.02	0.59
1:I:78:GLU:OE1	1:I:78:GLU:HA	2.02	0.59
1:L:204:GLU:N	1:L:204:GLU:CD	2.55	0.59
1:Q:39:VAL:HG12	1:Q:60:LEU:HD12	1.84	0.59
1:F:155:LEU:HD12	1:F:162:TRP:NE1	2.16	0.59
1:H:141:MET:O	1:H:145:ILE:HG12	2.02	0.59
1:S:151:LEU:O	1:S:155:LEU:HD13	2.03	0.59
1:R:149:GLU:HG2	1:R:196:TRP:HZ2	1.68	0.59
1:C:171:PRO:HD2	1:C:214:GLY:O	2.02	0.59
1:B:97:SER:O	1:B:101:ARG:HB2	2.03	0.59
1:F:218:ASN:O	1:F:221:ASN:OD1	2.20	0.59
1:F:13:LYS:N	1:F:65:GLN:HE22	2.01	0.59
1:I:250:ASP:O	1:I:254:LYS:HD3	2.03	0.59
1:L:236:VAL:CG1	1:L:239:ALA:HB3	2.33	0.59
1:M:244:GLU:O	1:M:247:THR:HB	2.03	0.59
1:O:222:ASP:OD1	1:O:225:LEU:HD12	2.03	0.59
1:K:222:ASP:OD1	1:K:234:PHE:CZ	2.55	0.59
1:R:250:ASP:HA	1:R:253:THR:HG22	1.85	0.59
1:M:7:PHE:HB2	1:M:210:ARG:HH11	1.68	0.59
1:A:143:VAL:O	1:A:147:GLN:HG3	2.03	0.59
1:R:239:ALA:O	1:R:245:PHE:HB2	2.03	0.59
1:C:187:GLU:OE1	1:C:228:CYS:HB3	2.02	0.59
1:O:218:ASN:HD22	1:O:220:SER:N	1.90	0.59
1:L:177:THR:CB	1:L:179:VAL:HG23	2.33	0.58
1:E:171:PRO:HG2	1:E:215:GLY:CA	2.10	0.58
1:K:218:ASN:ND2	1:K:219:GLY:H	2.00	0.58
1:Q:173:TRP:CZ3	1:Q:174:SER:HB3	2.37	0.58
1:O:14:CYS:SG	1:P:78:GLU:O	2.53	0.58
1:M:81:VAL:HG13	1:M:122:MET:SD	2.43	0.58
1:E:254:LYS:C	1:E:255:THR:OG1	2.36	0.58
1:K:165:VAL:O	1:K:209:ILE:CD1	2.49	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:195:LYS:O	1:K:199:GLU:HG3	2.03	0.58
1:N:21:ILE:O	1:N:25:VAL:HG23	2.02	0.58
1:E:171:PRO:HD2	1:E:214:GLY:O	2.03	0.58
1:P:221:ASN:OD1	1:P:222:ASP:N	2.36	0.58
1:R:228:CYS:SG	1:R:231:ILE:HG13	2.43	0.58
1:Q:173:TRP:CE3	1:Q:174:SER:HB3	2.38	0.58
1:M:13:LYS:N	1:M:65:GLN:HE22	2.01	0.58
1:F:196:TRP:O	1:F:200:LYS:HB2	2.03	0.58
1:P:159:LYS:O	1:P:162:TRP:HD1	1.85	0.58
1:C:76:THR:CG2	1:D:98:GLU:CD	2.57	0.58
1:R:174:SER:O	1:R:175:ILE:HG22	2.04	0.58
1:B:97:SER:CB	1:B:170:GLU:OE1	2.51	0.58
1:B:171:PRO:HG3	1:B:215:GLY:HA2	1.83	0.58
1:M:13:LYS:N	1:M:65:GLN:NE2	2.51	0.58
1:D:37:VAL:CG1	1:D:252:LEU:HD21	2.33	0.58
1:L:8:ILE:HB	1:L:252:LEU:HD22	1.85	0.58
1:F:108:GLU:O	1:F:112:LYS:HG3	2.04	0.58
1:S:221:ASN:O	1:S:224:LYS:HG3	2.02	0.58
1:I:130:GLU:OE2	1:I:135:ARG:NE	2.31	0.58
1:K:69:LEU:HD23	1:K:70:GLU:HG2	1.86	0.58
1:G:187:GLU:O	1:G:191:VAL:HG23	2.03	0.58
1:D:218:ASN:C	1:D:218:ASN:ND2	2.57	0.58
1:K:221:ASN:H	1:K:221:ASN:ND2	2.01	0.58
1:F:18:LEU:O	1:F:22:LYS:HG3	2.04	0.58
1:E:141:MET:HA	1:E:141:MET:CE	2.34	0.58
1:E:171:PRO:O	1:E:175:ILE:HG13	2.03	0.58
1:Q:7:PHE:HE2	1:Q:210:ARG:HG3	1.67	0.58
1:A:74:ALA:HB1	1:B:98:GLU:OE2	2.04	0.58
1:K:130:GLU:OE1	1:K:169:TYR:HE1	1.85	0.58
1:Q:183:PRO:HG3	1:Q:225:LEU:HD21	1.86	0.58
1:Q:218:ASN:N	1:Q:221:ASN:OD1	2.36	0.58
1:Q:91:HIS:CD2	1:Q:123:THR:HG21	2.39	0.58
1:M:225:LEU:O	1:M:231:ILE:CD1	2.52	0.58
1:L:18:LEU:O	1:L:22:LYS:HG3	2.04	0.58
1:E:190:HIS:ND1	1:E:211:ILE:HG22	2.17	0.58
1:R:225:LEU:CB	1:R:234:PHE:CZ	2.85	0.58
1:J:11:ASN:HD22	1:J:13:LYS:HG3	1.68	0.58
1:F:13:LYS:N	1:F:65:GLN:NE2	2.52	0.58
1:C:187:GLU:OE2	1:C:229:PRO:HG2	2.04	0.58
1:S:34:PRO:HG2	1:S:253:THR:OG1	2.02	0.58
1:M:194:ARG:HD3	1:M:206:ALA:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:66:ASN:ND2	1:R:99:ARG:NE	2.51	0.57
1:M:83:MET:O	1:M:87:MET:HG3	2.04	0.57
1:O:247:THR:O	1:O:251:ILE:HD13	2.04	0.57
1:S:130:GLU:CD	1:S:140:THR:HG23	2.25	0.57
1:Q:248:MET:HA	1:Q:251:ILE:HG22	1.85	0.57
1:R:28:ILE:HG12	1:R:246:MET:HE3	1.85	0.57
1:O:100:ARG:NH1	1:O:128:VAL:HA	2.19	0.57
1:T:246:MET:HA	1:T:249:ILE:CD1	2.34	0.57
1:P:64:ALA:HB3	1:P:92:VAL:HG23	1.84	0.57
1:I:81:VAL:O	1:I:85:GLN:HG3	2.04	0.57
1:E:128:VAL:HG11	1:E:148:LEU:HD13	1.85	0.57
1:R:66:ASN:ND2	1:R:99:ARG:CD	2.67	0.57
1:R:12:PHE:O	1:R:15:ASN:OD1	2.23	0.57
1:I:57:SER:HB3	1:I:60:LEU:HB3	1.86	0.57
1:R:186:ALA:O	1:R:189:VAL:HG22	2.04	0.57
1:O:139:ARG:HD2	1:O:142:GLU:OE2	2.03	0.57
1:S:75:TRP:HD1	1:T:14:CYS:SG	2.28	0.57
1:H:95:GLY:O	1:H:100:ARG:HG3	2.04	0.57
1:K:195:LYS:CG	1:K:196:TRP:N	2.68	0.57
1:R:15:ASN:ND2	1:R:241:LEU:HD11	2.19	0.57
1:L:251:ILE:HA	1:L:254:LYS:HD2	1.86	0.57
1:O:195:LYS:O	1:O:199:GLU:HG3	2.04	0.57
1:A:7:PHE:O	1:A:233:GLY:HA3	2.05	0.57
1:S:46:VAL:HG23	1:S:47:HIS:CD2	2.38	0.57
1:S:186:ALA:HB2	1:S:213:TYR:CE1	2.40	0.57
1:I:4:ARG:CG	1:I:4:ARG:NH1	2.63	0.57
1:K:251:ILE:HA	1:K:254:LYS:HE3	1.85	0.57
1:J:222:ASP:OD1	1:J:222:ASP:N	2.36	0.57
1:C:135:ARG:HA	1:C:140:THR:HG22	1.87	0.57
1:P:68:TYR:CE2	1:P:70:GLU:HB2	2.39	0.57
1:I:155:LEU:HD12	1:I:162:TRP:CE2	2.39	0.57
1:A:222:ASP:HA	1:A:225:LEU:HB2	1.87	0.57
1:J:182:THR:CG2	1:J:184:GLU:OE1	2.53	0.57
1:N:130:GLU:O	1:N:130:GLU:HG2	2.04	0.57
1:B:5:ARG:NH1	1:B:35:ASP:O	2.32	0.57
1:T:137:ALA:O	1:T:138:ASN:HB3	2.04	0.57
1:I:48:LEU:HD23	1:I:89:LEU:HD11	1.86	0.57
1:Q:177:THR:HG23	1:Q:177:THR:O	2.05	0.57
1:S:6:PRO:HG2	1:S:37:VAL:CA	2.29	0.57
1:Q:61:ARG:CG	1:Q:61:ARG:HH11	2.18	0.57
1:Q:62:ILE:O	1:Q:89:LEU:HD11	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:4:ARG:CD	1:I:208:HIS:HA	2.34	0.57
1:R:169:TYR:CE2	1:R:189:VAL:HG21	2.40	0.57
1:K:160:MET:HA	1:K:163:LYS:HG2	1.87	0.57
1:R:69:LEU:HD23	1:R:69:LEU:N	2.18	0.57
1:R:51:ALA:HB1	1:R:62:ILE:HD13	1.86	0.57
1:G:9:GLY:O	1:G:235:LEU:HD12	2.05	0.57
1:Q:7:PHE:HE1	1:Q:38:ASP:CG	2.07	0.56
1:S:151:LEU:HD23	1:S:162:TRP:CH2	2.40	0.56
1:P:130:GLU:HG3	1:P:144:ASN:HD21	1.68	0.56
1:S:25:VAL:HA	1:S:28:ILE:HG13	1.87	0.56
1:I:76:THR:HG23	1:J:65:GLN:HB3	1.87	0.56
1:H:126:PHE:CZ	1:H:151:LEU:HD21	2.40	0.56
1:T:239:ALA:O	1:T:245:PHE:HB2	2.05	0.56
1:B:5:ARG:O	1:B:210:ARG:HD2	2.05	0.56
1:I:236:VAL:CG1	1:I:239:ALA:HB3	2.35	0.56
1:E:72:ASN:ND2	1:E:80:SER:OG	2.38	0.56
1:M:105:GLU:HG2	1:M:110:SER:OG	2.04	0.56
1:F:174:SER:OG	1:F:175:ILE:HD12	2.06	0.56
1:I:194:ARG:HD2	1:I:230:ASN:OD1	2.05	0.56
1:R:66:ASN:ND2	1:R:99:ARG:HD2	2.20	0.56
1:D:221:ASN:O	1:D:224:LYS:HG2	2.04	0.56
1:M:98:GLU:HG2	1:N:74:ALA:O	2.05	0.56
1:M:210:ARG:HG3	1:M:232:ASP:CB	2.36	0.56
1:R:116:ARG:O	1:R:119:GLU:OE1	2.22	0.56
1:P:145:ILE:O	1:P:149:GLU:HG2	2.05	0.56
1:C:57:SER:HB3	1:C:60:LEU:HB3	1.88	0.56
1:J:223:GLU:OE2	1:J:254:LYS:HE3	2.05	0.56
1:E:143:VAL:O	1:E:147:GLN:HG3	2.05	0.56
1:Q:18:LEU:O	1:Q:22:LYS:HG3	2.05	0.56
1:F:90:LYS:HD3	1:F:91:HIS:CE1	2.39	0.56
1:Q:114:ALA:O	1:Q:118:LEU:HG	2.05	0.56
1:G:217:ALA:HB1	1:G:248:MET:HE1	1.87	0.56
1:S:31:HIS:CB	1:S:246:MET:HG2	2.36	0.56
1:I:155:LEU:HD12	1:I:162:TRP:NE1	2.20	0.56
1:C:64:ALA:HB3	1:C:92:VAL:HG23	1.88	0.56
1:P:198:ALA:HA	1:P:202:ALA:O	2.06	0.56
1:E:90:LYS:HG3	1:E:90:LYS:O	2.05	0.56
1:J:180:VAL:HG22	1:J:181:ALA:N	2.19	0.56
1:O:220:SER:O	1:O:221:ASN:CB	2.52	0.56
1:S:172:VAL:HA	1:S:175:ILE:CG1	2.34	0.56
1:R:63:ALA:CB	1:R:91:HIS:HB2	2.31	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:131:THR:OG1	1:N:134:GLU:HG3	2.06	0.56
1:P:145:ILE:HG13	1:P:196:TRP:CD1	2.41	0.56
1:M:222:ASP:OD1	1:M:223:GLU:N	2.38	0.56
1:C:95:GLY:HA2	1:C:110:SER:OG	2.05	0.56
1:G:189:VAL:O	1:G:193:LEU:HG	2.05	0.56
1:Q:183:PRO:HG3	1:Q:225:LEU:HD23	1.87	0.56
1:R:81:VAL:HG13	1:R:122:MET:SD	2.46	0.56
1:J:114:ALA:O	1:J:118:LEU:HG	2.05	0.56
1:E:95:GLY:C	1:E:127:CYS:HB2	2.26	0.56
1:Q:248:MET:O	1:Q:251:ILE:CG2	2.54	0.56
1:O:69:LEU:H	1:O:69:LEU:HD22	1.69	0.56
1:N:139:ARG:HD2	1:N:142:GLU:OE1	2.03	0.56
1:C:215:GLY:O	1:C:216:SER:C	2.41	0.56
1:I:4:ARG:NH1	1:I:194:ARG:NH2	2.53	0.56
1:D:221:ASN:O	1:D:224:LYS:CG	2.54	0.56
1:O:108:GLU:O	1:O:112:LYS:HB2	2.06	0.56
1:J:191:VAL:HG22	1:J:230:ASN:ND2	2.21	0.56
1:O:148:LEU:HD23	1:O:193:LEU:HD22	1.88	0.56
1:N:15:ASN:N	1:N:15:ASN:ND2	2.50	0.56
1:P:135:ARG:HE	1:P:173:TRP:HZ2	1.52	0.56
1:K:213:TYR:HD2	1:K:234:PHE:HE1	1.53	0.56
1:R:216:SER:O	1:R:217:ALA:HB3	2.06	0.56
1:D:67:VAL:O	1:D:113:LYS:HD3	2.06	0.56
1:Q:21:ILE:O	1:Q:25:VAL:HG23	2.05	0.56
1:K:42:ALA:HB1	1:K:65:GLN:HG3	1.88	0.56
1:T:222:ASP:HA	1:T:225:LEU:HD12	1.88	0.56
1:D:24:HIS:O	1:D:28:ILE:HG13	2.06	0.56
1:C:128:VAL:HG11	1:C:148:LEU:HD13	1.86	0.56
1:L:169:TYR:CE2	1:L:189:VAL:HG21	2.41	0.55
1:C:215:GLY:O	1:C:217:ALA:N	2.39	0.55
1:A:218:ASN:ND2	1:A:221:ASN:H	2.05	0.55
1:T:242:LYS:CB	1:T:243:PRO:HD2	2.35	0.55
1:K:41:ILE:HG12	1:K:62:ILE:HD12	1.87	0.55
1:P:62:ILE:N	1:P:62:ILE:HD12	2.21	0.55
1:R:127:CYS:HB3	1:R:170:GLU:OE2	2.07	0.55
1:F:17:SER:O	1:F:21:ILE:HG12	2.06	0.55
1:T:99:ARG:HA	1:T:103:MET:HB2	1.88	0.55
1:Q:166:VAL:HG22	1:Q:210:ARG:NE	2.21	0.55
1:D:158:SER:OG	1:D:160:MET:CE	2.54	0.55
1:S:91:HIS:HA	1:S:123:THR:O	2.06	0.55
1:J:155:LEU:HD22	1:J:161:LEU:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:197:PHE:HD1	1:P:206:ALA:HB2	1.71	0.55
1:D:40:VAL:HG22	1:D:61:ARG:HB2	1.88	0.55
1:J:90:LYS:HG2	1:J:90:LYS:O	2.04	0.55
1:R:66:ASN:HD22	1:R:99:ARG:CZ	2.19	0.55
1:S:74:ALA:HB1	1:T:98:GLU:OE2	2.06	0.55
1:O:160:MET:HG2	1:O:161:LEU:N	2.21	0.55
1:D:37:VAL:HG11	1:D:252:LEU:CD2	2.37	0.55
1:S:253:THR:HG22	1:S:254:LYS:N	2.20	0.55
1:M:218:ASN:O	1:M:222:ASP:HB3	2.07	0.55
1:F:240:SER:HA	1:F:245:PHE:CD1	2.41	0.55
1:M:74:ALA:HB1	1:N:98:GLU:OE2	2.05	0.55
1:O:65:GLN:HB3	1:P:76:THR:CG2	2.36	0.55
1:J:81:VAL:HG13	1:J:122:MET:SD	2.46	0.55
1:J:187:GLU:OE1	1:J:228:CYS:HB3	2.05	0.55
1:G:225:LEU:O	1:G:228:CYS:HB2	2.05	0.55
1:S:145:ILE:HG23	1:S:196:TRP:CD1	2.42	0.55
1:G:77:GLY:HA3	1:H:99:ARG:HH11	1.70	0.55
1:C:4:ARG:CG	1:C:207:GLN:O	2.53	0.55
1:P:184:GLU:H	1:P:184:GLU:CD	2.10	0.55
1:R:251:ILE:N	1:R:251:ILE:CD1	2.69	0.55
1:A:218:ASN:HD22	1:A:220:SER:N	2.05	0.55
1:L:251:ILE:HD13	1:L:254:LYS:HD2	1.89	0.55
1:E:175:ILE:HG12	1:I:176:GLY:O	2.07	0.55
1:F:174:SER:O	1:F:179:VAL:HB	2.06	0.55
1:G:236:VAL:HG21	1:G:248:MET:SD	2.46	0.55
1:A:218:ASN:ND2	1:A:220:SER:H	2.05	0.55
1:K:213:TYR:CE2	1:K:215:GLY:HA2	2.41	0.55
1:I:215:GLY:O	1:I:216:SER:C	2.45	0.55
1:P:247:THR:O	1:P:251:ILE:HD13	2.07	0.55
1:S:204:GLU:OE1	1:S:208:HIS:HE1	1.89	0.55
1:L:244:GLU:O	1:L:245:PHE:C	2.43	0.55
1:Q:234:PHE:CD2	1:Q:248:MET:HE2	2.40	0.55
1:Q:248:MET:C	1:Q:251:ILE:HG22	2.27	0.55
1:T:81:VAL:O	1:T:85:GLN:HG3	2.05	0.55
1:S:197:PHE:CD1	1:S:206:ALA:HA	2.42	0.55
1:N:226:GLY:C	1:N:255:THR:CG2	2.66	0.55
1:M:141:MET:O	1:M:145:ILE:HB	2.07	0.55
1:G:229:PRO:HB2	1:G:230:ASN:HD22	1.71	0.55
1:F:9:GLY:HA2	1:F:40:VAL:O	2.07	0.55
1:S:55:ASN:OD1	1:S:60:LEU:HD23	2.07	0.55
1:C:98:GLU:OE1	1:D:76:THR:N	2.34	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:37:VAL:HG11	1:I:252:LEU:HD23	1.88	0.55
1:C:2:PRO:HD2	1:C:207:GLN:HG2	1.87	0.55
1:I:132:LEU:O	1:I:136:LYS:HG3	2.06	0.55
1:R:141:MET:HE1	1:R:193:LEU:HD23	1.89	0.55
1:E:198:ALA:HB2	1:E:206:ALA:CB	2.37	0.55
1:R:228:CYS:HB2	1:R:231:ILE:HB	1.89	0.55
1:H:158:SER:HB2	1:H:161:LEU:HG	1.88	0.55
1:C:244:GLU:O	1:C:247:THR:HB	2.07	0.55
1:P:114:ALA:O	1:P:118:LEU:HG	2.07	0.55
1:C:173:TRP:O	1:C:177:THR:HG21	2.07	0.55
1:R:85:GLN:HE22	1:R:120:LYS:HB3	1.71	0.55
1:I:236:VAL:HG11	1:I:239:ALA:HB3	1.89	0.54
1:T:24:HIS:O	1:T:27:ALA:HB3	2.07	0.54
1:Q:236:VAL:HG12	1:Q:240:SER:HB3	1.89	0.54
1:C:33:ILE:HB	1:C:59:GLN:HE21	1.72	0.54
1:O:58:LYS:CG	1:O:59:GLN:OE1	2.55	0.54
1:C:215:GLY:C	1:C:217:ALA:N	2.56	0.54
1:H:197:PHE:CZ	1:H:201:VAL:HG11	2.42	0.54
1:M:5:ARG:HH12	1:M:36:SER:C	2.11	0.54
1:L:37:VAL:CG1	1:L:252:LEU:HD23	2.38	0.54
1:B:95:GLY:C	1:B:127:CYS:HB2	2.28	0.54
1:Q:27:ALA:O	1:Q:30:ALA:HB3	2.07	0.54
1:P:31:HIS:CE1	1:P:246:MET:HB3	2.42	0.54
1:I:67:VAL:O	1:I:113:LYS:HD3	2.07	0.54
1:R:15:ASN:ND2	1:R:241:LEU:CD1	2.70	0.54
1:A:137:ALA:HB3	1:A:139:ARG:HG3	1.90	0.54
1:Q:139:ARG:O	1:Q:143:VAL:HG23	2.07	0.54
1:S:72:ASN:ND2	1:S:80:SER:OG	2.40	0.54
1:E:187:GLU:O	1:E:191:VAL:HG23	2.06	0.54
1:O:98:GLU:O	1:O:102:ILE:HB	2.07	0.54
1:L:244:GLU:O	1:L:247:THR:N	2.40	0.54
1:A:99:ARG:HD2	1:B:76:THR:O	2.08	0.54
1:E:4:ARG:NH2	1:E:229:PRO:O	2.41	0.54
1:D:159:LYS:C	1:D:161:LEU:N	2.61	0.54
1:A:4:ARG:HH22	1:A:230:ASN:HA	1.73	0.54
1:F:40:VAL:HG22	1:F:61:ARG:HB2	1.90	0.54
1:G:137:ALA:HB3	1:G:139:ARG:HG3	1.90	0.54
1:S:5:ARG:HG2	1:S:6:PRO:HD2	1.88	0.54
1:Q:79:THR:CG2	1:Q:84:LEU:HD21	2.36	0.54
1:I:12:PHE:O	1:I:13:LYS:HB2	2.07	0.54
1:B:217:ALA:HB1	1:B:222:ASP:CG	2.28	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:197:PHE:HE2	1:S:209:ILE:HD13	1.72	0.54
1:N:141:MET:O	1:N:145:ILE:CG1	2.56	0.54
1:L:90:LYS:HE3	1:L:91:HIS:HE1	1.73	0.54
1:S:115:LYS:HD2	1:S:154:GLU:O	2.08	0.54
1:T:64:ALA:CB	1:T:84:LEU:HD11	2.38	0.54
1:L:200:LYS:C	1:L:200:LYS:HD2	2.11	0.54
1:Q:83:MET:O	1:Q:87:MET:HG2	2.07	0.54
1:E:169:TYR:CZ	1:E:189:VAL:HG11	2.42	0.54
1:C:47:HIS:CE1	1:D:83:MET:HG2	2.42	0.54
1:A:131:THR:HG22	1:A:132:LEU:N	2.22	0.54
1:D:102:ILE:HD11	1:N:179:VAL:HA	1.88	0.54
1:P:24:HIS:O	1:P:28:ILE:HG13	2.07	0.54
1:Q:7:PHE:CD1	1:Q:38:ASP:CB	2.87	0.54
1:N:226:GLY:HA3	1:N:255:THR:HG21	1.87	0.54
1:D:218:ASN:HD21	1:D:220:SER:H	1.53	0.54
1:Q:175:ILE:O	1:Q:177:THR:HB	2.06	0.54
1:G:93:ILE:HD11	1:G:96:HIS:HB2	1.89	0.54
1:P:162:TRP:HA	1:P:165:VAL:CG2	2.38	0.54
1:O:132:LEU:HD22	1:O:177:THR:HB	1.90	0.54
1:T:44:SER:O	1:T:48:LEU:HD13	2.08	0.54
1:H:144:ASN:HB3	1:H:193:LEU:HD21	1.90	0.54
1:A:108:GLU:OE2	1:A:112:LYS:NZ	2.40	0.54
1:Q:73:GLY:N	1:R:14:CYS:SG	2.81	0.54
1:P:180:VAL:HG22	1:P:181:ALA:N	2.22	0.54
1:P:21:ILE:O	1:P:25:VAL:HG23	2.08	0.54
1:O:6:PRO:HB2	1:O:37:VAL:HG13	1.90	0.54
1:Q:218:ASN:O	1:Q:221:ASN:OD1	2.26	0.54
1:Q:234:PHE:CD2	1:Q:248:MET:HE3	2.41	0.54
1:N:223:GLU:OE1	1:N:251:ILE:HD11	2.08	0.54
1:A:162:TRP:CE3	1:A:197:PHE:HE2	2.26	0.54
1:M:5:ARG:NH2	1:M:35:ASP:O	2.40	0.54
1:M:170:GLU:CB	1:M:175:ILE:HD11	2.38	0.54
1:O:103:MET:CE	1:P:78:GLU:HG3	2.38	0.54
1:P:162:TRP:HA	1:P:165:VAL:HG23	1.90	0.54
1:M:18:LEU:HD23	1:M:47:HIS:HD2	1.72	0.54
1:C:253:THR:HG22	1:C:254:LYS:N	2.23	0.54
1:G:145:ILE:O	1:G:149:GLU:HG2	2.08	0.54
1:F:219:GLY:HA2	1:F:222:ASP:OD2	2.08	0.54
1:S:5:ARG:CG	1:S:6:PRO:HD2	2.37	0.53
1:D:218:ASN:O	1:D:222:ASP:HB3	2.07	0.53
1:A:111:ALA:HB1	1:A:151:LEU:HA	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:243:PRO:O	1:S:246:MET:HE3	2.07	0.53
1:D:6:PRO:HB3	1:D:252:LEU:HD11	1.90	0.53
1:G:123:THR:HA	1:G:164:GLU:HB3	1.89	0.53
1:Q:55:ASN:HD22	1:Q:62:ILE:HD13	1.73	0.53
1:A:4:ARG:HD2	1:A:207:GLN:O	2.08	0.53
1:L:233:GLY:HA2	1:L:252:LEU:HD11	1.91	0.53
1:T:48:LEU:O	1:T:52:ILE:HD12	2.09	0.53
1:H:98:GLU:O	1:H:102:ILE:HB	2.08	0.53
1:S:6:PRO:CG	1:S:37:VAL:HG12	2.38	0.53
1:Q:63:ALA:HB2	1:Q:91:HIS:HB2	1.90	0.53
1:T:245:PHE:HA	1:T:248:MET:HG3	1.91	0.53
1:O:66:ASN:ND2	1:O:67:VAL:H	2.07	0.53
1:K:115:LYS:HG3	1:K:155:LEU:HD23	1.90	0.53
1:E:83:MET:HE1	1:F:14:CYS:HA	1.90	0.53
1:H:24:HIS:O	1:H:28:ILE:HG13	2.09	0.53
1:G:213:TYR:CB	1:G:234:PHE:CE1	2.88	0.53
1:S:224:LYS:HG3	1:S:225:LEU:H	1.73	0.53
1:F:145:ILE:HG23	1:F:196:TRP:CD1	2.44	0.53
1:O:46:VAL:HB	1:P:87:MET:SD	2.48	0.53
1:A:72:ASN:N	1:A:72:ASN:HD22	2.06	0.53
1:J:203:ALA:HB3	1:M:200:LYS:HE3	1.91	0.53
1:R:83:MET:O	1:R:86:ASP:HB3	2.07	0.53
1:E:171:PRO:HG3	1:E:213:TYR:CE1	2.44	0.53
1:S:38:ASP:OD2	1:S:210:ARG:NH2	2.40	0.53
1:S:151:LEU:HD23	1:S:162:TRP:CZ3	2.43	0.53
1:L:69:LEU:CD2	1:L:70:GLU:HG2	2.35	0.53
1:B:144:ASN:HD22	1:B:193:LEU:CD2	2.21	0.53
1:S:83:MET:HG2	1:T:46:VAL:HG21	1.91	0.53
1:Q:31:HIS:O	1:Q:33:ILE:HG13	2.09	0.53
1:Q:92:VAL:CG1	1:Q:124:VAL:HG22	2.38	0.53
1:T:82:GLU:CD	1:T:116:ARG:HH12	2.12	0.53
1:N:84:LEU:O	1:N:89:LEU:HB2	2.09	0.53
1:H:85:GLN:HE22	1:H:120:LYS:HB3	1.74	0.53
1:E:187:GLU:OE1	1:E:228:CYS:HB3	2.09	0.53
1:S:158:SER:HB2	1:S:161:LEU:CD2	2.29	0.53
1:O:182:THR:H	1:O:185:GLN:NE2	2.05	0.53
1:F:67:VAL:O	1:F:113:LYS:HD3	2.09	0.53
1:E:96:HIS:HB3	1:F:76:THR:HG21	1.89	0.53
1:J:251:ILE:HD12	1:J:254:LYS:NZ	2.23	0.53
1:C:4:ARG:HG2	1:C:207:GLN:O	2.07	0.53
1:L:24:HIS:O	1:L:28:ILE:HG13	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:84:LEU:HD22	1:J:89:LEU:HD12	1.90	0.53
1:J:217:ALA:O	1:J:248:MET:CE	2.57	0.53
1:O:197:PHE:HE2	1:O:205:GLY:C	2.12	0.53
1:G:96:HIS:CE1	1:G:98:GLU:HG3	2.44	0.53
1:Q:81:VAL:HG23	1:Q:116:ARG:HH11	1.74	0.53
1:F:95:GLY:O	1:F:127:CYS:HB2	2.09	0.53
1:K:116:ARG:O	1:K:119:GLU:HB2	2.08	0.53
1:M:41:ILE:HG12	1:M:60:LEU:HD11	1.91	0.53
1:P:37:VAL:HG21	1:P:253:THR:OG1	2.09	0.53
1:E:194:ARG:NH1	1:E:211:ILE:HD12	2.24	0.53
1:I:148:LEU:HG	1:I:196:TRP:CZ3	2.43	0.53
1:L:155:LEU:HD22	1:L:161:LEU:HB2	1.91	0.53
1:O:66:ASN:ND2	1:O:67:VAL:N	2.56	0.53
1:C:4:ARG:HD3	1:C:207:GLN:O	2.09	0.53
1:M:18:LEU:O	1:M:22:LYS:HG3	2.07	0.53
1:P:8:ILE:HB	1:P:252:LEU:HD22	1.91	0.53
1:Q:12:PHE:HB2	1:Q:42:ALA:O	2.09	0.53
1:S:2:PRO:HD2	1:S:207:GLN:HB2	1.91	0.53
1:Q:242:LYS:O	1:Q:245:PHE:HB3	2.09	0.53
1:O:139:ARG:CB	1:O:142:GLU:HB3	2.39	0.53
1:L:34:PRO:HG3	1:L:253:THR:OG1	2.08	0.53
1:Q:221:ASN:O	1:Q:225:LEU:HG	2.09	0.53
1:L:174:SER:O	1:L:215:GLY:HA3	2.09	0.53
1:N:255:THR:HG22	1:N:255:THR:O	2.09	0.53
1:E:130:GLU:OE2	1:E:140:THR:HB	2.09	0.53
1:H:187:GLU:OE1	1:H:228:CYS:HB3	2.08	0.53
1:J:69:LEU:HB3	1:J:113:LYS:HG2	1.91	0.53
1:A:160:MET:H	1:A:160:MET:CE	2.22	0.53
1:S:243:PRO:HA	1:S:246:MET:HE1	1.91	0.53
1:K:69:LEU:CD2	1:K:70:GLU:HG2	2.39	0.53
1:S:99:ARG:NH2	1:T:78:GLU:OE2	2.42	0.53
1:S:139:ARG:O	1:S:143:VAL:HG23	2.09	0.53
1:G:5:ARG:HG3	1:G:36:SER:O	2.09	0.53
1:F:236:VAL:CG1	1:F:239:ALA:HB3	2.39	0.53
1:P:131:THR:HG22	1:P:172:VAL:HG11	1.91	0.52
1:A:109:GLN:O	1:A:113:LYS:HG3	2.08	0.52
1:K:187:GLU:O	1:K:191:VAL:HG23	2.09	0.52
1:L:155:LEU:HD12	1:L:162:TRP:NE1	2.23	0.52
1:T:127:CYS:HA	1:T:168:ALA:O	2.09	0.52
1:O:21:ILE:O	1:O:25:VAL:HG23	2.08	0.52
1:Q:99:ARG:HD3	1:R:76:THR:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:242:LYS:HB3	1:R:243:PRO:HD2	1.91	0.52
1:T:115:LYS:HG2	1:T:155:LEU:HG	1.90	0.52
1:L:221:ASN:HD22	1:L:221:ASN:C	2.11	0.52
1:D:176:GLY:HA3	1:N:174:SER:O	2.09	0.52
1:S:241:LEU:HD23	1:S:241:LEU:N	2.24	0.52
1:A:115:LYS:CE	1:A:119:GLU:OE2	2.57	0.52
1:C:76:THR:CG2	1:D:13:LYS:HD3	2.36	0.52
1:T:217:ALA:HB1	1:T:248:MET:HE1	1.91	0.52
1:B:213:TYR:HB2	1:B:231:ILE:HD13	1.91	0.52
1:T:37:VAL:HG11	1:T:252:LEU:HD23	1.91	0.52
1:S:17:SER:O	1:S:21:ILE:HG12	2.09	0.52
1:E:206:ALA:O	1:E:209:ILE:HG22	2.09	0.52
1:O:217:ALA:HB1	1:O:222:ASP:OD1	2.09	0.52
1:I:13:LYS:HA	1:J:76:THR:HG22	1.90	0.52
1:E:178:GLY:HA3	1:I:172:VAL:CG1	2.39	0.52
1:E:69:LEU:HD23	1:E:70:GLU:HG2	1.91	0.52
1:D:180:VAL:HG13	1:D:181:ALA:N	2.24	0.52
1:Q:183:PRO:HA	1:Q:225:LEU:HD22	1.91	0.52
1:S:6:PRO:CG	1:S:37:VAL:HA	2.31	0.52
1:S:185:GLN:HA	1:S:188:GLU:OE1	2.10	0.52
1:R:11:ASN:OD1	1:R:13:LYS:N	2.42	0.52
1:J:56:THR:HG22	1:K:19:ASP:OD1	2.10	0.52
1:E:236:VAL:CG1	1:E:239:ALA:HB3	2.39	0.52
1:P:171:PRO:HB2	1:P:174:SER:OG	2.09	0.52
1:A:131:THR:HG22	1:A:132:LEU:H	1.74	0.52
1:R:81:VAL:HG21	1:R:116:ARG:HG2	1.92	0.52
1:A:90:LYS:HE2	1:A:123:THR:OG1	2.09	0.52
1:A:115:LYS:HE3	1:A:119:GLU:OE2	2.10	0.52
1:F:244:GLU:O	1:F:248:MET:HG3	2.09	0.52
1:S:55:ASN:HB2	1:S:62:ILE:HD11	1.89	0.52
1:S:182:THR:OG1	1:S:185:GLN:HB2	2.10	0.52
1:T:213:TYR:CD2	1:T:225:LEU:HD13	2.45	0.52
1:F:236:VAL:HG11	1:F:239:ALA:HB3	1.91	0.52
1:J:7:PHE:O	1:J:233:GLY:HA3	2.10	0.52
1:A:68:TYR:HD1	1:A:78:GLU:OE1	1.93	0.52
1:E:217:ALA:CB	1:I:178:GLY:HA3	2.38	0.52
1:S:118:LEU:HD13	1:S:161:LEU:CD1	2.39	0.52
1:G:69:LEU:CD1	1:G:69:LEU:C	2.77	0.52
1:I:37:VAL:HG11	1:I:252:LEU:CD2	2.40	0.52
1:R:230:ASN:N	1:R:230:ASN:ND2	2.58	0.52
1:B:4:ARG:HD3	1:B:207:GLN:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:194:ARG:HE	1:P:230:ASN:HD22	1.58	0.52
1:L:12:PHE:HB2	1:L:42:ALA:O	2.08	0.52
1:C:84:LEU:HD22	1:C:89:LEU:HD12	1.90	0.52
1:E:222:ASP:HB2	1:E:251:ILE:HG21	1.91	0.52
1:F:179:VAL:HG12	1:F:180:VAL:N	2.24	0.52
1:Q:7:PHE:HD1	1:Q:38:ASP:CB	2.13	0.52
1:G:69:LEU:HD12	1:G:70:GLU:N	2.24	0.52
1:C:68:TYR:HB2	1:C:78:GLU:HB3	1.92	0.52
1:I:13:LYS:HG2	1:J:74:ALA:HA	1.93	0.52
1:I:69:LEU:HB3	1:I:113:LYS:HG2	1.91	0.52
1:T:243:PRO:HA	1:T:246:MET:HE2	1.92	0.52
1:S:171:PRO:HA	1:S:173:TRP:NE1	2.23	0.52
1:J:11:ASN:HD21	1:J:13:LYS:HG3	1.72	0.51
1:O:61:ARG:NE	1:O:62:ILE:H	2.03	0.51
1:F:155:LEU:HD12	1:F:162:TRP:CE2	2.45	0.51
1:A:13:LYS:N	1:A:65:GLN:NE2	2.58	0.51
1:M:41:ILE:O	1:M:43:PRO:HD3	2.09	0.51
1:G:244:GLU:O	1:G:247:THR:HB	2.10	0.51
1:R:175:ILE:O	1:R:177:THR:HG23	2.10	0.51
1:I:4:ARG:HB2	1:I:4:ARG:NH1	2.24	0.51
1:T:13:LYS:H	1:T:65:GLN:NE2	2.08	0.51
1:F:69:LEU:HB3	1:F:113:LYS:HG2	1.91	0.51
1:J:21:ILE:HG13	1:J:47:HIS:HB3	1.92	0.51
1:N:141:MET:O	1:N:145:ILE:HG13	2.10	0.51
1:H:130:GLU:OE2	1:H:140:THR:HG23	2.10	0.51
1:B:139:ARG:HD2	1:B:142:GLU:OE1	2.10	0.51
1:C:134:GLU:O	1:C:139:ARG:HG3	2.09	0.51
1:G:83:MET:O	1:G:87:MET:HG3	2.10	0.51
1:R:175:ILE:CG2	1:R:177:THR:OG1	2.57	0.51
1:S:61:ARG:HH22	1:S:90:LYS:HB2	1.75	0.51
1:A:139:ARG:NH1	1:A:142:GLU:CD	2.63	0.51
1:E:46:VAL:HB	1:F:87:MET:SD	2.51	0.51
1:A:6:PRO:HB2	1:A:37:VAL:HG22	1.92	0.51
1:G:41:ILE:HG23	1:G:60:LEU:HD11	1.91	0.51
1:R:128:VAL:HG11	1:R:148:LEU:HD13	1.92	0.51
1:S:210:ARG:NH1	1:S:210:ARG:CG	2.55	0.51
1:I:194:ARG:HH12	1:I:211:ILE:HG13	1.74	0.51
1:I:4:ARG:CB	1:I:4:ARG:HH11	2.22	0.51
1:R:15:ASN:HD21	1:R:241:LEU:CD1	2.21	0.51
1:G:71:GLY:O	1:G:75:TRP:NE1	2.44	0.51
1:N:141:MET:HE3	1:N:145:ILE:HD11	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:134:GLU:HG2	1:C:143:VAL:HG21	1.92	0.51
1:A:246:MET:HA	1:A:249:ILE:HD12	1.92	0.51
1:O:58:LYS:CG	1:O:59:GLN:CD	2.66	0.51
1:F:181:ALA:HB3	1:F:213:TYR:OH	2.11	0.51
1:M:228:CYS:CB	1:M:231:ILE:HD12	2.38	0.51
1:R:194:ARG:NH1	1:R:209:ILE:HG23	2.23	0.51
1:S:160:MET:O	1:S:163:LYS:HB3	2.10	0.51
1:M:37:VAL:HG12	1:M:38:ASP:N	2.25	0.51
1:N:199:GLU:O	1:N:200:LYS:HD2	2.11	0.51
1:M:174:SER:HA	1:M:179:VAL:O	2.10	0.51
1:C:24:HIS:NE2	1:C:240:SER:O	2.42	0.51
1:A:239:ALA:HA	1:A:242:LYS:HG2	1.91	0.51
1:A:77:GLY:H	1:B:65:GLN:HE21	1.59	0.51
1:F:134:GLU:OE1	1:F:143:VAL:HG11	2.10	0.51
1:G:213:TYR:CB	1:G:234:PHE:CD1	2.80	0.51
1:T:106:THR:OG1	1:T:109:GLN:HG3	2.11	0.51
1:J:221:ASN:OD1	1:J:222:ASP:N	2.43	0.51
1:S:202:ALA:O	1:S:206:ALA:HB2	2.11	0.51
1:H:145:ILE:HG23	1:H:196:TRP:CD1	2.45	0.51
1:O:139:ARG:HD2	1:O:142:GLU:CD	2.31	0.51
1:B:37:VAL:CG1	1:B:252:LEU:HD23	2.41	0.51
1:P:81:VAL:O	1:P:85:GLN:HG3	2.11	0.51
1:S:112:LYS:O	1:S:116:ARG:HB2	2.11	0.51
1:R:68:TYR:CG	1:R:78:GLU:HG3	2.46	0.51
1:C:24:HIS:O	1:C:28:ILE:HG13	2.10	0.51
1:S:108:GLU:O	1:S:112:LYS:HG3	2.10	0.51
1:B:187:GLU:O	1:B:191:VAL:HG23	2.11	0.51
1:Q:7:PHE:HE2	1:Q:210:ARG:HH11	1.59	0.51
1:P:135:ARG:NE	1:P:173:TRP:CZ2	2.78	0.51
1:A:159:LYS:O	1:A:162:TRP:HB2	2.11	0.51
1:T:158:SER:HB3	1:T:161:LEU:HG	1.93	0.51
1:S:5:ARG:HH22	1:S:35:ASP:C	2.14	0.51
1:E:4:ARG:CD	1:E:207:GLN:O	2.54	0.51
1:K:209:ILE:HD12	1:K:210:ARG:H	1.75	0.51
1:B:171:PRO:HB2	1:B:174:SER:OG	2.10	0.51
1:J:67:VAL:O	1:J:113:LYS:HD3	2.10	0.51
1:A:155:LEU:HD12	1:A:162:TRP:NE1	2.26	0.51
1:K:187:GLU:HB2	1:K:228:CYS:SG	2.51	0.51
1:L:135:ARG:O	1:L:138:ASN:HA	2.11	0.51
1:D:139:ARG:O	1:D:143:VAL:HG23	2.10	0.51
1:Q:197:PHE:HD2	1:Q:206:ALA:CA	2.22	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:76:THR:CG2	1:P:65:GLN:HB3	2.39	0.51
1:Q:175:ILE:O	1:Q:176:GLY:C	2.49	0.51
1:S:31:HIS:HB2	1:S:246:MET:HG2	1.93	0.51
1:C:58:LYS:HB2	1:C:59:GLN:OE1	2.11	0.51
1:M:213:TYR:CE2	1:M:214:GLY:O	2.64	0.51
1:O:184:GLU:CD	1:O:184:GLU:H	2.14	0.51
1:E:190:HIS:CE1	1:E:211:ILE:HG22	2.46	0.50
1:Q:89:LEU:HD12	1:Q:91:HIS:H	1.74	0.50
1:A:172:VAL:CA	1:A:175:ILE:HG13	2.41	0.50
1:R:187:GLU:OE2	1:R:230:ASN:N	2.44	0.50
1:F:128:VAL:HG11	1:F:148:LEU:HD13	1.92	0.50
1:T:187:GLU:OE2	1:T:229:PRO:HG2	2.10	0.50
1:G:150:ALA:O	1:G:154:GLU:HG2	2.11	0.50
1:G:37:VAL:HG12	1:G:38:ASP:N	2.26	0.50
1:L:218:ASN:HB2	1:L:221:ASN:CG	2.31	0.50
1:A:172:VAL:CG1	1:A:175:ILE:HD12	2.37	0.50
1:Q:230:ASN:N	1:Q:230:ASN:ND2	2.58	0.50
1:D:69:LEU:O	1:D:116:ARG:HD2	2.10	0.50
1:B:244:GLU:O	1:B:247:THR:HB	2.11	0.50
1:L:141:MET:CE	1:L:141:MET:HA	2.41	0.50
1:L:137:ALA:O	1:L:138:ASN:CB	2.59	0.50
1:B:2:PRO:HB3	1:B:207:GLN:HG2	1.93	0.50
1:T:108:GLU:OE2	1:T:112:LYS:HE3	2.10	0.50
1:G:82:GLU:OE1	1:G:82:GLU:N	2.44	0.50
1:I:13:LYS:HG3	1:J:76:THR:HG23	1.92	0.50
1:N:222:ASP:O	1:N:223:GLU:C	2.48	0.50
1:T:7:PHE:C	1:T:7:PHE:CD1	2.85	0.50
1:S:173:TRP:HD1	1:S:173:TRP:H	1.49	0.50
1:O:139:ARG:NH1	1:O:142:GLU:OE2	2.44	0.50
1:E:176:GLY:HA3	1:I:132:LEU:HB2	1.93	0.50
1:E:6:PRO:HB2	1:E:37:VAL:HG13	1.92	0.50
1:N:70:GLU:OE1	1:N:70:GLU:HA	2.12	0.50
1:E:190:HIS:HE2	1:E:213:TYR:CB	2.14	0.50
1:R:24:HIS:O	1:R:27:ALA:HB3	2.11	0.50
1:N:196:TRP:O	1:N:200:LYS:HB2	2.11	0.50
1:E:141:MET:HE2	1:E:145:ILE:HD12	1.94	0.50
1:L:180:VAL:HG22	1:L:181:ALA:N	2.26	0.50
1:L:206:ALA:O	1:L:209:ILE:HG22	2.12	0.50
1:E:254:LYS:C	1:E:255:THR:HG1	2.11	0.50
1:O:224:LYS:O	1:O:227:GLN:HB2	2.11	0.50
1:A:138:ASN:HD22	1:A:138:ASN:C	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:243:PRO:HA	1:Q:246:MET:HE2	1.94	0.50
1:D:37:VAL:HG13	1:D:252:LEU:HD21	1.94	0.50
1:J:251:ILE:HD12	1:J:254:LYS:HZ1	1.76	0.50
1:I:4:ARG:NE	1:I:207:GLN:O	2.43	0.50
1:R:91:HIS:CD2	1:R:123:THR:CG2	2.94	0.50
1:K:223:GLU:CG	1:K:254:LYS:HZ1	2.18	0.50
1:T:7:PHE:CD1	1:T:8:ILE:N	2.80	0.50
1:I:141:MET:CE	1:I:192:GLY:HA3	2.42	0.50
1:R:227:GLN:CA	1:R:227:GLN:HE21	2.21	0.50
1:Q:39:VAL:HG12	1:Q:60:LEU:CD1	2.41	0.50
1:K:152:GLY:HA2	1:K:162:TRP:HZ2	1.77	0.50
1:T:64:ALA:HB2	1:T:84:LEU:HD11	1.94	0.50
1:M:18:LEU:HD23	1:M:47:HIS:CD2	2.47	0.50
1:K:174:SER:HA	1:K:179:VAL:O	2.11	0.50
1:I:51:ALA:HB1	1:I:62:ILE:HD12	1.94	0.50
1:P:137:ALA:O	1:P:138:ASN:HB3	2.11	0.50
1:E:194:ARG:CZ	1:E:211:ILE:HD12	2.42	0.50
1:F:21:ILE:HG13	1:F:47:HIS:HB3	1.93	0.50
1:T:84:LEU:HB3	1:T:122:MET:HE1	1.93	0.50
1:H:147:GLN:O	1:H:151:LEU:HD13	2.12	0.50
1:K:218:ASN:H	1:K:221:ASN:HD21	1.59	0.50
1:D:158:SER:HA	1:D:160:MET:HE1	1.94	0.50
1:M:9:GLY:HA2	1:M:40:VAL:O	2.12	0.50
1:M:17:SER:O	1:M:21:ILE:HG12	2.12	0.50
1:Q:166:VAL:HG23	1:Q:210:ARG:NH2	2.27	0.49
1:K:42:ALA:O	1:K:65:GLN:NE2	2.44	0.49
1:E:134:GLU:HB3	1:E:143:VAL:HG21	1.94	0.49
1:E:198:ALA:HB2	1:E:206:ALA:HB2	1.93	0.49
1:F:99:ARG:HA	1:F:103:MET:HB2	1.93	0.49
1:O:58:LYS:CD	1:O:59:GLN:OE1	2.60	0.49
1:H:100:ARG:NH2	1:H:126:PHE:CE2	2.80	0.49
1:K:209:ILE:HD12	1:K:210:ARG:N	2.27	0.49
1:L:251:ILE:HA	1:L:254:LYS:CD	2.42	0.49
1:J:250:ASP:O	1:J:254:LYS:HG2	2.12	0.49
1:I:40:VAL:HG22	1:I:61:ARG:HB2	1.94	0.49
1:P:106:THR:OG1	1:P:109:GLN:HG3	2.12	0.49
1:H:156:GLY:O	1:H:159:LYS:HG2	2.12	0.49
1:C:46:VAL:HB	1:D:87:MET:SD	2.53	0.49
1:K:213:TYR:O	1:K:215:GLY:N	2.36	0.49
1:P:42:ALA:HB1	1:P:65:GLN:HG2	1.93	0.49
1:M:5:ARG:O	1:M:210:ARG:NH1	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:190:HIS:ND1	1:N:211:ILE:HG22	2.28	0.49
1:O:67:VAL:HG22	1:O:68:TYR:H	1.77	0.49
1:Q:33:ILE:HB	1:Q:59:GLN:HE21	1.76	0.49
1:D:197:PHE:HD1	1:D:206:ALA:HB2	1.78	0.49
1:H:167:ILE:HB	1:H:211:ILE:HG23	1.94	0.49
1:K:40:VAL:CG1	1:K:63:ALA:HB2	2.42	0.49
1:I:149:GLU:O	1:I:153:LYS:N	2.42	0.49
1:L:169:TYR:CZ	1:L:189:VAL:HG21	2.47	0.49
1:H:126:PHE:CD2	1:H:151:LEU:HD21	2.47	0.49
1:Q:248:MET:CA	1:Q:251:ILE:HG22	2.41	0.49
1:N:218:ASN:HD22	1:N:221:ASN:HD22	1.61	0.49
1:P:141:MET:O	1:P:145:ILE:HB	2.12	0.49
1:S:75:TRP:HD1	1:T:14:CYS:CB	2.25	0.49
1:A:251:ILE:O	1:A:255:THR:HB	2.12	0.49
1:Q:68:TYR:HB2	1:Q:78:GLU:HB3	1.94	0.49
1:K:83:MET:CE	1:L:44:SER:OG	2.61	0.49
1:K:150:ALA:O	1:K:154:GLU:HG2	2.12	0.49
1:P:172:VAL:HG12	1:P:173:TRP:N	2.27	0.49
1:R:24:HIS:O	1:R:28:ILE:HG13	2.12	0.49
1:N:139:ARG:NH1	1:N:143:VAL:CG2	2.76	0.49
1:P:155:LEU:HD22	1:P:161:LEU:HB2	1.94	0.49
1:S:195:LYS:HD3	1:S:199:GLU:OE2	2.13	0.49
1:T:118:LEU:HD13	1:T:155:LEU:HD11	1.94	0.49
1:S:6:PRO:CG	1:S:36:SER:O	2.60	0.49
1:O:218:ASN:HB3	1:O:220:SER:O	2.12	0.49
1:S:7:PHE:CE1	1:S:40:VAL:CG2	2.95	0.49
1:R:246:MET:HA	1:R:249:ILE:CD1	2.35	0.49
1:J:109:GLN:O	1:J:113:LYS:HG3	2.13	0.49
1:R:36:SER:OG	1:R:37:VAL:HG23	2.12	0.49
1:J:180:VAL:CG2	1:J:181:ALA:N	2.75	0.49
1:H:64:ALA:HB3	1:H:92:VAL:HG23	1.93	0.49
1:L:99:ARG:HA	1:L:103:MET:SD	2.53	0.49
1:L:149:GLU:HA	1:L:149:GLU:OE1	2.12	0.49
1:B:66:ASN:HD22	1:B:67:VAL:H	0.58	0.49
1:F:171:PRO:HG2	1:F:213:TYR:OH	2.11	0.49
1:J:132:LEU:HD22	1:J:177:THR:CG2	2.41	0.49
1:B:128:VAL:HG11	1:B:148:LEU:HD13	1.95	0.49
1:N:98:GLU:O	1:N:102:ILE:HB	2.12	0.49
1:Q:236:VAL:CG1	1:Q:240:SER:N	2.76	0.49
1:P:180:VAL:HG22	1:P:181:ALA:H	1.78	0.49
1:S:2:PRO:HD2	1:S:207:GLN:CB	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:221:ASN:O	1:O:221:ASN:OD1	2.31	0.49
1:D:218:ASN:ND2	1:D:220:SER:N	2.56	0.49
1:D:222:ASP:HA	1:D:225:LEU:HD12	1.94	0.49
1:I:141:MET:HE1	1:I:192:GLY:HA3	1.94	0.49
1:T:182:THR:OG1	1:T:185:GLN:HG3	2.12	0.49
1:T:227:GLN:NE2	1:T:255:THR:HG22	2.28	0.49
1:S:221:ASN:CA	1:S:224:LYS:HE2	2.43	0.49
1:A:132:LEU:HG	1:A:136:LYS:HE3	1.95	0.49
1:Q:31:HIS:HE2	1:Q:250:ASP:CG	2.16	0.49
1:P:55:ASN:HD22	1:P:62:ILE:CD1	2.25	0.49
1:Q:186:ALA:HB2	1:Q:213:TYR:CE1	2.48	0.49
1:B:167:ILE:O	1:B:211:ILE:HA	2.13	0.49
1:M:79:THR:HG21	1:M:84:LEU:HD21	1.95	0.49
1:T:235:LEU:C	1:T:235:LEU:HD23	2.33	0.49
1:M:164:GLU:OE1	1:M:164:GLU:HA	2.13	0.49
1:E:214:GLY:HA3	1:E:235:LEU:O	2.13	0.49
1:R:228:CYS:HB2	1:R:231:ILE:CB	2.43	0.49
1:Q:198:ALA:HB2	1:Q:206:ALA:HB2	1.95	0.49
1:L:218:ASN:CB	1:L:221:ASN:ND2	2.76	0.49
1:S:228:CYS:CB	1:S:231:ILE:HG13	2.43	0.49
1:J:219:GLY:O	1:J:222:ASP:OD1	2.30	0.49
1:L:137:ALA:HB3	1:L:139:ARG:HG3	1.95	0.49
1:M:240:SER:HA	1:M:245:PHE:HB2	1.95	0.49
1:F:132:LEU:O	1:F:136:LYS:HB2	2.13	0.49
1:O:59:GLN:N	1:O:59:GLN:HE21	1.98	0.48
1:Q:5:ARG:NH2	1:Q:35:ASP:O	2.44	0.48
1:Q:85:GLN:NE2	1:Q:120:LYS:HB3	2.20	0.48
1:M:5:ARG:CG	1:M:5:ARG:NH1	2.69	0.48
1:L:21:ILE:O	1:L:25:VAL:HG23	2.12	0.48
1:E:115:LYS:HE3	1:E:119:GLU:OE2	2.12	0.48
1:P:190:HIS:CE1	1:P:231:ILE:HG12	2.48	0.48
1:E:179:VAL:HG13	1:E:179:VAL:O	2.12	0.48
1:E:99:ARG:HG3	1:F:76:THR:HG23	1.93	0.48
1:N:209:ILE:HG23	1:N:211:ILE:CD1	2.43	0.48
1:K:130:GLU:OE1	1:K:169:TYR:CE1	2.66	0.48
1:E:176:GLY:N	1:I:175:ILE:O	2.43	0.48
1:E:116:ARG:NH2	1:E:120:LYS:HZ1	2.12	0.48
1:E:81:VAL:HG11	1:E:120:LYS:HB2	1.94	0.48
1:Q:80:SER:O	1:Q:83:MET:HB2	2.14	0.48
1:I:194:ARG:HH12	1:I:209:ILE:HG23	1.78	0.48
1:P:40:VAL:HG11	1:P:63:ALA:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:145:ILE:O	1:S:149:GLU:HG2	2.13	0.48
1:F:68:TYR:HB2	1:F:78:GLU:HB3	1.96	0.48
1:R:114:ALA:HB3	1:R:151:LEU:HD13	1.94	0.48
1:N:130:GLU:OE1	1:N:140:THR:HG23	2.14	0.48
1:Q:31:HIS:NE2	1:Q:250:ASP:OD1	2.39	0.48
1:O:123:THR:HG23	1:O:164:GLU:O	2.13	0.48
1:M:187:GLU:OE2	1:M:230:ASN:OD1	2.31	0.48
1:N:139:ARG:HH12	1:N:143:VAL:CG2	2.26	0.48
1:K:81:VAL:O	1:K:85:GLN:HG3	2.13	0.48
1:R:236:VAL:CG1	1:R:239:ALA:HB3	2.44	0.48
1:E:141:MET:CE	1:E:145:ILE:HD12	2.43	0.48
1:E:139:ARG:O	1:E:143:VAL:HG23	2.13	0.48
1:H:229:PRO:HG2	1:H:230:ASN:HD22	1.78	0.48
1:T:198:ALA:HA	1:T:202:ALA:O	2.13	0.48
1:D:52:ILE:HA	1:D:62:ILE:HD13	1.95	0.48
1:S:243:PRO:HA	1:S:246:MET:CE	2.42	0.48
1:M:145:ILE:HG13	1:M:196:TRP:CD1	2.48	0.48
1:P:151:LEU:HD12	1:P:151:LEU:O	2.13	0.48
1:A:72:ASN:ND2	1:A:80:SER:OG	2.47	0.48
1:Q:145:ILE:O	1:Q:149:GLU:HG3	2.12	0.48
1:R:20:PHE:CE1	1:R:24:HIS:HB2	2.49	0.48
1:N:90:LYS:HE3	1:N:91:HIS:HE1	1.76	0.48
1:T:244:GLU:O	1:T:247:THR:HB	2.14	0.48
1:L:5:ARG:NH1	1:L:35:ASP:O	2.46	0.48
1:L:79:THR:HG21	1:L:84:LEU:HD21	1.93	0.48
1:R:226:GLY:N	1:R:234:PHE:CZ	2.78	0.48
1:G:236:VAL:HG13	1:G:239:ALA:HB3	1.91	0.48
1:Q:248:MET:HA	1:Q:251:ILE:CG2	2.44	0.48
1:A:250:ASP:O	1:A:254:LYS:HE2	2.12	0.48
1:K:9:GLY:HA2	1:K:40:VAL:O	2.14	0.48
1:J:57:SER:HB3	1:J:60:LEU:HB3	1.95	0.48
1:D:187:GLU:OE1	1:D:228:CYS:HB3	2.14	0.48
1:S:221:ASN:N	1:S:221:ASN:ND2	2.62	0.48
1:S:244:GLU:HG3	1:S:245:PHE:N	2.29	0.48
1:S:196:TRP:CE3	1:S:197:PHE:HA	2.48	0.48
1:O:103:MET:HE2	1:P:78:GLU:HG3	1.95	0.48
1:O:132:LEU:O	1:O:136:LYS:HG3	2.14	0.48
1:G:24:HIS:O	1:G:28:ILE:HG13	2.14	0.48
1:T:145:ILE:O	1:T:149:GLU:HG3	2.14	0.48
1:K:48:LEU:O	1:K:52:ILE:HG13	2.14	0.48
1:K:14:CYS:SG	1:L:80:SER:HB3	2.54	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:246:MET:O	1:K:249:ILE:HB	2.14	0.48
1:E:251:ILE:HD12	1:E:254:LYS:HE3	1.96	0.48
1:E:171:PRO:CD	1:E:215:GLY:HA2	2.34	0.48
1:D:219:GLY:O	1:D:222:ASP:OD1	2.31	0.48
1:A:4:ARG:NH2	1:A:229:PRO:O	2.46	0.48
1:L:118:LEU:HD23	1:L:122:MET:O	2.14	0.48
1:L:251:ILE:HD13	1:L:254:LYS:HZ2	1.76	0.48
1:S:43:PRO:HG2	1:S:48:LEU:CD1	2.43	0.48
1:B:37:VAL:HG12	1:B:38:ASP:N	2.29	0.48
1:O:184:GLU:N	1:O:184:GLU:CD	2.67	0.48
1:K:18:LEU:O	1:K:22:LYS:HG3	2.13	0.48
1:B:168:ALA:HA	1:B:212:ILE:O	2.14	0.48
1:R:64:ALA:CB	1:R:84:LEU:HD11	2.44	0.48
1:R:171:PRO:HD2	1:R:214:GLY:O	2.13	0.48
1:N:32:LYS:HG3	1:N:32:LYS:O	2.14	0.48
1:F:179:VAL:CG1	1:F:180:VAL:N	2.76	0.48
1:Q:197:PHE:CD2	1:Q:206:ALA:CA	2.94	0.48
1:M:2:PRO:HG2	1:M:207:GLN:CG	2.43	0.48
1:S:7:PHE:CE1	1:S:40:VAL:HG21	2.49	0.48
1:S:7:PHE:CD1	1:S:7:PHE:C	2.87	0.48
1:K:171:PRO:HG2	1:K:213:TYR:CE1	2.48	0.48
1:N:139:ARG:HD2	1:N:142:GLU:CD	2.35	0.48
1:D:226:GLY:O	1:D:255:THR:HG21	2.14	0.48
1:T:55:ASN:OD1	1:T:60:LEU:HD23	2.13	0.48
1:I:72:ASN:HD21	1:I:82:GLU:HB2	1.79	0.48
1:R:39:VAL:O	1:R:60:LEU:HD12	2.14	0.48
1:K:24:HIS:O	1:K:28:ILE:HG13	2.14	0.48
1:S:247:THR:O	1:S:251:ILE:HG12	2.14	0.48
1:B:116:ARG:O	1:B:120:LYS:HG3	2.14	0.48
1:O:131:THR:HG23	1:O:134:GLU:OE1	2.13	0.48
1:M:2:PRO:CB	1:M:207:GLN:HB3	2.43	0.47
1:I:4:ARG:HH12	1:I:194:ARG:NH2	2.12	0.47
1:S:188:GLU:HG2	1:S:189:VAL:N	2.28	0.47
1:B:144:ASN:ND2	1:B:193:LEU:HD21	2.29	0.47
1:O:100:ARG:HH12	1:O:128:VAL:HA	1.78	0.47
1:S:12:PHE:HB2	1:S:43:PRO:HA	1.96	0.47
1:S:76:THR:O	1:T:99:ARG:HD2	2.14	0.47
1:D:114:ALA:O	1:D:118:LEU:HG	2.14	0.47
1:N:123:THR:HA	1:N:164:GLU:HB3	1.96	0.47
1:M:69:LEU:HD12	1:M:70:GLU:HG2	1.96	0.47
1:E:190:HIS:CD2	1:E:231:ILE:HG12	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:97:SER:O	1:G:101:ARG:HG2	2.14	0.47
1:M:99:ARG:CA	1:M:103:MET:HB2	2.37	0.47
1:C:68:TYR:HE2	1:C:70:GLU:HG3	1.79	0.47
1:O:66:ASN:HD22	1:O:67:VAL:H	1.60	0.47
1:J:254:LYS:HG3	1:J:255:THR:H	1.79	0.47
1:F:40:VAL:CG1	1:F:63:ALA:HB2	2.44	0.47
1:A:68:TYR:CD1	1:A:78:GLU:HG3	2.49	0.47
1:H:7:PHE:O	1:H:233:GLY:HA3	2.14	0.47
1:L:187:GLU:OE1	1:L:228:CYS:HB3	2.13	0.47
1:R:250:ASP:HA	1:R:253:THR:HG23	1.96	0.47
1:D:190:HIS:CE1	1:D:211:ILE:O	2.67	0.47
1:E:196:TRP:O	1:E:200:LYS:N	2.38	0.47
1:B:99:ARG:HA	1:B:103:MET:HB2	1.97	0.47
1:Q:183:PRO:HB3	1:Q:225:LEU:CD2	2.15	0.47
1:E:251:ILE:CA	1:E:254:LYS:HE3	2.24	0.47
1:H:151:LEU:O	1:H:155:LEU:HG	2.15	0.47
1:F:218:ASN:C	1:F:220:SER:N	2.65	0.47
1:Q:85:GLN:HE22	1:Q:120:LYS:CB	2.24	0.47
1:L:43:PRO:HB2	1:L:47:HIS:HB2	1.97	0.47
1:G:98:GLU:O	1:G:102:ILE:HB	2.14	0.47
1:G:164:GLU:OE1	1:G:164:GLU:HA	2.12	0.47
1:S:4:ARG:HD3	1:S:207:GLN:O	2.14	0.47
1:G:80:SER:OG	1:G:83:MET:HG3	2.14	0.47
1:M:236:VAL:CG1	1:M:239:ALA:HB3	2.45	0.47
1:E:183:PRO:HG2	1:E:224:LYS:CD	2.45	0.47
1:O:41:ILE:HG23	1:O:60:LEU:HD11	1.96	0.47
1:S:6:PRO:HD2	1:S:36:SER:O	2.14	0.47
1:R:225:LEU:C	1:R:234:PHE:CZ	2.80	0.47
1:Q:73:GLY:O	1:R:14:CYS:SG	2.73	0.47
1:I:4:ARG:HH12	1:I:232:ASP:CG	2.17	0.47
1:R:123:THR:HA	1:R:164:GLU:HB3	1.96	0.47
1:D:254:LYS:HG3	1:D:255:THR:N	2.29	0.47
1:I:7:PHE:O	1:I:233:GLY:HA3	2.14	0.47
1:I:37:VAL:CG1	1:I:252:LEU:CD2	2.92	0.47
1:I:83:MET:HG2	1:J:47:HIS:HE1	1.79	0.47
1:P:221:ASN:OD1	1:P:221:ASN:C	2.53	0.47
1:P:222:ASP:OD1	1:P:223:GLU:N	2.48	0.47
1:J:158:SER:HG	1:J:161:LEU:HG	1.80	0.47
1:M:90:LYS:HE3	1:M:123:THR:OG1	2.15	0.47
1:O:174:SER:HA	1:O:179:VAL:O	2.13	0.47
1:O:74:ALA:O	1:P:98:GLU:HG2	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:VAL:HG11	1:A:148:LEU:HD13	1.97	0.47
1:K:67:VAL:O	1:K:113:LYS:HD3	2.14	0.47
1:R:71:GLY:HA3	1:R:116:ARG:NH2	2.29	0.47
1:M:81:VAL:O	1:M:85:GLN:HG3	2.14	0.47
1:Q:216:SER:O	1:Q:221:ASN:ND2	2.46	0.47
1:R:174:SER:C	1:R:175:ILE:CG2	2.83	0.47
1:K:218:ASN:OD1	1:K:244:GLU:OE1	2.32	0.47
1:K:197:PHE:HD1	1:K:206:ALA:HB2	1.80	0.47
1:L:98:GLU:O	1:L:102:ILE:HB	2.15	0.47
1:O:100:ARG:CZ	1:O:127:CYS:O	2.62	0.47
1:R:57:SER:HB2	1:R:60:LEU:HB3	1.97	0.47
1:N:190:HIS:NE2	1:N:213:TYR:HB2	2.30	0.47
1:P:145:ILE:O	1:P:149:GLU:N	2.42	0.47
1:R:85:GLN:HE22	1:R:120:LYS:CB	2.28	0.47
1:T:84:LEU:HD22	1:T:89:LEU:HD12	1.97	0.47
1:A:239:ALA:O	1:A:242:LYS:HG3	2.14	0.47
1:T:132:LEU:O	1:T:136:LYS:HG3	2.15	0.47
1:C:145:ILE:O	1:C:149:GLU:HG2	2.15	0.47
1:E:109:GLN:O	1:E:113:LYS:HG3	2.14	0.47
1:R:117:ALA:HB3	1:R:124:VAL:HG21	1.96	0.47
1:D:132:LEU:O	1:D:136:LYS:HG3	2.15	0.47
1:F:175:ILE:CD1	1:F:175:ILE:N	2.68	0.47
1:R:213:TYR:O	1:R:234:PHE:HA	2.14	0.47
1:L:141:MET:HB3	1:L:141:MET:HE2	1.56	0.47
1:O:198:ALA:CA	1:O:206:ALA:HB2	2.45	0.47
1:Q:115:LYS:HG3	1:Q:155:LEU:HD23	1.96	0.47
1:N:4:ARG:NE	1:N:232:ASP:OD1	2.45	0.47
1:N:100:ARG:NH2	1:N:127:CYS:O	2.45	0.47
1:I:197:PHE:HD2	1:I:206:ALA:HB2	1.80	0.47
1:C:76:THR:O	1:D:99:ARG:HD2	2.15	0.47
1:S:186:ALA:CB	1:S:213:TYR:CE1	2.98	0.47
1:A:222:ASP:O	1:A:226:GLY:N	2.44	0.47
1:R:236:VAL:HG21	1:R:248:MET:SD	2.55	0.47
1:O:11:ASN:OD1	1:O:65:GLN:HG2	2.15	0.47
1:P:37:VAL:HG11	1:P:252:LEU:HD23	1.97	0.47
1:F:134:GLU:OE1	1:F:143:VAL:HG21	2.14	0.47
1:E:116:ARG:CZ	1:E:120:LYS:NZ	2.78	0.47
1:E:173:TRP:O	1:E:177:THR:OG1	2.26	0.47
1:C:48:LEU:O	1:C:52:ILE:HG13	2.14	0.47
1:P:169:TYR:CE2	1:P:189:VAL:HG21	2.49	0.47
1:Q:165:VAL:C	1:Q:210:ARG:HE	2.18	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:187:GLU:OE1	1:O:228:CYS:HB3	2.15	0.47
1:G:69:LEU:CD1	1:G:70:GLU:CG	2.88	0.47
1:H:126:PHE:CE2	1:H:151:LEU:HD21	2.50	0.47
1:N:191:VAL:CG2	1:N:230:ASN:HD22	2.22	0.47
1:K:148:LEU:CD2	1:K:193:LEU:HD22	2.45	0.47
1:J:17:SER:H	1:J:20:PHE:HB3	1.79	0.47
1:N:167:ILE:O	1:N:212:ILE:N	2.41	0.47
1:N:29:ALA:HB1	1:N:57:SER:HB2	1.97	0.47
1:S:61:ARG:CG	1:S:61:ARG:HH11	2.11	0.46
1:D:222:ASP:OD1	1:D:223:GLU:N	2.48	0.46
1:N:222:ASP:O	1:N:225:LEU:N	2.48	0.46
1:C:15:ASN:N	1:D:83:MET:HE1	2.31	0.46
1:I:196:TRP:CD1	1:I:200:LYS:HG3	2.50	0.46
1:A:2:PRO:HG2	1:A:207:GLN:HB3	1.96	0.46
1:D:148:LEU:O	1:D:151:LEU:HB3	2.15	0.46
1:D:151:LEU:O	1:D:155:LEU:HG	2.15	0.46
1:J:254:LYS:HG3	1:J:255:THR:N	2.31	0.46
1:L:240:SER:HA	1:L:245:PHE:HB2	1.97	0.46
1:K:80:SER:HB3	1:L:14:CYS:SG	2.55	0.46
1:G:4:ARG:HD3	1:G:207:GLN:O	2.15	0.46
1:I:4:ARG:HH12	1:I:194:ARG:HH21	1.63	0.46
1:Q:223:GLU:HB2	1:Q:251:ILE:HD11	1.97	0.46
1:P:192:GLY:O	1:P:195:LYS:HB3	2.16	0.46
1:J:251:ILE:HA	1:J:254:LYS:NZ	2.30	0.46
1:C:198:ALA:HA	1:C:203:ALA:HA	1.97	0.46
1:Q:95:GLY:C	1:Q:127:CYS:HB2	2.36	0.46
1:B:184:GLU:N	1:B:184:GLU:OE1	2.48	0.46
1:S:130:GLU:OE2	1:S:169:TYR:OH	2.30	0.46
1:A:197:PHE:HD1	1:A:206:ALA:HB2	1.81	0.46
1:Q:4:ARG:NH2	1:Q:229:PRO:O	2.47	0.46
1:S:196:TRP:O	1:S:200:LYS:HG2	2.15	0.46
1:D:37:VAL:HG11	1:D:252:LEU:HD21	1.96	0.46
1:Q:69:LEU:HD12	1:Q:113:LYS:HG3	1.98	0.46
1:Q:186:ALA:HB1	1:Q:213:TYR:CD1	2.51	0.46
1:E:183:PRO:HG2	1:E:224:LYS:CE	2.45	0.46
1:T:218:ASN:N	1:T:218:ASN:HD22	2.13	0.46
1:O:221:ASN:HA	1:O:224:LYS:HZ1	1.80	0.46
1:Q:71:GLY:O	1:Q:75:TRP:NE1	2.35	0.46
1:B:128:VAL:HG21	1:B:144:ASN:ND2	2.31	0.46
1:K:41:ILE:O	1:K:43:PRO:HD3	2.15	0.46
1:L:155:LEU:HD23	1:L:155:LEU:HA	1.75	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:171:PRO:CD	1:C:214:GLY:O	2.63	0.46
1:F:197:PHE:CZ	1:F:201:VAL:HG11	2.50	0.46
1:N:9:GLY:HA2	1:N:40:VAL:O	2.15	0.46
1:C:18:LEU:HA	1:C:18:LEU:HD23	1.77	0.46
1:Q:201:VAL:CG1	1:Q:202:ALA:H	2.26	0.46
1:H:111:ALA:HB2	1:H:151:LEU:HD12	1.97	0.46
1:I:4:ARG:NH1	1:I:232:ASP:CG	2.69	0.46
1:A:145:ILE:O	1:A:149:GLU:N	2.42	0.46
1:C:177:THR:OG1	1:C:179:VAL:HG13	2.16	0.46
1:N:81:VAL:HG13	1:N:122:MET:SD	2.56	0.46
1:J:99:ARG:HA	1:J:103:MET:HB2	1.96	0.46
1:F:171:PRO:HB2	1:F:174:SER:OG	2.14	0.46
1:O:222:ASP:HA	1:O:225:LEU:HB2	1.96	0.46
1:S:158:SER:CB	1:S:161:LEU:HD23	2.30	0.46
1:C:69:LEU:H	1:C:69:LEU:CD2	2.26	0.46
1:R:2:PRO:HB3	1:R:207:GLN:CG	2.41	0.46
1:D:48:LEU:O	1:D:52:ILE:HG13	2.15	0.46
1:M:98:GLU:HG3	1:M:102:ILE:HD12	1.97	0.46
1:T:243:PRO:HA	1:T:246:MET:HE1	1.98	0.46
1:S:84:LEU:O	1:S:89:LEU:HB2	2.15	0.46
1:G:135:ARG:HB2	1:G:135:ARG:HE	1.55	0.46
1:Q:186:ALA:CB	1:Q:213:TYR:CE1	2.99	0.46
1:K:72:ASN:HA	1:L:14:CYS:O	2.16	0.46
1:I:224:LYS:O	1:I:227:GLN:HB2	2.16	0.46
1:E:11:ASN:OD1	1:E:65:GLN:HG2	2.15	0.46
1:G:114:ALA:HB3	1:G:151:LEU:HD13	1.97	0.46
1:L:184:GLU:CD	1:L:184:GLU:H	2.19	0.46
1:F:135:ARG:HE	1:F:135:ARG:HB2	1.58	0.46
1:K:76:THR:HG22	1:L:98:GLU:HB2	1.98	0.46
1:D:161:LEU:C	1:D:163:LYS:H	2.19	0.46
1:I:218:ASN:O	1:I:222:ASP:CB	2.61	0.46
1:L:251:ILE:O	1:L:254:LYS:HG2	2.16	0.46
1:R:127:CYS:HA	1:R:168:ALA:O	2.16	0.46
1:N:29:ALA:CB	1:N:57:SER:HB2	2.46	0.46
1:T:180:VAL:CG2	1:T:181:ALA:N	2.78	0.46
1:Q:148:LEU:HA	1:Q:148:LEU:HD13	1.73	0.46
1:T:155:LEU:HD13	1:T:161:LEU:HB2	1.96	0.46
1:Q:210:ARG:CD	1:Q:210:ARG:N	2.67	0.46
1:O:213:TYR:CE2	1:O:215:GLY:O	2.69	0.46
1:L:141:MET:CE	1:L:141:MET:CA	2.94	0.46
1:T:63:ALA:CB	1:T:91:HIS:HB2	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:39:VAL:HG12	1:T:60:LEU:HD13	1.97	0.46
1:S:164:GLU:OE1	1:S:164:GLU:HA	2.15	0.46
1:T:213:TYR:O	1:T:234:PHE:HA	2.16	0.46
1:E:90:LYS:HE2	1:E:91:HIS:CE1	2.51	0.46
1:A:72:ASN:H	1:A:72:ASN:HD22	1.63	0.46
1:M:137:ALA:HA	1:P:137:ALA:HA	1.97	0.46
1:O:40:VAL:HG11	1:O:63:ALA:HB2	1.97	0.46
1:R:182:THR:OG1	1:R:185:GLN:HG3	2.15	0.46
1:Q:75:TRP:NE1	1:R:14:CYS:SG	2.82	0.46
1:S:61:ARG:NH2	1:S:90:LYS:HB2	2.31	0.46
1:H:111:ALA:HA	1:H:151:LEU:HG	1.97	0.46
1:N:244:GLU:O	1:N:248:MET:CG	2.64	0.46
1:O:198:ALA:HA	1:O:206:ALA:HB2	1.97	0.46
1:R:161:LEU:C	1:R:163:LYS:N	2.68	0.46
1:F:111:ALA:HB1	1:F:151:LEU:HA	1.96	0.46
1:O:21:ILE:HG13	1:O:47:HIS:HB3	1.98	0.46
1:E:236:VAL:HG11	1:E:239:ALA:HB3	1.97	0.46
1:P:187:GLU:OE1	1:P:228:CYS:HB3	2.15	0.46
1:S:213:TYR:HB2	1:S:231:ILE:HD13	1.98	0.46
1:R:250:ASP:O	1:R:253:THR:HG23	2.16	0.46
1:G:224:LYS:HB3	1:G:224:LYS:HE3	1.33	0.46
1:S:198:ALA:HB2	1:S:206:ALA:CB	2.46	0.46
1:N:140:THR:HG22	1:N:141:MET:N	2.29	0.46
1:L:244:GLU:OE1	1:L:244:GLU:HA	2.16	0.46
1:C:244:GLU:O	1:C:248:MET:HG3	2.16	0.46
1:M:181:ALA:HB3	1:M:213:TYR:OH	2.16	0.46
1:T:187:GLU:OE2	1:T:191:VAL:HG23	2.16	0.46
1:C:196:TRP:NE1	1:C:200:LYS:HG3	2.30	0.46
1:P:134:GLU:CD	1:P:143:VAL:HG21	2.37	0.46
1:J:218:ASN:N	1:J:218:ASN:OD1	2.49	0.46
1:B:109:GLN:O	1:B:113:LYS:HG3	2.16	0.45
1:H:197:PHE:HB3	1:H:206:ALA:HB2	1.99	0.45
1:A:218:ASN:H	1:A:222:ASP:CG	2.18	0.45
1:E:136:LYS:HE2	1:E:136:LYS:HB3	1.79	0.45
1:D:158:SER:CB	1:D:160:MET:HE1	2.46	0.45
1:O:196:TRP:CE3	1:O:197:PHE:N	2.84	0.45
1:G:128:VAL:HG11	1:G:148:LEU:HD13	1.98	0.45
1:S:15:ASN:OD1	1:T:72:ASN:HB3	2.15	0.45
1:P:204:GLU:O	1:P:208:HIS:CE1	2.69	0.45
1:G:76:THR:HG22	1:H:65:GLN:HB3	1.96	0.45
1:T:197:PHE:CD1	1:T:201:VAL:HG21	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:9:GLY:HA2	1:B:40:VAL:O	2.16	0.45
1:N:114:ALA:O	1:N:118:LEU:HG	2.17	0.45
1:T:118:LEU:CD1	1:T:155:LEU:HD11	2.46	0.45
1:K:159:LYS:O	1:K:160:MET:HB3	2.14	0.45
1:Q:251:ILE:HG23	1:Q:252:LEU:N	2.31	0.45
1:K:198:ALA:HB2	1:K:206:ALA:CB	2.46	0.45
1:G:221:ASN:O	1:G:224:LYS:HB2	2.17	0.45
1:M:34:PRO:HB2	1:M:36:SER:OG	2.16	0.45
1:M:34:PRO:HG3	1:M:253:THR:HG21	1.99	0.45
1:J:137:ALA:O	1:J:138:ASN:HB2	2.17	0.45
1:N:72:ASN:ND2	1:N:80:SER:OG	2.50	0.45
1:O:81:VAL:O	1:O:85:GLN:HG3	2.15	0.45
1:O:240:SER:HA	1:O:245:PHE:CD1	2.51	0.45
1:A:81:VAL:O	1:A:85:GLN:HG3	2.16	0.45
1:B:114:ALA:HB2	1:B:126:PHE:CE1	2.51	0.45
1:L:196:TRP:O	1:L:200:LYS:N	2.45	0.45
1:P:5:ARG:NH1	1:P:35:ASP:O	2.43	0.45
1:E:171:PRO:HG3	1:E:213:TYR:HE1	1.80	0.45
1:Q:5:ARG:HA	1:Q:6:PRO:HD2	1.61	0.45
1:N:17:SER:O	1:N:21:ILE:HG12	2.17	0.45
1:P:159:LYS:O	1:P:162:TRP:CD1	2.69	0.45
1:J:158:SER:OG	1:J:161:LEU:HG	2.16	0.45
1:A:13:LYS:HG2	1:B:76:THR:OG1	2.16	0.45
1:P:4:ARG:HD2	1:P:207:GLN:O	2.15	0.45
1:M:24:HIS:O	1:M:28:ILE:HG13	2.15	0.45
1:T:18:LEU:O	1:T:22:LYS:HG3	2.17	0.45
1:G:190:HIS:ND1	1:G:231:ILE:HG12	2.31	0.45
1:F:228:CYS:HA	1:F:229:PRO:HD3	1.83	0.45
1:O:210:ARG:HB2	1:O:210:ARG:HE	1.68	0.45
1:P:164:GLU:OE1	1:P:164:GLU:HA	2.15	0.45
1:Q:218:ASN:N	1:Q:218:ASN:HD22	2.14	0.45
1:E:228:CYS:HB2	1:E:231:ILE:HD12	1.99	0.45
1:K:221:ASN:C	1:K:221:ASN:HD22	2.20	0.45
1:I:233:GLY:HA2	1:I:252:LEU:HD11	1.95	0.45
1:E:151:LEU:O	1:E:155:LEU:HG	2.17	0.45
1:L:37:VAL:HG11	1:L:252:LEU:HD23	1.98	0.45
1:C:71:GLY:O	1:C:75:TRP:NE1	2.49	0.45
1:R:190:HIS:NE2	1:R:231:ILE:HD13	2.31	0.45
1:I:68:TYR:CE2	1:I:70:GLU:HG3	2.51	0.45
1:S:171:PRO:HD3	1:S:214:GLY:O	2.17	0.45
1:L:131:THR:HA	1:L:172:VAL:HB	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:45:ALA:HA	1:T:48:LEU:HD22	1.98	0.45
1:K:83:MET:O	1:K:87:MET:HG3	2.17	0.45
1:S:141:MET:HE1	1:S:193:LEU:HD23	1.99	0.45
1:F:12:PHE:CD1	1:F:12:PHE:N	2.85	0.45
1:G:155:LEU:HD12	1:G:162:TRP:NE1	2.31	0.45
1:I:139:ARG:NH1	1:I:142:GLU:OE1	2.49	0.45
1:J:171:PRO:HB2	1:J:174:SER:OG	2.17	0.45
1:Q:217:ALA:HA	1:Q:221:ASN:HD21	1.80	0.45
1:M:228:CYS:HB2	1:M:231:ILE:CG1	2.46	0.45
1:S:7:PHE:HD1	1:S:7:PHE:C	2.19	0.45
1:S:194:ARG:HD3	1:S:206:ALA:O	2.16	0.45
1:P:45:ALA:HA	1:P:48:LEU:HD22	1.98	0.45
1:Q:12:PHE:HB2	1:Q:43:PRO:HA	1.99	0.45
1:S:2:PRO:CD	1:S:207:GLN:HB2	2.47	0.45
1:P:194:ARG:NE	1:P:230:ASN:HD22	2.14	0.45
1:C:196:TRP:CD1	1:C:200:LYS:HG3	2.52	0.45
1:J:18:LEU:O	1:J:22:LYS:HG3	2.16	0.45
1:K:13:LYS:HD3	1:L:74:ALA:HA	1.99	0.45
1:R:221:ASN:N	1:R:221:ASN:OD1	2.50	0.45
1:D:96:HIS:CE1	1:D:98:GLU:CD	2.90	0.45
1:Q:91:HIS:HA	1:Q:123:THR:O	2.16	0.45
1:Q:46:VAL:CG2	1:Q:47:HIS:CD2	2.98	0.45
1:S:171:PRO:CD	1:S:214:GLY:O	2.64	0.45
1:E:97:SER:CB	1:E:170:GLU:OE1	2.64	0.45
1:M:155:LEU:HD12	1:M:162:TRP:NE1	2.31	0.45
1:B:5:ARG:NH2	1:B:38:ASP:OD1	2.48	0.45
1:Q:74:ALA:HB1	1:R:98:GLU:OE2	2.17	0.45
1:T:184:GLU:OE1	1:T:184:GLU:N	2.49	0.45
1:L:193:LEU:O	1:L:196:TRP:HB3	2.16	0.45
1:Q:72:ASN:ND2	1:Q:80:SER:OG	2.50	0.45
1:Q:75:TRP:HD1	1:R:14:CYS:SG	2.29	0.45
1:M:228:CYS:HA	1:M:229:PRO:HD3	1.82	0.45
1:D:251:ILE:HA	1:D:254:LYS:HG2	1.98	0.45
1:F:177:THR:CG2	1:F:177:THR:O	2.63	0.45
1:L:136:LYS:C	1:L:138:ASN:N	2.69	0.45
1:G:77:GLY:HA3	1:H:99:ARG:NH1	2.31	0.45
1:T:128:VAL:HG11	1:T:148:LEU:HD13	1.99	0.45
1:H:83:MET:O	1:H:87:MET:HG3	2.17	0.45
1:A:36:SER:HB3	1:G:160:MET:CE	2.47	0.45
1:O:97:SER:CB	1:O:170:GLU:OE1	2.64	0.45
1:F:184:GLU:CD	1:F:184:GLU:H	2.20	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:8:ILE:HG22	1:S:252:LEU:CD2	2.47	0.45
1:R:68:TYR:CZ	1:R:69:LEU:HD21	2.52	0.45
1:B:217:ALA:HB1	1:B:222:ASP:OD2	2.17	0.45
1:S:101:ARG:N	1:S:101:ARG:HD3	2.31	0.45
1:S:163:LYS:HG2	1:S:164:GLU:HG2	1.98	0.45
1:S:106:THR:HG23	1:S:109:GLN:CD	2.37	0.45
1:A:160:MET:N	1:A:160:MET:HE3	2.32	0.45
1:S:95:GLY:C	1:S:127:CYS:HB2	2.37	0.45
1:A:91:HIS:CD2	1:A:123:THR:HB	2.52	0.45
1:G:166:VAL:HG13	1:G:210:ARG:HB3	1.98	0.45
1:F:175:ILE:HG12	1:F:215:GLY:HA2	1.98	0.45
1:S:190:HIS:CE1	1:S:213:TYR:HB2	2.52	0.45
1:C:68:TYR:CE2	1:C:70:GLU:HG3	2.52	0.45
1:J:243:PRO:HA	1:J:246:MET:CE	2.46	0.45
1:N:244:GLU:O	1:N:248:MET:HG3	2.17	0.45
1:M:210:ARG:HG3	1:M:232:ASP:OD2	2.16	0.45
1:I:6:PRO:HB2	1:I:37:VAL:HG13	1.98	0.45
1:P:67:VAL:HB	1:P:92:VAL:HG21	1.99	0.45
1:I:9:GLY:HA2	1:I:40:VAL:O	2.16	0.45
1:G:90:LYS:HB3	1:G:91:HIS:CE1	2.52	0.45
1:I:180:VAL:HG23	1:I:181:ALA:N	2.30	0.45
1:Q:4:ARG:HD2	1:Q:232:ASP:CG	2.37	0.44
1:Q:171:PRO:HB2	1:Q:174:SER:HG	1.83	0.44
1:P:200:LYS:HG2	1:P:200:LYS:O	2.17	0.44
1:H:145:ILE:O	1:H:149:GLU:HG2	2.17	0.44
1:D:145:ILE:HG23	1:D:149:GLU:OE2	2.17	0.44
1:S:187:GLU:OE2	1:S:229:PRO:HG2	2.17	0.44
1:H:163:LYS:H	1:H:163:LYS:HG3	1.44	0.44
1:H:111:ALA:HB1	1:H:151:LEU:HA	1.98	0.44
1:R:183:PRO:HG2	1:R:224:LYS:CD	2.40	0.44
1:I:68:TYR:HB2	1:I:78:GLU:HB3	2.00	0.44
1:B:190:HIS:ND1	1:B:231:ILE:HG12	2.32	0.44
1:N:139:ARG:HB3	1:N:139:ARG:NH1	2.24	0.44
1:T:227:GLN:N	1:T:227:GLN:OE1	2.50	0.44
1:N:33:ILE:O	1:N:59:GLN:HG2	2.17	0.44
1:L:58:LYS:HD2	1:L:58:LYS:O	2.16	0.44
1:S:245:PHE:HA	1:S:248:MET:HG3	1.99	0.44
1:I:96:HIS:CE1	1:I:98:GLU:OE1	2.70	0.44
1:T:8:ILE:HB	1:T:252:LEU:HD22	1.98	0.44
1:I:200:LYS:HE2	1:I:200:LYS:HB3	1.55	0.44
1:A:187:GLU:HB2	1:A:228:CYS:SG	2.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:187:GLU:OE1	1:R:187:GLU:HA	2.17	0.44
1:G:11:ASN:OD1	1:G:65:GLN:HG2	2.18	0.44
1:G:9:GLY:C	1:G:235:LEU:HD12	2.37	0.44
1:D:197:PHE:O	1:D:201:VAL:HB	2.17	0.44
1:P:218:ASN:O	1:P:222:ASP:HB3	2.18	0.44
1:O:139:ARG:HB3	1:O:142:GLU:HB3	1.99	0.44
1:O:81:VAL:HG11	1:O:120:LYS:HD3	1.99	0.44
1:C:82:GLU:OE1	1:C:116:ARG:NH1	2.51	0.44
1:H:247:THR:O	1:H:251:ILE:HG13	2.16	0.44
1:K:84:LEU:HD22	1:K:89:LEU:HD12	2.00	0.44
1:N:184:GLU:CD	1:N:184:GLU:H	2.21	0.44
1:N:58:LYS:O	1:N:58:LYS:HG2	2.17	0.44
1:B:201:VAL:O	1:B:202:ALA:HB2	2.17	0.44
1:L:218:ASN:N	1:L:221:ASN:ND2	2.39	0.44
1:R:195:LYS:HB3	1:R:195:LYS:HE3	1.82	0.44
1:T:57:SER:HB3	1:T:60:LEU:HB3	1.99	0.44
1:T:194:ARG:NH1	1:T:206:ALA:O	2.49	0.44
1:O:67:VAL:O	1:O:113:LYS:HD3	2.17	0.44
1:G:4:ARG:HB2	1:G:4:ARG:HE	1.40	0.44
1:P:130:GLU:O	1:P:172:VAL:HB	2.17	0.44
1:I:194:ARG:NH1	1:I:211:ILE:HG13	2.33	0.44
1:D:226:GLY:C	1:D:255:THR:HG21	2.38	0.44
1:M:166:VAL:HG22	1:M:210:ARG:HB3	2.00	0.44
1:O:65:GLN:HB3	1:P:76:THR:HG23	1.99	0.44
1:M:145:ILE:CG1	1:M:196:TRP:CD1	3.01	0.44
1:E:69:LEU:HD12	1:E:112:LYS:CB	2.47	0.44
1:D:140:THR:HG22	1:D:141:MET:N	2.32	0.44
1:P:171:PRO:HD2	1:P:214:GLY:O	2.18	0.44
1:A:140:THR:O	1:A:144:ASN:ND2	2.50	0.44
1:P:149:GLU:OE1	1:P:200:LYS:CE	2.65	0.44
1:D:5:ARG:HA	1:D:6:PRO:HD3	1.86	0.44
1:G:145:ILE:HG23	1:G:196:TRP:NE1	2.32	0.44
1:G:160:MET:H	1:G:160:MET:HG3	1.33	0.44
1:L:140:THR:O	1:L:144:ASN:ND2	2.50	0.44
1:R:222:ASP:OD1	1:R:223:GLU:N	2.50	0.44
1:E:174:SER:O	1:I:176:GLY:CA	2.65	0.44
1:I:190:HIS:CE1	1:I:211:ILE:HG22	2.52	0.44
1:J:173:TRP:HH2	1:J:185:GLN:OE1	2.00	0.44
1:D:106:THR:OG1	1:D:109:GLN:HG3	2.18	0.44
1:A:91:HIS:HA	1:A:123:THR:O	2.17	0.44
1:P:251:ILE:HD12	1:P:251:ILE:N	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:41:ILE:O	1:O:43:PRO:HD3	2.18	0.44
1:E:24:HIS:O	1:E:27:ALA:HB3	2.17	0.44
1:K:242:LYS:HE2	1:K:242:LYS:HB3	1.68	0.44
1:P:177:THR:HG21	1:P:179:VAL:HG22	1.98	0.44
1:K:160:MET:HA	1:K:163:LYS:HZ2	1.83	0.44
1:J:246:MET:HA	1:J:249:ILE:HD12	1.99	0.44
1:E:44:SER:O	1:E:48:LEU:HD22	2.18	0.44
1:J:91:HIS:CD2	1:J:123:THR:HB	2.53	0.44
1:M:83:MET:HE2	1:N:44:SER:HB2	2.00	0.44
1:G:74:ALA:HB1	1:H:98:GLU:OE2	2.17	0.44
1:E:116:ARG:NH1	1:E:120:LYS:HZ3	2.16	0.44
1:L:5:ARG:HE	1:L:38:ASP:CG	2.21	0.44
1:G:28:ILE:HD13	1:G:245:PHE:CD2	2.52	0.44
1:D:172:VAL:HA	1:D:175:ILE:HG12	2.00	0.44
1:P:5:ARG:HE	1:P:38:ASP:CG	2.21	0.44
1:H:94:VAL:HG11	1:H:114:ALA:HB2	2.00	0.44
1:E:45:ALA:HA	1:E:48:LEU:HD21	1.95	0.44
1:B:144:ASN:HD22	1:B:193:LEU:HD21	1.83	0.44
1:J:96:HIS:HA	1:J:127:CYS:HB2	2.00	0.44
1:L:37:VAL:HG13	1:L:252:LEU:HD23	2.00	0.44
1:D:9:GLY:HA2	1:D:40:VAL:O	2.18	0.44
1:C:174:SER:HA	1:C:177:THR:HG1	1.83	0.44
1:A:13:LYS:H	1:A:65:GLN:NE2	2.16	0.44
1:H:148:LEU:HD12	1:H:148:LEU:HA	1.80	0.44
1:O:63:ALA:HB2	1:O:91:HIS:HB2	1.99	0.44
1:A:167:ILE:HB	1:A:211:ILE:HG23	1.99	0.44
1:E:184:GLU:N	1:E:184:GLU:OE1	2.51	0.44
1:Q:70:GLU:HB2	1:Q:75:TRP:CE2	2.53	0.43
1:T:66:ASN:HD21	1:T:113:LYS:NZ	2.16	0.43
1:N:218:ASN:ND2	1:N:221:ASN:ND2	2.65	0.43
1:N:45:ALA:HA	1:N:48:LEU:CD2	2.45	0.43
1:Q:229:PRO:HB2	1:Q:230:ASN:HD22	1.82	0.43
1:M:98:GLU:HA	1:M:102:ILE:HD12	2.00	0.43
1:L:180:VAL:CG2	1:L:181:ALA:N	2.81	0.43
1:P:190:HIS:ND1	1:P:231:ILE:HG12	2.33	0.43
1:B:82:GLU:OE2	1:B:116:ARG:NH2	2.45	0.43
1:F:197:PHE:O	1:F:201:VAL:N	2.50	0.43
1:C:222:ASP:OD1	1:C:223:GLU:N	2.51	0.43
1:F:52:ILE:HA	1:F:62:ILE:HD13	2.00	0.43
1:F:212:ILE:CD1	1:F:235:LEU:HB2	2.48	0.43
1:C:221:ASN:HD22	1:C:221:ASN:N	2.14	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:72:ASN:HA	1:R:14:CYS:O	2.17	0.43
1:D:221:ASN:O	1:D:224:LYS:HG3	2.18	0.43
1:N:218:ASN:HD22	1:N:221:ASN:ND2	2.16	0.43
1:Q:4:ARG:NH1	1:Q:194:ARG:CZ	2.81	0.43
1:T:39:VAL:HG12	1:T:60:LEU:CD1	2.48	0.43
1:I:5:ARG:HA	1:I:6:PRO:HD3	1.86	0.43
1:Q:31:HIS:CE1	1:Q:246:MET:HB3	2.52	0.43
1:E:80:SER:HG	1:E:83:MET:H	1.66	0.43
1:M:21:ILE:HG13	1:M:47:HIS:HB3	2.00	0.43
1:E:46:VAL:HG23	1:E:47:HIS:CD2	2.53	0.43
1:P:81:VAL:HG21	1:P:117:ALA:HA	1.99	0.43
1:A:127:CYS:HB3	1:A:170:GLU:OE2	2.18	0.43
1:D:7:PHE:O	1:D:233:GLY:HA3	2.18	0.43
1:Q:183:PRO:HG2	1:Q:224:LYS:HD3	2.00	0.43
1:Q:64:ALA:N	1:Q:89:LEU:HD21	2.33	0.43
1:E:130:GLU:CD	1:E:140:THR:HB	2.39	0.43
1:N:222:ASP:OD2	1:N:248:MET:HE3	2.19	0.43
1:S:67:VAL:HG23	1:S:79:THR:HG22	2.01	0.43
1:B:172:VAL:O	1:O:176:GLY:HA2	2.18	0.43
1:E:239:ALA:HA	1:E:242:LYS:HE3	2.01	0.43
1:P:81:VAL:HG13	1:P:122:MET:SD	2.58	0.43
1:I:77:GLY:HA3	1:J:99:ARG:HH11	1.83	0.43
1:O:40:VAL:CG1	1:O:63:ALA:HB2	2.47	0.43
1:O:97:SER:HB3	1:O:170:GLU:OE1	2.18	0.43
1:M:128:VAL:HG12	1:M:147:GLN:HB2	1.99	0.43
1:I:48:LEU:CD2	1:I:89:LEU:HD11	2.48	0.43
1:O:100:ARG:NH1	1:O:147:GLN:CD	2.72	0.43
1:O:197:PHE:HE2	1:O:205:GLY:O	2.00	0.43
1:O:182:THR:HG23	1:O:185:GLN:NE2	2.33	0.43
1:I:228:CYS:HA	1:I:229:PRO:HD2	1.91	0.43
1:L:40:VAL:HG11	1:L:63:ALA:HB2	1.99	0.43
1:D:151:LEU:HD23	1:D:162:TRP:CH2	2.53	0.43
1:S:143:VAL:O	1:S:147:GLN:HG3	2.18	0.43
1:K:13:LYS:HG2	1:L:76:THR:OG1	2.18	0.43
1:A:252:LEU:HA	1:A:252:LEU:HD12	1.78	0.43
1:Q:166:VAL:CG2	1:Q:210:ARG:NH2	2.81	0.43
1:Q:7:PHE:HE1	1:Q:38:ASP:OD1	2.02	0.43
1:O:181:ALA:HB3	1:O:213:TYR:OH	2.18	0.43
1:J:69:LEU:HD22	1:J:113:LYS:HE2	2.00	0.43
1:A:151:LEU:O	1:A:155:LEU:HG	2.19	0.43
1:M:63:ALA:HB2	1:M:91:HIS:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:40:VAL:HA	1:K:61:ARG:O	2.18	0.43
1:R:214:GLY:HA2	1:R:235:LEU:HB3	2.00	0.43
1:E:183:PRO:HG2	1:E:224:LYS:HE2	2.01	0.43
1:I:197:PHE:CD2	1:I:206:ALA:HA	2.53	0.43
1:T:180:VAL:HG22	1:T:181:ALA:N	2.34	0.43
1:M:167:ILE:O	1:M:211:ILE:HA	2.18	0.43
1:J:166:VAL:HG13	1:J:210:ARG:HB3	1.99	0.43
1:T:111:ALA:HB1	1:T:151:LEU:HA	2.01	0.43
1:F:118:LEU:HB3	1:F:161:LEU:HD22	2.00	0.43
1:F:80:SER:OG	1:F:83:MET:HG3	2.19	0.43
1:I:182:THR:OG1	1:I:185:GLN:HG3	2.19	0.43
1:E:251:ILE:O	1:E:254:LYS:HG2	2.18	0.43
1:H:94:VAL:HG12	1:H:126:PHE:CD1	2.54	0.43
1:R:184:GLU:OE1	1:R:224:LYS:NZ	2.48	0.43
1:B:144:ASN:HD22	1:B:193:LEU:HD22	1.83	0.43
1:O:100:ARG:HH11	1:O:147:GLN:NE2	2.17	0.43
1:E:155:LEU:HD12	1:E:162:TRP:NE1	2.33	0.43
1:L:117:ALA:O	1:L:122:MET:HB2	2.18	0.43
1:Q:81:VAL:HG11	1:Q:117:ALA:HA	2.01	0.43
1:M:223:GLU:O	1:M:227:GLN:HG3	2.19	0.43
1:P:151:LEU:HD12	1:P:155:LEU:HG	2.01	0.43
1:S:24:HIS:NE2	1:S:241:LEU:HA	2.34	0.43
1:Q:189:VAL:O	1:Q:193:LEU:HG	2.19	0.43
1:B:21:ILE:O	1:B:25:VAL:HG23	2.19	0.43
1:L:246:MET:HA	1:L:249:ILE:HD12	1.99	0.43
1:L:189:VAL:O	1:L:193:LEU:HG	2.19	0.43
1:S:39:VAL:HG12	1:S:60:LEU:CD1	2.47	0.43
1:Q:85:GLN:NE2	1:Q:120:LYS:O	2.52	0.43
1:G:221:ASN:HA	1:G:224:LYS:HG3	2.00	0.43
1:J:69:LEU:H	1:J:69:LEU:CD2	2.27	0.43
1:N:134:GLU:OE1	1:N:143:VAL:HG11	2.19	0.43
1:P:83:MET:O	1:P:87:MET:HG3	2.18	0.43
1:I:115:LYS:HD2	1:I:154:GLU:O	2.18	0.43
1:F:82:GLU:H	1:F:82:GLU:HG2	1.41	0.43
1:B:197:PHE:HD2	1:B:206:ALA:HB2	1.83	0.43
1:A:172:VAL:HA	1:A:175:ILE:HD12	1.95	0.43
1:C:78:GLU:HA	1:C:78:GLU:OE1	2.19	0.43
1:Q:16:GLY:O	1:Q:47:HIS:HE1	2.01	0.43
1:M:210:ARG:HE	1:M:210:ARG:HB2	1.19	0.43
1:L:250:ASP:O	1:L:254:LYS:HE3	2.19	0.43
1:T:99:ARG:HB3	1:T:99:ARG:HE	1.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:127:CYS:HB3	1:T:170:GLU:OE2	2.19	0.43
1:Q:14:CYS:SG	1:R:80:SER:HB3	2.59	0.43
1:Q:77:GLY:H	1:R:65:GLN:NE2	2.17	0.43
1:C:160:MET:O	1:C:163:LYS:HB2	2.19	0.43
1:K:135:ARG:HB2	1:K:135:ARG:HE	1.58	0.43
1:N:13:LYS:O	1:N:15:ASN:N	2.51	0.43
1:J:132:LEU:HA	1:J:173:TRP:HB3	2.01	0.43
1:R:187:GLU:OE2	1:R:229:PRO:HB2	2.18	0.43
1:B:130:GLU:O	1:B:172:VAL:HB	2.19	0.43
1:Q:33:ILE:HB	1:Q:59:GLN:NE2	2.34	0.43
1:C:195:LYS:HB2	1:C:195:LYS:HE3	1.76	0.43
1:T:157:GLU:OE1	1:T:157:GLU:CA	2.67	0.43
1:F:151:LEU:HD23	1:F:162:TRP:CH2	2.54	0.43
1:S:2:PRO:HG2	1:S:207:GLN:HB2	2.01	0.43
1:S:10:GLY:HA2	1:S:236:VAL:HB	2.00	0.43
1:N:250:ASP:O	1:N:253:THR:HB	2.19	0.43
1:P:12:PHE:N	1:P:12:PHE:CD1	2.87	0.43
1:M:71:GLY:O	1:M:75:TRP:NE1	2.52	0.43
1:O:4:ARG:HD2	1:O:209:ILE:O	2.18	0.43
1:T:118:LEU:HD13	1:T:155:LEU:CD1	2.49	0.43
1:T:115:LYS:CD	1:T:155:LEU:HD21	2.39	0.43
1:O:83:MET:HE1	1:P:14:CYS:C	2.40	0.43
1:S:155:LEU:CG	1:S:161:LEU:HD11	2.46	0.43
1:R:91:HIS:HA	1:R:123:THR:O	2.18	0.43
1:D:55:ASN:HD22	1:D:62:ILE:HD12	1.84	0.43
1:S:246:MET:H	1:S:246:MET:HE3	1.83	0.43
1:D:37:VAL:HG11	1:D:252:LEU:HD23	2.00	0.43
1:Q:69:LEU:HD12	1:Q:113:LYS:HE2	2.01	0.43
1:F:90:LYS:HE2	1:F:123:THR:OG1	2.19	0.43
1:K:154:GLU:HA	1:K:154:GLU:OE1	2.19	0.43
1:G:4:ARG:HD2	1:G:194:ARG:HH12	1.82	0.43
1:E:42:ALA:O	1:E:65:GLN:NE2	2.45	0.43
1:J:71:GLY:O	1:J:75:TRP:NE1	2.49	0.43
1:F:198:ALA:HA	1:F:202:ALA:O	2.18	0.43
1:K:93:ILE:HG12	1:K:125:ILE:HD12	2.01	0.43
1:P:15:ASN:ND2	1:P:15:ASN:N	2.56	0.42
1:I:4:ARG:NH1	1:I:4:ARG:HG2	2.22	0.42
1:R:66:ASN:ND2	1:R:99:ARG:CZ	2.82	0.42
1:N:221:ASN:O	1:N:223:GLU:N	2.52	0.42
1:N:142:GLU:HG3	1:N:143:VAL:N	2.32	0.42
1:S:13:LYS:O	1:S:65:GLN:NE2	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:115:LYS:NZ	1:E:154:GLU:O	2.49	0.42
1:D:148:LEU:HA	1:D:148:LEU:HD12	1.72	0.42
1:B:162:TRP:HA	1:B:165:VAL:HG23	2.00	0.42
1:B:37:VAL:HG13	1:B:252:LEU:HD23	2.01	0.42
1:B:37:VAL:HG11	1:B:252:LEU:HD23	2.01	0.42
1:P:118:LEU:HD13	1:P:161:LEU:O	2.19	0.42
1:H:148:LEU:CD2	1:H:193:LEU:HD22	2.49	0.42
1:S:141:MET:CE	1:S:193:LEU:HD23	2.49	0.42
1:F:12:PHE:O	1:F:15:ASN:ND2	2.52	0.42
1:L:115:LYS:O	1:L:119:GLU:HG3	2.19	0.42
1:L:71:GLY:O	1:L:75:TRP:NE1	2.52	0.42
1:H:204:GLU:HG3	1:H:204:GLU:O	2.18	0.42
1:K:7:PHE:CD1	1:K:7:PHE:C	2.93	0.42
1:T:115:LYS:O	1:T:119:GLU:HG3	2.19	0.42
1:Q:91:HIS:CD2	1:Q:123:THR:CG2	3.02	0.42
1:P:177:THR:O	1:P:179:VAL:N	2.46	0.42
1:S:8:ILE:HG23	1:S:39:VAL:HG22	2.01	0.42
1:R:197:PHE:CD2	1:R:206:ALA:HA	2.54	0.42
1:N:221:ASN:OD1	1:N:222:ASP:OD1	2.36	0.42
1:T:11:ASN:HD21	1:T:13:LYS:HG3	1.84	0.42
1:T:8:ILE:HG22	1:T:39:VAL:HG22	2.01	0.42
1:S:92:VAL:HG13	1:S:124:VAL:HG22	1.97	0.42
1:S:128:VAL:HG12	1:S:147:GLN:HB2	1.99	0.42
1:A:246:MET:O	1:A:249:ILE:HB	2.19	0.42
1:T:149:GLU:O	1:T:153:LYS:HB3	2.19	0.42
1:R:181:ALA:HA	1:R:185:GLN:OE1	2.19	0.42
1:I:114:ALA:O	1:I:118:LEU:HG	2.19	0.42
1:O:246:MET:O	1:O:249:ILE:HB	2.18	0.42
1:D:97:SER:O	1:D:101:ARG:HB2	2.18	0.42
1:E:84:LEU:HD22	1:E:89:LEU:HD12	2.00	0.42
1:L:177:THR:C	1:L:179:VAL:H	2.20	0.42
1:L:196:TRP:O	1:L:200:LYS:HB3	2.19	0.42
1:O:227:GLN:O	1:O:228:CYS:C	2.56	0.42
1:R:198:ALA:HB2	1:R:206:ALA:CB	2.50	0.42
1:K:76:THR:OG1	1:L:65:GLN:HB3	2.18	0.42
1:R:6:PRO:HD2	1:R:36:SER:O	2.18	0.42
1:R:236:VAL:HG11	1:R:239:ALA:HB3	2.00	0.42
1:S:73:GLY:O	1:T:14:CYS:HB3	2.19	0.42
1:E:71:GLY:O	1:E:72:ASN:C	2.54	0.42
1:L:5:ARG:O	1:L:210:ARG:CD	2.67	0.42
1:T:162:TRP:CD2	1:T:197:PHE:HE1	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:148:LEU:HD12	1:T:148:LEU:HA	1.87	0.42
1:I:116:ARG:O	1:I:120:LYS:HG3	2.20	0.42
1:T:40:VAL:HG12	1:T:41:ILE:N	2.34	0.42
1:S:58:LYS:N	1:S:58:LYS:HD2	2.34	0.42
1:Q:183:PRO:CG	1:Q:225:LEU:HD21	2.48	0.42
1:L:171:PRO:CG	1:L:174:SER:HG	2.28	0.42
1:R:28:ILE:HG12	1:R:246:MET:CE	2.49	0.42
1:K:251:ILE:CD1	1:K:251:ILE:N	2.83	0.42
1:H:115:LYS:CE	1:H:119:GLU:OE2	2.64	0.42
1:O:141:MET:O	1:O:145:ILE:HG13	2.20	0.42
1:A:139:ARG:HH11	1:A:142:GLU:CD	2.22	0.42
1:E:141:MET:HA	1:E:141:MET:HE3	2.00	0.42
1:F:219:GLY:HA2	1:F:222:ASP:CG	2.39	0.42
1:H:4:ARG:HH22	1:H:230:ASN:HA	1.84	0.42
1:D:190:HIS:CE1	1:D:231:ILE:HG12	2.55	0.42
1:E:57:SER:HB3	1:E:60:LEU:HB3	2.02	0.42
1:S:85:GLN:NE2	1:S:120:LYS:O	2.52	0.42
1:L:218:ASN:HB3	1:L:220:SER:H	1.85	0.42
1:P:131:THR:CA	1:P:172:VAL:HG11	2.41	0.42
1:L:69:LEU:HB3	1:L:113:LYS:HG2	2.02	0.42
1:K:221:ASN:O	1:K:225:LEU:HD12	2.19	0.42
1:J:242:LYS:CB	1:J:244:GLU:OE1	2.59	0.42
1:R:218:ASN:N	1:R:218:ASN:HD22	2.16	0.42
1:N:142:GLU:CG	1:N:143:VAL:N	2.82	0.42
1:E:99:ARG:HH11	1:F:77:GLY:HA3	1.85	0.42
1:I:218:ASN:OD1	1:I:221:ASN:N	2.48	0.42
1:Q:132:LEU:O	1:Q:136:LYS:HG3	2.20	0.42
1:C:5:ARG:HA	1:C:6:PRO:HD3	1.79	0.42
1:P:156:GLY:O	1:P:159:LYS:HG3	2.19	0.42
1:J:118:LEU:HD13	1:J:161:LEU:O	2.20	0.42
1:F:139:ARG:O	1:F:143:VAL:HG23	2.19	0.42
1:J:5:ARG:HA	1:J:6:PRO:HD3	1.80	0.42
1:C:138:ASN:HD22	1:C:138:ASN:HA	1.68	0.42
1:L:78:GLU:OE1	1:L:78:GLU:HA	2.20	0.42
1:O:255:THR:O	1:O:255:THR:HG22	2.19	0.42
1:S:7:PHE:CE1	1:S:40:VAL:HG23	2.55	0.42
1:D:221:ASN:HA	1:D:224:LYS:HG2	2.00	0.42
1:D:161:LEU:HD23	1:D:161:LEU:HA	1.83	0.42
1:A:187:GLU:CD	1:A:229:PRO:HD2	2.40	0.42
1:L:21:ILE:HG13	1:L:47:HIS:HB3	2.01	0.42
1:N:4:ARG:NH2	1:N:232:ASP:OD1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:253:THR:HG22	1:T:254:LYS:N	2.33	0.42
1:J:251:ILE:HA	1:J:254:LYS:HZ3	1.83	0.42
1:D:116:ARG:O	1:D:120:LYS:HG3	2.20	0.42
1:Q:76:THR:N	1:R:98:GLU:OE1	2.47	0.42
1:B:67:VAL:O	1:B:113:LYS:HD3	2.19	0.42
1:S:5:ARG:O	1:S:210:ARG:NH1	2.52	0.42
1:D:183:PRO:CG	1:D:224:LYS:HD3	2.50	0.42
1:J:244:GLU:O	1:J:248:MET:HG3	2.19	0.42
1:J:173:TRP:CH2	1:J:185:GLN:OE1	2.73	0.42
1:R:43:PRO:HG2	1:R:51:ALA:CB	2.50	0.42
1:A:106:THR:OG1	1:A:109:GLN:HG3	2.19	0.42
1:B:215:GLY:O	1:B:217:ALA:N	2.53	0.42
1:D:171:PRO:CD	1:D:214:GLY:O	2.66	0.42
1:P:62:ILE:N	1:P:62:ILE:CD1	2.82	0.42
1:T:197:PHE:CE1	1:T:201:VAL:HG21	2.55	0.42
1:T:139:ARG:HG2	1:T:142:GLU:OE1	2.20	0.42
1:Q:48:LEU:HD12	1:Q:48:LEU:HA	1.70	0.42
1:R:25:VAL:HA	1:R:28:ILE:HG13	2.01	0.42
1:R:12:PHE:CD1	1:R:12:PHE:N	2.88	0.42
1:C:90:LYS:HG2	1:C:90:LYS:O	2.18	0.42
1:S:145:ILE:O	1:S:149:GLU:CG	2.68	0.42
1:H:43:PRO:HG2	1:H:48:LEU:CD1	2.49	0.42
1:G:80:SER:HG	1:G:83:MET:HG3	1.84	0.42
1:N:95:GLY:O	1:N:127:CYS:HB2	2.18	0.42
1:O:116:ARG:O	1:O:120:LYS:HG3	2.19	0.42
1:F:212:ILE:HD11	1:F:235:LEU:HB2	2.01	0.42
1:H:8:ILE:HB	1:H:252:LEU:HD23	2.01	0.42
1:E:245:PHE:HA	1:E:248:MET:HG3	2.02	0.42
1:D:221:ASN:HA	1:D:224:LYS:HE3	2.02	0.42
1:D:218:ASN:OD1	1:D:221:ASN:OD1	2.38	0.42
1:I:144:ASN:O	1:I:148:LEU:HB2	2.19	0.42
1:L:97:SER:OG	1:L:175:ILE:HD11	2.18	0.42
1:B:4:ARG:HB2	1:B:4:ARG:HE	1.43	0.42
1:P:134:GLU:HG2	1:P:143:VAL:HG21	2.00	0.42
1:Q:34:PRO:HG2	1:Q:37:VAL:HG23	2.02	0.42
1:I:212:ILE:CD1	1:I:235:LEU:HB2	2.50	0.42
1:I:87:MET:HE2	1:I:87:MET:HB3	1.92	0.42
1:M:141:MET:HE3	1:M:141:MET:HB3	1.93	0.42
1:Q:236:VAL:HG11	1:Q:240:SER:N	2.35	0.42
1:K:5:ARG:HE	1:K:38:ASP:CG	2.21	0.42
1:L:177:THR:HG21	1:L:179:VAL:HG21	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:66:ASN:ND2	1:T:67:VAL:H	2.18	0.41
1:K:197:PHE:CD1	1:K:206:ALA:CA	3.02	0.41
1:T:242:LYS:HB2	1:T:243:PRO:CD	2.43	0.41
1:R:116:ARG:NH1	1:R:116:ARG:HG3	2.35	0.41
1:M:151:LEU:HD23	1:M:162:TRP:CH2	2.55	0.41
1:G:196:TRP:O	1:G:200:LYS:HB2	2.20	0.41
1:G:37:VAL:CG1	1:G:38:ASP:N	2.83	0.41
1:N:32:LYS:O	1:N:32:LYS:CG	2.67	0.41
1:D:68:TYR:HB2	1:D:78:GLU:HB3	2.01	0.41
1:S:5:ARG:HE	1:S:38:ASP:CG	2.23	0.41
1:L:219:GLY:HA2	1:L:222:ASP:HB2	2.02	0.41
1:R:34:PRO:C	1:R:36:SER:N	2.73	0.41
1:N:141:MET:O	1:N:145:ILE:HG12	2.20	0.41
1:F:145:ILE:HD13	1:F:196:TRP:CD1	2.55	0.41
1:F:148:LEU:HB3	1:F:196:TRP:CH2	2.54	0.41
1:I:76:THR:CG2	1:J:65:GLN:HB3	2.49	0.41
1:F:21:ILE:O	1:F:25:VAL:HG23	2.20	0.41
1:M:145:ILE:O	1:M:149:GLU:HG2	2.20	0.41
1:D:101:ARG:CZ	1:D:131:THR:HG23	2.50	0.41
1:B:83:MET:O	1:B:87:MET:HG3	2.20	0.41
1:Q:65:GLN:O	1:Q:93:ILE:HG22	2.20	0.41
1:R:33:ILE:O	1:R:59:GLN:NE2	2.53	0.41
1:M:148:LEU:HD12	1:M:148:LEU:HA	1.82	0.41
1:Q:138:ASN:ND2	1:Q:138:ASN:O	2.53	0.41
1:S:6:PRO:HG3	1:S:37:VAL:HG12	2.02	0.41
1:O:218:ASN:CG	1:O:219:GLY:N	2.74	0.41
1:S:74:ALA:HA	1:T:13:LYS:HD3	2.02	0.41
1:T:7:PHE:O	1:T:233:GLY:HA3	2.20	0.41
1:T:242:LYS:CB	1:T:243:PRO:CD	2.98	0.41
1:R:34:PRO:C	1:R:36:SER:H	2.22	0.41
1:R:151:LEU:HD12	1:R:151:LEU:O	2.21	0.41
1:J:164:GLU:HA	1:J:164:GLU:OE1	2.20	0.41
1:J:228:CYS:HA	1:J:229:PRO:HD2	1.80	0.41
1:O:116:ARG:HH11	1:O:116:ARG:HG2	1.84	0.41
1:N:11:ASN:OD1	1:N:65:GLN:HG2	2.20	0.41
1:N:61:ARG:HD2	1:N:61:ARG:HA	1.87	0.41
1:S:7:PHE:HE1	1:S:40:VAL:CG2	2.32	0.41
1:B:128:VAL:CG2	1:B:144:ASN:HD21	2.33	0.41
1:E:131:THR:OG1	1:E:134:GLU:HG3	2.21	0.41
1:M:69:LEU:HG	1:M:69:LEU:H	1.71	0.41
1:K:193:LEU:HA	1:K:193:LEU:HD23	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:5:ARG:O	1:J:210:ARG:HD2	2.21	0.41
1:B:115:LYS:O	1:B:119:GLU:HB2	2.20	0.41
1:S:180:VAL:HG23	1:S:216:SER:HB3	2.01	0.41
1:B:145:ILE:HG12	1:B:196:TRP:CD1	2.55	0.41
1:G:12:PHE:CD1	1:G:12:PHE:N	2.88	0.41
1:A:12:PHE:N	1:A:12:PHE:CD1	2.88	0.41
1:N:107:ASP:OD1	1:N:107:ASP:N	2.53	0.41
1:L:218:ASN:HB3	1:L:220:SER:OG	2.21	0.41
1:A:218:ASN:O	1:A:222:ASP:CG	2.59	0.41
1:S:182:THR:HB	1:S:184:GLU:OE1	2.21	0.41
1:J:217:ALA:HB1	1:J:234:PHE:CD1	2.56	0.41
1:J:243:PRO:HD2	1:J:244:GLU:OE1	2.21	0.41
1:K:197:PHE:HE1	1:K:206:ALA:N	2.18	0.41
1:B:247:THR:O	1:B:251:ILE:HD13	2.21	0.41
1:H:221:ASN:HD22	1:H:224:LYS:HB2	1.85	0.41
1:A:190:HIS:HB3	1:A:230:ASN:O	2.20	0.41
1:R:229:PRO:HB2	1:R:230:ASN:HD22	1.85	0.41
1:S:33:ILE:HA	1:S:34:PRO:HD3	1.91	0.41
1:B:95:GLY:O	1:B:127:CYS:HB2	2.21	0.41
1:A:167:ILE:HG13	1:A:211:ILE:HG12	2.02	0.41
1:D:34:PRO:HB2	1:D:36:SER:OG	2.21	0.41
1:T:217:ALA:O	1:T:248:MET:HE1	2.21	0.41
1:A:137:ALA:HB3	1:A:139:ARG:CG	2.49	0.41
1:K:142:GLU:HG2	1:K:143:VAL:N	2.36	0.41
1:K:67:VAL:HG22	1:K:68:TYR:H	1.85	0.41
1:K:43:PRO:C	1:K:65:GLN:NE2	2.74	0.41
1:R:161:LEU:C	1:R:163:LYS:H	2.22	0.41
1:O:67:VAL:HG22	1:O:68:TYR:N	2.36	0.41
1:K:202:ALA:HB1	1:K:204:GLU:CD	2.41	0.41
1:C:72:ASN:N	1:C:72:ASN:HD22	2.17	0.41
1:C:228:CYS:HA	1:C:229:PRO:HD2	1.90	0.41
1:C:174:SER:HB2	1:C:180:VAL:HA	2.02	0.41
1:K:8:ILE:HG13	1:K:9:GLY:N	2.36	0.41
1:K:229:PRO:HB2	1:K:230:ASN:HD22	1.86	0.41
1:Q:130:GLU:CD	1:Q:140:THR:HG23	2.41	0.41
1:G:213:TYR:CD2	1:G:234:PHE:HD1	2.36	0.41
1:L:221:ASN:HD22	1:L:222:ASP:H	1.61	0.41
1:A:218:ASN:HD22	1:A:220:SER:H	1.64	0.41
1:R:4:ARG:NH2	1:R:194:ARG:NH2	2.68	0.41
1:J:8:ILE:HD13	1:J:245:PHE:CE1	2.55	0.41
1:K:195:LYS:HE3	1:K:195:LYS:HB2	1.70	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:128:VAL:HB	1:B:147:GLN:OE1	2.20	0.41
1:D:161:LEU:C	1:D:163:LYS:N	2.72	0.41
1:I:253:THR:HG22	1:I:254:LYS:HD2	2.02	0.41
1:G:7:PHE:CZ	1:G:40:VAL:HG11	2.56	0.41
1:I:143:VAL:O	1:I:147:GLN:HG3	2.20	0.41
1:B:159:LYS:HG2	1:B:160:MET:N	2.35	0.41
1:K:190:HIS:CE1	1:K:211:ILE:HG22	2.56	0.41
1:J:145:ILE:HG22	1:J:149:GLU:HG2	2.01	0.41
1:I:189:VAL:O	1:I:193:LEU:HG	2.21	0.41
1:C:169:TYR:CE1	1:C:189:VAL:HG11	2.56	0.41
1:R:7:PHE:CD1	1:R:7:PHE:C	2.93	0.41
1:F:171:PRO:HG2	1:F:213:TYR:CZ	2.54	0.41
1:Q:166:VAL:CG2	1:Q:210:ARG:CZ	2.99	0.41
1:O:221:ASN:O	1:O:225:LEU:HG	2.21	0.41
1:N:134:GLU:HB3	1:N:143:VAL:HG21	2.01	0.41
1:K:204:GLU:HG2	1:K:205:GLY:H	1.83	0.41
1:P:189:VAL:O	1:P:193:LEU:HG	2.20	0.41
1:T:197:PHE:O	1:T:201:VAL:HB	2.21	0.41
1:E:250:ASP:O	1:E:254:LYS:HG2	2.20	0.41
1:H:163:LYS:HE2	1:H:163:LYS:HB2	1.89	0.41
1:I:194:ARG:NH1	1:I:209:ILE:HG23	2.36	0.41
1:R:67:VAL:HG23	1:R:79:THR:HG22	2.02	0.41
1:A:218:ASN:ND2	1:A:218:ASN:O	2.53	0.41
1:Q:222:ASP:O	1:Q:226:GLY:N	2.49	0.41
1:R:48:LEU:HA	1:R:48:LEU:HD12	1.75	0.41
1:B:128:VAL:HG21	1:B:144:ASN:HD21	1.86	0.41
1:M:95:GLY:O	1:M:100:ARG:NE	2.50	0.41
1:I:72:ASN:HD22	1:I:72:ASN:N	2.18	0.41
1:E:96:HIS:CG	1:F:76:THR:HG21	2.56	0.41
1:I:218:ASN:OD1	1:I:221:ASN:ND2	2.53	0.41
1:R:116:ARG:HG3	1:R:116:ARG:HH11	1.86	0.41
1:R:118:LEU:HD21	1:R:165:VAL:HG23	2.02	0.41
1:P:128:VAL:HG12	1:P:147:GLN:OE1	2.20	0.41
1:K:130:GLU:OE2	1:K:169:TYR:OH	2.34	0.41
1:C:250:ASP:O	1:C:253:THR:HB	2.21	0.41
1:G:74:ALA:HA	1:H:13:LYS:HD3	2.03	0.41
1:E:178:GLY:HA3	1:I:172:VAL:HG13	2.03	0.41
1:S:195:LYS:O	1:S:199:GLU:HG3	2.21	0.41
1:I:137:ALA:HB3	1:I:139:ARG:HG3	2.02	0.41
1:O:31:HIS:HB2	1:O:246:MET:HG2	2.03	0.41
1:C:169:TYR:CZ	1:C:189:VAL:HG11	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:236:VAL:CG1	1:C:239:ALA:HB3	2.51	0.41
1:C:166:VAL:CG1	1:C:212:ILE:HD13	2.51	0.41
1:H:223:GLU:O	1:H:227:GLN:HG3	2.21	0.41
1:M:180:VAL:HG23	1:M:215:GLY:O	2.21	0.41
1:S:5:ARG:NH1	1:S:35:ASP:O	2.47	0.41
1:Q:61:ARG:HD2	1:Q:61:ARG:HA	1.50	0.41
1:S:224:LYS:O	1:S:227:GLN:HB2	2.21	0.41
1:M:183:PRO:HA	1:M:225:LEU:HD23	2.03	0.41
1:H:155:LEU:HD12	1:H:162:TRP:CE2	2.55	0.41
1:D:224:LYS:HG3	1:D:225:LEU:N	2.36	0.41
1:D:160:MET:O	1:D:163:LYS:HB2	2.21	0.41
1:A:130:GLU:O	1:A:173:TRP:HD1	2.04	0.41
1:C:13:LYS:HA	1:C:65:GLN:OE1	2.21	0.41
1:G:96:HIS:ND1	1:G:98:GLU:HG3	2.36	0.41
1:K:202:ALA:HB1	1:K:204:GLU:OE1	2.20	0.41
1:S:246:MET:CE	1:S:246:MET:H	2.34	0.41
1:H:66:ASN:HD21	1:H:113:LYS:NZ	2.19	0.41
1:J:247:THR:O	1:J:251:ILE:HD13	2.21	0.41
1:I:63:ALA:HB2	1:I:91:HIS:HB2	2.03	0.41
1:P:57:SER:HB3	1:P:60:LEU:HB3	2.03	0.41
1:B:66:ASN:ND2	1:B:67:VAL:O	2.53	0.40
1:E:175:ILE:HG23	1:I:176:GLY:O	2.21	0.40
1:N:187:GLU:O	1:N:191:VAL:HG23	2.21	0.40
1:L:204:GLU:O	1:L:207:GLN:HB2	2.22	0.40
1:O:194:ARG:CG	1:O:206:ALA:O	2.69	0.40
1:G:65:GLN:HB3	1:H:76:THR:HG23	2.03	0.40
1:P:69:LEU:CD2	1:P:70:GLU:HG2	2.50	0.40
1:B:118:LEU:HD12	1:B:155:LEU:HD21	2.03	0.40
1:M:141:MET:HE2	1:M:192:GLY:HA3	2.03	0.40
1:G:111:ALA:HB1	1:G:154:GLU:CG	2.51	0.40
1:C:116:ARG:O	1:C:120:LYS:HG3	2.20	0.40
1:E:184:GLU:CD	1:E:184:GLU:H	2.24	0.40
1:D:68:TYR:CE2	1:D:75:TRP:HB3	2.55	0.40
1:O:125:ILE:HG21	1:O:235:LEU:HD13	2.02	0.40
1:L:59:GLN:HE21	1:L:59:GLN:HB2	1.71	0.40
1:Q:195:LYS:O	1:Q:199:GLU:CB	2.60	0.40
1:R:68:TYR:CE1	1:R:69:LEU:CD2	3.04	0.40
1:F:68:TYR:CE1	1:F:69:LEU:HD22	2.57	0.40
1:I:130:GLU:O	1:I:130:GLU:HG2	2.18	0.40
1:M:83:MET:HG2	1:N:47:HIS:HE1	1.86	0.40
1:A:251:ILE:HA	1:A:251:ILE:HD12	1.80	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:186:ALA:HB1	1:P:231:ILE:HD11	2.03	0.40
1:P:242:LYS:C	1:P:244:GLU:N	2.74	0.40
1:O:226:GLY:C	1:O:255:THR:HG21	2.40	0.40
1:H:222:ASP:OD1	1:H:234:PHE:CZ	2.74	0.40
1:O:218:ASN:ND2	1:O:219:GLY:N	2.70	0.40
1:L:218:ASN:N	1:L:222:ASP:OD1	2.55	0.40
1:L:112:LYS:HE3	1:L:154:GLU:OE2	2.22	0.40
1:T:12:PHE:O	1:T:13:LYS:HB2	2.20	0.40
1:M:5:ARG:HH12	1:M:37:VAL:N	2.19	0.40
1:F:90:LYS:O	1:F:90:LYS:HG2	2.21	0.40
1:T:117:ALA:O	1:T:122:MET:HB2	2.21	0.40
1:M:240:SER:HA	1:M:245:PHE:CD1	2.57	0.40
1:N:168:ALA:HA	1:N:212:ILE:O	2.21	0.40
1:Q:24:HIS:NE2	1:Q:28:ILE:HD11	2.36	0.40
1:N:150:ALA:O	1:N:154:GLU:HG2	2.22	0.40
1:M:33:ILE:O	1:M:59:GLN:HG2	2.20	0.40
1:M:52:ILE:HD11	1:M:89:LEU:HD21	2.04	0.40
1:L:190:HIS:CE1	1:L:211:ILE:HG22	2.57	0.40
1:F:5:ARG:O	1:F:210:ARG:HD2	2.21	0.40
1:E:61:ARG:HA	1:E:61:ARG:HD2	1.85	0.40
1:E:187:GLU:HG3	1:E:187:GLU:O	2.21	0.40
1:S:158:SER:O	1:S:161:LEU:HD23	2.22	0.40
1:S:225:LEU:O	1:S:228:CYS:HB2	2.21	0.40
1:L:68:TYR:CE2	1:L:70:GLU:HB2	2.56	0.40
1:S:185:GLN:O	1:S:188:GLU:CD	2.60	0.40
1:K:196:TRP:CE3	1:K:197:PHE:N	2.89	0.40
1:T:249:ILE:O	1:T:252:LEU:HB3	2.21	0.40
1:G:75:TRP:HD1	1:H:14:CYS:HB3	1.86	0.40
1:P:149:GLU:HA	1:P:149:GLU:OE1	2.21	0.40
1:D:37:VAL:HG12	1:D:38:ASP:N	2.36	0.40
1:S:21:ILE:HD13	1:S:21:ILE:N	2.37	0.40
1:R:65:GLN:O	1:R:93:ILE:O	2.40	0.40
1:P:12:PHE:HA	1:P:241:LEU:HD21	2.02	0.40
1:I:97:SER:N	1:I:170:GLU:OE1	2.54	0.40
1:O:228:CYS:HA	1:O:229:PRO:HD3	1.79	0.40
1:S:186:ALA:HB1	1:S:213:TYR:CD1	2.57	0.40
1:S:8:ILE:CG2	1:S:39:VAL:HG22	2.52	0.40
1:J:132:LEU:O	1:J:136:LYS:HB2	2.22	0.40
1:G:93:ILE:HA	1:G:125:ILE:HB	2.04	0.40
1:T:84:LEU:HD23	1:T:84:LEU:HA	1.67	0.40
1:S:128:VAL:HG11	1:S:148:LEU:HD13	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:12:PHE:N	1:L:12:PHE:CD1	2.90	0.40
1:K:72:ASN:ND2	1:K:80:SER:OG	2.55	0.40
1:C:114:ALA:O	1:C:118:LEU:HG	2.21	0.40
1:K:46:VAL:HG13	1:L:45:ALA:HB1	2.04	0.40
1:J:33:ILE:HB	1:J:59:GLN:HE21	1.86	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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	252/255 (99%)	241 (96%)	10 (4%)	1 (0%)	39	69
1	B	252/255 (99%)	247 (98%)	5 (2%)	0	100	100
1	C	252/255 (99%)	240 (95%)	11 (4%)	1 (0%)	39	69
1	D	252/255 (99%)	244 (97%)	7 (3%)	1 (0%)	39	69
1	E	252/255 (99%)	240 (95%)	11 (4%)	1 (0%)	39	69
1	F	252/255 (99%)	244 (97%)	7 (3%)	1 (0%)	39	69
1	G	252/255 (99%)	243 (96%)	8 (3%)	1 (0%)	39	69
1	H	252/255 (99%)	240 (95%)	12 (5%)	0	100	100
1	I	252/255 (99%)	243 (96%)	9 (4%)	0	100	100
1	J	252/255 (99%)	244 (97%)	8 (3%)	0	100	100
1	K	252/255 (99%)	240 (95%)	11 (4%)	1 (0%)	39	69
1	L	252/255 (99%)	239 (95%)	13 (5%)	0	100	100
1	M	252/255 (99%)	244 (97%)	8 (3%)	0	100	100
1	N	252/255 (99%)	239 (95%)	11 (4%)	2 (1%)	24	51
1	O	252/255 (99%)	237 (94%)	14 (6%)	1 (0%)	39	69
1	P	252/255 (99%)	233 (92%)	18 (7%)	1 (0%)	39	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	252/255 (99%)	237 (94%)	14 (6%)	1 (0%)	39	69
1	R	252/255 (99%)	242 (96%)	7 (3%)	3 (1%)	16	39
1	S	252/255 (99%)	238 (94%)	14 (6%)	0	100	100
1	T	252/255 (99%)	246 (98%)	6 (2%)	0	100	100
All	All	5040/5100 (99%)	4821 (96%)	204 (4%)	15 (0%)	46	75

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	218	ASN
1	E	220	SER
1	G	219	GLY
1	R	218	ASN
1	Q	201	VAL
1	R	13	LYS
1	K	214	GLY
1	N	13	LYS
1	O	138	ASN
1	R	156	GLY
1	A	156	GLY
1	P	243	PRO
1	D	201	VAL
1	N	156	GLY
1	F	201	VAL

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	202/203 (100%)	178 (88%)	24 (12%)	6	15
1	B	202/203 (100%)	187 (93%)	15 (7%)	17	39
1	C	202/203 (100%)	180 (89%)	22 (11%)	8	18
1	D	202/203 (100%)	176 (87%)	26 (13%)	5	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	202/203 (100%)	177 (88%)	25 (12%)	6	13
1	F	202/203 (100%)	186 (92%)	16 (8%)	15	34
1	G	202/203 (100%)	181 (90%)	21 (10%)	9	20
1	H	202/203 (100%)	180 (89%)	22 (11%)	8	18
1	I	202/203 (100%)	177 (88%)	25 (12%)	6	13
1	J	202/203 (100%)	184 (91%)	18 (9%)	12	27
1	K	202/203 (100%)	181 (90%)	21 (10%)	9	20
1	L	202/203 (100%)	184 (91%)	18 (9%)	12	27
1	M	202/203 (100%)	176 (87%)	26 (13%)	5	12
1	N	202/203 (100%)	176 (87%)	26 (13%)	5	12
1	O	202/203 (100%)	176 (87%)	26 (13%)	5	12
1	P	202/203 (100%)	180 (89%)	22 (11%)	8	18
1	Q	202/203 (100%)	169 (84%)	33 (16%)	3	7
1	R	202/203 (100%)	181 (90%)	21 (10%)	9	20
1	S	202/203 (100%)	160 (79%)	42 (21%)	1	4
1	T	202/203 (100%)	168 (83%)	34 (17%)	2	6
All	All	4040/4060 (100%)	3557 (88%)	483 (12%)	6	14

All (483) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ARG
1	A	18	LEU
1	A	32	LYS
1	A	48	LEU
1	A	49	SER
1	A	57	SER
1	A	69	LEU
1	A	72	ASN
1	A	99	ARG
1	A	138	ASN
1	A	139	ARG
1	A	142	GLU
1	A	149	GLU
1	A	157	GLU
1	A	160	MET

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Mol	Chain	Res	Type
1	A	167	ILE
1	A	179	VAL
1	A	210	ARG
1	A	218	ASN
1	A	221	ASN
1	A	246	MET
1	A	251	ILE
1	A	252	LEU
1	A	255	THR
1	B	4	ARG
1	B	5	ARG
1	B	35	ASP
1	B	66	ASN
1	B	69	LEU
1	B	101	ARG
1	B	138	ASN
1	B	148	LEU
1	B	159	LYS
1	B	160	MET
1	B	177	THR
1	B	179	VAL
1	B	184	GLU
1	B	210	ARG
1	B	221	ASN
1	C	44	SER
1	C	48	LEU
1	C	49	SER
1	C	59	GLN
1	C	61	ARG
1	C	62	ILE
1	C	69	LEU
1	C	86	ASP
1	C	110	SER
1	C	116	ARG
1	C	138	ASN
1	C	139	ARG
1	C	140	THR
1	C	148	LEU
1	C	158	SER
1	C	159	LYS
1	C	160	MET
1	C	179	VAL

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Mol	Chain	Res	Type
1	C	207	GLN
1	C	210	ARG
1	C	218	ASN
1	C	251	ILE
1	D	4	ARG
1	D	8	ILE
1	D	32	LYS
1	D	36	SER
1	D	44	SER
1	D	48	LEU
1	D	58	LYS
1	D	67	VAL
1	D	68	TYR
1	D	69	LEU
1	D	99	ARG
1	D	100	ARG
1	D	135	ARG
1	D	138	ASN
1	D	140	THR
1	D	145	ILE
1	D	148	LEU
1	D	160	MET
1	D	180	VAL
1	D	188	GLU
1	D	194	ARG
1	D	210	ARG
1	D	218	ASN
1	D	222	ASP
1	D	244	GLU
1	D	252	LEU
1	E	49	SER
1	E	62	ILE
1	E	69	LEU
1	E	89	LEU
1	E	115	LYS
1	E	116	ARG
1	E	130	GLU
1	E	131	THR
1	E	138	ASN
1	E	140	THR
1	E	141	MET
1	E	145	ILE

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Mol	Chain	Res	Type
1	E	148	LEU
1	E	149	GLU
1	E	157	GLU
1	E	158	SER
1	E	160	MET
1	E	184	GLU
1	E	195	LYS
1	E	199	GLU
1	E	220	SER
1	E	222	ASP
1	E	225	LEU
1	E	248	MET
1	E	255	THR
1	F	5	ARG
1	F	44	SER
1	F	48	LEU
1	F	58	LYS
1	F	61	ARG
1	F	69	LEU
1	F	82	GLU
1	F	112	LYS
1	F	135	ARG
1	F	148	LEU
1	F	159	LYS
1	F	160	MET
1	F	185	GLN
1	F	209	ILE
1	F	210	ARG
1	F	221	ASN
1	G	4	ARG
1	G	8	ILE
1	G	23	SER
1	G	40	VAL
1	G	62	ILE
1	G	93	ILE
1	G	116	ARG
1	G	130	GLU
1	G	135	ARG
1	G	139	ARG
1	G	148	LEU
1	G	159	LYS
1	G	160	MET

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Mol	Chain	Res	Type
1	G	179	VAL
1	G	210	ARG
1	G	211	ILE
1	G	224	LYS
1	G	225	LEU
1	G	242	LYS
1	G	252	LEU
1	G	254	LYS
1	H	4	ARG
1	H	32	LYS
1	H	48	LEU
1	H	49	SER
1	H	58	LYS
1	H	69	LEU
1	H	86	ASP
1	H	109	GLN
1	H	112	LYS
1	H	115	LYS
1	H	138	ASN
1	H	142	GLU
1	H	148	LEU
1	H	154	GLU
1	H	158	SER
1	H	159	LYS
1	H	160	MET
1	H	164	GLU
1	H	180	VAL
1	H	210	ARG
1	H	248	MET
1	H	252	LEU
1	I	4	ARG
1	I	8	ILE
1	I	13	LYS
1	I	32	LYS
1	I	36	SER
1	I	44	SER
1	I	46	VAL
1	I	69	LEU
1	I	130	GLU
1	I	138	ASN
1	I	145	ILE
1	I	148	LEU

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Mol	Chain	Res	Type
1	I	157	GLU
1	I	160	MET
1	I	167	ILE
1	I	194	ARG
1	I	200	LYS
1	I	209	ILE
1	I	210	ARG
1	I	218	ASN
1	I	227	GLN
1	I	240	SER
1	I	244	GLU
1	I	251	ILE
1	I	252	LEU
1	J	17	SER
1	J	23	SER
1	J	48	LEU
1	J	49	SER
1	J	58	LYS
1	J	61	ARG
1	J	110	SER
1	J	112	LYS
1	J	115	LYS
1	J	148	LEU
1	J	153	LYS
1	J	159	LYS
1	J	160	MET
1	J	163	LYS
1	J	210	ARG
1	J	218	ASN
1	J	224	LYS
1	J	240	SER
1	K	4	ARG
1	K	46	VAL
1	K	48	LEU
1	K	62	ILE
1	K	69	LEU
1	K	116	ARG
1	K	135	ARG
1	K	148	LEU
1	K	157	GLU
1	K	195	LYS
1	K	209	ILE

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Mol	Chain	Res	Type
1	K	210	ARG
1	K	218	ASN
1	K	220	SER
1	K	221	ASN
1	K	225	LEU
1	K	242	LYS
1	K	248	MET
1	K	251	ILE
1	K	254	LYS
1	K	255	THR
1	L	4	ARG
1	L	49	SER
1	L	59	GLN
1	L	69	LEU
1	L	99	ARG
1	L	100	ARG
1	L	138	ASN
1	L	148	LEU
1	L	173	TRP
1	L	179	VAL
1	L	189	VAL
1	L	199	GLU
1	L	204	GLU
1	L	208	HIS
1	L	218	ASN
1	L	221	ASN
1	L	232	ASP
1	L	240	SER
1	M	5	ARG
1	M	32	LYS
1	M	35	ASP
1	M	44	SER
1	M	48	LEU
1	M	49	SER
1	M	58	LYS
1	M	68	TYR
1	M	69	LEU
1	M	75	TRP
1	M	97	SER
1	M	98	GLU
1	M	106	THR
1	M	145	ILE

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Mol	Chain	Res	Type
1	M	148	LEU
1	M	159	LYS
1	M	160	MET
1	M	170	GLU
1	M	179	VAL
1	M	194	ARG
1	M	209	ILE
1	M	210	ARG
1	M	224	LYS
1	M	251	ILE
1	M	253	THR
1	M	255	THR
1	N	15	ASN
1	N	32	LYS
1	N	36	SER
1	N	44	SER
1	N	48	LEU
1	N	49	SER
1	N	62	ILE
1	N	69	LEU
1	N	89	LEU
1	N	107	ASP
1	N	120	LYS
1	N	130	GLU
1	N	139	ARG
1	N	142	GLU
1	N	145	ILE
1	N	148	LEU
1	N	160	MET
1	N	179	VAL
1	N	180	VAL
1	N	184	GLU
1	N	224	LYS
1	N	225	LEU
1	N	240	SER
1	N	244	GLU
1	N	247	THR
1	N	248	MET
1	O	8	ILE
1	O	13	LYS
1	O	14	CYS
1	O	36	SER

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Mol	Chain	Res	Type
1	O	48	LEU
1	O	49	SER
1	O	59	GLN
1	O	69	LEU
1	O	86	ASP
1	O	112	LYS
1	O	120	LYS
1	O	131	THR
1	O	138	ASN
1	O	139	ARG
1	O	145	ILE
1	O	148	LEU
1	O	160	MET
1	O	163	LYS
1	O	167	ILE
1	O	204	GLU
1	O	210	ARG
1	O	223	GLU
1	O	244	GLU
1	O	247	THR
1	O	248	MET
1	O	251	ILE
1	P	4	ARG
1	P	15	ASN
1	P	35	ASP
1	P	48	LEU
1	P	59	GLN
1	P	61	ARG
1	P	69	LEU
1	P	89	LEU
1	P	108	GLU
1	P	115	LYS
1	P	116	ARG
1	P	128	VAL
1	P	130	GLU
1	P	145	ILE
1	P	148	LEU
1	P	160	MET
1	P	172	VAL
1	P	173	TRP
1	P	199	GLU
1	P	210	ARG

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Mol	Chain	Res	Type
1	P	221	ASN
1	P	223	GLU
1	Q	8	ILE
1	Q	19	ASP
1	Q	23	SER
1	Q	28	ILE
1	Q	37	VAL
1	Q	38	ASP
1	Q	46	VAL
1	Q	48	LEU
1	Q	50	THR
1	Q	58	LYS
1	Q	59	GLN
1	Q	61	ARG
1	Q	75	TRP
1	Q	81	VAL
1	Q	103	MET
1	Q	106	THR
1	Q	115	LYS
1	Q	116	ARG
1	Q	139	ARG
1	Q	148	LEU
1	Q	153	LYS
1	Q	158	SER
1	Q	159	LYS
1	Q	160	MET
1	Q	177	THR
1	Q	189	VAL
1	Q	195	LYS
1	Q	210	ARG
1	Q	220	SER
1	Q	230	ASN
1	Q	236	VAL
1	Q	252	LEU
1	Q	255	THR
1	R	8	ILE
1	R	28	ILE
1	R	35	ASP
1	R	48	LEU
1	R	49	SER
1	R	69	LEU
1	R	80	SER

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Mol	Chain	Res	Type
1	R	87	MET
1	R	89	LEU
1	R	119	GLU
1	R	120	LYS
1	R	135	ARG
1	R	148	LEU
1	R	153	LYS
1	R	210	ARG
1	R	222	ASP
1	R	230	ASN
1	R	244	GLU
1	R	251	ILE
1	R	253	THR
1	R	255	THR
1	S	7	PHE
1	S	8	ILE
1	S	23	SER
1	S	28	ILE
1	S	32	LYS
1	S	44	SER
1	S	48	LEU
1	S	49	SER
1	S	59	GLN
1	S	61	ARG
1	S	69	LEU
1	S	86	ASP
1	S	87	MET
1	S	89	LEU
1	S	99	ARG
1	S	101	ARG
1	S	102	ILE
1	S	106	THR
1	S	108	GLU
1	S	116	ARG
1	S	128	VAL
1	S	130	GLU
1	S	138	ASN
1	S	148	LEU
1	S	157	GLU
1	S	158	SER
1	S	159	LYS
1	S	160	MET

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Mol	Chain	Res	Type
1	S	163	LYS
1	S	180	VAL
1	S	185	GLN
1	S	188	GLU
1	S	207	GLN
1	S	210	ARG
1	S	220	SER
1	S	221	ASN
1	S	241	LEU
1	S	244	GLU
1	S	246	MET
1	S	247	THR
1	S	253	THR
1	S	254	LYS
1	T	22	LYS
1	T	23	SER
1	T	28	ILE
1	T	32	LYS
1	T	33	ILE
1	T	48	LEU
1	T	49	SER
1	T	67	VAL
1	T	87	MET
1	T	99	ARG
1	T	115	LYS
1	T	135	ARG
1	T	136	LYS
1	T	148	LEU
1	T	153	LYS
1	T	157	GLU
1	T	158	SER
1	T	160	MET
1	T	163	LYS
1	T	164	GLU
1	T	170	GLU
1	T	174	SER
1	T	180	VAL
1	T	199	GLU
1	T	209	ILE
1	T	210	ARG
1	T	216	SER
1	T	220	SER

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Mol	Chain	Res	Type
1	T	223	GLU
1	T	240	SER
1	T	242	LYS
1	T	244	GLU
1	T	248	MET
1	T	253	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (112) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	GLN
1	A	72	ASN
1	A	91	HIS
1	A	138	ASN
1	A	208	HIS
1	A	218	ASN
1	B	65	GLN
1	B	66	ASN
1	B	72	ASN
1	B	144	ASN
1	C	47	HIS
1	C	72	ASN
1	C	91	HIS
1	C	138	ASN
1	C	221	ASN
1	D	47	HIS
1	D	72	ASN
1	D	144	ASN
1	D	207	GLN
1	D	218	ASN
1	E	66	ASN
1	E	72	ASN
1	E	91	HIS
1	F	47	HIS
1	F	65	GLN
1	F	91	HIS
1	G	66	ASN
1	G	72	ASN
1	G	230	ASN
1	H	47	HIS
1	H	66	ASN
1	H	85	GLN

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Mol	Chain	Res	Type
1	H	221	ASN
1	H	230	ASN
1	I	11	ASN
1	I	72	ASN
1	I	91	HIS
1	I	138	ASN
1	I	221	ASN
1	J	11	ASN
1	J	47	HIS
1	J	72	ASN
1	J	91	HIS
1	J	207	GLN
1	K	59	GLN
1	K	66	ASN
1	K	72	ASN
1	K	218	ASN
1	K	221	ASN
1	K	230	ASN
1	L	47	HIS
1	L	59	GLN
1	L	72	ASN
1	L	91	HIS
1	L	138	ASN
1	L	144	ASN
1	L	221	ASN
1	M	47	HIS
1	M	59	GLN
1	M	65	GLN
1	M	66	ASN
1	M	72	ASN
1	N	15	ASN
1	N	47	HIS
1	N	66	ASN
1	N	72	ASN
1	N	91	HIS
1	N	218	ASN
1	O	59	GLN
1	O	66	ASN
1	O	72	ASN
1	O	185	GLN
1	O	190	HIS
1	O	208	HIS

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Mol	Chain	Res	Type
1	O	218	ASN
1	P	15	ASN
1	P	59	GLN
1	P	66	ASN
1	P	72	ASN
1	P	91	HIS
1	P	96	HIS
1	P	138	ASN
1	P	144	ASN
1	P	230	ASN
1	Q	47	HIS
1	Q	59	GLN
1	Q	66	ASN
1	Q	72	ASN
1	Q	85	GLN
1	Q	91	HIS
1	Q	190	HIS
1	Q	218	ASN
1	Q	230	ASN
1	R	47	HIS
1	R	72	ASN
1	R	85	GLN
1	R	190	HIS
1	R	218	ASN
1	R	230	ASN
1	S	47	HIS
1	S	72	ASN
1	S	144	ASN
1	S	190	HIS
1	S	221	ASN
1	S	230	ASN
1	T	47	HIS
1	T	65	GLN
1	T	66	ASN
1	T	72	ASN
1	T	85	GLN
1	T	190	HIS
1	T	218	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	254/255 (99%)	0.10	9 (3%) 48 48	26, 40, 72, 88	0
1	B	254/255 (99%)	0.11	7 (2%) 56 57	21, 37, 70, 89	0
1	C	254/255 (99%)	0.11	8 (3%) 52 52	22, 39, 72, 93	0
1	D	254/255 (99%)	0.08	4 (1%) 74 75	25, 40, 71, 84	0
1	E	254/255 (99%)	0.18	11 (4%) 39 38	24, 44, 75, 90	0
1	F	254/255 (99%)	0.09	4 (1%) 74 75	23, 39, 71, 88	0
1	G	254/255 (99%)	0.18	10 (3%) 43 43	24, 38, 70, 92	0
1	H	254/255 (99%)	0.07	3 (1%) 81 81	24, 39, 73, 91	0
1	I	254/255 (99%)	0.13	6 (2%) 62 62	25, 40, 70, 85	0
1	J	254/255 (99%)	0.05	6 (2%) 62 62	24, 38, 72, 93	0
1	K	254/255 (99%)	0.26	15 (5%) 26 24	25, 48, 76, 93	0
1	L	254/255 (99%)	0.36	14 (5%) 29 27	27, 52, 79, 90	0
1	M	254/255 (99%)	0.12	3 (1%) 81 81	24, 42, 75, 87	0
1	N	254/255 (99%)	0.16	8 (3%) 52 52	23, 43, 76, 92	0
1	O	254/255 (99%)	0.35	17 (6%) 21 19	24, 45, 77, 93	0
1	P	254/255 (99%)	0.30	12 (4%) 35 34	27, 51, 80, 95	0
1	Q	254/255 (99%)	0.65	34 (13%) 4 3	40, 65, 86, 96	0
1	R	254/255 (99%)	0.56	28 (11%) 7 5	35, 64, 87, 95	0
1	S	254/255 (99%)	0.34	10 (3%) 43 43	41, 64, 85, 96	0
1	T	254/255 (99%)	0.51	28 (11%) 7 5	36, 62, 87, 96	0
All	All	5080/5100 (99%)	0.23	237 (4%) 35 34	21, 46, 79, 96	0

All (237) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	N	2	PRO	11.8
1	R	217	ALA	11.0
1	K	219	GLY	9.2
1	Q	40	VAL	7.9
1	A	217	ALA	7.8
1	O	2	PRO	7.8
1	R	176	GLY	7.8
1	P	175	ILE	7.6
1	C	2	PRO	7.3
1	T	2	PRO	6.7
1	E	216	SER	6.6
1	O	219	GLY	6.5
1	A	222	ASP	6.4
1	L	2	PRO	6.4
1	Q	210	ARG	6.4
1	T	40	VAL	6.0
1	G	2	PRO	5.9
1	J	2	PRO	5.8
1	R	234	PHE	5.6
1	E	217	ALA	5.6
1	G	219	GLY	5.5
1	L	180	VAL	5.4
1	K	218	ASN	5.4
1	Q	166	VAL	5.4
1	Q	25	VAL	5.3
1	Q	176	GLY	5.2
1	C	3	ALA	5.1
1	O	252	LEU	5.0
1	K	235	LEU	4.9
1	H	222	ASP	4.9
1	R	33	ILE	4.9
1	E	215	GLY	4.8
1	S	166	VAL	4.8
1	K	2	PRO	4.8
1	Q	42	ALA	4.7
1	O	225	LEU	4.6
1	I	219	GLY	4.5
1	Q	124	VAL	4.5
1	T	41	ILE	4.4
1	Q	63	ALA	4.4
1	R	40	VAL	4.3
1	I	176	GLY	4.2
1	T	42	ALA	4.2

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Mol	Chain	Res	Type	RSRZ
1	E	219	GLY	4.2
1	R	2	PRO	4.1
1	P	253	THR	4.1
1	T	217	ALA	4.1
1	I	2	PRO	4.1
1	Q	168	ALA	4.0
1	T	12	PHE	4.0
1	Q	196	TRP	4.0
1	T	52	ILE	3.9
1	D	216	SER	3.9
1	I	216	SER	3.9
1	Q	125	ILE	3.8
1	A	175	ILE	3.7
1	C	219	GLY	3.7
1	L	111	ALA	3.7
1	C	81	VAL	3.7
1	M	255	THR	3.7
1	S	252	LEU	3.7
1	P	128	VAL	3.7
1	R	216	SER	3.6
1	K	248	MET	3.6
1	H	2	PRO	3.6
1	Q	37	VAL	3.6
1	R	55	ASN	3.6
1	T	29	ALA	3.6
1	J	219	GLY	3.6
1	Q	249	ILE	3.5
1	L	175	ILE	3.5
1	A	225	LEU	3.5
1	N	227	GLN	3.5
1	P	95	GLY	3.5
1	O	3	ALA	3.4
1	T	166	VAL	3.4
1	Q	8	ILE	3.4
1	T	63	ALA	3.4
1	K	3	ALA	3.3
1	R	209	ILE	3.3
1	C	175	ILE	3.2
1	G	217	ALA	3.2
1	R	38	ASP	3.2
1	R	25	VAL	3.2
1	E	2	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
1	G	220	SER	3.1
1	G	252	LEU	3.1
1	T	37	VAL	3.1
1	L	255	THR	3.1
1	O	198	ALA	3.1
1	R	148	LEU	3.1
1	A	226	GLY	3.1
1	N	3	ALA	3.0
1	Q	179	VAL	3.0
1	T	155	LEU	3.0
1	P	110	SER	3.0
1	D	2	PRO	3.0
1	G	234	PHE	3.0
1	R	245	PHE	2.9
1	A	220	SER	2.9
1	B	63	ALA	2.9
1	R	236	VAL	2.9
1	R	7	PHE	2.9
1	Q	94	VAL	2.9
1	Q	89	LEU	2.9
1	B	176	GLY	2.9
1	D	3	ALA	2.9
1	P	2	PRO	2.8
1	K	83	MET	2.8
1	K	225	LEU	2.8
1	R	37	VAL	2.8
1	N	218	ASN	2.8
1	T	252	LEU	2.8
1	E	202	ALA	2.8
1	Q	51	ALA	2.8
1	R	235	LEU	2.8
1	L	222	ASP	2.8
1	E	225	LEU	2.7
1	R	177	THR	2.7
1	Q	41	ILE	2.7
1	P	249	ILE	2.7
1	F	177	THR	2.7
1	N	216	SER	2.7
1	T	39	VAL	2.7
1	Q	7	PHE	2.7
1	L	101	ARG	2.7
1	R	52	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
1	T	49	SER	2.7
1	Q	84	LEU	2.7
1	S	128	VAL	2.7
1	I	129	GLY	2.6
1	T	25	VAL	2.6
1	Q	26	ALA	2.6
1	R	218	ASN	2.6
1	L	234	PHE	2.6
1	S	25	VAL	2.6
1	O	215	GLY	2.6
1	G	255	THR	2.6
1	O	221	ASN	2.5
1	K	217	ALA	2.5
1	P	174	SER	2.5
1	F	206	ALA	2.5
1	Q	22	LYS	2.5
1	Q	39	VAL	2.5
1	Q	178	GLY	2.5
1	F	137	ALA	2.5
1	T	168	ALA	2.5
1	L	197	PHE	2.5
1	J	111	ALA	2.5
1	Q	177	THR	2.5
1	T	8	ILE	2.5
1	O	220	SER	2.5
1	G	236	VAL	2.4
1	T	203	ALA	2.4
1	A	221	ASN	2.4
1	I	151	LEU	2.4
1	B	171	PRO	2.4
1	S	127	CYS	2.4
1	S	4	ARG	2.4
1	N	254	LYS	2.4
1	E	168	ALA	2.4
1	M	221	ASN	2.3
1	R	34	PRO	2.3
1	B	252	LEU	2.3
1	Q	2	PRO	2.3
1	K	255	THR	2.3
1	R	8	ILE	2.3
1	T	28	ILE	2.3
1	T	195	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	R	165	VAL	2.3
1	T	21	ILE	2.3
1	O	214	GLY	2.3
1	B	223	GLU	2.3
1	L	223	GLU	2.3
1	T	165	VAL	2.3
1	J	165	VAL	2.3
1	T	163	LYS	2.3
1	K	223	GLU	2.2
1	O	197	PHE	2.2
1	T	254	LYS	2.2
1	A	212	ILE	2.2
1	K	252	LEU	2.2
1	E	171	PRO	2.2
1	O	205	GLY	2.2
1	Q	64	ALA	2.2
1	T	202	ALA	2.2
1	N	167	ILE	2.2
1	T	50	THR	2.2
1	S	235	LEU	2.2
1	J	3	ALA	2.2
1	A	218	ASN	2.2
1	C	218	ASN	2.2
1	Q	3	ALA	2.2
1	O	249	ILE	2.2
1	R	252	LEU	2.2
1	B	2	PRO	2.2
1	L	246	MET	2.2
1	E	126	PHE	2.2
1	F	111	ALA	2.2
1	O	137	ALA	2.2
1	O	253	THR	2.2
1	R	175	ILE	2.2
1	O	216	SER	2.2
1	R	147	GLN	2.2
1	R	5	ARG	2.1
1	O	157	GLU	2.1
1	L	252	LEU	2.1
1	P	129	GLY	2.1
1	Q	91	HIS	2.1
1	C	222	ASP	2.1
1	P	117	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	151	LEU	2.1
1	Q	201	VAL	2.1
1	Q	28	ILE	2.1
1	Q	95	GLY	2.1
1	N	193	LEU	2.1
1	R	212	ILE	2.1
1	S	167	ILE	2.1
1	E	200	LYS	2.1
1	G	216	SER	2.1
1	P	140	THR	2.1
1	L	211	ILE	2.1
1	M	222	ASP	2.1
1	T	62	ILE	2.1
1	B	172	VAL	2.0
1	K	126	PHE	2.0
1	S	41	ILE	2.0
1	K	222	ASP	2.0
1	C	216	SER	2.0
1	J	136	LYS	2.0
1	P	255	THR	2.0
1	G	222	ASP	2.0
1	K	162	TRP	2.0
1	Q	241	LEU	2.0
1	L	128	VAL	2.0
1	H	197	PHE	2.0
1	S	34	PRO	2.0

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

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.