



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:15 PM GMT

PDB ID : 1WUU
Title : crystal structure of human galactokinase complexed with MgAMPPNP and galactose
Authors : Thoden, J.B.; Timson, D.J.; Reece, R.J.; Holden, H.M.
Deposited on : 2004-12-08
Resolution : 2.50 Å(reported)

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

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

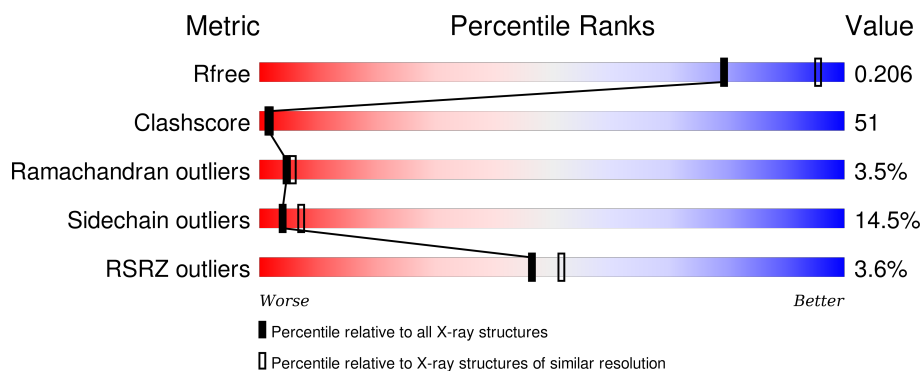
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	399	<div> <div>2%</div> <div> <div></div> <div>28%</div> <div>55%</div> <div>13%</div> <div>..</div> </div> </div>
1	B	399	<div> <div>6%</div> <div> <div></div> <div>27%</div> <div>52%</div> <div>17%</div> <div>..</div> </div> </div>
1	C	399	<div> <div>3%</div> <div> <div></div> <div>29%</div> <div>55%</div> <div>11%</div> <div>..</div> </div> </div>
1	D	399	<div> <div>2%</div> <div> <div></div> <div>28%</div> <div>50%</div> <div>18%</div> <div>..</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GLA	B	393	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12358 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 Galactokinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	391	Total	C	N	O	S	Se	0	0	0
			2960	1847	538	559	8	8			
1	B	390	Total	C	N	O	S	Se	0	0	0
			2942	1838	530	558	8	8			
1	C	390	Total	C	N	O	S	Se	0	0	0
			2944	1838	532	558	8	8			
1	D	390	Total	C	N	O	S	Se	0	1	0
			2952	1842	535	559	8	8			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MSE	-	EXPRESSION TAG	UNP P51570
A	-5	ALA	-	EXPRESSION TAG	UNP P51570
A	-4	HIS	-	EXPRESSION TAG	UNP P51570
A	-3	HIS	-	EXPRESSION TAG	UNP P51570
A	-2	HIS	-	EXPRESSION TAG	UNP P51570
A	-1	HIS	-	EXPRESSION TAG	UNP P51570
A	0	HIS	-	EXPRESSION TAG	UNP P51570
A	1	HIS	-	EXPRESSION TAG	UNP P51570
A	55	MSE	MET	MODIFIED RESIDUE	UNP P51570
A	60	MSE	MET	MODIFIED RESIDUE	UNP P51570
A	180	MSE	MET	MODIFIED RESIDUE	UNP P51570
A	185	MSE	MET	MODIFIED RESIDUE	UNP P51570
A	192	MSE	MET	MODIFIED RESIDUE	UNP P51570
A	307	MSE	MET	MODIFIED RESIDUE	UNP P51570
A	343	MSE	MET	MODIFIED RESIDUE	UNP P51570
A	365	MSE	MET	MODIFIED RESIDUE	UNP P51570
B	-6	MSE	-	EXPRESSION TAG	UNP P51570
B	-5	ALA	-	EXPRESSION TAG	UNP P51570
B	-4	HIS	-	EXPRESSION TAG	UNP P51570
B	-3	HIS	-	EXPRESSION TAG	UNP P51570
B	-2	HIS	-	EXPRESSION TAG	UNP P51570

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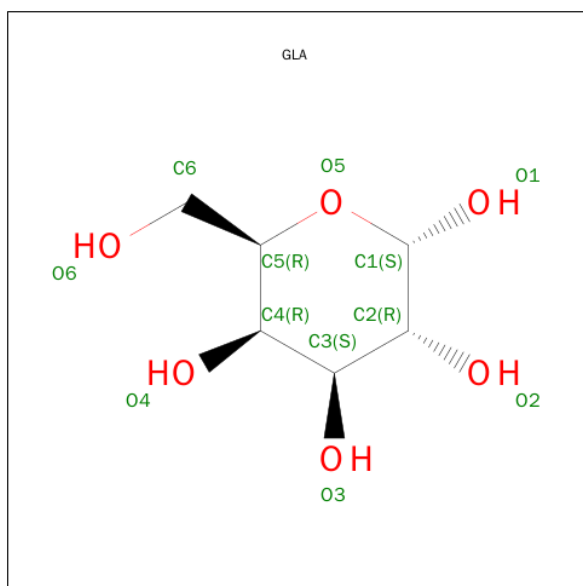
Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	HIS	-	EXPRESSION TAG	UNP P51570
B	0	HIS	-	EXPRESSION TAG	UNP P51570
B	1	HIS	-	EXPRESSION TAG	UNP P51570
B	55	MSE	MET	MODIFIED RESIDUE	UNP P51570
B	60	MSE	MET	MODIFIED RESIDUE	UNP P51570
B	180	MSE	MET	MODIFIED RESIDUE	UNP P51570
B	185	MSE	MET	MODIFIED RESIDUE	UNP P51570
B	192	MSE	MET	MODIFIED RESIDUE	UNP P51570
B	307	MSE	MET	MODIFIED RESIDUE	UNP P51570
B	343	MSE	MET	MODIFIED RESIDUE	UNP P51570
B	365	MSE	MET	MODIFIED RESIDUE	UNP P51570
C	-6	MSE	-	EXPRESSION TAG	UNP P51570
C	-5	ALA	-	EXPRESSION TAG	UNP P51570
C	-4	HIS	-	EXPRESSION TAG	UNP P51570
C	-3	HIS	-	EXPRESSION TAG	UNP P51570
C	-2	HIS	-	EXPRESSION TAG	UNP P51570
C	-1	HIS	-	EXPRESSION TAG	UNP P51570
C	0	HIS	-	EXPRESSION TAG	UNP P51570
C	1	HIS	-	EXPRESSION TAG	UNP P51570
C	55	MSE	MET	MODIFIED RESIDUE	UNP P51570
C	60	MSE	MET	MODIFIED RESIDUE	UNP P51570
C	180	MSE	MET	MODIFIED RESIDUE	UNP P51570
C	185	MSE	MET	MODIFIED RESIDUE	UNP P51570
C	192	MSE	MET	MODIFIED RESIDUE	UNP P51570
C	307	MSE	MET	MODIFIED RESIDUE	UNP P51570
C	343	MSE	MET	MODIFIED RESIDUE	UNP P51570
C	365	MSE	MET	MODIFIED RESIDUE	UNP P51570
D	-6	MSE	-	EXPRESSION TAG	UNP P51570
D	-5	ALA	-	EXPRESSION TAG	UNP P51570
D	-4	HIS	-	EXPRESSION TAG	UNP P51570
D	-3	HIS	-	EXPRESSION TAG	UNP P51570
D	-2	HIS	-	EXPRESSION TAG	UNP P51570
D	-1	HIS	-	EXPRESSION TAG	UNP P51570
D	0	HIS	-	EXPRESSION TAG	UNP P51570
D	1	HIS	-	EXPRESSION TAG	UNP P51570
D	55	MSE	MET	MODIFIED RESIDUE	UNP P51570
D	60	MSE	MET	MODIFIED RESIDUE	UNP P51570
D	180	MSE	MET	MODIFIED RESIDUE	UNP P51570
D	185	MSE	MET	MODIFIED RESIDUE	UNP P51570
D	192	MSE	MET	MODIFIED RESIDUE	UNP P51570
D	307	MSE	MET	MODIFIED RESIDUE	UNP P51570
D	343	MSE	MET	MODIFIED RESIDUE	UNP P51570

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Chain	Residue	Modelled	Actual	Comment	Reference
D	365	MSE	MET	MODIFIED RESIDUE	UNP P51570

- Molecule 2 is SUGAR (D-GALACTOSE) (three-letter code: GLA) (formula: $C_6H_{12}O_6$).

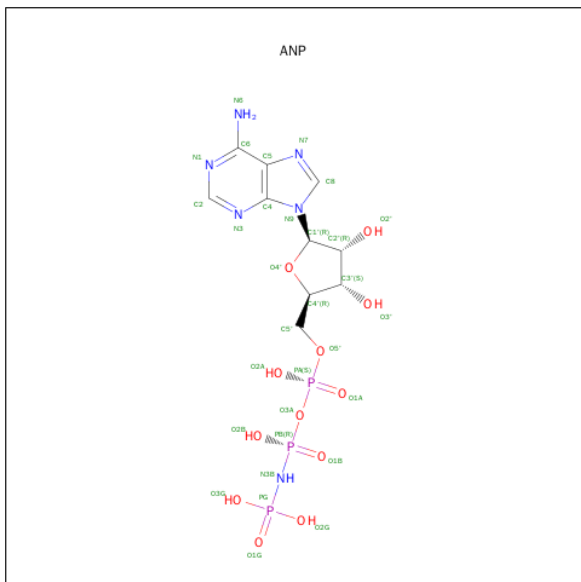


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			12	6	6		
2	B	1	Total	C	O	0	0
			12	6	6		
2	C	1	Total	C	O	0	0
			12	6	6		
2	D	1	Total	C	O	0	0
			12	6	6		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		

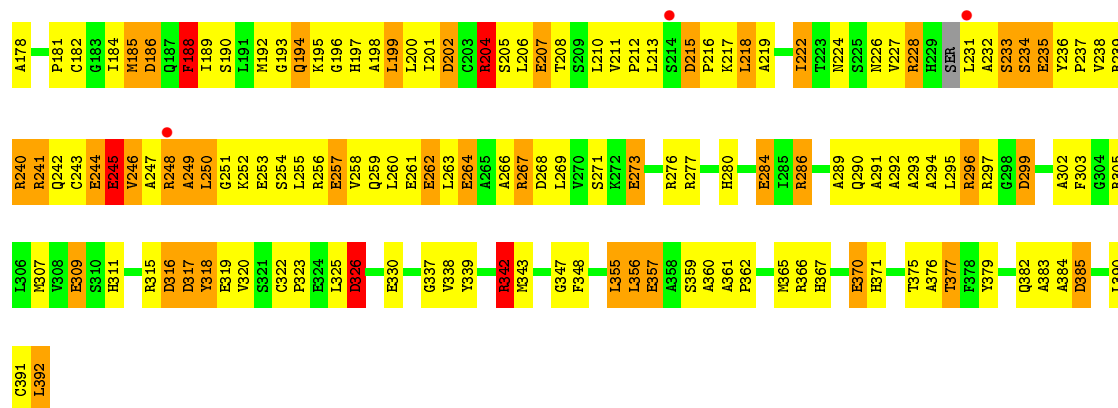
- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $\text{C}_{10}\text{H}_{17}\text{N}_6\text{O}_{12}\text{P}_3$).



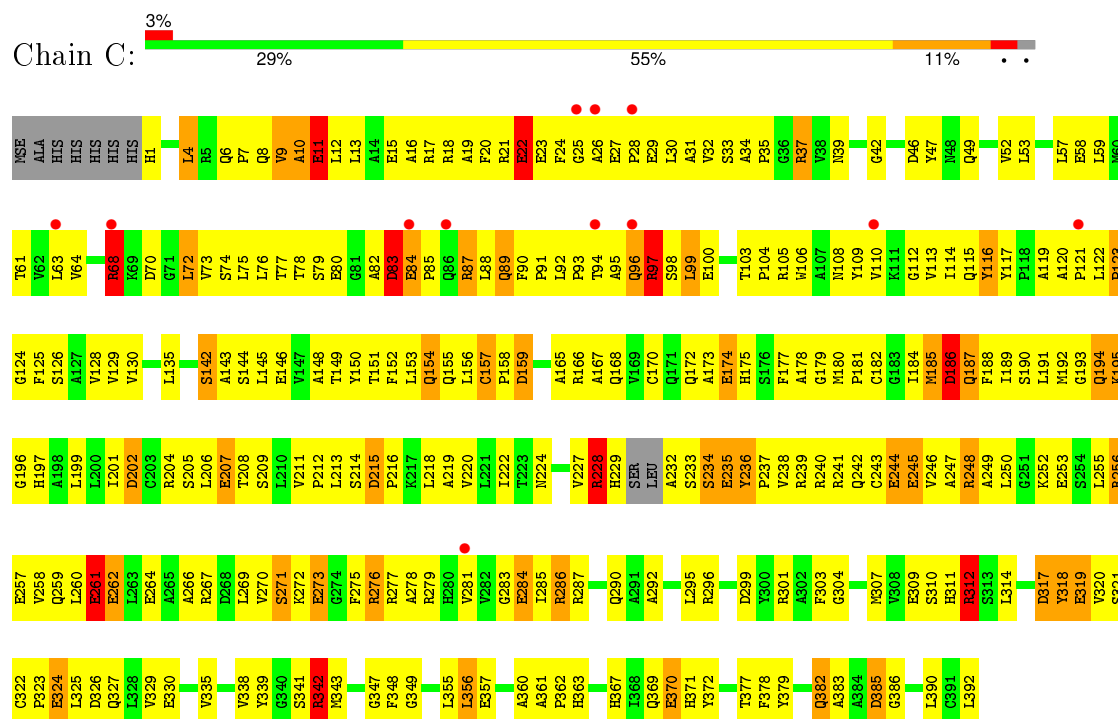
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 31	C 10	N 6	O 12	P 3	0	0
4	B	1	Total 31	C 10	N 6	O 12	P 3	0	0
4	C	1	Total 31	C 10	N 6	O 12	P 3	0	0
4	D	1	Total 31	C 10	N 6	O 12	P 3	0	0

- Molecule 5 is water.

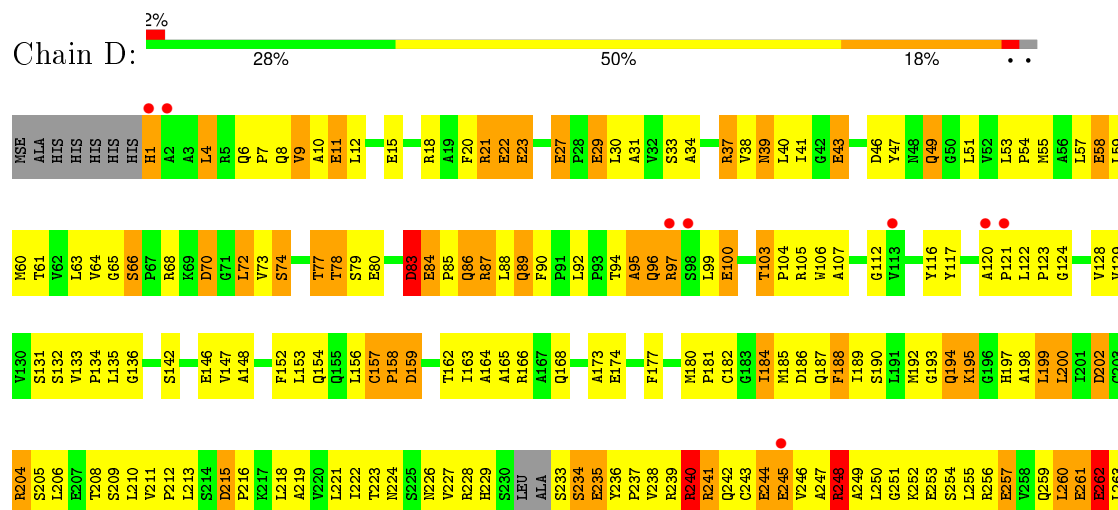
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	94	Total O 94 94	0	0
5	B	89	Total O 89 89	0	0
5	C	105	Total O 105 105	0	0
5	D	96	Total O 96 96	0	0



• Molecule 1: Galactokinase



• Molecule 1: Galactokinase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.20Å 109.60Å 115.80Å 90.00° 95.90° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 19.95 – 2.50	Depositor EDS
% Data completeness (in resolution range)	95.2 (20.00-2.50) 97.9 (19.95-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.02 (at 2.50Å)	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.201 , 0.258 0.201 , 0.206	Depositor DCC
R_{free} test set	6099 reflections (11.00%)	DCC
Wilson B-factor (Å ²)	41.6	Xtriage
Anisotropy	0.546	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 118.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 61550 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12358	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.05	24/3007 (0.8%)	1.32	28/4062 (0.7%)
1	B	1.02	28/2987 (0.9%)	1.39	38/4036 (0.9%)
1	C	1.05	29/2990 (1.0%)	1.31	31/4040 (0.8%)
1	D	1.05	26/3002 (0.9%)	1.33	32/4055 (0.8%)
All	All	1.04	107/11986 (0.9%)	1.34	129/16193 (0.8%)

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

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

All (107) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	244	GLU	CD-OE2	7.87	1.34	1.25
1	A	194	GLN	CA-CB	-7.86	1.36	1.53
1	A	84	GLU	CD-OE2	7.60	1.34	1.25
1	C	261	GLU	CD-OE2	7.42	1.33	1.25
1	D	174	GLU	CD-OE2	7.38	1.33	1.25
1	B	319	GLU	CD-OE2	7.35	1.33	1.25
1	B	23	GLU	CD-OE2	7.24	1.33	1.25
1	C	253	GLU	CD-OE2	7.14	1.33	1.25
1	C	284	GLU	CD-OE2	6.96	1.33	1.25
1	B	264	GLU	CD-OE2	6.94	1.33	1.25
1	B	22	GLU	CD-OE2	6.88	1.33	1.25
1	A	261	GLU	CD-OE2	6.85	1.33	1.25
1	C	80	GLU	CD-OE2	6.82	1.33	1.25
1	D	245	GLU	CD-OE2	6.74	1.33	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	309	GLU	CD-OE2	6.71	1.33	1.25
1	A	22	GLU	CD-OE2	6.69	1.33	1.25
1	D	257	GLU	CD-OE2	6.65	1.32	1.25
1	D	319	GLU	CD-OE2	6.64	1.32	1.25
1	B	58	GLU	CD-OE2	6.62	1.32	1.25
1	A	309	GLU	CD-OE2	6.58	1.32	1.25
1	A	100	GLU	CD-OE2	6.55	1.32	1.25
1	A	11	GLU	CD-OE2	6.54	1.32	1.25
1	D	370	GLU	CD-OE2	6.49	1.32	1.25
1	C	15	GLU	CD-OE2	6.48	1.32	1.25
1	B	330	GLU	CD-OE2	6.45	1.32	1.25
1	A	244	GLU	CD-OE2	6.37	1.32	1.25
1	C	273	GLU	CD-OE2	6.36	1.32	1.25
1	D	235	GLU	CD-OE2	6.34	1.32	1.25
1	A	330	GLU	CD-OE2	6.33	1.32	1.25
1	C	23	GLU	CD-OE2	6.29	1.32	1.25
1	D	253	GLU	CD-OE2	6.28	1.32	1.25
1	A	15	GLU	CD-OE2	6.28	1.32	1.25
1	C	29	GLU	CD-OE2	6.27	1.32	1.25
1	D	261	GLU	CD-OE2	6.26	1.32	1.25
1	C	207	GLU	CD-OE2	6.25	1.32	1.25
1	B	235	GLU	CD-OE2	6.24	1.32	1.25
1	D	11	GLU	CD-OE2	6.17	1.32	1.25
1	B	207	GLU	CD-OE2	6.17	1.32	1.25
1	A	257	GLU	CD-OE2	6.12	1.32	1.25
1	B	84	GLU	CD-OE2	6.12	1.32	1.25
1	B	262	GLU	CD-OE2	6.10	1.32	1.25
1	D	29	GLU	CD-OE2	6.10	1.32	1.25
1	C	370	GLU	CD-OE2	6.05	1.32	1.25
1	D	309	GLU	CD-OE2	6.02	1.32	1.25
1	D	100	GLU	CD-OE2	6.01	1.32	1.25
1	B	15	GLU	CD-OE2	6.00	1.32	1.25
1	C	235	GLU	CD-OE2	5.99	1.32	1.25
1	C	324	GLU	CD-OE2	5.99	1.32	1.25
1	D	273	GLU	CD-OE2	5.97	1.32	1.25
1	C	58	GLU	CD-OE2	5.97	1.32	1.25
1	C	174	GLU	CD-OE2	5.94	1.32	1.25
1	D	23	GLU	CD-OE2	5.93	1.32	1.25
1	C	261	GLU	CD-OE1	-5.92	1.19	1.25
1	C	11	GLU	CD-OE2	5.92	1.32	1.25
1	C	319	GLU	CD-OE2	5.90	1.32	1.25
1	B	273	GLU	CD-OE2	5.89	1.32	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	27	GLU	CD-OE2	5.88	1.32	1.25
1	D	80	GLU	CD-OE2	5.88	1.32	1.25
1	C	22	GLU	CD-OE2	5.88	1.32	1.25
1	A	273	GLU	CD-OE2	5.86	1.32	1.25
1	D	27	GLU	CD-OE2	5.86	1.32	1.25
1	C	330	GLU	CD-OE2	5.85	1.32	1.25
1	D	15	GLU	CD-OE2	5.84	1.32	1.25
1	A	264	GLU	CD-OE2	5.84	1.32	1.25
1	B	27	GLU	CD-OE2	5.84	1.32	1.25
1	A	319	GLU	CD-OE2	5.77	1.31	1.25
1	C	309	GLU	CD-OE2	5.76	1.31	1.25
1	D	22	GLU	CD-OE2	5.76	1.31	1.25
1	B	29	GLU	CD-OE2	5.75	1.31	1.25
1	B	100	GLU	CD-OE2	5.71	1.31	1.25
1	B	245	GLU	CD-OE2	5.71	1.31	1.25
1	C	84	GLU	CD-OE2	5.70	1.31	1.25
1	C	245	GLU	CD-OE2	5.70	1.31	1.25
1	A	29	GLU	CD-OE2	5.66	1.31	1.25
1	B	146	GLU	CD-OE2	5.63	1.31	1.25
1	A	357	GLU	CD-OE2	5.61	1.31	1.25
1	C	257	GLU	CD-OE2	5.58	1.31	1.25
1	D	84	GLU	CD-OE2	5.58	1.31	1.25
1	C	100	GLU	CD-OE2	5.58	1.31	1.25
1	B	261	GLU	CD-OE2	5.56	1.31	1.25
1	B	257	GLU	CD-OE2	5.55	1.31	1.25
1	D	324	GLU	CD-OE2	5.54	1.31	1.25
1	B	43	GLU	CD-OE2	5.53	1.31	1.25
1	B	244	GLU	CD-OE2	5.53	1.31	1.25
1	C	262	GLU	CD-OE2	5.53	1.31	1.25
1	A	43	GLU	CD-OE2	5.48	1.31	1.25
1	D	264	GLU	CD-OE2	5.48	1.31	1.25
1	A	58	GLU	CD-OE2	5.46	1.31	1.25
1	A	235	GLU	CD-OE2	5.45	1.31	1.25
1	B	253	GLU	CD-OE2	5.39	1.31	1.25
1	D	284	GLU	CD-OE2	5.34	1.31	1.25
1	D	262	GLU	CD-OE2	5.33	1.31	1.25
1	B	174	GLU	CD-OE2	5.32	1.31	1.25
1	D	330	GLU	CD-OE2	5.31	1.31	1.25
1	C	357	GLU	CD-OE2	5.29	1.31	1.25
1	A	174	GLU	CD-OE2	5.29	1.31	1.25
1	D	244	GLU	CD-OE2	5.28	1.31	1.25
1	B	284	GLU	CD-OE2	5.26	1.31	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	370	GLU	CD-OE2	5.25	1.31	1.25
1	A	262	GLU	CD-OE2	5.24	1.31	1.25
1	B	11	GLU	CD-OE2	5.23	1.31	1.25
1	D	58	GLU	CD-OE2	5.21	1.31	1.25
1	B	357	GLU	CD-OE2	5.20	1.31	1.25
1	A	253	GLU	CD-OE2	5.20	1.31	1.25
1	A	207	GLU	CD-OE2	5.16	1.31	1.25
1	A	146	GLU	CD-OE2	5.14	1.31	1.25
1	C	284	GLU	CD-OE1	-5.08	1.20	1.25

All (129) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	70	ASP	N-CA-CB	-13.51	86.29	110.60
1	B	70	ASP	CB-CA-C	13.23	136.85	110.40
1	D	157	CYS	C-N-CD	-12.20	93.76	120.60
1	B	46	ASP	CB-CG-OD2	-8.62	110.54	118.30
1	B	204	ARG	NE-CZ-NH1	8.53	124.57	120.30
1	A	299	ASP	CB-CG-OD2	-8.26	110.86	118.30
1	A	83	ASP	CB-CG-OD2	-8.05	111.05	118.30
1	C	186	ASP	CB-CG-OD1	7.77	125.29	118.30
1	B	159	ASP	CB-CG-OD2	-7.61	111.45	118.30
1	B	215	ASP	CB-CG-OD2	-7.55	111.50	118.30
1	B	159	ASP	CB-CG-OD1	7.54	125.08	118.30
1	A	317	ASP	CB-CG-OD2	-7.46	111.58	118.30
1	A	317	ASP	CB-CG-OD1	7.46	125.01	118.30
1	B	46	ASP	CB-CG-OD1	7.36	124.93	118.30
1	C	186	ASP	CB-CG-OD2	-7.33	111.70	118.30
1	D	202	ASP	CB-CG-OD2	-7.29	111.74	118.30
1	C	342	ARG	NE-CZ-NH2	-7.28	116.66	120.30
1	B	241	ARG	NE-CZ-NH1	7.27	123.93	120.30
1	C	385	ASP	CB-CG-OD2	-7.25	111.77	118.30
1	A	46	ASP	CB-CA-C	-7.23	95.94	110.40
1	B	228	ARG	NE-CZ-NH1	7.14	123.87	120.30
1	B	186	ASP	CB-CG-OD2	-7.12	111.89	118.30
1	B	299	ASP	CB-CG-OD2	-7.11	111.90	118.30
1	C	83	ASP	CB-CG-OD2	-7.09	111.92	118.30
1	B	316	ASP	CB-CG-OD2	-7.03	111.97	118.30
1	D	215	ASP	CB-CG-OD2	-7.00	112.00	118.30
1	B	299	ASP	CB-CG-OD1	6.99	124.59	118.30
1	D	299	ASP	CB-CG-OD2	-6.99	112.01	118.30
1	A	215	ASP	CB-CG-OD2	-6.97	112.02	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	286	ARG	NE-CZ-NH1	6.91	123.75	120.30
1	D	202	ASP	CB-CG-OD1	6.90	124.51	118.30
1	C	215	ASP	CB-CG-OD2	-6.89	112.10	118.30
1	B	97	ARG	NE-CZ-NH1	6.88	123.74	120.30
1	C	276	ARG	NE-CZ-NH2	-6.86	116.87	120.30
1	C	286	ARG	NE-CZ-NH1	6.86	123.73	120.30
1	A	236	TYR	CB-CG-CD2	6.82	125.09	121.00
1	A	267	ARG	NE-CZ-NH1	6.81	123.70	120.30
1	B	342	ARG	NE-CZ-NH1	6.76	123.68	120.30
1	A	315	ARG	NE-CZ-NH2	-6.73	116.94	120.30
1	B	268	ASP	CB-CG-OD2	-6.72	112.25	118.30
1	D	301	ARG	NE-CZ-NH1	6.64	123.62	120.30
1	B	37	ARG	NE-CZ-NH2	-6.63	116.98	120.30
1	D	46	ASP	CB-CG-OD2	-6.63	112.33	118.30
1	A	17	ARG	NE-CZ-NH1	6.58	123.59	120.30
1	B	268	ASP	CB-CG-OD1	6.53	124.18	118.30
1	A	268	ASP	CB-CG-OD1	6.52	124.17	118.30
1	A	159	ASP	CB-CG-OD2	-6.50	112.45	118.30
1	A	316	ASP	CB-CG-OD2	-6.47	112.47	118.30
1	B	316	ASP	CB-CG-OD1	6.44	124.10	118.30
1	B	296	ARG	NE-CZ-NH1	6.42	123.51	120.30
1	C	385	ASP	CB-CG-OD1	6.38	124.05	118.30
1	D	229	HIS	N-CA-CB	6.35	122.03	110.60
1	D	268	ASP	CB-CG-OD2	-6.30	112.63	118.30
1	C	326	ASP	CB-CG-OD2	-6.27	112.66	118.30
1	A	301	ARG	NE-CZ-NH1	6.26	123.43	120.30
1	D	240	ARG	NE-CZ-NH1	6.25	123.42	120.30
1	B	385	ASP	CB-CG-OD2	-6.24	112.69	118.30
1	C	317	ASP	CB-CG-OD2	-6.23	112.69	118.30
1	A	299	ASP	CB-CG-OD1	6.18	123.87	118.30
1	C	261	GLU	OE1-CD-OE2	-6.17	115.89	123.30
1	A	236	TYR	CB-CG-CD1	-6.17	117.30	121.00
1	D	186	ASP	CB-CG-OD2	-6.14	112.78	118.30
1	C	317	ASP	CB-CG-OD1	6.13	123.82	118.30
1	C	97	ARG	NE-CZ-NH1	6.10	123.35	120.30
1	C	299	ASP	CB-CG-OD1	6.10	123.79	118.30
1	C	68	ARG	NE-CZ-NH1	6.05	123.33	120.30
1	A	159	ASP	CB-CG-OD1	6.03	123.72	118.30
1	A	316	ASP	CB-CG-OD1	6.00	123.70	118.30
1	B	215	ASP	CB-CG-OD1	5.98	123.68	118.30
1	C	312	ARG	NE-CZ-NH1	5.98	123.29	120.30
1	D	215	ASP	CB-CG-OD1	5.97	123.67	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	186	ASP	CB-CG-OD1	5.96	123.66	118.30
1	D	241	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	D	286	ARG	NE-CZ-NH1	5.91	123.26	120.30
1	A	202	ASP	CB-CG-OD2	-5.88	113.01	118.30
1	D	159	ASP	CB-CG-OD2	-5.86	113.03	118.30
1	B	83	ASP	CB-CG-OD2	-5.85	113.04	118.30
1	B	240	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	A	215	ASP	CB-CG-OD1	5.81	123.53	118.30
1	D	316	ASP	CB-CG-OD2	-5.79	113.09	118.30
1	C	215	ASP	CB-CG-OD1	5.78	123.50	118.30
1	B	326	ASP	CB-CG-OD1	5.72	123.45	118.30
1	B	317	ASP	CB-CG-OD2	-5.68	113.19	118.30
1	C	83	ASP	CB-CG-OD1	5.67	123.40	118.30
1	D	77	THR	N-CA-CB	5.67	121.07	110.30
1	B	202	ASP	CB-CG-OD2	-5.66	113.20	118.30
1	B	385	ASP	CB-CG-OD1	5.66	123.39	118.30
1	C	299	ASP	CB-CG-OD2	-5.63	113.23	118.30
1	B	391	CYS	N-CA-CB	5.62	120.72	110.60
1	C	17	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	A	312	ARG	NE-CZ-NH2	-5.61	117.50	120.30
1	C	228	ARG	NE-CZ-NH1	5.61	123.10	120.30
1	C	312	ARG	NE-CZ-NH2	-5.60	117.50	120.30
1	D	268	ASP	CB-CG-OD1	5.58	123.32	118.30
1	A	391	CYS	N-CA-CB	5.50	120.50	110.60
1	C	116	TYR	CG-CD1-CE1	5.49	125.69	121.30
1	D	299	ASP	CB-CG-OD1	5.47	123.23	118.30
1	C	46	ASP	CB-CG-OD2	-5.47	113.38	118.30
1	C	87	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	A	202	ASP	CB-CG-OD1	5.45	123.20	118.30
1	A	312	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	D	316	ASP	CB-CG-OD1	5.41	123.17	118.30
1	A	385	ASP	CB-CG-OD2	-5.41	113.44	118.30
1	D	83	ASP	CB-CG-OD2	-5.41	113.44	118.30
1	A	186	ASP	CB-CG-OD2	-5.40	113.44	118.30
1	B	241	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	D	74	SER	N-CA-CB	5.37	118.55	110.50
1	D	385	ASP	CB-CG-OD2	-5.36	113.47	118.30
1	A	355	LEU	CB-CA-C	-5.34	100.05	110.20
1	C	301	ARG	NE-CZ-NH1	5.33	122.97	120.30
1	C	326	ASP	CB-CG-OD1	5.33	123.10	118.30
1	D	186	ASP	CB-CG-OD1	5.30	123.07	118.30
1	D	317	ASP	CB-CG-OD2	-5.30	113.53	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	46	ASP	CB-CG-OD1	5.26	123.04	118.30
1	B	70	ASP	CB-CG-OD2	5.24	123.02	118.30
1	D	277	ARG	NE-CZ-NH2	-5.23	117.68	120.30
1	B	377	THR	CA-CB-CG2	-5.22	105.08	112.40
1	D	240	ARG	NE-CZ-NH2	-5.11	117.74	120.30
1	C	159	ASP	CB-CG-OD2	-5.10	113.71	118.30
1	D	312	ARG	NE-CZ-NH2	-5.09	117.75	120.30
1	C	202	ASP	CB-CG-OD2	-5.09	113.72	118.30
1	B	37	ARG	NE-CZ-NH1	5.09	122.84	120.30
1	D	21	ARG	NE-CZ-NH1	5.08	122.84	120.30
1	D	248	ARG	N-CA-CB	5.06	119.71	110.60
1	A	385	ASP	CB-CG-OD1	5.05	122.85	118.30
1	B	188	PHE	CB-CG-CD1	-5.03	117.28	120.80
1	D	159	ASP	CB-CG-OD1	5.02	122.82	118.30
1	C	342	ARG	NE-CZ-NH1	5.01	122.81	120.30
1	B	317	ASP	CB-CG-OD1	5.00	122.81	118.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	D	229	HIS	CA

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2960	0	2947	286	0
1	B	2942	0	2930	328	0
1	C	2944	0	2929	302	0
1	D	2952	0	2939	311	0
2	A	12	0	12	1	0
2	B	12	0	12	0	0
2	C	12	0	12	0	0
2	D	12	0	12	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	31	0	13	6	0
4	B	31	0	13	7	0
4	C	31	0	13	8	0
4	D	31	0	13	3	0
5	A	94	0	0	6	0
5	B	89	0	0	7	0
5	C	105	0	0	9	0
5	D	96	0	0	14	0
All	All	12358	0	11845	1220	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 51.

All (1220) 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:B:201:ILE:HG23	1:B:208:THR:HG22	1.24	1.18
1:B:250:LEU:HD21	1:B:266:ALA:HB2	1.20	1.16
1:A:266:ALA:HB1	1:A:269:LEU:HB2	1.29	1.14
1:A:307:MSE:HE1	1:A:355:LEU:HB2	1.30	1.13
1:A:246:VAL:HG22	1:A:270:VAL:HG11	1.27	1.12
1:A:304:GLY:HA2	1:A:307:MSE:HE3	1.22	1.10
1:B:259:GLN:HB2	1:B:262:GLU:HG3	1.33	1.09
1:B:153:LEU:HA	1:B:156:LEU:HD12	1.33	1.08
1:D:266:ALA:HA	1:D:269:LEU:HD12	1.35	1.08
1:D:77:THR:HG22	1:D:79:SER:H	1.23	1.04
1:C:97:ARG:HB2	1:C:97:ARG:HH11	1.22	1.04
1:B:2:ALA:HB2	1:D:334:ALA:HB1	1.35	1.03
1:D:198:ALA:HB2	1:D:213:LEU:HD11	1.44	0.99
1:B:150:TYR:HE2	1:B:166:ARG:HD3	1.26	0.99
1:A:98:SER:HB3	1:A:115:GLN:HE22	1.28	0.97
1:C:94:THR:HG22	1:C:96:GLN:H	1.27	0.97
1:C:135:LEU:HD22	4:C:395:ANP:H3'	1.48	0.96
1:D:88:LEU:HD12	1:D:89:GLN:H	1.27	0.95
1:A:100:GLU:HG3	1:A:101:PRO:HD2	1.50	0.93
1:C:188:PHE:CE2	1:C:192:MSE:HE3	2.04	0.93
1:A:188:PHE:CD2	1:A:192:MSE:HG3	2.05	0.92
1:B:14:ALA:HB1	1:B:18:ARG:NH1	1.84	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:113:VAL:HG11	1:C:149:THR:HG22	1.50	0.91
1:C:115:GLN:HG2	1:C:177:PHE:HZ	1.36	0.91
1:B:197:HIS:HD2	1:B:210:LEU:HB3	1.34	0.90
1:B:77:THR:HG22	1:B:79:SER:H	1.37	0.89
1:B:152:PHE:CD2	1:B:156:LEU:HD11	2.08	0.89
1:D:85:PRO:HD2	1:D:104:PRO:HG3	1.53	0.89
1:C:49:GLN:HE21	1:C:204:ARG:HG3	1.34	0.89
1:C:361:ALA:HB3	1:C:362:PRO:HD3	1.55	0.89
1:A:184:ILE:H	1:A:184:ILE:HD12	1.35	0.89
1:B:93:PRO:HA	1:B:97:ARG:HG2	1.55	0.88
1:B:150:TYR:CE2	1:B:166:ARG:HD3	2.08	0.88
1:D:221:LEU:HB3	1:D:354:THR:HB	1.54	0.88
1:A:361:ALA:HB3	1:A:362:PRO:HD3	1.55	0.88
1:B:120:ALA:HB1	1:B:121:PRO:HA	1.55	0.87
1:B:83:ASP:HB3	1:B:106:TRP:HD1	1.38	0.87
1:B:16:ALA:HB1	1:B:64:VAL:HG22	1.56	0.86
1:C:184:ILE:HG21	1:C:206:LEU:HD21	1.58	0.86
1:B:94:THR:HG22	1:B:95:ALA:H	1.39	0.86
1:C:150:TYR:CE2	1:C:166:ARG:HD3	2.10	0.85
1:A:307:MSE:HE1	1:A:355:LEU:CB	2.06	0.85
1:C:49:GLN:NE2	1:C:204:ARG:HG3	1.92	0.84
1:A:116:TYR:O	1:A:117:TYR:C	2.16	0.84
1:B:259:GLN:HB2	1:B:262:GLU:CG	2.08	0.84
1:B:201:ILE:HG23	1:B:208:THR:CG2	2.06	0.83
1:A:188:PHE:HD2	1:A:192:MSE:HG3	1.42	0.83
1:C:33:SER:HB3	1:C:390:LEU:HD11	1.58	0.83
1:B:2:ALA:CB	1:D:334:ALA:HB1	2.08	0.83
1:A:287:ARG:HG2	1:A:306:LEU:HD23	1.58	0.83
1:D:21:ARG:HE	1:D:27:GLU:HG3	1.43	0.83
1:A:266:ALA:CB	1:A:269:LEU:HB2	2.07	0.82
1:D:218:LEU:HD12	1:D:219:ALA:H	1.42	0.82
1:D:266:ALA:HB1	1:D:269:LEU:HB2	1.60	0.82
1:B:224:ASN:HB3	1:B:377:THR:HB	1.61	0.82
1:C:237:PRO:HB2	1:C:241:ARG:HH21	1.46	0.81
1:B:366:ARG:HH11	1:B:366:ARG:HG3	1.44	0.81
1:B:188:PHE:CE1	1:B:206:LEU:HD11	2.15	0.81
1:C:213:LEU:HD13	1:C:295:LEU:HD21	1.62	0.81
1:B:14:ALA:HB1	1:B:18:ARG:HH12	1.41	0.81
1:B:150:TYR:CE2	1:B:166:ARG:HB3	2.16	0.81
1:D:291:ALA:HB1	1:D:303:PHE:CE1	2.15	0.80
1:D:266:ALA:CA	1:D:269:LEU:HD12	2.11	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:115:GLN:HG2	1:C:177:PHE:CZ	2.15	0.80
1:C:150:TYR:HE2	1:C:166:ARG:HD3	1.44	0.80
1:A:291:ALA:HB1	1:A:303:PHE:CE1	2.17	0.80
1:D:311:HIS:CD2	1:D:329:VAL:HG21	2.16	0.80
1:C:135:LEU:HD21	4:C:395:ANP:C5	2.13	0.79
1:A:304:GLY:HA2	1:A:307:MSE:CE	2.10	0.79
1:D:332:ALA:HB2	1:D:368:ILE:HD11	1.65	0.79
1:D:240:ARG:O	1:D:244:GLU:HG3	1.83	0.79
1:D:74:SER:HB2	1:D:89:GLN:HG3	1.64	0.79
1:B:188:PHE:HE1	1:B:206:LEU:HD21	1.47	0.78
1:D:304:GLY:HA2	1:D:307:MSE:HG3	1.64	0.78
1:D:37:ARG:HA	1:D:57:LEU:HG	1.65	0.78
1:C:63:LEU:CD1	1:C:129:VAL:HG22	2.13	0.78
1:D:236:TYR:HB3	1:D:237:PRO:HD3	1.66	0.78
1:B:338:VAL:HA	1:B:356:LEU:HB3	1.65	0.78
1:A:49:GLN:O	1:A:256:ARG:HD2	1.84	0.78
1:C:175:HIS:CE1	1:C:181:PRO:HA	2.19	0.77
1:B:4:LEU:HD23	1:B:379:TYR:CE2	2.20	0.77
1:C:90:PHE:HB2	1:C:91:PRO:HD2	1.66	0.77
1:C:92:LEU:HD11	1:C:123:PRO:O	1.83	0.77
1:D:49:GLN:O	1:D:256:ARG:HD3	1.84	0.77
1:D:68:ARG:HH12	1:D:72:LEU:HD12	1.50	0.77
1:B:198:ALA:HB2	1:B:213:LEU:HD11	1.67	0.76
1:B:361:ALA:O	1:B:365:MSE:HG3	1.86	0.76
1:D:219:ALA:HB3	1:D:356:LEU:HD13	1.66	0.76
1:B:142:SER:O	1:B:146:GLU:HG3	1.86	0.76
1:B:188:PHE:CE1	1:B:206:LEU:HD21	2.19	0.76
1:A:232:ALA:O	1:A:235:GLU:HB2	1.85	0.76
1:B:47:TYR:CD1	1:B:240:ARG:HG3	2.21	0.75
1:C:103:THR:HG23	1:C:104:PRO:HA	1.67	0.75
1:C:237:PRO:HB2	1:C:241:ARG:NH2	2.00	0.75
1:B:250:LEU:CD2	1:B:266:ALA:HB2	2.10	0.75
1:B:23:GLU:OE2	1:B:87:ARG:HD3	1.86	0.75
1:A:308:VAL:HG22	1:A:333:LEU:HD11	1.69	0.75
1:D:87:ARG:HG2	1:D:87:ARG:HH11	1.52	0.75
1:D:30:LEU:HD21	5:D:464:HOH:O	1.86	0.75
1:B:73:VAL:CG1	1:B:75:LEU:HD21	2.17	0.75
1:B:29:GLU:OE1	1:B:67:PRO:HD2	1.87	0.75
1:B:250:LEU:HD21	1:B:266:ALA:CB	2.09	0.74
1:D:260:LEU:O	1:D:260:LEU:HD12	1.87	0.74
1:A:246:VAL:CG2	1:A:270:VAL:HG11	2.15	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:70:ASP:OD1	5:D:465:HOH:O	2.05	0.74
1:C:292:ALA:O	1:C:296:ARG:HG3	1.87	0.74
1:C:264:GLU:OE2	1:C:267:ARG:HD3	1.87	0.74
1:B:116:TYR:O	1:B:117:TYR:C	2.22	0.74
1:A:236:TYR:HB3	1:A:237:PRO:HD3	1.68	0.74
1:B:164:ALA:O	1:B:168:GLN:HG3	1.88	0.74
1:A:8:GLN:O	1:A:11:GLU:HB2	1.87	0.73
1:A:120:ALA:HB1	1:A:121:PRO:HA	1.68	0.73
1:C:74:SER:HB2	1:C:89:GLN:CG	2.19	0.73
1:B:105:ARG:HH11	1:B:105:ARG:HG3	1.51	0.73
1:C:99:LEU:HD23	1:C:99:LEU:H	1.54	0.73
1:C:72:LEU:HD23	1:C:91:PRO:HA	1.69	0.73
1:A:384:ALA:HB1	5:A:465:HOH:O	1.89	0.73
1:A:31:ALA:HB3	1:A:390:LEU:O	1.88	0.73
1:B:250:LEU:O	1:B:252:LYS:HG2	1.89	0.73
1:A:94:THR:HG22	1:A:96:GLN:H	1.53	0.73
1:B:16:ALA:HB1	1:B:64:VAL:CG2	2.19	0.72
1:D:241:ARG:O	1:D:245:GLU:HG3	1.88	0.72
1:A:162:THR:HG23	1:A:165:ALA:H	1.53	0.72
1:D:6:GLN:OE1	1:D:58:GLU:HB2	1.89	0.72
1:C:120:ALA:HB1	1:C:121:PRO:HA	1.70	0.72
1:D:162:THR:O	1:D:165:ALA:HB3	1.89	0.72
1:C:72:LEU:CD2	1:C:91:PRO:HA	2.20	0.72
1:B:92:LEU:O	1:B:97:ARG:HD3	1.89	0.72
1:B:198:ALA:HB2	1:B:213:LEU:CD1	2.19	0.72
1:A:189:ILE:HD13	1:A:199:LEU:HG	1.72	0.72
1:A:187:GLN:O	1:A:191:LEU:HD12	1.90	0.71
1:B:286:ARG:O	1:B:290:GLN:HG3	1.89	0.71
1:A:49:GLN:HE21	1:A:204:ARG:HG3	1.55	0.71
1:C:113:VAL:HG11	1:C:149:THR:CG2	2.21	0.71
1:D:343:MSE:HE1	1:D:347:GLY:HA2	1.71	0.71
1:C:97:ARG:CB	1:C:97:ARG:HH11	2.00	0.71
1:B:122:LEU:HD12	1:B:157:CYS:HB3	1.72	0.71
1:D:185:MSE:O	1:D:189:ILE:HG22	1.91	0.71
1:A:8:GLN:HB2	1:A:11:GLU:OE1	1.89	0.71
1:A:322:CYS:HB2	1:A:323:PRO:HD2	1.72	0.71
1:D:302:ALA:O	1:D:306:LEU:HD12	1.89	0.71
1:B:245:GLU:O	1:B:246:VAL:C	2.27	0.71
1:C:267:ARG:HD2	1:C:275:PHE:CE1	2.25	0.71
1:C:21:ARG:HA	1:C:26:ALA:O	1.90	0.71
1:D:88:LEU:HD12	1:D:89:GLN:N	2.02	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:293:ALA:O	1:B:297:ARG:HB2	1.91	0.71
1:D:122:LEU:HD12	1:D:123:PRO:HD2	1.72	0.70
1:C:327:GLN:NE2	5:C:497:HOH:O	2.23	0.70
1:D:332:ALA:HB2	1:D:368:ILE:CD1	2.20	0.70
1:B:117:TYR:CD1	1:B:118:PRO:HD2	2.26	0.70
1:A:100:GLU:CG	1:A:101:PRO:HD2	2.20	0.70
1:A:198:ALA:HB2	1:A:213:LEU:HD13	1.74	0.70
1:B:192:MSE:HE3	1:B:192:MSE:HA	1.72	0.70
1:C:241:ARG:O	1:C:245:GLU:HG3	1.91	0.70
1:C:28:PRO:CB	1:C:64:VAL:HG13	2.22	0.70
1:B:273:GLU:HA	1:B:276:ARG:CZ	2.22	0.70
1:B:197:HIS:CD2	1:B:210:LEU:HB3	2.24	0.70
1:C:99:LEU:HD23	1:C:99:LEU:N	2.06	0.70
1:B:7:PRO:HB2	1:B:12:LEU:HG	1.72	0.70
1:C:323:PRO:O	1:C:327:GLN:HG3	1.91	0.69
1:B:258:VAL:HG11	1:B:263:LEU:HD12	1.74	0.69
1:B:235:GLU:O	1:B:238:VAL:HB	1.93	0.69
1:B:73:VAL:HG12	1:B:75:LEU:HD21	1.74	0.69
1:D:343:MSE:HE1	1:D:347:GLY:CA	2.22	0.69
1:C:311:HIS:HB2	1:C:342:ARG:CB	2.21	0.69
1:B:242:GLN:OE1	1:B:277:ARG:HG3	1.93	0.69
1:D:263:LEU:HG	1:D:275:PHE:CE1	2.27	0.69
1:D:195:LYS:HB2	1:D:385:ASP:OD1	1.93	0.69
1:C:184:ILE:HA	5:C:477:HOH:O	1.92	0.68
1:D:197:HIS:HD2	1:D:210:LEU:HB3	1.58	0.68
1:A:312:ARG:HE	1:A:315:ARG:NH1	1.91	0.68
1:A:150:TYR:HD2	1:A:154:GLN:HE21	1.38	0.68
1:B:188:PHE:HD2	1:B:192:MSE:HG3	1.59	0.68
1:C:91:PRO:HG2	1:C:97:ARG:NH2	2.08	0.68
1:B:88:LEU:HD12	1:B:107:ALA:CB	2.23	0.68
1:A:117:TYR:CD1	1:A:118:PRO:HD2	2.29	0.68
1:D:218:LEU:HD22	1:D:300:TYR:CE1	2.29	0.68
1:D:339:TYR:CD1	1:D:356:LEU:HA	2.29	0.68
1:A:338:VAL:HA	1:A:356:LEU:HB3	1.75	0.68
1:C:74:SER:HB2	1:C:89:GLN:HG3	1.76	0.68
1:D:227:VAL:HG21	1:D:324:GLU:HG2	1.75	0.67
1:D:12:LEU:HD12	1:D:60:MSE:HE3	1.76	0.67
1:C:146:GLU:O	1:C:149:THR:HB	1.95	0.67
1:D:361:ALA:HB3	1:D:362:PRO:HD3	1.77	0.67
1:C:103:THR:CG2	1:C:104:PRO:HA	2.24	0.67
1:C:47:TYR:CD1	1:C:240:ARG:HG3	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:74:SER:CB	1:D:89:GLN:HG3	2.25	0.67
1:A:366:ARG:O	1:A:367:HIS:C	2.30	0.67
4:C:395:ANP:N7	5:C:439:HOH:O	2.28	0.67
1:D:147:VAL:HG21	1:D:190:SER:HB3	1.77	0.67
1:B:32:VAL:HA	1:B:390:LEU:HG	1.77	0.67
1:D:224:ASN:HB3	1:D:377:THR:HB	1.77	0.67
1:A:110:VAL:O	1:A:114:ILE:HG13	1.94	0.67
1:D:332:ALA:CB	1:D:368:ILE:HD11	2.24	0.67
1:D:20:PHE:HD1	1:D:128:VAL:HG23	1.60	0.67
1:C:34:ALA:HB3	1:C:148:ALA:HB2	1.76	0.67
1:A:164:ALA:O	1:A:168:GLN:HG3	1.94	0.67
1:A:117:TYR:CG	1:A:118:PRO:HD2	2.30	0.66
1:D:29:GLU:HB2	1:D:66:SER:OG	1.96	0.66
1:C:4:LEU:HG	1:C:377:THR:CG2	2.24	0.66
1:A:322:CYS:SG	1:A:325:LEU:HG	2.35	0.66
1:B:152:PHE:CE2	1:B:156:LEU:HD11	2.31	0.66
1:A:117:TYR:OH	1:A:154:GLN:HA	1.96	0.66
1:B:83:ASP:CB	1:B:106:TRP:HD1	2.09	0.66
1:D:273:GLU:O	1:D:274:GLY:C	2.34	0.66
1:D:266:ALA:CB	1:D:269:LEU:HB2	2.26	0.66
1:D:218:LEU:HD12	1:D:219:ALA:N	2.10	0.66
1:A:33:SER:HB3	1:A:390:LEU:HD11	1.76	0.66
1:A:356:LEU:N	1:A:356:LEU:HD12	2.10	0.66
1:C:360:ALA:O	1:C:361:ALA:C	2.34	0.66
1:A:45:THR:O	1:A:48:ASN:N	2.29	0.66
1:D:107:ALA:HB3	5:D:430:HOH:O	1.96	0.66
1:C:205:SER:HB2	1:C:207:GLU:HG3	1.77	0.65
1:D:68:ARG:HH12	1:D:72:LEU:CD1	2.08	0.65
1:D:236:TYR:HB3	1:D:237:PRO:CD	2.26	0.65
1:D:343:MSE:CE	1:D:347:GLY:HA2	2.26	0.65
1:B:273:GLU:HA	1:B:276:ARG:NH2	2.12	0.65
1:B:153:LEU:N	1:B:153:LEU:HD23	2.11	0.65
1:D:117:TYR:OH	1:D:154:GLN:HA	1.96	0.65
1:B:366:ARG:NH1	1:B:366:ARG:HG3	2.10	0.65
1:B:234:SER:O	1:B:238:VAL:HG23	1.96	0.65
1:C:6:GLN:HG2	1:C:59:LEU:HD21	1.78	0.65
1:D:273:GLU:O	1:D:276:ARG:N	2.30	0.65
1:B:266:ALA:O	1:B:269:LEU:N	2.30	0.65
1:B:29:GLU:HB2	1:B:66:SER:OG	1.97	0.65
1:B:94:THR:HG22	1:B:95:ALA:N	2.10	0.65
1:A:68:ARG:N	1:A:124:GLY:O	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:279:ARG:NH2	1:C:317:ASP:OD1	2.30	0.65
1:C:19:ALA:O	1:C:22:GLU:HB3	1.97	0.65
1:A:250:LEU:HD21	1:A:266:ALA:HB3	1.78	0.65
1:D:198:ALA:HB2	1:D:213:LEU:CD1	2.22	0.65
1:D:85:PRO:HD2	1:D:104:PRO:CG	2.26	0.65
1:D:259:GLN:N	1:D:262:GLU:OE1	2.30	0.65
1:B:248:ARG:O	1:B:249:ALA:C	2.36	0.65
1:D:39:ASN:HD22	1:D:40:LEU:N	1.94	0.64
1:D:242:GLN:OE1	1:D:277:ARG:NE	2.29	0.64
1:B:6:GLN:HG2	1:B:59:LEU:HD21	1.79	0.64
1:D:266:ALA:O	1:D:269:LEU:N	2.30	0.64
1:D:250:LEU:N	1:D:250:LEU:HD23	2.11	0.64
1:A:92:LEU:HD11	1:A:123:PRO:O	1.97	0.64
1:C:135:LEU:HD22	4:C:395:ANP:C3'	2.26	0.64
1:C:110:VAL:O	1:C:114:ILE:HG13	1.98	0.64
1:C:356:LEU:HD12	1:C:356:LEU:N	2.13	0.64
1:A:243:CYS:O	1:A:246:VAL:N	2.30	0.64
1:A:68:ARG:HD2	1:A:125:PHE:C	2.17	0.64
1:C:242:GLN:OE1	1:C:277:ARG:NE	2.30	0.64
1:A:272:LYS:O	1:A:275:PHE:N	2.29	0.64
1:C:286:ARG:O	1:C:290:GLN:HG3	1.96	0.64
1:B:83:ASP:OD1	1:B:105:ARG:NH1	2.31	0.64
1:D:335:VAL:HG13	1:D:363:HIS:ND1	2.12	0.64
1:A:18:ARG:NH2	5:A:469:HOH:O	2.23	0.64
1:C:202:ASP:O	1:C:206:LEU:N	2.30	0.64
1:A:307:MSE:HE2	1:A:355:LEU:HD22	1.80	0.64
1:B:27:GLU:OE1	1:B:27:GLU:HA	1.97	0.64
1:B:117:TYR:CE2	1:B:119:ALA:HB3	2.33	0.63
1:B:88:LEU:HD12	1:B:107:ALA:HB2	1.81	0.63
1:C:63:LEU:HD11	1:C:129:VAL:HG22	1.79	0.63
1:A:189:ILE:CD1	1:A:199:LEU:HG	2.28	0.63
1:D:283:GLY:O	1:D:287:ARG:HB2	1.97	0.63
1:A:227:VAL:HG21	1:A:324:GLU:HG2	1.81	0.63
1:C:68:ARG:NH1	1:C:70:ASP:HB2	2.14	0.63
1:A:302:ALA:O	1:A:306:LEU:HD12	1.96	0.63
1:B:4:LEU:HD23	1:B:379:TYR:HE2	1.63	0.63
1:D:226:ASN:ND2	1:D:375:THR:O	2.30	0.63
1:A:49:GLN:NE2	1:A:204:ARG:HG3	2.13	0.63
1:B:248:ARG:O	1:B:251:GLY:N	2.30	0.63
1:B:103:THR:HG23	1:B:104:PRO:HA	1.81	0.63
1:B:188:PHE:CD2	1:B:192:MSE:HG3	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:280:HIS:HA	5:D:412:HOH:O	1.98	0.63
1:B:337:GLY:O	1:B:357:GLU:HG3	1.99	0.63
1:D:7:PRO:HG2	1:D:12:LEU:HD21	1.79	0.63
1:D:20:PHE:CD1	1:D:128:VAL:HG23	2.33	0.63
1:A:250:LEU:HD21	1:A:266:ALA:CB	2.28	0.63
1:A:98:SER:HB3	1:A:115:GLN:NE2	2.09	0.63
1:D:259:GLN:HB2	1:D:262:GLU:CD	2.18	0.63
1:D:21:ARG:NE	1:D:27:GLU:HG3	2.11	0.63
1:D:304:GLY:HA2	1:D:307:MSE:HE2	1.79	0.63
1:B:215:ASP:OD1	1:B:216:PRO:HD2	1.99	0.63
1:B:248:ARG:O	1:B:250:LEU:N	2.32	0.62
1:B:259:GLN:CB	1:B:262:GLU:HG3	2.21	0.62
1:B:29:GLU:O	1:B:30:LEU:HD23	1.99	0.62
1:C:234:SER:O	1:C:238:VAL:HG23	1.98	0.62
1:C:356:LEU:H	1:C:356:LEU:HD12	1.63	0.62
1:A:182:CYS:O	1:A:240:ARG:NH1	2.31	0.62
1:D:357:GLU:O	1:D:358:ALA:C	2.36	0.62
1:A:266:ALA:O	1:A:267:ARG:C	2.36	0.62
1:C:97:ARG:HB2	1:C:97:ARG:NH1	2.04	0.62
1:C:250:LEU:HD12	1:C:250:LEU:N	2.13	0.62
1:A:296:ARG:HG2	5:A:461:HOH:O	1.98	0.62
1:C:335:VAL:HG13	1:C:363:HIS:ND1	2.14	0.62
1:B:42:GLY:O	1:B:52:VAL:HG12	1.98	0.62
1:D:4:LEU:HD13	5:D:457:HOH:O	1.99	0.62
1:B:97:ARG:HG3	1:B:97:ARG:HH11	1.64	0.62
1:C:154:GLN:C	1:C:155:GLN:HE21	2.03	0.62
1:D:271:SER:OG	1:D:274:GLY:N	2.33	0.62
1:A:194:GLN:OE1	1:B:192:MSE:HE1	2.00	0.62
1:D:237:PRO:O	1:D:241:ARG:HG3	2.00	0.62
1:A:28:PRO:CB	1:A:64:VAL:HG12	2.29	0.62
1:A:202:ASP:OD1	1:A:256:ARG:NH1	2.30	0.61
1:C:372:TYR:HA	5:C:497:HOH:O	1.99	0.61
1:B:105:ARG:NH1	1:B:105:ARG:HG3	2.13	0.61
1:B:322:CYS:HB2	1:B:323:PRO:HD2	1.81	0.61
1:C:194:GLN:HG2	1:D:163:ILE:CD1	2.30	0.61
1:C:312:ARG:HH11	1:C:312:ARG:HG2	1.65	0.61
1:C:92:LEU:O	1:C:97:ARG:HD3	2.00	0.61
1:D:361:ALA:O	1:D:364:ALA:HB3	1.99	0.61
1:A:291:ALA:HB1	1:A:303:PHE:CD1	2.35	0.61
1:A:266:ALA:O	1:A:269:LEU:N	2.30	0.61
1:D:23:GLU:CD	1:D:87:ARG:HH12	2.04	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:89:GLN:HB2	5:D:469:HOH:O	2.01	0.61
1:C:219:ALA:HB3	1:C:356:LEU:HD13	1.81	0.61
1:C:283:GLY:HA3	5:C:414:HOH:O	2.00	0.61
1:D:238:VAL:O	1:D:239:ARG:C	2.38	0.61
1:D:277:ARG:HB3	1:D:318:TYR:CE1	2.36	0.61
1:B:339:TYR:CD1	1:B:356:LEU:HA	2.35	0.61
1:C:270:VAL:HG23	1:C:271:SER:O	2.01	0.61
1:A:252:LYS:HG2	1:A:257:GLU:HB3	1.82	0.61
1:D:95:ALA:O	1:D:96:GLN:C	2.38	0.61
1:C:149:THR:O	1:C:152:PHE:HB3	2.01	0.61
1:D:182:CYS:O	1:D:240:ARG:NH1	2.34	0.61
1:A:343:MSE:HE1	1:A:347:GLY:CA	2.30	0.61
1:D:77:THR:HG21	4:D:395:ANP:N1	2.16	0.60
1:A:202:ASP:O	1:A:206:LEU:N	2.30	0.60
1:A:232:ALA:HB1	1:A:235:GLU:CG	2.31	0.60
1:C:49:GLN:HE21	1:C:204:ARG:CG	2.12	0.60
1:D:307:MSE:O	1:D:310:SER:HB3	2.00	0.60
1:C:64:VAL:HG22	1:C:392:LEU:HD11	1.82	0.60
1:A:138:GLY:HA2	4:A:395:ANP:O2G	2.00	0.60
1:B:254:SER:OG	1:B:256:ARG:HB3	2.00	0.60
1:C:188:PHE:CD2	1:C:192:MSE:HE3	2.35	0.60
1:D:311:HIS:HB2	1:D:342:ARG:HB3	1.83	0.60
1:D:261:GLU:OE1	1:D:261:GLU:N	2.34	0.60
1:C:232:ALA:HB1	1:C:235:GLU:HG2	1.84	0.60
1:B:120:ALA:CB	1:B:121:PRO:HA	2.20	0.60
1:A:236:TYR:HB3	1:A:237:PRO:CD	2.31	0.60
1:C:105:ARG:O	1:C:108:ASN:HB2	2.01	0.60
1:B:34:ALA:HB3	1:B:144:SER:O	2.01	0.60
1:D:106:TRP:HB2	4:D:395:ANP:N3	2.16	0.60
1:D:43:GLU:HA	1:D:43:GLU:OE1	2.01	0.60
1:B:23:GLU:HG3	1:B:23:GLU:O	2.02	0.60
1:C:335:VAL:HG13	1:C:363:HIS:CE1	2.37	0.60
1:B:169:VAL:HG12	1:B:170:CYS:N	2.15	0.60
1:B:188:PHE:CZ	1:B:206:LEU:HD11	2.36	0.60
1:B:224:ASN:O	1:B:376:ALA:HA	2.01	0.60
1:B:61:THR:HG23	1:B:130:VAL:O	2.02	0.60
1:A:303:PHE:HD2	1:A:307:MSE:HE2	1.66	0.60
1:D:77:THR:HG22	1:D:78:THR:N	2.17	0.60
1:D:49:GLN:HG3	1:D:254:SER:CB	2.32	0.60
1:C:279:ARG:HH21	1:C:317:ASP:CG	2.04	0.60
1:C:325:LEU:HD11	1:C:349:GLY:O	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:258:VAL:HG12	1:C:259:GLN:N	2.16	0.59
1:D:23:GLU:OE2	1:D:87:ARG:NH1	2.34	0.59
1:C:167:ALA:HB2	1:C:191:LEU:HD12	1.83	0.59
1:B:93:PRO:HG3	1:B:99:LEU:HG	1.84	0.59
1:B:8:GLN:O	1:B:9:VAL:C	2.39	0.59
1:B:162:THR:O	1:B:165:ALA:HB3	2.01	0.59
1:B:237:PRO:HB2	1:B:241:ARG:NH2	2.17	0.59
1:B:152:PHE:HD2	1:B:153:LEU:CD2	2.14	0.59
1:D:264:GLU:O	1:D:266:ALA:N	2.35	0.59
1:D:234:SER:O	1:D:238:VAL:HG23	2.02	0.59
1:A:254:SER:OG	1:A:256:ARG:N	2.30	0.59
1:B:188:PHE:O	1:B:192:MSE:N	2.30	0.59
1:C:338:VAL:HA	1:C:356:LEU:HB3	1.84	0.59
1:D:322:CYS:O	1:D:325:LEU:N	2.36	0.59
1:D:31:ALA:CB	1:D:64:VAL:HG12	2.32	0.59
1:B:41:ILE:HG22	1:B:53:LEU:HB3	1.85	0.59
1:D:277:ARG:O	1:D:280:HIS:HB3	2.02	0.59
1:C:224:ASN:HB3	1:C:377:THR:HB	1.85	0.59
1:B:138:GLY:H	4:B:395:ANP:HNB1	1.50	0.59
1:B:149:THR:O	1:B:150:TYR:C	2.39	0.59
1:C:185:MSE:HG2	1:C:186:ASP:N	2.17	0.59
1:D:39:ASN:ND2	1:D:41:ILE:H	2.01	0.59
1:A:259:GLN:O	1:A:262:GLU:N	2.35	0.59
1:A:339:TYR:HB2	1:A:355:LEU:HB3	1.84	0.59
1:C:135:LEU:HD21	4:C:395:ANP:C4	2.33	0.59
1:A:77:THR:O	1:A:86:GLN:HG2	2.02	0.59
1:B:370:GLU:HB3	1:B:371:HIS:CD2	2.38	0.59
1:A:9:VAL:HG22	1:A:60:MSE:CE	2.33	0.59
1:B:21:ARG:HA	1:B:26:ALA:O	2.03	0.58
1:D:329:VAL:O	1:D:332:ALA:N	2.36	0.58
1:A:23:GLU:HG3	1:A:23:GLU:O	2.02	0.58
1:A:335:VAL:HG13	1:A:363:HIS:ND1	2.18	0.58
1:D:49:GLN:HB3	1:D:204:ARG:HB2	1.84	0.58
1:A:295:LEU:HD12	1:A:295:LEU:O	2.04	0.58
1:D:4:LEU:HD22	1:D:377:THR:CG2	2.34	0.58
1:B:245:GLU:O	1:B:248:ARG:N	2.37	0.58
1:D:103:THR:HA	1:D:104:PRO:C	2.24	0.58
1:D:310:SER:OG	1:D:342:ARG:NH1	2.36	0.58
1:B:258:VAL:HG11	1:B:263:LEU:CD1	2.32	0.58
1:B:147:VAL:HG21	1:B:190:SER:HB3	1.84	0.58
1:D:266:ALA:HA	1:D:269:LEU:CD1	2.22	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:94:THR:N	1:C:97:ARG:O	2.35	0.58
1:B:83:ASP:HB3	1:B:106:TRP:CD1	2.29	0.58
1:A:143:ALA:HB2	1:A:186:ASP:HB3	1.85	0.58
1:D:242:GLN:OE1	1:D:277:ARG:HG3	2.03	0.58
1:C:184:ILE:CG2	1:C:206:LEU:HD21	2.33	0.58
1:D:362:PRO:HA	1:D:365:MSE:HE3	1.85	0.58
1:A:66:SER:HB3	1:A:67:PRO:HD2	1.86	0.58
1:D:248:ARG:O	1:D:249:ALA:C	2.41	0.58
1:B:356:LEU:HD12	1:B:356:LEU:N	2.18	0.58
1:C:175:HIS:NE2	1:C:181:PRO:HA	2.18	0.58
1:B:23:GLU:OE1	1:B:87:ARG:NH1	2.36	0.58
1:C:18:ARG:O	1:C:19:ALA:C	2.41	0.58
1:C:117:TYR:OH	1:C:154:GLN:HA	2.04	0.58
1:C:49:GLN:O	1:C:256:ARG:HD3	2.04	0.58
1:B:105:ARG:O	1:B:108:ASN:HB2	2.04	0.58
1:C:311:HIS:HB2	1:C:342:ARG:HB3	1.86	0.58
1:A:45:THR:HB	1:A:50:GLY:HA3	1.85	0.58
1:B:58:GLU:HG2	1:B:384:ALA:HB2	1.85	0.57
1:B:145:LEU:O	1:B:146:GLU:C	2.41	0.57
1:C:4:LEU:HD23	1:C:4:LEU:N	2.18	0.57
1:D:304:GLY:HA3	1:D:339:TYR:O	2.04	0.57
1:A:188:PHE:CZ	1:A:206:LEU:HD23	2.39	0.57
1:B:150:TYR:HD2	1:B:154:GLN:HE21	1.51	0.57
1:B:338:VAL:HA	1:B:356:LEU:CB	2.34	0.57
1:A:335:VAL:HG13	1:A:363:HIS:CE1	2.39	0.57
1:B:73:VAL:HG23	1:B:92:LEU:HD12	1.86	0.57
1:B:97:ARG:NH1	1:B:97:ARG:HG3	2.20	0.57
1:A:331:ALA:O	1:A:334:ALA:HB3	2.04	0.57
1:C:189:ILE:HG23	1:C:190:SER:N	2.20	0.57
1:B:117:TYR:CG	1:B:118:PRO:HD2	2.40	0.57
1:C:37:ARG:HA	1:C:57:LEU:HG	1.87	0.57
1:D:135:LEU:N	1:D:135:LEU:HD23	2.19	0.57
1:B:142:SER:HB3	4:B:395:ANP:O2A	2.05	0.57
1:D:369:GLN:O	1:D:372:TYR:N	2.34	0.57
1:C:32:VAL:HG11	1:C:151:THR:HG22	1.86	0.57
1:B:13:LEU:O	1:B:16:ALA:N	2.38	0.57
1:D:242:GLN:O	1:D:245:GLU:N	2.36	0.57
1:C:88:LEU:HD22	1:C:104:PRO:HD2	1.87	0.57
1:D:197:HIS:CD2	1:D:210:LEU:HB3	2.38	0.57
1:A:192:MSE:HA	1:A:192:MSE:HE3	1.87	0.56
1:D:271:SER:HG	1:D:274:GLY:H	1.52	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:320:VAL:O	1:A:348:PHE:N	2.38	0.56
1:C:18:ARG:O	1:C:21:ARG:N	2.38	0.56
1:A:94:THR:HG22	1:A:95:ALA:N	2.20	0.56
1:C:284:GLU:OE1	1:C:287:ARG:NH2	2.35	0.56
1:C:76:LEU:HD13	1:C:87:ARG:CG	2.35	0.56
1:B:153:LEU:HD22	1:B:156:LEU:CD1	2.35	0.56
1:B:73:VAL:HG23	1:B:92:LEU:CD1	2.35	0.56
1:C:91:PRO:HG2	1:C:97:ARG:CZ	2.35	0.56
1:B:41:ILE:HG12	1:B:42:GLY:N	2.21	0.56
1:B:59:LEU:CB	1:B:133:VAL:HG22	2.35	0.56
1:C:76:LEU:HD13	1:C:87:ARG:HG3	1.88	0.56
1:C:343:MSE:HE1	1:C:347:GLY:CA	2.36	0.56
1:B:68:ARG:HD2	1:B:126:SER:OG	2.06	0.56
1:B:104:PRO:HB2	1:B:106:TRP:CD1	2.40	0.56
1:B:77:THR:HG21	4:B:395:ANP:N1	2.21	0.56
1:A:9:VAL:HG22	1:A:60:MSE:HE3	1.88	0.56
1:A:38:VAL:HG23	1:A:344:THR:HG21	1.86	0.56
1:B:77:THR:HG22	1:B:78:THR:N	2.20	0.56
1:A:94:THR:N	1:A:97:ARG:O	2.27	0.56
1:D:259:GLN:HB2	1:D:262:GLU:OE2	2.06	0.56
1:A:107:ALA:O	1:A:111:LYS:HG3	2.05	0.56
1:C:188:PHE:HZ	1:C:206:LEU:HD13	1.70	0.56
1:C:165:ALA:O	1:C:166:ARG:C	2.42	0.56
1:D:163:ILE:O	1:D:166:ARG:HB2	2.05	0.56
1:C:205:SER:CB	1:C:207:GLU:HG3	2.36	0.56
1:D:218:LEU:HD22	1:D:300:TYR:CZ	2.41	0.56
1:A:307:MSE:CE	1:A:355:LEU:HD22	2.35	0.55
1:B:103:THR:HA	1:B:104:PRO:C	2.27	0.55
1:A:143:ALA:HA	1:A:146:GLU:OE1	2.06	0.55
1:D:330:GLU:O	1:D:331:ALA:C	2.43	0.55
1:C:236:TYR:HB3	1:C:237:PRO:HD3	1.86	0.55
1:B:231:LEU:C	1:B:233:SER:H	2.09	0.55
1:C:235:GLU:O	1:C:238:VAL:N	2.39	0.55
1:B:226:ASN:ND2	1:B:375:THR:O	2.30	0.55
1:A:59:LEU:HD23	1:A:59:LEU:N	2.20	0.55
1:A:304:GLY:HA3	1:A:339:TYR:O	2.05	0.55
1:A:204:ARG:CZ	1:A:256:ARG:HD3	2.36	0.55
1:C:39:ASN:HD21	1:C:53:LEU:H	1.54	0.55
1:C:367:HIS:O	1:C:370:GLU:HB2	2.06	0.55
1:C:109:TYR:HB2	1:C:145:LEU:HD21	1.88	0.55
1:C:174:GLU:O	1:C:178:ALA:HB3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:180:MSE:O	1:C:182:CYS:N	2.36	0.55
1:A:93:PRO:HB3	1:A:99:LEU:H	1.71	0.55
1:B:241:ARG:O	1:B:244:GLU:N	2.39	0.55
1:A:284:GLU:HB2	1:A:287:ARG:HH21	1.71	0.55
1:B:23:GLU:CD	1:B:87:ARG:HH11	2.10	0.55
1:C:329:VAL:HG21	1:C:342:ARG:HA	1.89	0.55
1:A:43:GLU:OE2	1:A:342:ARG:NH2	2.29	0.55
1:B:273:GLU:O	1:B:277:ARG:HG2	2.07	0.55
1:C:37:ARG:HD2	1:C:37:ARG:C	2.27	0.55
1:C:98:SER:O	1:C:99:LEU:C	2.46	0.55
1:A:136:GLY:HA3	1:A:228:ARG:HD2	1.89	0.55
1:A:27:GLU:HA	1:A:27:GLU:OE2	2.07	0.55
1:A:219:ALA:O	1:A:356:LEU:HD12	2.06	0.55
1:A:304:GLY:HA3	1:A:339:TYR:C	2.27	0.55
1:C:91:PRO:HG2	1:C:97:ARG:HH21	1.72	0.55
1:D:246:VAL:O	1:D:249:ALA:HB3	2.07	0.55
1:C:103:THR:HA	1:C:104:PRO:C	2.26	0.55
1:A:37:ARG:O	1:A:37:ARG:NH1	2.30	0.55
1:D:208:THR:HG22	1:D:209:SER:N	2.21	0.55
1:C:120:ALA:CB	1:C:121:PRO:HA	2.33	0.55
1:B:247:ALA:HB2	1:B:255:LEU:HD23	1.88	0.54
1:A:266:ALA:HA	1:A:269:LEU:HD12	1.89	0.54
1:B:2:ALA:HB3	1:D:334:ALA:O	2.06	0.54
1:A:308:VAL:CG2	1:A:333:LEU:HD11	2.38	0.54
1:A:75:LEU:CD2	1:A:127:ALA:HB3	2.38	0.54
1:D:63:LEU:C	1:D:63:LEU:HD23	2.27	0.54
1:C:77:THR:HG22	1:C:79:SER:H	1.70	0.54
1:B:30:LEU:O	1:B:64:VAL:HA	2.06	0.54
1:D:248:ARG:O	1:D:251:GLY:N	2.30	0.54
1:B:33:SER:HB3	1:B:390:LEU:HD11	1.88	0.54
1:A:112:GLY:HA3	1:A:173:ALA:HB1	1.89	0.54
1:D:325:LEU:HD11	1:D:349:GLY:H	1.71	0.54
1:D:339:TYR:HD1	1:D:356:LEU:HA	1.73	0.54
1:C:117:TYR:CE1	1:C:153:LEU:HB2	2.42	0.54
1:D:302:ALA:O	1:D:305:ARG:HB2	2.07	0.54
1:B:31:ALA:HA	1:B:63:LEU:O	2.08	0.54
1:D:327:GLN:OE1	1:D:372:TYR:HA	2.07	0.54
1:A:20:PHE:CE1	1:A:65:GLY:HA2	2.42	0.54
1:A:0:HIS:O	1:A:1:HIS:C	2.44	0.54
1:A:205:SER:OG	1:A:207:GLU:HB2	2.08	0.54
1:D:304:GLY:HA2	1:D:307:MSE:CG	2.35	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:122:LEU:CD1	1:B:157:CYS:HB3	2.37	0.54
1:A:68:ARG:NH1	1:A:70:ASP:OD2	2.41	0.54
1:D:215:ASP:OD1	1:D:216:PRO:HD2	2.07	0.54
1:A:51:LEU:HD21	1:A:256:ARG:NH2	2.23	0.54
1:D:38:VAL:HG12	1:D:57:LEU:HD21	1.89	0.54
1:B:311:HIS:HB2	1:B:342:ARG:CB	2.38	0.54
1:C:167:ALA:HB2	1:C:191:LEU:CD1	2.38	0.54
1:B:266:ALA:HA	1:B:269:LEU:HB2	1.89	0.54
1:A:272:LYS:O	1:A:273:GLU:C	2.47	0.54
1:C:259:GLN:O	1:C:262:GLU:N	2.41	0.54
1:B:305:ARG:O	1:B:309:GLU:HG3	2.07	0.54
1:C:256:ARG:HG3	1:C:256:ARG:O	2.06	0.53
1:C:20:PHE:HD1	1:C:128:VAL:CG2	2.21	0.53
1:C:93:PRO:HG3	1:C:99:LEU:HG	1.90	0.53
1:A:122:LEU:HD12	1:A:123:PRO:HD2	1.88	0.53
1:A:287:ARG:O	1:A:306:LEU:HD22	2.07	0.53
1:D:218:LEU:CD1	1:D:219:ALA:H	2.17	0.53
1:D:49:GLN:CB	1:D:204:ARG:HB2	2.38	0.53
1:D:133:VAL:CG1	1:D:134:PRO:HD2	2.39	0.53
1:B:45:THR:HG21	1:B:284:GLU:HB3	1.90	0.53
1:C:135:LEU:CD2	4:C:395:ANP:H3'	2.32	0.53
1:A:188:PHE:CE1	1:A:206:LEU:HD23	2.43	0.53
1:D:259:GLN:HB2	1:D:262:GLU:OE1	2.08	0.53
1:A:368:ILE:O	1:A:369:GLN:C	2.45	0.53
1:B:175:HIS:CE1	1:B:181:PRO:HA	2.43	0.53
1:B:236:TYR:HB3	1:B:237:PRO:HD3	1.90	0.53
1:A:87:ARG:HG3	5:A:444:HOH:O	2.07	0.53
1:C:281:VAL:O	1:C:285:ILE:HG13	2.08	0.53
1:C:201:ILE:HG12	1:C:208:THR:HG22	1.90	0.53
1:B:49:GLN:OE1	1:B:254:SER:HB3	2.09	0.53
1:C:94:THR:HG22	1:C:95:ALA:N	2.23	0.53
1:D:89:GLN:NE2	5:D:469:HOH:O	2.41	0.53
1:D:43:GLU:HB3	1:D:314:LEU:HD21	1.91	0.53
1:B:149:THR:O	1:B:152:PHE:N	2.42	0.53
1:A:150:TYR:CE2	1:A:166:ARG:HG2	2.44	0.53
1:C:367:HIS:O	1:C:371:HIS:HD2	1.91	0.53
1:D:39:ASN:HA	1:D:54:PRO:HA	1.90	0.53
1:D:327:GLN:OE1	1:D:373:GLY:N	2.33	0.53
1:B:39:ASN:HD21	1:B:53:LEU:H	1.55	0.53
1:D:335:VAL:HG13	1:D:363:HIS:CE1	2.44	0.53
1:D:202:ASP:O	1:D:206:LEU:N	2.35	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:367:HIS:O	1:B:371:HIS:HD2	1.91	0.53
1:B:17:ARG:HG2	1:B:27:GLU:OE2	2.09	0.53
1:D:249:ALA:C	1:D:250:LEU:HD23	2.29	0.53
1:C:320:VAL:O	1:C:347:GLY:HA3	2.08	0.53
1:A:247:ALA:HB2	1:A:255:LEU:CD2	2.40	0.52
1:B:322:CYS:SG	1:B:325:LEU:HG	2.49	0.52
1:D:193:GLY:O	1:D:194:GLN:HG2	2.09	0.52
1:D:342:ARG:O	1:D:352:THR:HB	2.10	0.52
1:D:242:GLN:O	1:D:243:CYS:C	2.47	0.52
1:D:254:SER:OG	1:D:256:ARG:HB3	2.09	0.52
1:C:19:ALA:HB3	1:C:128:VAL:HG11	1.91	0.52
1:A:98:SER:CB	1:A:115:GLN:HE22	2.11	0.52
1:B:343:MSE:HE1	1:B:347:GLY:CA	2.39	0.52
1:C:259:GLN:H	1:C:262:GLU:HB2	1.74	0.52
1:A:307:MSE:O	1:A:310:SER:HB3	2.09	0.52
1:B:101:PRO:HG3	1:B:177:PHE:CD2	2.45	0.52
1:D:162:THR:HB	5:D:449:HOH:O	2.09	0.52
1:A:45:THR:O	1:A:48:ASN:HB2	2.10	0.52
1:D:18:ARG:HG3	1:D:22:GLU:OE2	2.10	0.52
1:D:78:THR:HB	1:D:129:VAL:O	2.10	0.52
1:A:192:MSE:HE1	1:B:194:GLN:HG2	1.92	0.52
1:C:90:PHE:HB2	1:C:91:PRO:CD	2.38	0.52
1:B:143:ALA:HB2	1:B:186:ASP:HB3	1.92	0.52
1:D:324:GLU:N	1:D:324:GLU:OE1	2.37	0.52
1:C:218:LEU:HD11	1:C:355:LEU:HG	1.91	0.52
1:A:279:ARG:NH2	1:A:317:ASP:OD1	2.42	0.52
1:B:315:ARG:HG2	1:B:316:ASP:OD1	2.10	0.52
1:B:116:TYR:CE1	1:B:177:PHE:HE1	2.27	0.52
1:D:83:ASP:OD2	1:D:105:ARG:N	2.30	0.52
1:C:20:PHE:HD1	1:C:128:VAL:HG23	1.75	0.52
1:D:285:ILE:O	1:D:288:THR:N	2.42	0.52
1:B:239:ARG:HH11	1:B:239:ARG:HG2	1.74	0.52
1:B:222:ILE:HB	1:B:379:TYR:HB2	1.92	0.52
1:C:20:PHE:HB2	1:C:128:VAL:HG21	1.91	0.52
1:B:239:ARG:HG2	1:B:239:ARG:NH1	2.25	0.52
1:A:40:LEU:HB2	1:A:53:LEU:O	2.10	0.52
1:B:31:ALA:HB2	1:B:392:LEU:HD21	1.92	0.52
1:A:72:LEU:HD23	1:A:91:PRO:HA	1.92	0.52
1:C:304:GLY:O	1:C:307:MSE:HB2	2.11	0.52
1:A:356:LEU:H	1:A:356:LEU:HD12	1.73	0.51
1:C:91:PRO:HG2	1:C:97:ARG:NE	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:339:TYR:OH	1:B:357:GLU:HG2	2.09	0.51
1:C:239:ARG:HG2	1:C:239:ARG:HH11	1.76	0.51
1:B:32:VAL:N	1:B:390:LEU:HD12	2.25	0.51
1:D:181:PRO:O	1:D:240:ARG:NH1	2.37	0.51
1:D:47:TYR:CD1	1:D:240:ARG:HG3	2.45	0.51
1:D:221:LEU:HD13	1:D:380:LEU:HD21	1.92	0.51
1:C:74:SER:HB2	1:C:89:GLN:HG2	1.91	0.51
1:D:88:LEU:HD22	1:D:104:PRO:HD2	1.93	0.51
1:D:202:ASP:OD1	1:D:204:ARG:HB3	2.10	0.51
1:A:335:VAL:HG13	1:A:336:PRO:HD2	1.92	0.51
1:A:245:GLU:HG3	1:A:248:ARG:HH21	1.74	0.51
1:A:207:GLU:CD	1:B:296:ARG:HD3	2.31	0.51
1:B:206:LEU:O	5:B:397:HOH:O	2.19	0.51
1:C:264:GLU:O	1:C:267:ARG:HB2	2.11	0.51
1:C:68:ARG:N	1:C:124:GLY:O	2.44	0.51
1:A:29:GLU:O	1:A:30:LEU:HD23	2.11	0.51
1:B:250:LEU:O	1:B:251:GLY:C	2.49	0.51
1:D:264:GLU:O	1:D:267:ARG:N	2.29	0.51
1:D:87:ARG:HG2	1:D:87:ARG:NH1	2.22	0.51
1:C:249:ALA:C	1:C:250:LEU:HD12	2.31	0.51
1:A:34:ALA:O	1:A:144:SER:OG	2.29	0.51
1:B:152:PHE:CD2	1:B:153:LEU:HD23	2.46	0.51
1:B:97:ARG:HH11	1:B:97:ARG:CG	2.24	0.51
1:A:252:LYS:HG2	1:A:257:GLU:CB	2.40	0.51
1:C:382:GLN:O	1:C:383:ALA:C	2.49	0.51
1:B:244:GLU:O	1:B:245:GLU:C	2.47	0.51
1:D:260:LEU:HD12	1:D:260:LEU:C	2.31	0.51
1:C:264:GLU:OE2	1:C:267:ARG:NH1	2.30	0.51
1:A:23:GLU:OE2	1:A:87:ARG:NE	2.31	0.51
1:A:294:ALA:HA	1:A:297:ARG:CZ	2.41	0.51
1:D:157:CYS:O	1:D:158:PRO:C	2.49	0.51
1:D:365:MSE:HG2	1:D:378:PHE:CD2	2.46	0.51
1:C:83:ASP:O	1:C:85:PRO:O	2.29	0.51
1:C:276:ARG:O	1:C:277:ARG:C	2.48	0.50
1:A:53:LEU:O	1:A:53:LEU:HG	2.11	0.50
1:A:175:HIS:CE1	1:A:181:PRO:HA	2.45	0.50
1:D:120:ALA:HB1	1:D:121:PRO:HA	1.93	0.50
1:C:94:THR:HG22	1:C:96:GLN:N	2.12	0.50
1:A:100:GLU:HG3	1:A:101:PRO:CD	2.31	0.50
1:B:29:GLU:C	1:B:30:LEU:HD23	2.32	0.50
1:D:226:ASN:ND2	1:D:377:THR:OG1	2.33	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:GLU:HB2	1:A:314:LEU:HD11	1.92	0.50
1:A:361:ALA:HB3	1:A:362:PRO:CD	2.36	0.50
1:D:7:PRO:CG	1:D:12:LEU:HD21	2.42	0.50
1:D:9:VAL:CG2	1:D:60:MSE:HE1	2.42	0.50
1:A:367:HIS:O	1:A:371:HIS:HD2	1.94	0.50
1:D:133:VAL:HG12	1:D:134:PRO:HD2	1.93	0.50
1:D:308:VAL:O	1:D:312:ARG:HG3	2.11	0.50
1:A:215:ASP:OD1	1:A:216:PRO:HD2	2.11	0.50
1:B:185:MSE:HG2	1:B:186:ASP:N	2.26	0.50
1:D:205:SER:O	1:D:206:LEU:HB2	2.11	0.50
1:B:31:ALA:CB	1:B:390:LEU:HB2	2.42	0.50
1:A:75:LEU:HD23	1:A:127:ALA:HB3	1.94	0.50
1:C:325:LEU:HD21	1:C:349:GLY:O	2.12	0.50
1:C:77:THR:HG21	4:C:395:ANP:N1	2.27	0.50
1:B:184:ILE:HD12	1:B:184:ILE:N	2.26	0.50
1:D:280:HIS:CD2	1:D:281:VAL:N	2.80	0.50
1:D:279:ARG:HG2	1:D:317:ASP:OD2	2.12	0.50
1:A:33:SER:HA	1:A:61:THR:O	2.12	0.50
1:A:180:MSE:O	1:A:182:CYS:N	2.44	0.50
1:C:187:GLN:O	1:C:191:LEU:HG	2.12	0.50
1:A:169:VAL:HG12	1:A:170:CYS:N	2.26	0.50
1:B:241:ARG:O	1:B:242:GLN:C	2.49	0.50
1:B:116:TYR:CZ	1:B:177:PHE:HE1	2.30	0.50
1:B:150:TYR:CE2	1:B:154:GLN:NE2	2.80	0.50
1:A:77:THR:HG22	1:A:79:SER:H	1.76	0.50
1:C:82:ALA:O	1:C:83:ASP:O	2.30	0.50
1:D:213:LEU:HD21	1:D:295:LEU:HD21	1.93	0.50
1:D:181:PRO:O	1:D:240:ARG:HD2	2.12	0.50
1:C:322:CYS:HB2	1:C:323:PRO:HD2	1.93	0.50
1:B:109:TYR:O	1:B:113:VAL:HG23	2.12	0.50
1:A:205:SER:OG	1:A:207:GLU:N	2.37	0.50
1:A:146:GLU:O	1:A:149:THR:HB	2.12	0.50
1:B:339:TYR:CZ	1:B:357:GLU:HG2	2.47	0.50
1:B:116:TYR:CE1	1:B:177:PHE:CE1	3.00	0.49
1:B:135:LEU:HB3	4:B:395:ANP:H3'	1.93	0.49
1:C:37:ARG:HD2	1:C:37:ARG:O	2.12	0.49
1:D:293:ALA:O	1:D:294:ALA:C	2.49	0.49
1:B:35:PRO:O	1:B:144:SER:HB2	2.11	0.49
1:C:371:HIS:CD2	1:C:371:HIS:N	2.80	0.49
1:D:312:ARG:NH2	5:D:418:HOH:O	2.44	0.49
1:A:247:ALA:HB2	1:A:255:LEU:HD23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:117:TYR:HE2	1:C:119:ALA:HB3	1.77	0.49
1:A:184:ILE:H	1:A:184:ILE:CD1	2.06	0.49
1:A:273:GLU:O	1:A:277:ARG:HG2	2.13	0.49
1:C:177:PHE:CD1	1:C:177:PHE:N	2.80	0.49
1:B:361:ALA:HB3	1:B:362:PRO:HD3	1.94	0.49
1:B:371:HIS:CD2	1:B:371:HIS:N	2.80	0.49
1:C:243:CYS:O	1:C:244:GLU:C	2.49	0.49
1:C:261:GLU:OE2	1:C:286:ARG:NH1	2.43	0.49
1:A:34:ALA:HB3	1:A:148:ALA:HB2	1.94	0.49
1:C:320:VAL:O	1:C:348:PHE:N	2.45	0.49
1:D:142:SER:O	1:D:146:GLU:HG3	2.13	0.49
1:D:291:ALA:HB1	1:D:303:PHE:CD1	2.46	0.49
1:A:270:VAL:O	1:A:271:SER:O	2.30	0.49
1:B:13:LEU:O	1:B:16:ALA:HB3	2.13	0.49
1:C:188:PHE:O	1:C:189:ILE:C	2.48	0.49
1:C:98:SER:O	1:C:99:LEU:O	2.31	0.49
1:B:6:GLN:O	1:B:7:PRO:C	2.50	0.49
1:B:136:GLY:N	4:B:395:ANP:O2B	2.46	0.49
1:C:37:ARG:HG2	1:C:189:ILE:HG21	1.95	0.49
1:A:116:TYR:O	1:A:117:TYR:O	2.30	0.49
1:B:143:ALA:CB	1:B:186:ASP:HB3	2.43	0.49
1:D:68:ARG:HD3	1:D:70:ASP:HB2	1.95	0.49
1:B:35:PRO:HA	1:B:60:MSE:CB	2.43	0.49
1:B:294:ALA:O	1:B:299:ASP:N	2.36	0.49
1:B:205:SER:HB2	1:B:207:GLU:OE2	2.12	0.49
1:C:236:TYR:O	1:C:237:PRO:C	2.50	0.48
1:A:77:THR:HG21	4:A:395:ANP:C2	2.43	0.48
1:B:280:HIS:CD2	1:B:318:TYR:CD1	3.00	0.48
1:D:51:LEU:HB3	1:D:200:LEU:HD11	1.94	0.48
1:B:181:PRO:O	1:B:236:TYR:HE2	1.97	0.48
1:C:94:THR:O	1:C:97:ARG:O	2.31	0.48
1:C:192:MSE:HB2	1:C:199:LEU:CD2	2.43	0.48
1:C:113:VAL:CG1	1:C:149:THR:HG22	2.33	0.48
1:C:112:GLY:O	1:C:116:TYR:HD1	1.95	0.48
1:B:53:LEU:N	1:B:54:PRO:HD3	2.28	0.48
1:B:59:LEU:HB2	1:B:133:VAL:HG22	1.94	0.48
1:C:220:VAL:HG22	1:C:355:LEU:HD12	1.95	0.48
1:B:239:ARG:HD2	1:B:318:TYR:CE2	2.47	0.48
1:B:246:VAL:O	1:B:247:ALA:C	2.52	0.48
1:D:85:PRO:HG2	1:D:87:ARG:O	2.12	0.48
1:C:21:ARG:O	1:C:25:GLY:N	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:194:GLN:O	1:C:195:LYS:O	2.31	0.48
1:D:163:ILE:O	1:D:166:ARG:N	2.42	0.48
1:D:95:ALA:O	1:D:96:GLN:O	2.30	0.48
1:A:35:PRO:HA	1:A:60:MSE:CB	2.43	0.48
1:C:314:LEU:O	1:C:319:GLU:N	2.47	0.48
1:D:366:ARG:O	1:D:370:GLU:HG3	2.13	0.48
1:B:152:PHE:HD2	1:B:153:LEU:HD23	1.77	0.48
1:C:177:PHE:HD1	1:C:177:PHE:N	2.11	0.48
1:A:235:GLU:O	1:A:238:VAL:HB	2.13	0.48
1:D:8:GLN:O	1:D:9:VAL:C	2.49	0.48
1:D:375:THR:HG22	1:D:375:THR:O	2.12	0.48
1:C:318:TYR:O	1:C:319:GLU:HB2	2.13	0.48
1:D:73:VAL:HG11	1:D:90:PHE:CZ	2.48	0.48
1:C:37:ARG:NH2	1:C:186:ASP:OD1	2.42	0.48
1:D:281:VAL:O	1:D:284:GLU:N	2.47	0.48
1:D:43:GLU:OE2	1:D:345:GLY:N	2.44	0.48
1:C:16:ALA:HB1	1:C:64:VAL:HB	1.95	0.48
1:B:232:ALA:O	1:B:235:GLU:N	2.31	0.48
1:A:312:ARG:HE	1:A:315:ARG:HH12	1.59	0.48
1:C:4:LEU:N	1:C:378:PHE:O	2.38	0.48
1:C:242:GLN:OE1	1:C:277:ARG:HG2	2.14	0.48
1:B:9:VAL:HG23	5:B:479:HOH:O	2.13	0.48
1:A:260:LEU:N	1:A:282:VAL:HG11	2.29	0.48
1:B:24:PHE:CE1	1:B:126:SER:HB3	2.48	0.48
1:A:239:ARG:HD3	1:A:242:GLN:OE1	2.13	0.48
1:A:207:GLU:OE2	1:B:296:ARG:HD3	2.14	0.48
1:B:7:PRO:HG2	1:B:132:SER:HB3	1.95	0.48
1:B:33:SER:HA	1:B:61:THR:O	2.13	0.48
1:A:1:HIS:HD2	1:A:3:ALA:HB3	1.78	0.48
1:D:94:THR:O	1:D:97:ARG:O	2.31	0.48
1:D:77:THR:HG22	1:D:79:SER:N	2.08	0.48
1:B:125:PHE:CG	1:B:152:PHE:HE2	2.31	0.48
1:B:186:ASP:HB2	5:B:446:HOH:O	2.14	0.48
1:C:20:PHE:CD1	1:C:128:VAL:HG23	2.49	0.48
1:D:328:LEU:HD21	1:D:372:TYR:CG	2.48	0.48
1:A:49:GLN:HE21	1:A:204:ARG:CG	2.26	0.48
1:B:54:PRO:HD2	1:B:199:LEU:O	2.14	0.48
1:A:321:SER:OG	1:A:322:CYS:N	2.44	0.48
1:A:77:THR:HG21	4:A:395:ANP:H2	1.96	0.48
1:C:347:GLY:O	1:C:348:PHE:HB2	2.14	0.48
1:C:188:PHE:CZ	1:C:206:LEU:HD22	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:304:GLY:CA	1:D:307:MSE:HE2	2.41	0.48
1:B:258:VAL:CG1	1:B:263:LEU:HD12	2.42	0.48
1:A:43:GLU:CB	1:A:314:LEU:HD11	2.44	0.48
1:C:369:GLN:HA	1:C:369:GLN:NE2	2.29	0.48
1:D:285:ILE:O	1:D:286:ARG:C	2.50	0.47
1:A:146:GLU:OE2	1:A:174:GLU:HB2	2.13	0.47
1:D:277:ARG:O	1:D:280:HIS:N	2.47	0.47
1:A:249:ALA:C	1:A:251:GLY:H	2.17	0.47
1:B:259:GLN:O	1:B:260:LEU:C	2.53	0.47
1:B:85:PRO:HA	5:B:453:HOH:O	2.13	0.47
1:D:358:ALA:O	1:D:360:ALA:N	2.48	0.47
1:B:171:GLN:HG2	1:B:175:HIS:HD2	1.78	0.47
1:B:204:ARG:HB2	1:B:256:ARG:NH1	2.30	0.47
1:C:84:GLU:HA	1:C:85:PRO:O	2.14	0.47
1:A:391:CYS:HB3	5:A:489:HOH:O	2.13	0.47
1:A:307:MSE:CE	1:A:355:LEU:HB2	2.21	0.47
1:B:138:GLY:HA2	4:B:395:ANP:O2G	2.13	0.47
1:C:63:LEU:HD12	1:C:129:VAL:HA	1.96	0.47
1:B:299:ASP:OD1	1:B:302:ALA:HB2	2.14	0.47
1:D:94:THR:OG1	1:D:97:ARG:HG2	2.15	0.47
1:C:273:GLU:HB2	5:C:397:HOH:O	2.13	0.47
1:C:32:VAL:CG1	1:C:151:THR:HG22	2.44	0.47
1:C:304:GLY:HA3	1:C:339:TYR:O	2.13	0.47
1:A:5:ARG:C	1:A:7:PRO:HD3	2.35	0.47
1:B:115:GLN:HG2	1:B:177:PHE:CZ	2.50	0.47
1:B:146:GLU:O	1:B:149:THR:HB	2.14	0.47
1:C:151:THR:O	1:C:154:GLN:HB2	2.14	0.47
1:B:356:LEU:HD22	1:B:360:ALA:HB3	1.95	0.47
1:C:59:LEU:HD11	1:C:379:TYR:CD2	2.50	0.47
1:C:370:GLU:HB3	1:C:371:HIS:CD2	2.49	0.47
1:D:1:HIS:CE1	1:D:366:ARG:HG2	2.49	0.47
1:C:227:VAL:HG21	1:C:324:GLU:HG2	1.96	0.47
1:D:292:ALA:O	1:D:296:ARG:N	2.45	0.47
1:B:124:GLY:O	1:B:125:PHE:HB3	2.15	0.47
1:D:266:ALA:CB	1:D:269:LEU:HD12	2.44	0.47
1:A:105:ARG:O	1:A:106:TRP:C	2.51	0.47
1:B:211:VAL:HA	1:B:212:PRO:HD2	1.71	0.47
1:B:267:ARG:HG3	5:B:410:HOH:O	2.15	0.47
1:B:112:GLY:HA3	1:B:173:ALA:HB1	1.97	0.47
1:D:266:ALA:CA	1:D:269:LEU:HB2	2.44	0.47
1:D:329:VAL:O	1:D:330:GLU:C	2.52	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:246:VAL:O	1:C:249:ALA:N	2.48	0.47
1:B:12:LEU:HD23	1:B:12:LEU:HA	1.75	0.47
1:D:20:PHE:HD1	1:D:128:VAL:CG2	2.27	0.47
1:D:136:GLY:HA3	1:D:228:ARG:CZ	2.45	0.47
1:C:213:LEU:HA	1:C:213:LEU:HD12	1.75	0.46
1:A:171:GLN:HG2	1:A:175:HIS:CD2	2.49	0.46
1:A:339:TYR:CD1	1:A:356:LEU:HA	2.51	0.46
1:C:142:SER:OG	4:C:395:ANP:O1B	2.33	0.46
1:A:35:PRO:HA	1:A:60:MSE:HB2	1.97	0.46
1:D:1:HIS:CG	1:D:366:ARG:HG2	2.50	0.46
1:B:196:GLY:HA2	1:B:383:ALA:HB3	1.95	0.46
1:B:146:GLU:OE2	1:B:174:GLU:HB2	2.15	0.46
1:B:85:PRO:O	1:B:104:PRO:HG3	2.15	0.46
1:A:33:SER:HB3	1:A:62:VAL:HG22	1.97	0.46
1:A:47:TYR:CD1	1:A:240:ARG:HG3	2.51	0.46
1:C:312:ARG:NH1	1:C:312:ARG:HG2	2.30	0.46
1:A:141:SER:OG	4:A:395:ANP:O2B	2.30	0.46
1:A:259:GLN:O	1:A:260:LEU:C	2.53	0.46
1:C:143:ALA:O	1:C:144:SER:C	2.52	0.46
1:B:111:LYS:O	1:B:114:ILE:HB	2.16	0.46
1:A:205:SER:HG	1:A:207:GLU:HB2	1.79	0.46
1:D:221:LEU:HD13	1:D:380:LEU:CD2	2.45	0.46
1:A:113:VAL:HB	1:A:149:THR:HG21	1.96	0.46
1:D:304:GLY:CA	1:D:307:MSE:HG3	2.39	0.46
1:A:57:LEU:O	1:A:384:ALA:HB3	2.15	0.46
1:D:199:LEU:HD21	1:D:208:THR:HG21	1.97	0.46
1:B:92:LEU:HG	1:B:93:PRO:HD2	1.96	0.46
1:A:188:PHE:HE1	1:A:206:LEU:CD2	2.28	0.46
1:D:222:ILE:HB	1:D:379:TYR:HB2	1.96	0.46
1:A:284:GLU:OE1	1:A:287:ARG:NH2	2.46	0.46
1:A:188:PHE:CE1	1:A:206:LEU:CD2	2.99	0.46
1:D:68:ARG:N	1:D:124:GLY:O	2.49	0.46
1:C:277:ARG:H	1:C:277:ARG:HD3	1.81	0.46
1:C:320:VAL:HG12	1:C:348:PHE:CE1	2.51	0.46
1:A:281:VAL:O	1:A:285:ILE:HG13	2.15	0.46
1:B:114:ILE:O	1:B:116:TYR:N	2.49	0.46
1:A:187:GLN:OE1	1:A:187:GLN:N	2.31	0.46
1:A:29:GLU:C	1:A:30:LEU:HD23	2.36	0.46
1:B:43:GLU:O	1:B:44:HIS:HB2	2.15	0.46
1:D:371:HIS:CD2	1:D:371:HIS:N	2.84	0.46
1:D:59:LEU:HD22	1:D:132:SER:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:GLU:CB	1:A:287:ARG:HH21	2.28	0.46
1:D:356:LEU:N	1:D:356:LEU:HD12	2.31	0.46
1:C:83:ASP:OD2	1:C:105:ARG:N	2.40	0.46
1:C:303:PHE:O	1:C:307:MSE:HG3	2.15	0.46
1:A:246:VAL:O	1:A:247:ALA:C	2.53	0.46
1:D:358:ALA:O	1:D:359:SER:C	2.55	0.46
1:A:46:ASP:OD2	2:A:393:GLA:H4	2.16	0.46
1:A:221:LEU:HD13	1:A:380:LEU:HD21	1.96	0.46
1:B:292:ALA:O	1:B:296:ARG:HG3	2.16	0.46
1:C:28:PRO:HB2	1:C:64:VAL:HG13	1.97	0.46
1:A:58:GLU:HG3	1:A:384:ALA:HB2	1.97	0.46
1:B:325:LEU:HD13	1:B:343:MSE:CB	2.46	0.46
1:C:123:PRO:HG2	1:C:156:LEU:HB3	1.97	0.45
1:C:112:GLY:HA2	1:C:115:GLN:HB3	1.98	0.45
1:B:21:ARG:HB2	1:B:27:GLU:OE1	2.15	0.45
1:D:302:ALA:C	1:D:306:LEU:HD12	2.35	0.45
1:B:34:ALA:HB2	1:B:147:VAL:HG12	1.97	0.45
1:D:208:THR:CG2	1:D:209:SER:N	2.80	0.45
1:B:16:ALA:O	1:B:17:ARG:C	2.53	0.45
1:A:284:GLU:HA	1:A:287:ARG:NH2	2.31	0.45
1:B:188:PHE:CZ	1:B:206:LEU:HG	2.51	0.45
1:B:356:LEU:CD2	1:B:360:ALA:HB3	2.46	0.45
1:C:276:ARG:HG2	1:C:317:ASP:OD1	2.16	0.45
1:A:335:VAL:HG12	1:A:336:PRO:N	2.31	0.45
1:C:76:LEU:CD1	1:C:87:ARG:HG3	2.46	0.45
1:C:170:CYS:O	1:C:173:ALA:HB3	2.16	0.45
1:B:356:LEU:H	1:B:356:LEU:HD12	1.81	0.45
1:B:311:HIS:HB2	1:B:342:ARG:HB2	1.97	0.45
1:B:37:ARG:O	1:B:139:LEU:HA	2.17	0.45
1:A:303:PHE:CD2	1:A:307:MSE:HE2	2.50	0.45
1:B:149:THR:O	1:B:152:PHE:HB3	2.16	0.45
1:C:184:ILE:HG21	1:C:206:LEU:CD2	2.38	0.45
1:A:192:MSE:HA	1:A:192:MSE:CE	2.46	0.45
1:C:361:ALA:N	1:C:362:PRO:CD	2.80	0.45
1:A:284:GLU:CA	1:A:287:ARG:NH2	2.79	0.45
1:B:192:MSE:HE3	1:B:192:MSE:CA	2.44	0.45
1:C:109:TYR:CB	1:C:145:LEU:HD21	2.47	0.45
1:A:44:HIS:ND1	1:A:318:TYR:HE2	2.14	0.45
1:D:173:ALA:O	1:D:177:PHE:HB2	2.17	0.45
1:B:242:GLN:O	1:B:243:CYS:C	2.52	0.45
1:B:141:SER:OG	4:B:395:ANP:O2B	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:360:ALA:C	1:C:362:PRO:HD2	2.37	0.45
1:C:246:VAL:O	1:C:247:ALA:C	2.54	0.45
1:D:239:ARG:NH2	1:D:319:GLU:O	2.48	0.45
1:D:297[A]:ARG:NH1	5:D:456:HOH:O	2.43	0.45
1:A:245:GLU:O	1:A:248:ARG:HB3	2.15	0.45
1:C:189:ILE:CG2	1:C:190:SER:N	2.80	0.45
1:D:53:LEU:N	1:D:54:PRO:CD	2.80	0.45
1:C:59:LEU:HD11	1:C:379:TYR:CE2	2.52	0.45
1:A:227:VAL:CG1	1:A:228:ARG:N	2.80	0.45
1:C:194:GLN:O	1:C:195:LYS:C	2.55	0.45
1:D:356:LEU:N	1:D:356:LEU:CD1	2.80	0.45
1:B:185:MSE:O	1:B:189:ILE:HG22	2.16	0.45
1:C:311:HIS:HB2	1:C:342:ARG:HB2	1.96	0.45
1:B:45:THR:CG2	1:B:284:GLU:HB3	2.46	0.45
1:C:307:MSE:O	1:C:310:SER:HB3	2.17	0.45
1:B:202:ASP:OD1	1:B:204:ARG:HB3	2.17	0.45
1:B:266:ALA:O	1:B:267:ARG:C	2.53	0.45
1:B:40:LEU:O	1:B:41:ILE:HB	2.17	0.45
1:B:188:PHE:CZ	1:B:206:LEU:CG	3.00	0.45
1:D:343:MSE:HE3	1:D:343:MSE:HB2	1.52	0.45
1:D:357:GLU:O	1:D:360:ALA:N	2.48	0.45
1:A:260:LEU:HG	1:A:282:VAL:HG12	1.99	0.45
1:A:218:LEU:HD11	1:A:355:LEU:HG	1.99	0.45
1:B:117:TYR:OH	1:B:159:ASP:HB3	2.16	0.45
1:D:41:ILE:HD12	1:D:307:MSE:HA	1.98	0.45
1:A:94:THR:CG2	1:A:95:ALA:N	2.80	0.45
1:D:287:ARG:HG3	1:D:287:ARG:HH11	1.82	0.45
1:A:75:LEU:HD11	1:A:110:VAL:HG11	1.99	0.45
1:A:122:LEU:HD21	1:A:153:LEU:HD22	1.98	0.45
1:C:258:VAL:CG1	1:C:259:GLN:N	2.80	0.45
1:A:13:LEU:HD12	1:A:13:LEU:HA	1.60	0.45
1:B:273:GLU:CA	1:B:276:ARG:NH2	2.80	0.44
1:B:51:LEU:HD23	1:B:202:ASP:HA	1.99	0.44
1:C:117:TYR:CE2	1:C:119:ALA:HB3	2.52	0.44
1:D:335:VAL:CG1	1:D:363:HIS:ND1	2.80	0.44
1:C:245:GLU:O	1:C:246:VAL:C	2.52	0.44
1:C:238:VAL:HG12	1:C:242:GLN:HE21	1.81	0.44
1:C:227:VAL:CG1	1:C:228:ARG:N	2.80	0.44
1:C:73:VAL:CG1	1:C:125:PHE:CZ	3.00	0.44
1:D:77:THR:O	1:D:86:GLN:HG2	2.18	0.44
1:C:119:ALA:HB2	1:C:159:ASP:HA	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:20:PHE:CE2	1:B:28:PRO:HA	2.52	0.44
1:A:185:MSE:HG2	1:A:186:ASP:N	2.31	0.44
1:B:198:ALA:HB2	1:B:213:LEU:HD12	1.97	0.44
1:D:63:LEU:HD23	1:D:63:LEU:O	2.18	0.44
1:A:20:PHE:HA	1:A:128:VAL:HG21	1.99	0.44
1:D:131:SER:N	5:D:432:HOH:O	2.49	0.44
1:A:328:LEU:HD23	1:A:328:LEU:HA	1.67	0.44
1:C:215:ASP:HA	1:C:216:PRO:HD2	1.73	0.44
1:D:364:ALA:O	1:D:368:ILE:HG13	2.18	0.44
1:D:68:ARG:NH1	1:D:72:LEU:HD12	2.26	0.44
1:B:31:ALA:HB3	1:B:390:LEU:HB2	1.99	0.44
1:B:320:VAL:O	1:B:348:PHE:N	2.45	0.44
1:B:49:GLN:NE2	1:B:204:ARG:CG	2.80	0.44
1:B:109:TYR:CE2	1:B:178:ALA:CB	3.00	0.44
1:C:94:THR:CG2	1:C:95:ALA:N	2.81	0.44
1:B:41:ILE:HG12	1:B:42:GLY:H	1.80	0.44
1:B:27:GLU:HA	1:B:28:PRO:HD3	1.75	0.44
1:D:272:LYS:O	1:D:276:ARG:HG3	2.17	0.44
1:A:232:ALA:HB3	1:A:348:PHE:CD2	2.53	0.44
1:A:336:PRO:HD2	1:A:363:HIS:CE1	2.52	0.44
1:D:97:ARG:NH2	1:D:99:LEU:HD23	2.33	0.44
1:C:227:VAL:HG13	1:C:229:HIS:CE1	2.53	0.44
1:B:227:VAL:CG1	1:B:228:ARG:N	2.80	0.44
1:A:219:ALA:HB3	1:A:356:LEU:HD13	2.00	0.44
1:A:243:CYS:O	1:A:245:GLU:N	2.51	0.44
1:D:105:ARG:O	1:D:106:TRP:C	2.53	0.44
1:B:41:ILE:CG1	1:B:42:GLY:N	2.80	0.44
1:D:47:TYR:CD1	1:D:240:ARG:CG	3.00	0.44
1:B:356:LEU:CD1	1:B:356:LEU:N	2.81	0.44
1:A:229:HIS:HB2	1:A:348:PHE:O	2.17	0.44
1:C:356:LEU:CD1	1:C:356:LEU:N	2.80	0.44
1:B:117:TYR:CD1	1:B:118:PRO:CD	3.00	0.44
1:C:113:VAL:O	1:C:117:TYR:N	2.50	0.44
1:C:250:LEU:N	1:C:250:LEU:CD1	2.81	0.44
1:C:261:GLU:HG3	5:C:480:HOH:O	2.17	0.44
1:A:1:HIS:CD2	1:A:3:ALA:H	2.36	0.44
1:D:136:GLY:HA3	1:D:228:ARG:NH1	2.33	0.44
1:D:34:ALA:HB3	1:D:148:ALA:HB2	1.99	0.44
1:B:260:LEU:HD12	1:B:260:LEU:HA	1.85	0.44
1:D:53:LEU:N	1:D:54:PRO:HD3	2.33	0.44
1:C:6:GLN:HG2	1:C:59:LEU:CD2	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:VAL:CG2	1:A:60:MSE:HE1	2.47	0.44
1:A:336:PRO:HD2	1:A:363:HIS:HE1	1.83	0.44
1:C:269:LEU:HD23	1:C:269:LEU:HA	1.69	0.44
1:A:188:PHE:HE1	1:A:206:LEU:HD21	1.82	0.44
1:A:51:LEU:HD21	1:A:256:ARG:HH22	1.82	0.44
1:C:116:TYR:CE2	1:C:172:GLN:HG2	2.52	0.44
1:C:49:GLN:HB3	1:C:204:ARG:HB2	2.00	0.44
1:C:361:ALA:HB3	1:C:362:PRO:CD	2.37	0.44
1:A:117:TYR:CD1	1:A:118:PRO:CD	3.00	0.44
1:C:245:GLU:O	1:C:248:ARG:HB3	2.17	0.44
1:B:286:ARG:O	1:B:289:ALA:HB3	2.18	0.44
1:A:34:ALA:HB3	1:A:144:SER:O	2.17	0.44
1:A:224:ASN:N	1:A:377:THR:O	2.41	0.44
1:C:35:PRO:HG3	1:C:385:ASP:O	2.17	0.44
1:B:115:GLN:HG2	1:B:177:PHE:HZ	1.82	0.43
1:D:362:PRO:O	1:D:363:HIS:C	2.55	0.43
1:C:24:PHE:HZ	1:C:74:SER:OG	2.01	0.43
1:B:232:ALA:O	1:B:235:GLU:HB2	2.17	0.43
1:D:259:GLN:O	1:D:262:GLU:N	2.50	0.43
1:C:261:GLU:OE2	1:C:286:ARG:NH2	2.49	0.43
1:A:28:PRO:HB3	1:A:64:VAL:HG12	2.00	0.43
1:B:311:HIS:ND1	1:B:343:MSE:HG2	2.33	0.43
1:A:56:ALA:O	1:A:383:ALA:HA	2.17	0.43
1:B:218:LEU:HD11	1:B:355:LEU:HG	2.00	0.43
1:B:150:TYR:HE1	1:B:169:VAL:HG21	1.83	0.43
1:C:72:LEU:HD22	1:C:91:PRO:HA	1.96	0.43
1:D:9:VAL:HA	1:D:60:MSE:HE1	2.00	0.43
1:C:255:LEU:HD23	1:C:255:LEU:HA	1.55	0.43
1:A:32:VAL:HG11	1:A:152:PHE:HA	1.99	0.43
1:D:159:ASP:HB2	5:D:472:HOH:O	2.18	0.43
1:B:116:TYR:O	1:B:117:TYR:O	2.37	0.43
1:B:113:VAL:HB	1:B:149:THR:HG21	1.99	0.43
1:A:204:ARG:NH2	1:A:257:GLU:OE2	2.51	0.43
1:A:113:VAL:HG11	1:A:150:TYR:N	2.34	0.43
1:A:149:THR:O	1:A:152:PHE:HB3	2.19	0.43
1:C:266:ALA:O	1:C:267:ARG:C	2.56	0.43
1:C:28:PRO:HB3	1:C:64:VAL:HG13	1.99	0.43
1:B:326:ASP:OD1	1:B:326:ASP:N	2.52	0.43
1:C:8:GLN:O	1:C:9:VAL:C	2.57	0.43
1:B:252:LYS:HB3	1:B:257:GLU:HB2	2.00	0.43
1:A:310:SER:O	1:A:311:HIS:C	2.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:236:TYR:HB3	1:C:237:PRO:CD	2.47	0.43
1:B:219:ALA:HB3	1:B:356:LEU:CD1	2.49	0.43
1:D:68:ARG:HB3	1:D:70:ASP:H	1.84	0.43
1:B:284:GLU:HA	1:B:284:GLU:OE1	2.18	0.43
1:C:189:ILE:HD13	1:C:199:LEU:HB3	2.01	0.43
1:D:54:PRO:HG3	1:D:185:MSE:HG3	2.00	0.43
1:B:188:PHE:CZ	1:B:206:LEU:CD1	2.99	0.43
1:D:279:ARG:O	1:D:280:HIS:C	2.57	0.43
1:C:20:PHE:CE1	1:C:24:PHE:CD1	3.07	0.43
1:A:239:ARG:O	1:A:242:GLN:HB2	2.18	0.43
1:C:192:MSE:HB2	1:C:199:LEU:HD21	2.00	0.43
1:B:222:ILE:HG21	1:B:222:ILE:HD12	1.77	0.43
1:D:164:ALA:O	1:D:168:GLN:HG3	2.18	0.43
1:A:77:THR:CG2	4:A:395:ANP:N1	2.82	0.43
1:A:6:GLN:HE21	1:A:6:GLN:HB2	1.47	0.43
1:D:77:THR:CG2	4:D:395:ANP:N1	2.80	0.43
1:C:68:ARG:NH1	1:C:70:ASP:CB	2.81	0.43
1:A:76:LEU:HD12	1:A:77:THR:H	1.83	0.43
1:C:9:VAL:O	1:C:13:LEU:N	2.51	0.43
1:B:88:LEU:HG	1:B:104:PRO:HD2	2.00	0.43
1:C:165:ALA:O	1:C:168:GLN:N	2.51	0.43
1:D:236:TYR:O	1:D:237:PRO:C	2.56	0.43
1:D:38:VAL:HG13	1:D:38:VAL:O	2.19	0.43
1:C:93:PRO:HG3	1:C:99:LEU:CG	2.49	0.43
1:D:287:ARG:HG2	1:D:306:LEU:HD23	1.99	0.43
1:A:295:LEU:HD12	1:A:295:LEU:C	2.39	0.43
1:C:222:ILE:HB	1:C:379:TYR:HB2	2.00	0.43
1:A:68:ARG:NH1	1:A:72:LEU:CB	2.82	0.43
1:C:211:VAL:O	1:C:212:PRO:C	2.55	0.43
1:A:250:LEU:O	1:A:251:GLY:C	2.57	0.42
1:D:266:ALA:O	1:D:267:ARG:C	2.58	0.42
1:C:206:LEU:HD23	1:C:206:LEU:HA	1.69	0.42
1:A:299:ASP:OD1	1:A:302:ALA:HB2	2.19	0.42
1:A:68:ARG:HH12	1:A:72:LEU:CB	2.32	0.42
1:A:28:PRO:HB2	1:A:64:VAL:HG12	2.00	0.42
1:B:325:LEU:HD13	1:B:343:MSE:HB2	2.01	0.42
1:B:9:VAL:O	1:B:10:ALA:C	2.56	0.42
1:D:199:LEU:CD2	1:D:208:THR:HG21	2.49	0.42
1:D:133:VAL:HA	1:D:134:PRO:HD3	1.75	0.42
1:A:88:LEU:HD13	1:A:104:PRO:HD2	2.01	0.42
1:B:266:ALA:CA	1:B:269:LEU:HB2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:ARG:NH2	1:A:256:ARG:HG2	2.34	0.42
1:D:218:LEU:HD12	1:D:356:LEU:O	2.18	0.42
1:C:245:GLU:HA	1:C:248:ARG:CZ	2.49	0.42
1:C:275:PHE:O	1:C:278:ALA:HB3	2.19	0.42
1:D:163:ILE:O	1:D:164:ALA:C	2.56	0.42
1:B:80:GLU:C	1:B:82:ALA:H	2.21	0.42
1:B:240:ARG:O	1:B:244:GLU:HG3	2.19	0.42
1:A:49:GLN:HB3	1:A:204:ARG:HB2	2.01	0.42
1:A:284:GLU:HB2	1:A:287:ARG:NH2	2.33	0.42
1:D:202:ASP:C	1:D:204:ARG:H	2.22	0.42
1:B:291:ALA:O	1:B:294:ALA:HB3	2.19	0.42
1:C:158:PRO:HB3	5:C:444:HOH:O	2.18	0.42
1:D:152:PHE:O	1:D:153:LEU:C	2.55	0.42
1:B:171:GLN:HG3	1:B:182:CYS:SG	2.59	0.42
1:D:221:LEU:O	1:D:354:THR:N	2.38	0.42
1:A:361:ALA:HB3	5:A:454:HOH:O	2.19	0.42
1:B:83:ASP:OD2	1:B:105:ARG:N	2.47	0.42
1:C:321:SER:OG	1:C:322:CYS:N	2.52	0.42
1:D:199:LEU:HD23	1:D:208:THR:HG23	2.01	0.42
1:D:153:LEU:O	1:D:156:LEU:N	2.50	0.42
1:D:333:LEU:HD23	1:D:333:LEU:HA	1.74	0.42
1:B:188:PHE:HZ	1:B:206:LEU:HG	1.83	0.42
1:D:246:VAL:O	1:D:247:ALA:C	2.57	0.42
1:B:219:ALA:HB3	1:B:356:LEU:HD13	2.01	0.42
1:A:68:ARG:HB3	1:A:70:ASP:HB3	2.02	0.42
1:C:68:ARG:HD2	1:C:126:SER:OG	2.19	0.42
1:C:314:LEU:HA	1:C:314:LEU:HD23	1.82	0.42
1:D:223:THR:O	1:D:351:CYS:HA	2.19	0.42
1:B:76:LEU:HD12	1:B:86:GLN:O	2.20	0.42
1:B:366:ARG:NH1	5:B:452:HOH:O	2.51	0.42
1:D:274:GLY:O	1:D:275:PHE:C	2.57	0.42
1:D:204:ARG:HB3	1:D:256:ARG:NH1	2.35	0.42
1:C:74:SER:HA	1:C:89:GLN:HA	2.02	0.42
1:A:213:LEU:HD11	1:A:295:LEU:HD21	2.02	0.42
1:A:18:ARG:O	1:A:19:ALA:C	2.57	0.42
1:B:247:ALA:HB2	1:B:255:LEU:CD2	2.49	0.42
1:A:243:CYS:O	1:A:244:GLU:C	2.58	0.42
1:C:32:VAL:CA	1:C:390:LEU:HD12	2.50	0.42
1:B:53:LEU:HD13	1:B:200:LEU:HD13	2.02	0.42
1:D:303:PHE:O	1:D:307:MSE:HG3	2.20	0.42
1:D:235:GLU:O	1:D:238:VAL:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:240:ARG:O	1:C:244:GLU:HG3	2.20	0.42
1:A:122:LEU:HD11	1:A:153:LEU:HD22	2.02	0.42
1:B:171:GLN:HG2	1:B:175:HIS:CD2	2.54	0.42
1:B:173:ALA:O	1:B:177:PHE:HB2	2.20	0.42
1:B:109:TYR:CE2	1:B:178:ALA:HB2	2.54	0.42
1:D:380:LEU:HD23	1:D:380:LEU:HA	1.70	0.42
1:D:39:ASN:C	1:D:39:ASN:HD22	2.22	0.42
1:C:110:VAL:O	1:C:110:VAL:HG12	2.19	0.42
1:B:370:GLU:CB	1:B:371:HIS:CD2	3.02	0.42
1:D:112:GLY:O	1:D:116:TYR:HD1	2.02	0.42
1:B:246:VAL:HG12	1:B:250:LEU:HD12	2.00	0.42
1:C:31:ALA:CB	1:C:390:LEU:HB2	2.50	0.42
1:B:49:GLN:HE21	1:B:204:ARG:CG	2.32	0.42
1:D:88:LEU:CD1	1:D:89:GLN:N	2.80	0.42
1:A:252:LYS:NZ	1:A:257:GLU:O	2.45	0.42
1:C:117:TYR:CD1	1:C:153:LEU:HB2	2.55	0.42
1:C:256:ARG:HD3	1:C:256:ARG:HH11	1.53	0.42
1:D:329:VAL:HG12	1:D:330:GLU:N	2.34	0.42
1:D:47:TYR:CE1	1:D:240:ARG:HG3	2.55	0.42
1:D:68:ARG:C	1:D:70:ASP:H	2.20	0.42
1:D:9:VAL:O	1:D:10:ALA:C	2.57	0.42
1:D:322:CYS:HA	1:D:323:PRO:HD2	1.77	0.42
1:D:84:GLU:HB2	5:D:446:HOH:O	2.19	0.42
1:D:252:LYS:CG	1:D:257:GLU:HB2	2.50	0.42
1:B:99:LEU:N	1:B:115:GLN:OE1	2.53	0.41
1:A:152:PHE:O	1:A:155:GLN:HB2	2.20	0.41
1:C:341:SER:O	1:C:342:ARG:HB3	2.20	0.41
1:C:4:LEU:HG	1:C:377:THR:HG23	2.02	0.41
1:A:293:ALA:O	1:A:297:ARG:HB3	2.20	0.41
1:D:184:ILE:HG22	1:D:188:PHE:CD1	2.55	0.41
1:C:122:LEU:HA	1:C:123:PRO:HD2	1.74	0.41
1:C:192:MSE:CB	1:C:199:LEU:HD21	2.50	0.41
1:A:361:ALA:N	1:A:362:PRO:CD	2.83	0.41
1:A:113:VAL:CG1	1:A:149:THR:HG22	2.50	0.41
1:C:295:LEU:HA	1:C:295:LEU:HD12	1.63	0.41
1:D:260:LEU:HB3	1:D:261:GLU:OE1	2.21	0.41
1:D:12:LEU:HD23	1:D:12:LEU:HA	1.64	0.41
1:A:34:ALA:HA	1:A:35:PRO:HD3	1.92	0.41
1:C:10:ALA:O	1:C:13:LEU:N	2.52	0.41
1:C:7:PRO:HB2	1:C:12:LEU:HG	2.02	0.41
1:C:184:ILE:HG12	1:C:184:ILE:H	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:238:VAL:HG12	1:D:242:GLN:HE21	1.85	0.41
1:D:314:LEU:O	1:D:319:GLU:N	2.44	0.41
1:A:227:VAL:HG12	1:A:228:ARG:N	2.35	0.41
1:C:260:LEU:HA	1:C:260:LEU:HD12	1.86	0.41
1:B:148:ALA:O	1:B:149:THR:C	2.57	0.41
1:B:117:TYR:OH	1:B:154:GLN:HA	2.21	0.41
1:B:199:LEU:HD11	1:B:210:LEU:CD2	2.51	0.41
1:A:361:ALA:O	1:A:364:ALA:HB3	2.20	0.41
1:D:245:GLU:O	1:D:246:VAL:C	2.57	0.41
1:C:175:HIS:CD2	1:C:181:PRO:HA	2.55	0.41
1:B:60:MSE:HE1	5:B:479:HOH:O	2.21	0.41
1:C:193:GLY:O	1:C:386:GLY:N	2.53	0.41
1:D:239:ARG:O	1:D:240:ARG:C	2.58	0.41
1:C:239:ARG:O	1:C:240:ARG:C	2.57	0.41
1:A:343:MSE:CE	1:A:347:GLY:HA2	2.50	0.41
1:A:140:SER:N	4:A:395:ANP:O3G	2.50	0.41
1:B:295:LEU:HD22	1:B:303:PHE:CE1	2.56	0.41
1:B:77:THR:CG2	1:B:78:THR:N	2.83	0.41
1:D:320:VAL:O	1:D:348:PHE:N	2.52	0.41
1:B:166:ARG:O	1:B:169:VAL:HB	2.20	0.41
1:D:77:THR:CG2	1:D:78:THR:N	2.83	0.41
1:C:189:ILE:HA	1:C:189:ILE:HD12	1.70	0.41
1:B:184:ILE:HG22	1:B:188:PHE:CD1	2.55	0.41
1:A:308:VAL:O	1:A:309:GLU:C	2.59	0.41
1:D:30:LEU:O	1:D:65:GLY:N	2.45	0.41
1:C:20:PHE:CD2	1:C:28:PRO:HB3	2.56	0.41
1:A:262:GLU:O	1:A:265:ALA:HB3	2.20	0.41
1:C:8:GLN:N	1:C:11:GLU:HG3	2.36	0.41
1:D:211:VAL:HA	1:D:212:PRO:HD2	1.57	0.41
1:B:276:ARG:O	1:B:317:ASP:HB3	2.20	0.41
1:C:205:SER:O	1:C:206:LEU:HB2	2.20	0.41
1:A:343:MSE:HE1	1:A:347:GLY:HA2	2.01	0.41
1:A:12:LEU:HD12	1:A:12:LEU:HA	1.85	0.41
1:D:92:LEU:HD23	1:D:92:LEU:HA	1.89	0.41
1:D:87:ARG:CG	1:D:87:ARG:NH1	2.79	0.41
1:A:205:SER:O	1:A:206:LEU:HB2	2.20	0.41
1:D:221:LEU:HD12	1:D:222:ILE:N	2.36	0.41
1:A:113:VAL:HG11	1:A:149:THR:HG22	2.02	0.41
1:B:184:ILE:HD12	1:B:184:ILE:H	1.85	0.41
1:D:49:GLN:HE21	1:D:49:GLN:HB3	1.44	0.41
1:B:63:LEU:HD12	1:B:129:VAL:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4:LEU:HD21	1:C:377:THR:HG23	2.03	0.41
1:B:325:LEU:HA	1:B:325:LEU:HD23	1.83	0.41
1:A:76:LEU:HD12	1:A:77:THR:N	2.36	0.41
1:D:322:CYS:O	1:D:323:PRO:C	2.59	0.41
1:B:239:ARG:HB3	1:B:318:TYR:CE2	2.54	0.41
1:A:53:LEU:N	1:A:54:PRO:CD	2.84	0.41
1:D:99:LEU:HA	1:D:99:LEU:HD23	1.89	0.41
1:C:61:THR:HA	1:C:130:VAL:O	2.20	0.41
1:D:382:GLN:HE21	1:D:382:GLN:HB3	1.63	0.41
1:C:78:THR:O	1:C:78:THR:HG22	2.21	0.41
1:D:33:SER:HA	1:D:61:THR:O	2.21	0.41
1:A:250:LEU:CD2	1:A:266:ALA:HB2	2.51	0.41
1:B:93:PRO:HA	1:B:97:ARG:CG	2.36	0.41
1:A:13:LEU:O	1:A:16:ALA:N	2.54	0.41
1:B:254:SER:O	1:B:257:GLU:HB2	2.21	0.40
1:A:202:ASP:HB3	1:A:205:SER:HG	1.86	0.40
1:D:59:LEU:HD11	1:D:379:TYR:CE2	2.56	0.40
1:C:20:PHE:CE2	1:C:28:PRO:HA	2.56	0.40
1:D:4:LEU:HD22	1:D:377:THR:HG22	2.02	0.40
1:D:20:PHE:CD1	1:D:128:VAL:CG2	3.03	0.40
1:B:307:MSE:HB3	1:B:342:ARG:HG2	2.03	0.40
1:B:77:THR:HG22	1:B:79:SER:N	2.18	0.40
1:D:70:ASP:N	1:D:70:ASP:OD2	2.54	0.40
1:C:372:TYR:HD1	5:C:497:HOH:O	2.03	0.40
1:D:328:LEU:HD21	1:D:372:TYR:CD1	2.56	0.40
1:A:39:ASN:HD22	1:A:40:LEU:N	2.19	0.40
1:D:315:ARG:NH1	5:D:418:HOH:O	2.51	0.40
1:C:42:GLY:O	1:C:52:VAL:HG12	2.21	0.40
1:A:250:LEU:CD2	1:A:266:ALA:CB	2.98	0.40
1:B:153:LEU:CD2	1:B:156:LEU:CD1	2.98	0.40
1:D:73:VAL:O	1:D:89:GLN:HA	2.21	0.40
1:D:122:LEU:HD12	1:D:122:LEU:HA	1.93	0.40
1:D:4:LEU:HA	1:D:4:LEU:HD12	1.59	0.40
1:A:259:GLN:O	1:A:261:GLU:N	2.54	0.40
1:C:229:HIS:HE2	1:C:324:GLU:CD	2.24	0.40
1:A:135:LEU:HD23	1:A:135:LEU:N	2.36	0.40
1:B:29:GLU:HB3	1:B:30:LEU:HG	2.03	0.40
1:D:276:ARG:HB3	1:D:317:ASP:OD1	2.20	0.40
1:C:175:HIS:O	1:C:179:GLY:HA2	2.22	0.40
1:C:20:PHE:CD1	1:C:128:VAL:CG2	3.04	0.40
1:C:195:LYS:O	1:C:197:HIS:N	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:335:VAL:CG1	1:A:336:PRO:HD2	2.51	0.40
1:A:52:VAL:HG23	1:A:54:PRO:CD	2.52	0.40
1:B:146:GLU:HB3	1:B:170:CYS:HB3	2.04	0.40
1:D:59:LEU:HA	1:D:59:LEU:HD23	1.83	0.40
1:B:85:PRO:HD2	1:B:104:PRO:HG3	2.04	0.40
1:D:361:ALA:N	1:D:362:PRO:CD	2.85	0.40
1:B:184:ILE:O	1:B:185:MSE:C	2.60	0.40
1:C:343:MSE:CE	1:C:347:GLY:HA2	2.51	0.40
1:C:157:CYS:O	1:C:157:CYS:SG	2.80	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	387/399 (97%)	326 (84%)	52 (13%)	9 (2%)	8	12
1	B	386/399 (97%)	320 (83%)	50 (13%)	16 (4%)	3	4
1	C	386/399 (97%)	331 (86%)	42 (11%)	13 (3%)	5	6
1	D	387/399 (97%)	319 (82%)	52 (13%)	16 (4%)	3	4
All	All	1546/1596 (97%)	1296 (84%)	196 (13%)	54 (4%)	4	6

All (54) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	99	LEU
1	A	271	SER
1	B	18	ARG
1	B	115	GLN
1	B	158	PRO
1	B	246	VAL

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Mol	Chain	Res	Type
1	C	83	ASP
1	C	99	LEU
1	C	185	MSE
1	D	265	ALA
1	A	161	GLY
1	A	196	GLY
1	A	244	GLU
1	A	250	LEU
1	B	22	GLU
1	B	249	ALA
1	C	195	LYS
1	C	233	SER
1	D	9	VAL
1	D	285	ILE
1	A	46	ASP
1	A	260	LEU
1	B	123	PRO
1	B	248	ARG
1	C	10	ALA
1	C	186	ASP
1	D	158	PRO
1	D	281	VAL
1	D	359	SER
1	A	181	PRO
1	B	10	ALA
1	B	13	LEU
1	B	185	MSE
1	B	245	GLU
1	C	22	GLU
1	C	96	GLN
1	C	123	PRO
1	D	96	GLN
1	D	188	PHE
1	D	264	GLU
1	D	273	GLU
1	B	149	THR
1	D	323	PRO
1	D	358	ALA
1	D	369	GLN
1	B	233	SER
1	D	95	ALA
1	D	361	ALA

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Mol	Chain	Res	Type
1	C	236	TYR
1	D	282	VAL
1	B	41	ILE
1	B	193	GLY
1	C	196	GLY
1	C	9	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	309/308 (100%)	261 (84%)	48 (16%)	3	6
1	B	307/308 (100%)	260 (85%)	47 (15%)	3	6
1	C	307/308 (100%)	276 (90%)	31 (10%)	9	17
1	D	309/308 (100%)	257 (83%)	52 (17%)	2	4
All	All	1232/1232 (100%)	1054 (86%)	178 (14%)	4	7

All (178) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	HIS
1	A	5	ARG
1	A	6	GLN
1	A	18	ARG
1	A	37	ARG
1	A	39	ASN
1	A	43	GLU
1	A	46	ASP
1	A	49	GLN
1	A	55	MSE
1	A	63	LEU
1	A	74	SER
1	A	86	GLN
1	A	89	GLN
1	A	97	ARG

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Mol	Chain	Res	Type
1	A	103	THR
1	A	105	ARG
1	A	135	LEU
1	A	140	SER
1	A	176	SER
1	A	184	ILE
1	A	188	PHE
1	A	192	MSE
1	A	206	LEU
1	A	207	GLU
1	A	212	PRO
1	A	213	LEU
1	A	233	SER
1	A	234	SER
1	A	250	LEU
1	A	252	LYS
1	A	254	SER
1	A	257	GLU
1	A	271	SER
1	A	286	ARG
1	A	287	ARG
1	A	290	GLN
1	A	297	ARG
1	A	306	LEU
1	A	312	ARG
1	A	313	SER
1	A	318	TYR
1	A	342	ARG
1	A	356	LEU
1	A	366	ARG
1	A	370	GLU
1	A	390	LEU
1	A	391	CYS
1	B	6	GLN
1	B	13	LEU
1	B	21	ARG
1	B	27	GLU
1	B	37	ARG
1	B	49	GLN
1	B	55	MSE
1	B	63	LEU
1	B	68	ARG

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Mol	Chain	Res	Type
1	B	69	LYS
1	B	75	LEU
1	B	76	LEU
1	B	79	SER
1	B	88	LEU
1	B	89	GLN
1	B	97	ARG
1	B	98	SER
1	B	100	GLU
1	B	105	ARG
1	B	122	LEU
1	B	140	SER
1	B	156	LEU
1	B	159	ASP
1	B	163	ILE
1	B	166	ARG
1	B	188	PHE
1	B	194	GLN
1	B	195	LYS
1	B	199	LEU
1	B	204	ARG
1	B	217	LYS
1	B	218	LEU
1	B	222	ILE
1	B	234	SER
1	B	250	LEU
1	B	264	GLU
1	B	267	ARG
1	B	271	SER
1	B	318	TYR
1	B	326	ASP
1	B	342	ARG
1	B	355	LEU
1	B	356	LEU
1	B	359	SER
1	B	382	GLN
1	B	385	ASP
1	B	392	LEU
1	C	1	HIS
1	C	4	LEU
1	C	11	GLU
1	C	30	LEU

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Mol	Chain	Res	Type
1	C	37	ARG
1	C	68	ARG
1	C	72	LEU
1	C	75	LEU
1	C	89	GLN
1	C	97	ARG
1	C	106	TRP
1	C	142	SER
1	C	154	GLN
1	C	157	CYS
1	C	187	GLN
1	C	194	GLN
1	C	209	SER
1	C	214	SER
1	C	228	ARG
1	C	234	SER
1	C	248	ARG
1	C	252	LYS
1	C	256	ARG
1	C	261	GLU
1	C	271	SER
1	C	272	LYS
1	C	312	ARG
1	C	318	TYR
1	C	342	ARG
1	C	356	LEU
1	C	382	GLN
1	D	1	HIS
1	D	4	LEU
1	D	11	GLU
1	D	37	ARG
1	D	39	ASN
1	D	43	GLU
1	D	49	GLN
1	D	55	MSE
1	D	66	SER
1	D	70	ASP
1	D	72	LEU
1	D	78	THR
1	D	83	ASP
1	D	86	GLN
1	D	87	ARG

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Mol	Chain	Res	Type
1	D	89	GLN
1	D	97	ARG
1	D	100	GLU
1	D	103	THR
1	D	180	MSE
1	D	184	ILE
1	D	187	GLN
1	D	192	MSE
1	D	194	GLN
1	D	195	LYS
1	D	199	LEU
1	D	200	LEU
1	D	204	ARG
1	D	233	SER
1	D	234	SER
1	D	240	ARG
1	D	248	ARG
1	D	255	LEU
1	D	260	LEU
1	D	262	GLU
1	D	264	GLU
1	D	272	LYS
1	D	277	ARG
1	D	279	ARG
1	D	286	ARG
1	D	290	GLN
1	D	306	LEU
1	D	312	ARG
1	D	313	SER
1	D	318	TYR
1	D	322	CYS
1	D	341	SER
1	D	342	ARG
1	D	343	MSE
1	D	356	LEU
1	D	381	SER
1	D	382	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	GLN

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Mol	Chain	Res	Type
1	A	39	ASN
1	A	49	GLN
1	A	89	GLN
1	A	115	GLN
1	A	175	HIS
1	A	327	GLN
1	A	369	GLN
1	A	371	HIS
1	A	382	GLN
1	B	8	GLN
1	B	39	ASN
1	B	49	GLN
1	B	89	GLN
1	B	371	HIS
1	B	382	GLN
1	C	39	ASN
1	C	49	GLN
1	C	89	GLN
1	C	154	GLN
1	C	155	GLN
1	C	168	GLN
1	C	171	GLN
1	C	187	GLN
1	C	194	GLN
1	C	259	GLN
1	C	327	GLN
1	C	369	GLN
1	C	371	HIS
1	C	382	GLN
1	D	39	ASN
1	D	49	GLN
1	D	154	GLN
1	D	187	GLN
1	D	194	GLN
1	D	197	HIS
1	D	226	ASN
1	D	259	GLN
1	D	371	HIS
1	D	382	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	GLA	A	393	-	12,12,12	0.70	0	17,17,17	1.08	0
4	ANP	A	395	3	27,33,33	1.58	7 (25%)	30,52,52	2.01	7 (23%)
2	GLA	B	393	-	12,12,12	0.52	0	17,17,17	1.45	4 (23%)
4	ANP	B	395	3	27,33,33	1.73	4 (14%)	30,52,52	2.02	6 (20%)
2	GLA	C	393	-	12,12,12	0.57	0	17,17,17	1.11	1 (5%)
4	ANP	C	395	3	27,33,33	1.62	6 (22%)	30,52,52	1.97	6 (20%)
2	GLA	D	393	-	12,12,12	0.53	0	17,17,17	1.12	1 (5%)
4	ANP	D	395	3	27,33,33	1.55	5 (18%)	30,52,52	2.08	5 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLA	A	393	-	-	0/2/22/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ANP	A	395	3	-	0/12/38/38	0/3/3/3
2	GLA	B	393	-	-	0/2/22/22	0/1/1/1
4	ANP	B	395	3	-	0/12/38/38	0/3/3/3
2	GLA	C	393	-	-	0/2/22/22	0/1/1/1
4	ANP	C	395	3	-	0/12/38/38	0/3/3/3
2	GLA	D	393	-	-	0/2/22/22	0/1/1/1
4	ANP	D	395	3	-	0/12/38/38	0/3/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	395	ANP	O4'-C1'	-4.08	1.36	1.41
4	A	395	ANP	C6-N6	-3.26	1.24	1.34
4	D	395	ANP	C6-N6	-3.22	1.25	1.34
4	B	395	ANP	C6-N6	-3.14	1.25	1.34
4	C	395	ANP	PG-O2G	-3.06	1.48	1.56
4	C	395	ANP	PB-O2B	-3.04	1.48	1.56
4	C	395	ANP	C6-N6	-3.02	1.25	1.34
4	C	395	ANP	O4'-C1'	-2.96	1.37	1.41
4	A	395	ANP	O4'-C1'	-2.78	1.37	1.41
4	D	395	ANP	PG-O2G	-2.41	1.50	1.56
4	A	395	ANP	PB-O2B	-2.27	1.50	1.56
4	D	395	ANP	O4'-C1'	-2.19	1.38	1.41
4	A	395	ANP	C4-N3	-2.01	1.32	1.35
4	A	395	ANP	PG-O2G	-2.00	1.51	1.56
4	C	395	ANP	PB-O1B	2.95	1.49	1.46
4	A	395	ANP	PG-O1G	3.06	1.49	1.46
4	A	395	ANP	PB-O1B	3.42	1.50	1.46
4	B	395	ANP	PG-O1G	3.74	1.50	1.46
4	C	395	ANP	PG-O1G	3.80	1.50	1.46
4	D	395	ANP	PB-O1B	3.97	1.50	1.46
4	D	395	ANP	PG-O1G	4.09	1.50	1.46
4	B	395	ANP	PB-O1B	4.23	1.51	1.46

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	395	ANP	N3-C2-N1	-7.65	123.03	128.89
4	B	395	ANP	N3-C2-N1	-7.33	123.28	128.89
4	C	395	ANP	N3-C2-N1	-6.59	123.84	128.89
4	A	395	ANP	N3-C2-N1	-6.33	124.05	128.89
4	A	395	ANP	O1B-PB-N3B	-4.34	105.25	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	395	ANP	O1B-PB-N3B	-4.03	105.72	111.90
4	D	395	ANP	O1B-PB-N3B	-3.14	107.08	111.90
2	C	393	GLA	O3-C3-C4	-3.05	103.47	110.34
4	B	395	ANP	O1G-PG-N3B	-3.00	107.30	111.90
2	B	393	GLA	O3-C3-C2	-2.59	104.50	110.34
4	B	395	ANP	C1'-N9-C4	-2.48	123.19	126.94
4	B	395	ANP	O3G-PG-O1G	-2.38	107.17	113.49
4	D	395	ANP	PA-O3A-PB	-2.37	124.71	132.67
2	B	393	GLA	O2-C2-C3	-2.37	105.01	110.34
4	A	395	ANP	O1G-PG-N3B	-2.32	108.34	111.90
4	C	395	ANP	C2'-C3'-C4'	-2.26	97.97	102.61
2	B	393	GLA	C3-C4-C5	-2.25	106.28	110.20
4	A	395	ANP	O3G-PG-O1G	-2.12	107.86	113.49
4	C	395	ANP	PA-O3A-PB	-2.09	125.66	132.67
4	B	395	ANP	C2'-C3'-C4'	-2.04	98.41	102.61
4	A	395	ANP	N6-C6-N1	2.05	123.60	119.20
2	D	393	GLA	C1-C2-C3	2.15	113.63	110.43
4	C	395	ANP	N6-C6-N1	2.15	123.83	119.20
2	B	393	GLA	O2-C2-C1	2.72	115.82	109.82
4	A	395	ANP	O3A-PA-O5'	2.99	110.86	102.94
4	D	395	ANP	O3A-PA-O5'	4.04	113.64	102.94
4	D	395	ANP	C2-N1-C6	4.10	126.10	118.77
4	B	395	ANP	C2-N1-C6	4.16	126.20	118.77
4	A	395	ANP	C2-N1-C6	4.27	126.40	118.77
4	C	395	ANP	C2-N1-C6	4.53	126.86	118.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	393	GLA	1	0
4	A	395	ANP	6	0
4	B	395	ANP	7	0
4	C	395	ANP	8	0
4	D	395	ANP	3	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	383/399 (95%)	-0.05	9 (2%) 64 67	22, 41, 69, 84	0
1	B	382/399 (95%)	0.27	25 (6%) 22 25	19, 48, 76, 93	0
1	C	382/399 (95%)	0.02	12 (3%) 52 57	15, 40, 73, 91	0
1	D	382/399 (95%)	-0.03	9 (2%) 62 66	21, 41, 68, 88	0
All	All	1529/1596 (95%)	0.05	55 (3%) 46 51	15, 43, 73, 93	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	98	SER	4.5
1	B	97	ARG	4.5
1	B	94	THR	4.2
1	C	121	PRO	4.1
1	B	2	ALA	4.1
1	A	157	CYS	4.0
1	B	63	LEU	3.9
1	A	232	ALA	3.8
1	B	158	PRO	3.8
1	C	96	GLN	3.8
1	D	266	ALA	3.7
1	B	21	ARG	3.6
1	C	94	THR	3.5
1	B	69	LYS	3.2
1	D	1	HIS	3.2
1	C	110	VAL	3.2
1	B	214	SER	3.0
1	B	119	ALA	3.0
1	C	26	ALA	2.9
1	B	231	LEU	2.9
1	B	70	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	97	ARG	2.8
1	B	75	LEU	2.8
1	A	391	CYS	2.8
1	D	120	ALA	2.7
1	B	96	GLN	2.7
1	B	160	SER	2.7
1	A	354	THR	2.7
1	A	63	LEU	2.6
1	C	63	LEU	2.6
1	B	22	GLU	2.6
1	B	95	ALA	2.6
1	D	2	ALA	2.6
1	C	86	GLN	2.5
1	B	18	ARG	2.5
1	D	98	SER	2.5
1	B	248	ARG	2.5
1	D	245	GLU	2.4
1	C	281	VAL	2.4
1	C	68	ARG	2.3
1	A	95	ALA	2.3
1	B	120	ALA	2.3
1	C	84	GLU	2.3
1	C	25	GLY	2.3
1	A	298	GLY	2.2
1	B	105	ARG	2.1
1	B	99	LEU	2.1
1	D	121	PRO	2.1
1	A	145	LEU	2.1
1	B	88	LEU	2.1
1	B	161	GLY	2.1
1	A	228	ARG	2.1
1	C	28	PRO	2.1
1	B	162	THR	2.1
1	D	113	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	GLA	B	393	12/12	0.95	0.22	2.43	22,34,54,71	0
2	GLA	D	393	12/12	0.98	0.17	0.34	2,22,31,55	0
4	ANP	B	395	31/31	0.88	0.16	-0.10	0,44,81,94	0
2	GLA	C	393	12/12	0.98	0.14	-0.55	6,19,58,80	0
2	GLA	A	393	12/12	0.96	0.14	-0.64	22,33,49,66	0
4	ANP	A	395	31/31	0.97	0.10	-1.16	19,34,50,66	0
4	ANP	D	395	31/31	0.98	0.10	-1.22	12,26,51,80	0
4	ANP	C	395	31/31	0.96	0.11	-1.44	0,36,57,92	0
3	MG	A	394	1/1	0.92	0.22	-	38,38,38,38	0
3	MG	C	394	1/1	0.94	0.05	-	26,26,26,26	0
3	MG	B	394	1/1	0.83	0.13	-	41,41,41,41	0
3	MG	D	394	1/1	0.95	0.09	-	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.