



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:32 AM GMT

PDB ID : 2R3V
Title : The Biochemical and Structural Basis for Feedback Inhibition of Mevalonate Kinase and Isoprenoid Metabolism
Authors : Fu, Z.; Voynova, N.E.; Mizioro, H.M.; Kim, J.P.
Deposited on : 2007-08-30
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

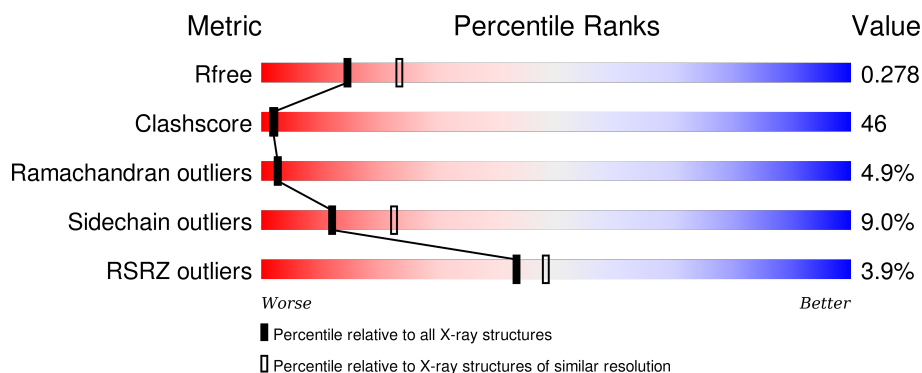
1 Overall quality at a glance

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	396	<div> <div>4%</div> <div>39% 50% 9% ..</div> </div>
1	B	396	<div> <div>%</div> <div>39% 48% 10% ..</div> </div>
1	C	396	<div> <div>6%</div> <div>37% 53% 7% ..</div> </div>
1	D	396	<div> <div>5%</div> <div>38% 53% 6% .</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11935 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 Mevalonate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	0	0
			2933	1849	519	552	13			
1	B	388	Total	C	N	O	S	0	0	0
			2918	1838	517	550	13			
1	C	390	Total	C	N	O	S	0	0	0
			2933	1849	519	552	13			
1	D	389	Total	C	N	O	S	0	0	0
			2926	1844	518	551	13			

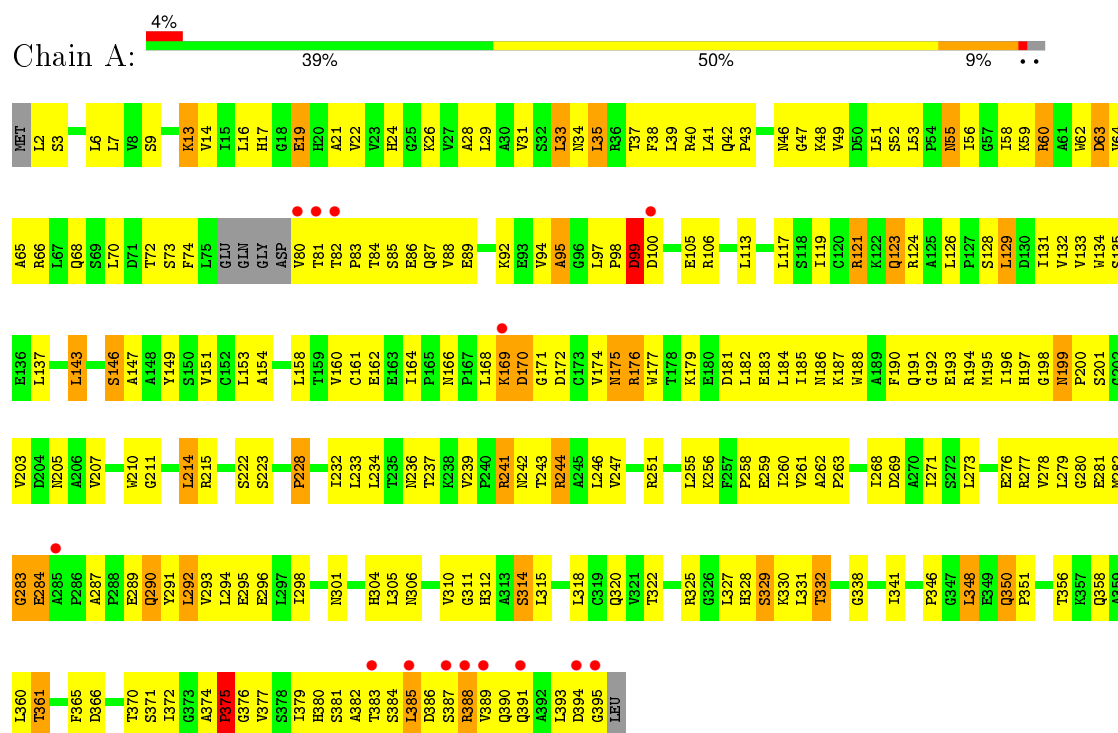
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	72	Total	O	0	0
			72	72		
2	B	63	Total	O	0	0
			63	63		
2	C	45	Total	O	0	0
			45	45		
2	D	45	Total	O	0	0
			45	45		

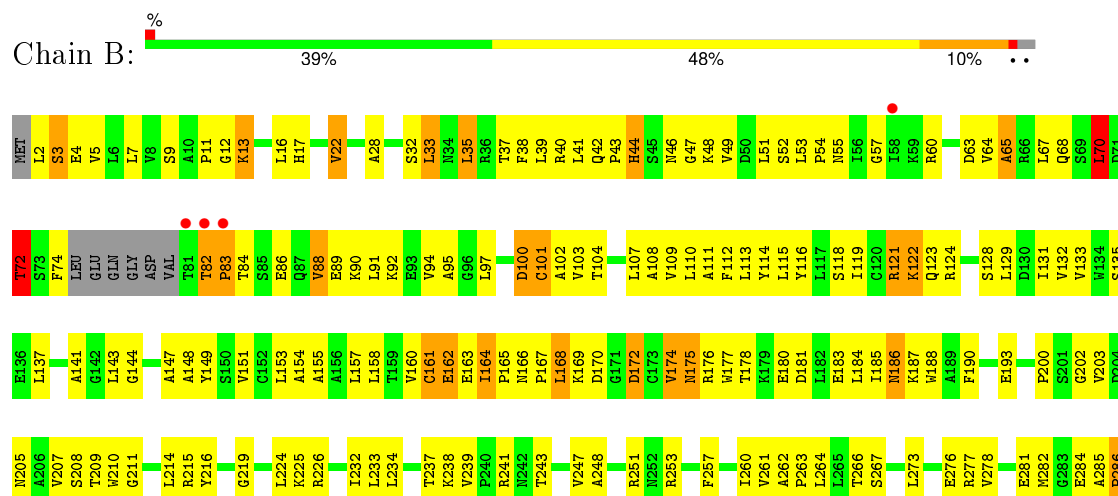
3 Residue-property plots

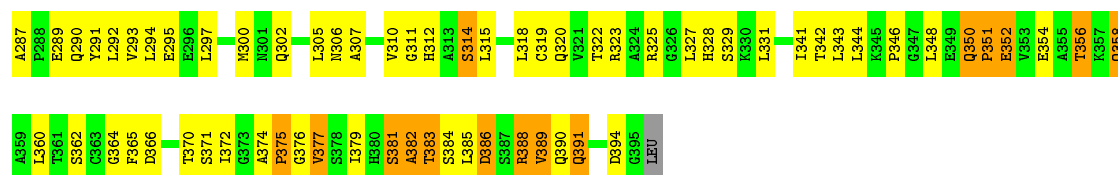
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

• Molecule 1: Mevalonate kinase

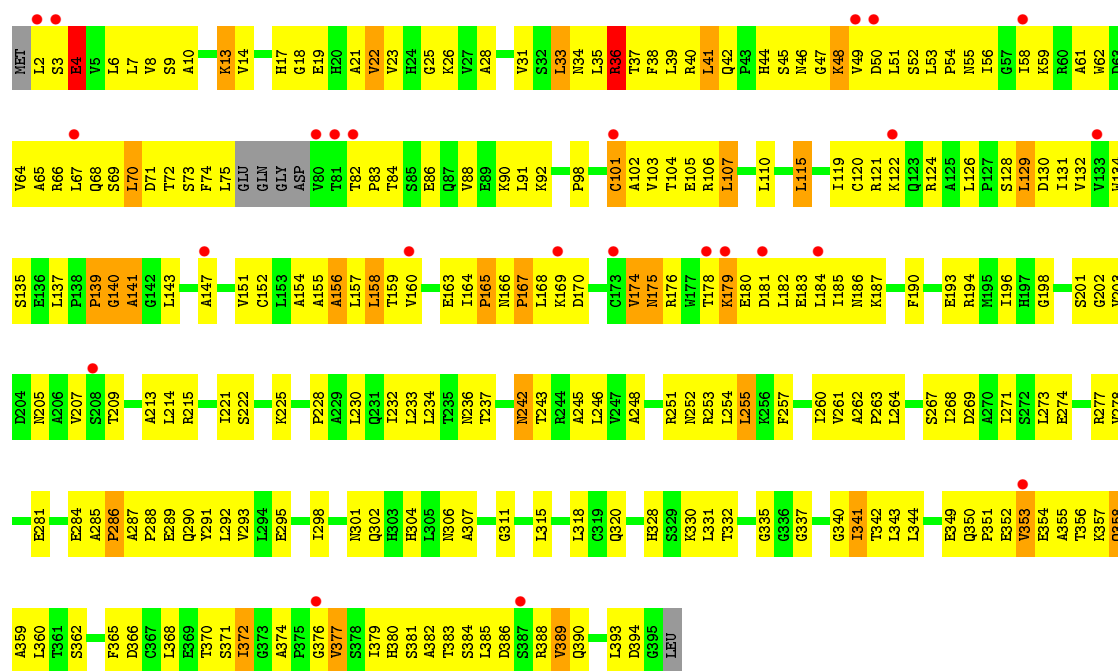


• Molecule 1: Mevalonate kinase

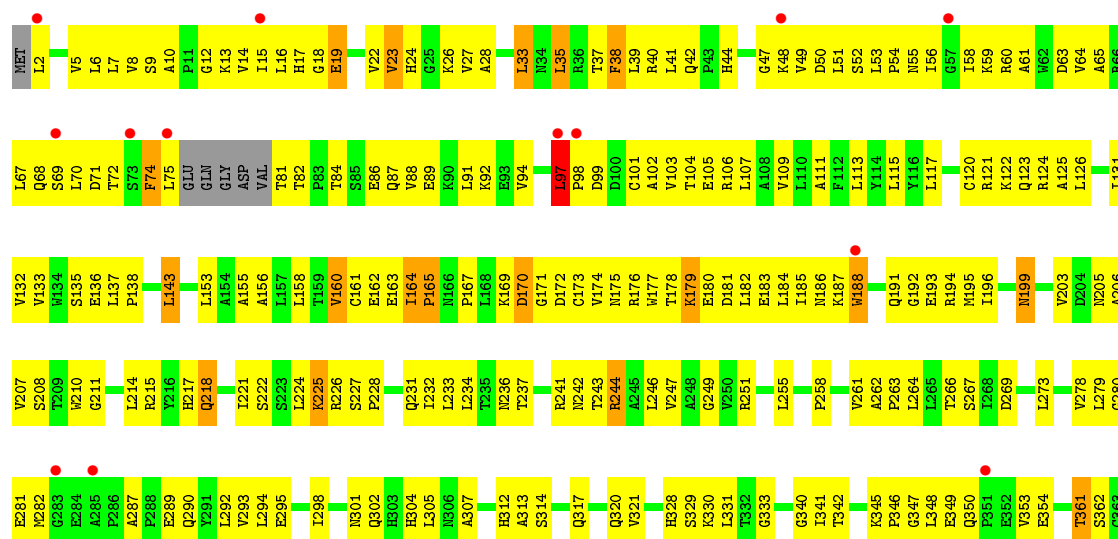


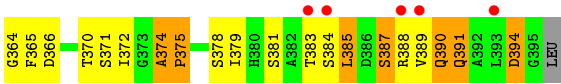


• Molecule 1: Mevalonate kinase



• Molecule 1: Mevalonate kinase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	102.03Å 78.20Å 109.45Å 90.00° 113.33° 90.00°	Depositor
Resolution (Å)	29.37 – 2.50 34.47 – 2.50	Depositor EDS
% Data completeness (in resolution range)	84.1 (29.37-2.50) 84.0 (34.47-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.01 (at 2.51Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.239 , 0.282 0.236 , 0.278	Depositor DCC
R_{free} test set	3916 reflections (8.46%)	DCC
Wilson B-factor (Å ²)	38.3	Xtriage
Anisotropy	0.733	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 53.1	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	4 of 46324 reflections (0.009%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11935	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.75 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.6120e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 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	0.39	0/2983	0.69	0/4055
1	B	0.39	0/2968	0.66	1/4034 (0.0%)
1	C	0.35	0/2983	0.62	0/4055
1	D	0.34	0/2976	0.65	2/4045 (0.0%)
All	All	0.37	0/11910	0.66	3/16189 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	97	LEU	CB-CG-CD2	-5.88	101.01	111.00
1	D	35	LEU	N-CA-C	-5.65	95.75	111.00
1	B	72	THR	N-CA-C	5.44	125.70	111.00

There are no chirality outliers.

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	2933	0	3003	278	0
1	B	2918	0	2983	272	0
1	C	2933	0	3003	290	0
1	D	2926	0	2994	273	0
2	A	72	0	0	7	0
2	B	63	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	45	0	0	4	0
2	D	45	0	0	5	0
All	All	11935	0	11983	1097	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 46.

All (1097) 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:119:ILE:HD11	1:C:158:LEU:HD13	1.27	1.08
1:C:50:ASP:HB2	1:C:130:ASP:HA	1.33	1.06
1:C:52:SER:HB3	1:C:132:VAL:HG22	1.35	1.06
1:B:232:ILE:HG12	1:B:372:ILE:HD13	1.36	1.04
1:A:52:SER:HB3	1:A:132:VAL:HG22	1.40	1.03
1:B:68:GLN:O	1:B:70:LEU:HD22	1.62	1.00
1:D:158:LEU:HD23	1:D:185:ILE:HD13	1.41	0.99
1:B:82:THR:HB	1:B:86:GLU:HB2	1.44	0.98
1:A:388:ARG:H	1:A:388:ARG:HE	1.02	0.97
1:B:115:LEU:HD23	1:B:153:LEU:HB3	1.43	0.96
1:C:386:ASP:HB2	1:C:389:VAL:HG23	1.47	0.96
1:B:55:ASN:HD21	1:B:135:SER:H	1.04	0.94
1:C:7:LEU:O	1:C:379:ILE:HD12	1.66	0.94
1:A:7:LEU:HD23	1:A:380:HIS:HB2	1.50	0.93
1:C:119:ILE:HD11	1:C:158:LEU:CD1	1.97	0.93
1:D:52:SER:HB3	1:D:132:VAL:HG22	1.50	0.93
1:C:66:ARG:O	1:C:70:LEU:HD23	1.69	0.92
1:B:388:ARG:HH21	1:B:391:GLN:HG3	1.34	0.92
1:B:164:ILE:HD11	1:B:177:TRP:HD1	1.32	0.92
1:C:56:ILE:HG22	1:C:58:ILE:HG23	1.52	0.91
1:C:233:LEU:HD13	1:C:344:LEU:HD21	1.52	0.91
1:B:70:LEU:HG	1:B:72:THR:CG2	2.00	0.90
1:B:39:LEU:HD11	1:B:153:LEU:HD12	1.54	0.90
1:D:164:ILE:HD11	1:D:181:ASP:CG	1.93	0.89
1:B:67:LEU:O	1:B:70:LEU:HD13	1.72	0.88
1:A:58:ILE:HD13	1:A:105:GLU:HB2	1.55	0.88
1:C:182:LEU:HD23	1:C:185:ILE:HD12	1.55	0.88
1:D:107:LEU:HD22	1:D:196:ILE:HG23	1.52	0.87
1:A:40:ARG:HH22	1:A:390:GLN:NE2	1.72	0.87
1:B:211:GLY:HA3	1:B:375:PRO:O	1.75	0.87
1:B:39:LEU:HG	1:B:133:VAL:HG22	1.55	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:84:THR:HG22	1:C:86:GLU:H	1.39	0.86
1:B:287:ALA:HB3	1:B:290:GLN:HG3	1.57	0.86
1:C:6:LEU:HD13	1:C:379:ILE:HD11	1.58	0.85
1:B:122:LYS:HD3	1:B:122:LYS:H	1.41	0.85
1:B:33:LEU:HD11	1:B:234:LEU:HD22	1.57	0.85
1:C:385:LEU:HD23	1:C:390:GLN:HB2	1.57	0.85
1:B:13:LYS:HB2	1:B:207:VAL:HG11	1.58	0.84
1:C:141:ALA:HB3	1:C:143:LEU:HD23	1.57	0.84
1:D:243:THR:O	1:D:247:VAL:HG23	1.78	0.84
1:A:175:ASN:HD22	1:A:176:ARG:H	1.25	0.83
1:A:84:THR:HG22	1:A:86:GLU:H	1.40	0.83
1:A:386:ASP:HB2	1:A:389:VAL:HG23	1.60	0.83
1:D:39:LEU:HD21	1:D:131:ILE:HG23	1.59	0.83
1:A:81:THR:HA	1:A:194:ARG:NH1	1.91	0.83
1:A:39:LEU:HD11	1:A:153:LEU:HD23	1.58	0.83
1:C:53:LEU:HD12	1:C:58:ILE:HD11	1.61	0.82
1:A:385:LEU:CD2	1:A:389:VAL:HG11	2.10	0.82
1:A:385:LEU:HD23	1:A:389:VAL:HG11	1.61	0.82
1:B:164:ILE:HD11	1:B:177:TRP:CD1	2.14	0.82
1:D:12:GLY:HA2	1:D:137:LEU:HD11	1.60	0.82
1:B:164:ILE:HD13	1:B:165:PRO:N	1.95	0.81
1:B:70:LEU:HD23	1:B:70:LEU:O	1.79	0.81
1:D:37:THR:HG23	1:D:135:SER:HB2	1.62	0.81
1:D:49:VAL:HG23	1:D:64:VAL:HG12	1.62	0.81
1:D:388:ARG:HE	1:D:389:VAL:HG23	1.45	0.81
1:D:12:GLY:CA	1:D:137:LEU:HD11	2.11	0.81
1:D:40:ARG:HD2	1:D:394:ASP:HB3	1.63	0.81
1:D:50:ASP:HB3	1:D:61:ALA:HB2	1.63	0.80
1:D:97:LEU:HB3	1:D:98:PRO:HD2	1.62	0.80
1:D:53:LEU:HD12	1:D:58:ILE:HD11	1.60	0.80
1:B:55:ASN:ND2	1:B:135:SER:H	1.79	0.79
1:C:225:LYS:HZ2	1:C:225:LYS:HB2	1.48	0.79
1:B:155:ALA:HA	1:B:185:ILE:HD12	1.64	0.79
1:D:39:LEU:HD11	1:D:153:LEU:HD23	1.64	0.79
1:B:2:LEU:HA	1:B:169:LYS:HG3	1.65	0.79
1:C:350:GLN:HE21	1:C:354:GLU:HG2	1.48	0.78
1:B:55:ASN:HD21	1:B:135:SER:N	1.80	0.78
1:A:60:ARG:NH1	1:A:60:ARG:HB2	1.99	0.78
1:D:164:ILE:HD12	1:D:177:TRP:HD1	1.46	0.78
1:B:233:LEU:HD13	1:B:344:LEU:HD11	1.64	0.78
1:A:262:ALA:HB3	1:A:263:PRO:HD3	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:268:ILE:HD11	1:A:304:HIS:CB	2.13	0.78
1:A:374:ALA:HB1	1:A:375:PRO:HD2	1.67	0.77
1:A:46:ASN:HD21	1:A:48:LYS:HB2	1.48	0.77
1:A:84:THR:HG22	1:A:86:GLU:N	1.99	0.77
1:C:207:VAL:HG22	1:C:214:LEU:HD22	1.65	0.77
1:A:46:ASN:ND2	1:A:48:LYS:HB2	1.99	0.77
1:A:168:LEU:O	1:A:170:ASP:N	2.17	0.77
1:D:6:LEU:HB2	1:D:41:LEU:CD2	2.15	0.77
1:A:56:ILE:HG22	1:A:58:ILE:HG23	1.67	0.77
1:D:33:LEU:HD11	1:D:234:LEU:HD22	1.66	0.76
1:C:180:GLU:H	1:C:180:GLU:CD	1.88	0.76
1:D:388:ARG:NE	1:D:389:VAL:HG23	2.00	0.76
1:A:81:THR:HA	1:A:194:ARG:HH11	1.46	0.76
1:A:40:ARG:HH22	1:A:390:GLN:HE21	1.31	0.76
1:A:97:LEU:HD13	1:A:106:ARG:HG3	1.68	0.76
1:B:119:ILE:O	1:B:122:LYS:HE2	1.86	0.76
1:A:287:ALA:H	1:A:290:GLN:NE2	1.83	0.75
1:A:147:ALA:HB2	1:A:193:GLU:OE2	1.86	0.75
1:B:12:GLY:HA3	1:B:137:LEU:HD11	1.69	0.75
1:C:147:ALA:O	1:C:151:VAL:HG23	1.87	0.75
1:A:84:THR:HB	1:A:87:GLN:HG3	1.69	0.75
1:D:244:ARG:H	1:D:244:ARG:NE	1.83	0.75
1:D:164:ILE:HD11	1:D:181:ASP:CB	2.17	0.75
1:D:251:ARG:O	1:D:255:LEU:HD23	1.87	0.74
1:C:175:ASN:HD22	1:C:176:ARG:H	1.35	0.74
1:C:47:GLY:O	1:C:48:LYS:HG2	1.87	0.74
1:A:35:LEU:O	1:A:137:LEU:HG	1.87	0.74
1:C:278:VAL:HG21	1:C:293:VAL:HG11	1.69	0.74
1:C:41:LEU:HD12	1:C:156:ALA:HB1	1.70	0.74
1:D:68:GLN:OE1	1:D:125:ALA:HB1	1.88	0.74
1:D:181:ASP:O	1:D:185:ILE:HG12	1.85	0.74
1:D:317:GLN:O	1:D:321:VAL:HG23	1.88	0.74
1:D:164:ILE:HD13	1:D:165:PRO:CD	2.18	0.74
1:D:164:ILE:HD11	1:D:181:ASP:HB3	1.70	0.74
1:A:40:ARG:NH2	1:A:390:GLN:HE21	1.86	0.74
1:B:164:ILE:CD1	1:B:177:TRP:CD1	2.71	0.74
1:B:183:GLU:O	1:B:187:LYS:HG2	1.88	0.74
1:D:88:VAL:O	1:D:92:LYS:HB2	1.88	0.74
1:A:244:ARG:HD2	1:C:289:GLU:HG2	1.69	0.74
1:B:176:ARG:NH1	1:D:89:GLU:HG2	2.03	0.73
1:B:295:GLU:HB3	1:B:328:HIS:CD2	2.24	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:164:ILE:HD12	1:D:177:TRP:CD1	2.23	0.73
1:D:289:GLU:O	1:D:293:VAL:HG23	1.88	0.73
1:C:295:GLU:HB3	1:C:328:HIS:ND1	2.04	0.73
1:B:388:ARG:NH2	1:B:391:GLN:HG3	2.03	0.73
1:A:129:LEU:HD13	1:A:131:ILE:HD11	1.71	0.72
1:B:158:LEU:C	1:B:164:ILE:HG22	2.10	0.72
1:B:158:LEU:O	1:B:164:ILE:HG22	1.87	0.72
1:A:33:LEU:HD21	1:A:370:THR:HG21	1.71	0.72
1:A:241:ARG:HG2	1:A:241:ARG:HH11	1.55	0.72
1:C:193:GLU:HG3	1:C:205:ASN:HD22	1.53	0.72
1:D:105:GLU:O	1:D:109:VAL:HG23	1.90	0.72
1:C:332:THR:CG2	1:C:341:ILE:HD13	2.18	0.72
1:C:83:PRO:HG3	1:C:198:GLY:HA2	1.70	0.72
1:B:233:LEU:HB2	1:B:342:THR:HB	1.70	0.71
1:A:199:ASN:C	1:A:199:ASN:HD22	1.93	0.71
1:B:385:LEU:HB3	1:B:389:VAL:HG11	1.72	0.71
1:C:41:LEU:HD13	1:C:160:VAL:HG21	1.73	0.71
1:D:164:ILE:HD11	1:D:181:ASP:OD1	1.90	0.71
1:A:22:VAL:HG11	1:A:28:ALA:HB2	1.72	0.71
1:D:231:GLN:NE2	1:D:371:SER:HB3	2.06	0.71
1:A:129:LEU:CD1	1:A:131:ILE:HD11	2.21	0.71
1:A:196:ILE:HG13	1:A:197:HIS:N	2.03	0.71
1:D:70:LEU:CD2	1:D:94:VAL:HG11	2.20	0.71
1:A:298:ILE:HG23	1:A:330:LYS:HB3	1.73	0.70
1:B:209:THR:HA	1:B:377:VAL:HG23	1.73	0.70
1:C:233:LEU:CD1	1:C:344:LEU:HD21	2.20	0.70
1:D:233:LEU:HB3	1:D:342:THR:HB	1.73	0.70
1:B:70:LEU:HG	1:B:72:THR:HG21	1.72	0.70
1:D:278:VAL:O	1:D:282:MET:HG3	1.92	0.70
1:C:51:LEU:O	1:C:59:LYS:HD2	1.91	0.70
1:D:9:SER:HA	1:D:37:THR:O	1.92	0.70
1:C:121:ARG:HG3	1:C:122:LYS:H	1.57	0.69
1:D:207:VAL:HG22	1:D:214:LEU:HD12	1.73	0.69
1:B:352:GLU:O	1:B:356:THR:HG23	1.92	0.69
1:D:51:LEU:HD21	1:D:53:LEU:HD21	1.72	0.69
1:A:22:VAL:CG1	1:A:28:ALA:HB2	2.22	0.69
1:B:112:PHE:HE1	1:B:131:ILE:HD12	1.54	0.69
1:D:6:LEU:HB2	1:D:41:LEU:HD21	1.74	0.69
1:D:203:VAL:O	1:D:207:VAL:HG23	1.92	0.69
1:D:236:ASN:HB3	1:D:366:ASP:HB2	1.72	0.69
1:B:233:LEU:CD1	1:B:344:LEU:HD11	2.23	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:348:LEU:HD21	2:B:431:HOH:O	1.93	0.69
1:A:13:LYS:HG2	1:A:14:VAL:N	2.07	0.69
1:A:117:LEU:O	1:A:121:ARG:HB2	1.93	0.69
1:D:86:GLU:O	1:D:89:GLU:HB3	1.93	0.69
1:A:73:SER:HA	1:A:121:ARG:HH22	1.58	0.69
1:D:22:VAL:HG13	1:D:28:ALA:HB2	1.73	0.69
1:C:41:LEU:HG	1:C:131:ILE:HG12	1.75	0.68
1:C:52:SER:HB3	1:C:132:VAL:CG2	2.20	0.68
1:C:154:ALA:O	1:C:158:LEU:HD22	1.93	0.68
1:B:176:ARG:HH11	1:D:89:GLU:HG2	1.58	0.68
1:C:232:ILE:HG12	1:C:372:ILE:HD13	1.75	0.68
1:A:360:LEU:O	1:A:365:PHE:HB2	1.93	0.68
1:C:65:ALA:O	1:C:68:GLN:HB3	1.94	0.68
1:B:39:LEU:HG	1:B:133:VAL:CG2	2.22	0.68
1:C:35:LEU:HB3	1:C:137:LEU:HD23	1.74	0.68
1:C:284:GLU:C	1:C:286:PRO:HD3	2.13	0.68
1:D:75:LEU:HD12	1:D:75:LEU:H	1.57	0.68
1:C:33:LEU:HD11	1:C:234:LEU:HD22	1.76	0.68
1:A:175:ASN:HD22	1:A:176:ARG:N	1.92	0.68
1:C:175:ASN:HD22	1:C:176:ARG:N	1.92	0.67
1:B:262:ALA:HB3	1:B:263:PRO:HD3	1.76	0.67
1:B:86:GLU:HG2	1:B:90:LYS:HD2	1.75	0.67
1:C:332:THR:HG21	1:C:341:ILE:HD13	1.75	0.67
1:C:34:ASN:HB2	1:C:374:ALA:HB2	1.76	0.67
1:D:84:THR:OG1	1:D:87:GLN:HG3	1.95	0.67
1:B:2:LEU:HA	1:B:169:LYS:CG	2.25	0.67
1:A:26:LYS:HD2	1:A:269:ASP:HB2	1.77	0.67
1:D:70:LEU:HD21	1:D:94:VAL:HG11	1.77	0.67
1:C:236:ASN:HB3	1:C:366:ASP:HB2	1.77	0.67
1:D:180:GLU:H	1:D:180:GLU:CD	1.98	0.67
1:D:282:MET:HG2	1:D:290:GLN:NE2	2.10	0.67
1:B:237:THR:HA	1:B:365:PHE:CD2	2.28	0.67
1:C:7:LEU:HD11	1:C:382:ALA:HB2	1.77	0.67
1:B:253:ARG:NH2	1:B:307:ALA:O	2.28	0.67
1:B:176:ARG:HG3	1:B:176:ARG:HH21	1.60	0.67
1:B:88:VAL:HG12	1:B:92:LYS:HE3	1.75	0.66
1:A:41:LEU:HD23	1:A:41:LEU:C	2.15	0.66
1:A:70:LEU:HD21	1:A:94:VAL:HG22	1.77	0.66
1:C:176:ARG:HB2	1:C:176:ARG:NH1	2.09	0.66
1:D:12:GLY:HA3	1:D:137:LEU:HD21	1.77	0.66
1:D:122:LYS:HD2	1:D:163:GLU:OE1	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:356:THR:HG22	1:C:360:LEU:CD1	2.25	0.66
1:A:33:LEU:HD11	1:A:234:LEU:HD22	1.76	0.66
1:C:306:ASN:HD22	1:C:311:GLY:HA3	1.61	0.66
1:A:381:SER:O	1:A:383:THR:N	2.27	0.66
1:C:51:LEU:N	1:C:59:LYS:HZ1	1.94	0.66
1:A:268:ILE:HD11	1:A:304:HIS:HB2	1.76	0.66
1:B:67:LEU:O	1:B:70:LEU:HB3	1.95	0.66
1:D:59:LYS:O	1:D:60:ARG:HG3	1.95	0.66
1:C:306:ASN:ND2	1:C:311:GLY:HA3	2.11	0.66
1:A:322:THR:HG22	1:A:327:LEU:O	1.94	0.66
1:B:33:LEU:HD23	1:B:372:ILE:CD1	2.26	0.66
1:A:121:ARG:HG2	1:A:121:ARG:HH11	1.61	0.66
1:C:39:LEU:C	1:C:39:LEU:HD23	2.17	0.65
1:B:39:LEU:HD11	1:B:153:LEU:CD1	2.22	0.65
1:D:70:LEU:HG	1:D:72:THR:HG23	1.76	0.65
1:A:215:ARG:NH1	1:A:276:GLU:OE1	2.29	0.65
1:C:187:LYS:HD3	1:C:187:LYS:C	2.16	0.65
1:A:174:VAL:HG12	1:A:380:HIS:ND1	2.11	0.65
1:A:268:ILE:HD11	1:A:304:HIS:HB3	1.77	0.65
1:B:168:LEU:HD23	1:B:172:ASP:OD1	1.96	0.65
1:D:298:ILE:HG23	1:D:330:LYS:HB3	1.78	0.65
1:C:48:LYS:H	1:C:128:SER:CB	2.09	0.65
1:D:33:LEU:HD21	1:D:370:THR:HG21	1.79	0.65
1:B:121:ARG:HB3	1:B:121:ARG:HH21	1.61	0.65
1:A:322:THR:HG23	1:A:327:LEU:HB2	1.79	0.65
1:D:224:LEU:HB3	1:D:227:SER:HB2	1.79	0.65
1:C:6:LEU:CD1	1:C:379:ILE:HD11	2.26	0.65
1:C:51:LEU:HA	1:C:131:ILE:O	1.97	0.65
1:B:158:LEU:HD21	1:B:184:LEU:HG	1.79	0.65
1:C:64:VAL:HG11	1:C:128:SER:HB3	1.79	0.65
1:B:22:VAL:HG13	1:B:28:ALA:HB2	1.77	0.65
1:B:70:LEU:HG	1:B:72:THR:HG23	1.76	0.64
1:C:243:THR:HA	1:C:246:LEU:HD23	1.79	0.64
1:A:168:LEU:HG	1:A:379:ILE:HG23	1.78	0.64
1:B:37:THR:HG23	1:B:135:SER:HB2	1.79	0.64
1:D:39:LEU:HG	1:D:133:VAL:HG22	1.79	0.64
1:A:291:TYR:CE1	1:A:346:PRO:HD2	2.32	0.64
1:C:233:LEU:HB2	1:C:342:THR:HB	1.78	0.64
1:C:203:VAL:O	1:C:207:VAL:HG23	1.97	0.64
1:D:251:ARG:HH11	1:D:251:ARG:HG2	1.63	0.64
1:D:98:PRO:HG2	1:D:101:CYS:HA	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2:LEU:HD12	1:B:2:LEU:N	2.12	0.64
1:C:193:GLU:HG3	1:C:205:ASN:ND2	2.13	0.63
1:A:277:ARG:HG2	1:A:281:GLU:OE1	1.98	0.63
1:C:390:GLN:HA	1:C:393:LEU:HD12	1.81	0.63
1:A:287:ALA:H	1:A:290:GLN:HE21	1.43	0.63
1:A:73:SER:HA	1:A:121:ARG:NH2	2.14	0.63
1:A:279:LEU:O	1:A:282:MET:HB3	1.98	0.63
1:D:53:LEU:HD12	1:D:58:ILE:CD1	2.27	0.63
1:C:298:ILE:HG23	1:C:330:LYS:HB3	1.80	0.63
1:D:41:LEU:HD13	1:D:156:ALA:HB1	1.79	0.63
1:D:255:LEU:O	1:D:258:PRO:HD3	1.99	0.63
1:C:52:SER:HB2	1:C:59:LYS:HD3	1.81	0.63
1:B:325:ARG:HG2	1:B:356:THR:HG22	1.80	0.63
1:C:262:ALA:HB3	1:C:263:PRO:HD3	1.80	0.63
1:D:176:ARG:HG2	1:D:378:SER:OG	1.99	0.63
1:B:389:VAL:HG12	1:B:390:GLN:N	2.13	0.63
1:D:215:ARG:NE	2:D:414:HOH:O	2.31	0.63
1:B:209:THR:HA	1:B:377:VAL:CG2	2.29	0.62
1:B:329:SER:HB2	1:B:341:ILE:O	1.99	0.62
1:B:103:VAL:O	1:B:107:LEU:HD13	1.97	0.62
1:B:260:ILE:O	1:B:263:PRO:HD2	1.97	0.62
1:C:62:TRP:HB2	1:C:67:LEU:HD11	1.80	0.62
1:C:52:SER:O	1:C:132:VAL:HA	1.99	0.62
1:B:263:PRO:O	1:B:266:THR:HB	1.99	0.62
1:C:71:ASP:O	1:C:73:SER:N	2.30	0.62
1:A:70:LEU:CD2	1:A:94:VAL:HG22	2.29	0.62
1:C:166:ASN:HB3	1:C:169:LYS:HE2	1.80	0.62
1:A:388:ARG:N	1:A:388:ARG:HE	1.87	0.62
1:C:331:LEU:HD12	1:C:331:LEU:C	2.20	0.62
1:B:186:ASN:OD1	1:B:210:TRP:HZ3	1.81	0.62
1:B:67:LEU:O	1:B:70:LEU:CD1	2.46	0.62
1:B:115:LEU:CD2	1:B:153:LEU:HB3	2.25	0.62
1:B:22:VAL:CG1	1:B:28:ALA:HB2	2.30	0.62
1:A:244:ARG:CD	1:C:289:GLU:HG2	2.29	0.62
1:A:22:VAL:HG11	1:A:28:ALA:CB	2.30	0.61
1:A:331:LEU:C	1:A:331:LEU:HD12	2.19	0.61
1:B:160:VAL:C	1:B:162:GLU:H	2.03	0.61
1:D:81:THR:HG22	1:D:82:THR:N	2.15	0.61
1:B:89:GLU:HA	1:B:92:LYS:HD2	1.82	0.61
1:C:70:LEU:HD22	1:C:70:LEU:H	1.65	0.61
1:C:287:ALA:HB3	1:C:290:GLN:NE2	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:325:ARG:HD3	1:A:356:THR:OG1	2.01	0.61
1:C:6:LEU:CD1	1:C:379:ILE:CD1	2.78	0.61
1:B:82:THR:HG22	1:B:83:PRO:HD2	1.83	0.61
1:D:98:PRO:HG2	1:D:101:CYS:CB	2.31	0.61
1:C:291:TYR:O	1:C:295:GLU:HG3	2.00	0.61
1:D:164:ILE:HD13	1:D:165:PRO:N	2.15	0.61
1:D:243:THR:HB	1:D:244:ARG:HH21	1.65	0.61
1:B:208:SER:O	1:B:377:VAL:HG23	2.00	0.61
1:A:70:LEU:HD12	1:A:70:LEU:H	1.66	0.61
1:B:168:LEU:HD13	1:B:168:LEU:O	2.01	0.61
1:D:81:THR:HG22	1:D:82:THR:H	1.65	0.61
1:C:164:ILE:HG23	1:C:165:PRO:HD2	1.81	0.61
1:C:33:LEU:HD11	1:C:234:LEU:CD2	2.30	0.61
1:C:165:PRO:O	1:C:166:ASN:HB2	2.01	0.61
1:D:35:LEU:O	1:D:137:LEU:HG	2.01	0.61
1:B:141:ALA:O	1:B:143:LEU:HD13	2.00	0.61
1:D:221:ILE:HG22	1:D:222:SER:N	2.16	0.61
1:B:193:GLU:HA	1:B:193:GLU:OE1	2.01	0.61
1:C:176:ARG:HB2	1:C:176:ARG:HH11	1.65	0.61
1:C:42:GLN:NE2	1:C:44:HIS:NE2	2.49	0.61
1:A:81:THR:HB	1:C:225:LYS:NZ	2.16	0.60
1:D:70:LEU:CG	1:D:72:THR:HG23	2.31	0.60
1:D:173:CYS:CB	1:D:384:SER:HB3	2.30	0.60
1:A:13:LYS:HG3	1:A:207:VAL:HG21	1.83	0.60
1:B:331:LEU:C	1:B:331:LEU:HD12	2.22	0.60
1:C:175:ASN:O	1:C:379:ILE:HG22	2.01	0.60
1:B:52:SER:HB3	1:B:132:VAL:HG23	1.82	0.60
1:B:112:PHE:HA	1:B:153:LEU:HD21	1.82	0.60
1:B:122:LYS:N	1:B:122:LYS:HD3	2.14	0.60
1:D:207:VAL:O	1:D:211:GLY:N	2.33	0.60
1:A:182:LEU:HA	1:A:185:ILE:HD12	1.81	0.60
1:B:118:SER:HB3	1:B:188:TRP:CH2	2.36	0.60
1:A:374:ALA:HB1	1:A:375:PRO:CD	2.32	0.60
1:C:356:THR:HG22	1:C:360:LEU:HD11	1.84	0.60
1:C:233:LEU:HD12	1:C:344:LEU:HD11	1.84	0.60
1:D:22:VAL:HG23	1:D:23:VAL:H	1.67	0.60
1:A:53:LEU:CD2	1:A:133:VAL:HB	2.32	0.59
1:D:98:PRO:HG2	1:D:101:CYS:CA	2.32	0.59
1:A:387:SER:H	1:A:388:ARG:HH21	1.50	0.59
1:A:49:VAL:HG13	1:A:62:TRP:HB2	1.84	0.59
1:B:232:ILE:CG1	1:B:372:ILE:HD13	2.22	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:164:ILE:CD1	1:D:177:TRP:HD1	2.15	0.59
1:B:375:PRO:HG3	1:D:89:GLU:OE1	2.02	0.59
1:D:237:THR:HA	1:D:365:PHE:CD2	2.36	0.59
1:D:58:ILE:HD12	1:D:105:GLU:HG3	1.83	0.59
1:D:262:ALA:HB3	1:D:263:PRO:HD3	1.83	0.59
1:C:82:THR:HB	1:C:83:PRO:HD2	1.82	0.59
1:B:35:LEU:O	1:B:137:LEU:HG	2.02	0.59
1:A:228:PRO:HD2	1:A:283:GLY:HA2	1.83	0.59
1:D:40:ARG:HD3	1:D:394:ASP:O	2.02	0.59
1:C:8:VAL:HG23	1:C:39:LEU:HB3	1.84	0.59
1:D:243:THR:CB	1:D:244:ARG:HH21	2.16	0.59
1:D:7:LEU:O	1:D:379:ILE:HG13	2.03	0.59
1:C:156:ALA:O	1:C:160:VAL:HG23	2.02	0.59
1:B:251:ARG:HH11	1:B:251:ARG:HG3	1.68	0.59
1:A:236:ASN:HB3	1:A:366:ASP:HB2	1.83	0.59
1:A:192:GLY:O	1:A:195:MET:HB3	2.02	0.59
1:C:158:LEU:HD23	1:C:164:ILE:CD1	2.32	0.59
1:C:332:THR:HG21	1:C:341:ILE:CD1	2.33	0.59
1:C:115:LEU:O	1:C:119:ILE:HG22	2.03	0.59
1:C:62:TRP:CB	1:C:67:LEU:HD11	2.33	0.59
1:C:106:ARG:O	1:C:110:LEU:HD13	2.02	0.59
1:A:38:PHE:O	1:A:133:VAL:HG13	2.02	0.58
1:B:33:LEU:HD23	1:B:372:ILE:HD12	1.85	0.58
1:A:146:SER:O	1:A:149:TYR:HB3	2.03	0.58
1:A:28:ALA:O	1:A:29:LEU:HD23	2.03	0.58
1:D:381:SER:HB2	1:D:383:THR:HG22	1.83	0.58
1:C:178:THR:HB	1:C:180:GLU:OE2	2.03	0.58
1:B:186:ASN:OD1	1:B:210:TRP:CZ3	2.57	0.58
1:A:179:LYS:HE2	1:A:183:GLU:OE2	2.04	0.58
1:A:386:ASP:HB2	1:A:389:VAL:CG2	2.33	0.58
1:B:9:SER:HB3	1:B:38:PHE:CD2	2.38	0.58
1:D:55:ASN:HB2	1:D:56:ILE:HD12	1.86	0.58
1:C:269:ASP:O	1:C:273:LEU:HD23	2.04	0.58
1:C:2:LEU:HD12	1:C:2:LEU:N	2.18	0.58
1:C:40:ARG:HH12	1:C:390:GLN:HG3	1.68	0.58
1:A:60:ARG:HB2	1:A:60:ARG:CZ	2.33	0.58
1:B:348:LEU:HD22	1:B:352:GLU:OE1	2.04	0.58
1:B:305:LEU:HD13	1:B:331:LEU:HD11	1.84	0.58
1:A:21:ALA:HB1	1:A:26:LYS:HB2	1.86	0.58
1:B:44:HIS:CD2	1:B:46:ASN:HD21	2.22	0.58
1:C:141:ALA:HB3	1:C:143:LEU:CD2	2.29	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:350:GLN:HA	1:C:353:VAL:CG1	2.34	0.57
1:B:147:ALA:O	1:B:151:VAL:HG23	2.03	0.57
1:B:257:PHE:HB3	1:B:260:ILE:HD12	1.84	0.57
1:A:187:LYS:O	1:A:191:GLN:HG2	2.04	0.57
1:C:55:ASN:ND2	1:C:134:TRP:CD1	2.71	0.57
1:B:154:ALA:O	1:B:158:LEU:HB2	2.04	0.57
1:A:388:ARG:H	1:A:388:ARG:NE	1.87	0.57
1:C:73:SER:O	1:C:75:LEU:N	2.38	0.57
1:C:119:ILE:HG23	1:C:120:CYS:N	2.20	0.57
1:C:355:ALA:O	1:C:358:GLN:HB3	2.05	0.57
1:B:386:ASP:O	1:B:389:VAL:HB	2.04	0.57
1:D:22:VAL:CG1	1:D:28:ALA:HB2	2.32	0.57
1:A:203:VAL:O	1:A:207:VAL:HG23	2.04	0.57
1:D:211:GLY:HA3	1:D:375:PRO:O	2.04	0.57
1:D:143:LEU:HD21	1:D:234:LEU:HD21	1.86	0.57
1:A:52:SER:OG	1:A:59:LYS:HE2	2.03	0.57
1:D:164:ILE:CD1	1:D:181:ASP:HB3	2.35	0.57
1:D:39:LEU:HD23	1:D:40:ARG:N	2.19	0.57
1:B:2:LEU:O	1:B:3:SER:HB2	2.03	0.57
1:B:291:TYR:CE2	1:B:346:PRO:HD3	2.40	0.57
1:A:241:ARG:HG2	1:A:241:ARG:NH1	2.19	0.57
1:D:295:GLU:HB2	1:D:328:HIS:CG	2.40	0.57
1:A:232:ILE:HG13	1:A:233:LEU:N	2.19	0.57
1:D:287:ALA:HB3	1:D:290:GLN:CD	2.26	0.57
1:C:9:SER:HB3	1:C:38:PHE:CD2	2.40	0.57
1:C:129:LEU:HD23	1:C:160:VAL:HG11	1.87	0.57
1:D:167:PRO:HG2	1:D:177:TRP:HA	1.86	0.57
1:B:54:PRO:O	1:B:57:GLY:N	2.37	0.57
1:B:315:LEU:HD22	1:B:331:LEU:HB3	1.87	0.57
1:A:158:LEU:HG	1:A:164:ILE:HD12	1.85	0.57
1:B:370:THR:OG1	1:B:371:SER:N	2.38	0.57
1:B:2:LEU:HA	1:B:169:LYS:CD	2.35	0.57
1:A:21:ALA:HB1	1:A:26:LYS:CB	2.35	0.57
1:C:164:ILE:HG23	1:C:181:ASP:CG	2.24	0.56
1:C:274:GLU:O	1:C:278:VAL:HG23	2.05	0.56
1:B:322:THR:CG2	1:B:360:LEU:HD11	2.35	0.56
1:B:38:PHE:O	1:B:133:VAL:HA	2.06	0.56
1:B:203:VAL:O	1:B:207:VAL:HG23	2.06	0.56
1:C:350:GLN:N	1:C:351:PRO:HD2	2.20	0.56
1:A:201:SER:OG	1:A:203:VAL:HG23	2.06	0.56
1:A:295:GLU:HB3	1:A:328:HIS:CD2	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:232:ILE:HD13	1:B:341:ILE:CD1	2.35	0.56
1:B:39:LEU:HD23	1:B:40:ARG:N	2.21	0.56
1:A:329:SER:HA	1:A:341:ILE:O	2.05	0.56
1:B:331:LEU:HD12	1:B:331:LEU:O	2.06	0.56
1:B:157:LEU:O	1:B:160:VAL:HG12	2.05	0.56
1:B:164:ILE:HD13	1:B:165:PRO:CD	2.36	0.56
1:A:60:ARG:NH2	1:A:105:GLU:OE2	2.39	0.56
1:D:173:CYS:HB3	1:D:384:SER:HB3	1.87	0.56
1:C:33:LEU:HD12	1:C:143:LEU:HD12	1.88	0.56
1:A:251:ARG:HG2	1:A:251:ARG:HH11	1.70	0.56
1:C:68:GLN:OE1	1:C:126:LEU:HD23	2.06	0.56
1:D:19:GLU:N	1:D:19:GLU:OE2	2.39	0.56
1:D:58:ILE:CD1	1:D:105:GLU:HG3	2.36	0.56
1:C:254:LEU:HD13	1:C:261:VAL:CG1	2.36	0.56
1:C:39:LEU:HD23	1:C:40:ARG:N	2.21	0.56
1:A:81:THR:HB	1:C:225:LYS:HZ1	1.71	0.56
1:D:186:ASN:HD21	1:D:206:ALA:HA	1.70	0.56
1:A:385:LEU:HD23	1:A:389:VAL:CG1	2.34	0.56
1:A:387:SER:H	1:A:388:ARG:NH2	2.03	0.56
1:C:318:LEU:HD11	1:C:340:GLY:HA3	1.87	0.56
1:D:234:LEU:HD12	1:D:340:GLY:O	2.06	0.56
1:A:13:LYS:HB2	1:A:207:VAL:HG11	1.88	0.56
1:A:92:LYS:O	1:A:95:ALA:HB3	2.06	0.56
1:C:50:ASP:HB2	1:C:130:ASP:CA	2.23	0.55
1:A:119:ILE:C	1:A:121:ARG:H	2.10	0.55
1:C:48:LYS:H	1:C:128:SER:HB2	1.70	0.55
1:C:233:LEU:CD1	1:C:344:LEU:HD11	2.36	0.55
1:A:322:THR:HG21	1:A:329:SER:OG	2.06	0.55
1:D:56:ILE:HG22	1:D:58:ILE:HG23	1.88	0.55
1:C:18:GLY:HA3	1:C:28:ALA:CB	2.36	0.55
1:D:50:ASP:HB3	1:D:61:ALA:CB	2.34	0.55
1:D:60:ARG:HH21	1:D:60:ARG:HG3	1.70	0.55
1:A:41:LEU:HA	2:A:419:HOH:O	2.06	0.55
1:B:322:THR:HG22	1:B:360:LEU:HD11	1.87	0.55
1:A:55:ASN:HD21	1:A:134:TRP:HE1	1.54	0.55
1:B:287:ALA:HB3	1:B:290:GLN:CG	2.33	0.55
1:B:158:LEU:CD2	1:B:185:ILE:HD13	2.36	0.55
1:C:167:PRO:HB2	1:C:379:ILE:HG21	1.89	0.55
1:B:164:ILE:HD13	1:B:164:ILE:C	2.27	0.55
1:A:121:ARG:CG	1:A:121:ARG:HH11	2.20	0.55
1:D:266:THR:O	1:D:269:ASP:HB3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:248:ALA:O	1:B:251:ARG:HB3	2.05	0.55
1:B:95:ALA:HB1	1:B:97:LEU:HG	1.88	0.55
1:B:224:LEU:O	1:B:225:LYS:C	2.46	0.55
1:C:88:VAL:HG12	1:C:92:LYS:HE3	1.88	0.55
1:A:84:THR:HB	1:A:87:GLN:CG	2.36	0.54
1:A:14:VAL:HG22	1:A:372:ILE:HD11	1.87	0.54
1:A:199:ASN:HB2	1:C:281:GLU:HG3	1.89	0.54
1:C:139:PRO:O	1:C:140:GLY:C	2.45	0.54
1:D:187:LYS:HD3	1:D:187:LYS:C	2.28	0.54
1:D:6:LEU:HB2	1:D:41:LEU:HD23	1.88	0.54
1:C:390:GLN:HA	1:C:393:LEU:HB2	1.88	0.54
1:B:168:LEU:HD11	1:B:381:SER:HA	1.89	0.54
1:B:238:LYS:HE3	1:B:366:ASP:CG	2.28	0.54
1:B:100:ASP:O	1:B:101:CYS:O	2.26	0.54
1:A:58:ILE:CD1	1:A:105:GLU:HB2	2.34	0.54
1:D:226:ARG:HB2	1:D:280:GLY:HA2	1.88	0.54
1:C:343:LEU:HD12	1:C:344:LEU:H	1.73	0.54
1:C:207:VAL:CG2	1:C:214:LEU:HD22	2.36	0.54
1:D:279:LEU:C	1:D:281:GLU:H	2.11	0.54
1:B:91:LEU:HD23	1:B:91:LEU:O	2.07	0.54
1:C:158:LEU:HD23	1:C:164:ILE:HD11	1.89	0.54
1:C:147:ALA:HB1	1:C:205:ASN:HA	1.88	0.54
1:D:188:TRP:O	1:D:191:GLN:HB2	2.07	0.54
1:B:225:LYS:HD2	1:B:226:ARG:N	2.22	0.54
1:C:251:ARG:HH11	1:C:251:ARG:HG3	1.73	0.54
1:A:85:SER:O	1:A:89:GLU:HB2	2.08	0.54
1:C:41:LEU:HD13	1:C:160:VAL:CG2	2.37	0.54
1:A:38:PHE:CE2	1:A:385:LEU:HD21	2.42	0.54
1:C:180:GLU:CD	1:C:180:GLU:N	2.60	0.54
1:B:158:LEU:HB3	1:B:164:ILE:HG21	1.88	0.54
1:A:197:HIS:O	1:A:200:PRO:HD3	2.08	0.54
1:C:384:SER:O	1:C:385:LEU:HD12	2.08	0.54
1:B:5:VAL:HG22	1:B:42:GLN:HG3	1.89	0.54
1:B:285:ALA:HB2	1:D:107:LEU:HD21	1.89	0.53
1:A:242:ASN:O	1:A:246:LEU:HD23	2.07	0.53
1:C:209:THR:O	1:C:376:GLY:HA3	2.09	0.53
1:C:50:ASP:CB	1:C:130:ASP:HA	2.23	0.53
1:D:295:GLU:HB2	1:D:328:HIS:CD2	2.43	0.53
1:C:119:ILE:HD13	1:C:157:LEU:CB	2.38	0.53
1:C:128:SER:C	1:C:129:LEU:HG	2.28	0.53
1:C:39:LEU:HD13	1:C:152:CYS:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:6:LEU:HD12	1:C:379:ILE:HD13	1.90	0.53
1:C:13:LYS:HD3	1:C:13:LYS:O	2.08	0.53
1:A:282:MET:O	1:A:284:GLU:N	2.42	0.53
1:C:73:SER:C	1:C:75:LEU:H	2.12	0.53
1:B:160:VAL:HG13	1:B:161:CYS:N	2.22	0.53
1:A:149:TYR:CZ	1:A:153:LEU:HD11	2.43	0.53
1:D:75:LEU:N	1:D:75:LEU:HD12	2.23	0.53
1:D:69:SER:C	1:D:71:ASP:H	2.11	0.53
1:A:350:GLN:N	1:A:351:PRO:HD2	2.24	0.53
1:D:48:LYS:HE3	2:D:421:HOH:O	2.09	0.53
1:C:164:ILE:CG2	1:C:165:PRO:HD2	2.38	0.53
1:B:47:GLY:O	1:B:64:VAL:HG22	2.08	0.53
1:A:174:VAL:HG12	1:A:380:HIS:HD1	1.72	0.53
1:B:350:GLN:N	1:B:351:PRO:HD2	2.24	0.53
1:C:164:ILE:HG23	1:C:181:ASP:OD1	2.09	0.53
1:C:70:LEU:CD2	1:C:70:LEU:H	2.20	0.53
1:C:18:GLY:HA3	1:C:28:ALA:HB2	1.91	0.53
1:D:331:LEU:HD12	1:D:331:LEU:C	2.29	0.53
1:A:60:ARG:NH1	1:A:60:ARG:CB	2.71	0.53
1:A:123:GLN:CA	1:A:123:GLN:HE21	2.21	0.53
1:C:164:ILE:HA	2:C:410:HOH:O	2.08	0.52
1:B:35:LEU:CD2	1:B:370:THR:HG21	2.39	0.52
1:D:59:LYS:HD2	1:D:59:LYS:N	2.24	0.52
1:C:349:GLU:N	1:C:349:GLU:OE2	2.42	0.52
1:A:158:LEU:HG	1:A:164:ILE:CD1	2.39	0.52
1:B:306:ASN:ND2	1:B:311:GLY:HA3	2.24	0.52
1:B:164:ILE:HD12	1:B:177:TRP:CD1	2.45	0.52
1:A:386:ASP:HB3	1:A:388:ARG:NE	2.24	0.52
1:B:52:SER:O	1:B:54:PRO:HD3	2.09	0.52
1:B:207:VAL:HG22	1:B:214:LEU:HD22	1.90	0.52
1:C:225:LYS:HZ2	1:C:225:LYS:CB	2.20	0.52
1:D:53:LEU:HB3	1:D:56:ILE:HD13	1.90	0.52
1:D:232:ILE:HG13	1:D:233:LEU:N	2.23	0.52
1:C:64:VAL:O	1:C:68:GLN:HB2	2.10	0.52
1:C:358:GLN:HG3	1:C:359:ALA:N	2.23	0.52
1:A:98:PRO:O	1:A:99:ASP:C	2.47	0.52
1:C:175:ASN:ND2	1:C:176:ARG:N	2.57	0.52
1:D:164:ILE:HD13	1:D:165:PRO:HD2	1.90	0.52
1:B:82:THR:CG2	1:B:83:PRO:HD2	2.39	0.52
1:D:75:LEU:HB2	1:D:121:ARG:CD	2.40	0.52
1:A:123:GLN:HA	1:A:123:GLN:NE2	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:10:ALA:HB2	1:C:377:VAL:HG13	1.91	0.52
1:B:237:THR:O	1:B:238:LYS:HB2	2.10	0.52
1:B:388:ARG:HH21	1:B:391:GLN:CG	2.16	0.52
1:D:12:GLY:HA3	1:D:137:LEU:HD11	1.90	0.52
1:C:356:THR:HG22	1:C:360:LEU:HD12	1.92	0.52
1:C:237:THR:HA	1:C:365:PHE:CD2	2.45	0.52
1:D:39:LEU:HD11	1:D:153:LEU:CD2	2.39	0.52
1:A:39:LEU:HD11	1:A:153:LEU:CD2	2.36	0.52
1:B:33:LEU:HD23	1:B:372:ILE:HD11	1.91	0.51
1:A:168:LEU:C	1:A:170:ASP:H	2.11	0.51
1:A:196:ILE:CG1	1:A:197:HIS:N	2.73	0.51
1:A:188:TRP:O	1:A:191:GLN:HB2	2.10	0.51
1:A:350:GLN:HG2	2:A:460:HOH:O	2.10	0.51
1:C:253:ARG:NH2	1:C:307:ALA:O	2.43	0.51
1:D:329:SER:HA	1:D:341:ILE:O	2.10	0.51
1:B:190:PHE:CE1	1:B:200:PRO:HG2	2.45	0.51
1:D:158:LEU:HD23	1:D:185:ILE:CD1	2.27	0.51
1:A:14:VAL:CG2	1:A:372:ILE:HD11	2.41	0.51
1:D:232:ILE:HD13	1:D:372:ILE:HD13	1.92	0.51
1:D:186:ASN:ND2	1:D:206:ALA:HA	2.25	0.51
1:A:243:THR:O	1:A:247:VAL:HG23	2.10	0.51
1:A:278:VAL:HG21	1:A:293:VAL:HG11	1.91	0.51
1:D:2:LEU:HD12	1:D:2:LEU:N	2.26	0.51
1:D:70:LEU:HD23	1:D:72:THR:HG21	1.92	0.51
1:B:305:LEU:O	1:B:310:VAL:HG22	2.11	0.51
1:D:385:LEU:HD22	1:D:391:GLN:CD	2.31	0.51
1:D:13:LYS:HD3	1:D:13:LYS:O	2.09	0.51
1:D:178:THR:O	1:D:179:LYS:C	2.49	0.51
1:D:370:THR:OG1	1:D:371:SER:N	2.42	0.51
1:D:278:VAL:HG12	1:D:282:MET:SD	2.51	0.51
1:A:16:LEU:HG	1:A:17:HIS:CD2	2.46	0.51
1:B:176:ARG:NH2	1:B:176:ARG:HG3	2.23	0.51
1:D:244:ARG:HE	1:D:244:ARG:H	1.59	0.51
1:C:225:LYS:NZ	1:C:225:LYS:HB2	2.22	0.51
1:D:374:ALA:HB1	1:D:375:PRO:HD2	1.93	0.51
1:A:284:GLU:N	1:A:284:GLU:OE1	2.43	0.51
1:D:26:LYS:HD2	1:D:269:ASP:HB2	1.93	0.51
1:C:242:ASN:C	1:C:242:ASN:HD22	2.12	0.51
1:D:184:LEU:HG	1:D:188:TRP:CD1	2.46	0.51
1:C:368:LEU:HD13	2:C:428:HOH:O	2.11	0.51
1:C:163:GLU:HA	1:C:163:GLU:OE2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:54:PRO:HD2	1:D:133:VAL:O	2.11	0.51
1:B:13:LYS:O	1:B:13:LYS:HD3	2.11	0.51
1:D:387:SER:HA	1:D:391:GLN:HG2	1.93	0.51
1:B:293:VAL:O	1:B:297:LEU:HG	2.11	0.51
1:B:165:PRO:O	1:B:167:PRO:HD3	2.12	0.50
1:B:39:LEU:HD21	1:B:131:ILE:HG23	1.92	0.50
1:D:40:ARG:HD2	1:D:394:ASP:CB	2.39	0.50
1:A:182:LEU:HD23	1:A:185:ILE:HD12	1.93	0.50
1:A:258:PRO:HG2	1:A:259:GLU:OE1	2.11	0.50
1:C:167:PRO:C	1:C:169:LYS:H	2.14	0.50
1:B:232:ILE:HD11	1:B:370:THR:HG23	1.93	0.50
1:A:84:THR:O	1:A:88:VAL:HG23	2.11	0.50
1:C:119:ILE:CG2	1:C:120:CYS:N	2.74	0.50
1:A:80:VAL:HG13	1:A:82:THR:HG23	1.93	0.50
1:B:384:SER:O	1:B:385:LEU:HG	2.11	0.50
1:C:246:LEU:HD22	1:C:246:LEU:H	1.75	0.50
1:A:31:VAL:HG21	1:A:372:ILE:HG12	1.93	0.50
1:A:70:LEU:H	1:A:70:LEU:CD1	2.23	0.50
1:B:232:ILE:C	1:B:232:ILE:HD12	2.32	0.50
1:A:83:PRO:HD2	1:A:194:ARG:HH11	1.75	0.50
1:A:375:PRO:HA	2:A:406:HOH:O	2.11	0.50
1:A:41:LEU:HG	2:A:419:HOH:O	2.12	0.50
1:D:178:THR:O	1:D:181:ASP:N	2.44	0.50
1:D:33:LEU:HD22	1:D:35:LEU:HD23	1.94	0.50
1:A:228:PRO:CD	1:A:283:GLY:HA2	2.41	0.50
1:D:249:GLY:HA3	2:D:428:HOH:O	2.12	0.50
1:B:158:LEU:HD23	1:B:185:ILE:HD13	1.93	0.50
1:D:158:LEU:HD21	1:D:184:LEU:HD23	1.92	0.50
1:A:60:ARG:HH11	1:A:60:ARG:CB	2.25	0.50
1:A:143:LEU:HD21	1:A:234:LEU:HD21	1.92	0.50
1:C:353:VAL:O	1:C:357:LYS:HG3	2.11	0.50
1:A:370:THR:OG1	1:A:371:SER:N	2.43	0.50
1:A:21:ALA:HB1	1:A:26:LYS:HG3	1.93	0.50
1:B:318:LEU:C	1:B:318:LEU:HD23	2.31	0.50
1:C:252:ASN:O	1:C:255:LEU:HD23	2.12	0.50
1:C:51:LEU:C	1:C:59:LYS:HD2	2.32	0.50
1:C:354:GLU:OE2	1:C:357:LYS:HD3	2.11	0.49
1:D:279:LEU:HD23	1:D:282:MET:SD	2.52	0.49
1:B:362:SER:C	1:B:364:GLY:H	2.15	0.49
1:C:48:LYS:H	1:C:128:SER:HB3	1.77	0.49
1:D:302:GLN:HE22	1:D:331:LEU:HD23	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:306:ASN:ND2	1:A:311:GLY:HA3	2.27	0.49
1:D:50:ASP:CB	1:D:61:ALA:HB2	2.39	0.49
1:A:282:MET:O	1:A:283:GLY:C	2.50	0.49
1:A:242:ASN:C	1:A:246:LEU:HD23	2.33	0.49
1:C:3:SER:OG	1:C:4:GLU:N	2.43	0.49
1:C:176:ARG:HG2	1:C:377:VAL:O	2.12	0.49
1:B:264:LEU:O	1:B:267:SER:N	2.44	0.49
1:B:215:ARG:HD2	1:B:276:GLU:OE1	2.12	0.49
1:B:161:CYS:O	1:B:163:GLU:N	2.45	0.49
1:A:83:PRO:HB2	2:C:404:HOH:O	2.12	0.49
1:A:237:THR:O	1:A:239:VAL:HG23	2.11	0.49
1:B:121:ARG:HH21	1:B:121:ARG:CB	2.26	0.49
1:A:259:GLU:OE1	1:A:259:GLU:N	2.46	0.49
1:D:361:THR:O	1:D:364:GLY:N	2.42	0.49
1:C:176:ARG:CB	1:C:176:ARG:HH11	2.26	0.49
1:A:244:ARG:CG	1:C:289:GLU:HG2	2.42	0.49
1:D:41:LEU:HB2	1:D:131:ILE:HG12	1.94	0.49
1:C:102:ALA:O	1:C:105:GLU:HB3	2.13	0.49
1:D:56:ILE:HD12	1:D:56:ILE:N	2.27	0.49
1:C:22:VAL:O	1:C:25:GLY:N	2.46	0.49
1:A:123:GLN:CA	1:A:123:GLN:NE2	2.76	0.49
1:B:278:VAL:HG11	1:B:294:LEU:HD13	1.95	0.49
1:C:52:SER:CB	1:C:132:VAL:HG22	2.25	0.49
1:C:349:GLU:C	1:C:351:PRO:HD2	2.33	0.49
1:A:131:ILE:N	1:A:131:ILE:HD12	2.27	0.49
1:A:22:VAL:HG12	1:A:26:LYS:O	2.13	0.49
1:B:32:SER:O	1:B:372:ILE:HA	2.14	0.48
1:A:86:GLU:HB2	2:A:449:HOH:O	2.12	0.48
1:D:37:THR:CG2	1:D:135:SER:HB2	2.40	0.48
1:C:232:ILE:HG12	1:C:372:ILE:CD1	2.41	0.48
1:C:263:PRO:HB2	1:D:267:SER:HB2	1.94	0.48
1:A:164:ILE:HD11	1:A:184:LEU:HD23	1.95	0.48
1:B:101:CYS:O	1:B:102:ALA:C	2.52	0.48
1:B:278:VAL:O	1:B:282:MET:HG3	2.13	0.48
1:B:47:GLY:HA2	1:B:128:SER:HB3	1.95	0.48
1:A:60:ARG:HG2	1:A:62:TRP:CZ2	2.49	0.48
1:C:213:ALA:O	1:C:214:LEU:HD12	2.13	0.48
1:A:193:GLU:HA	1:A:193:GLU:OE1	2.13	0.48
1:B:4:GLU:HB3	1:B:43:PRO:HG2	1.95	0.48
1:A:170:ASP:N	1:A:170:ASP:OD1	2.45	0.48
1:D:120:CYS:HA	1:D:161:CYS:SG	2.53	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:312:HIS:ND1	1:D:313:ALA:N	2.60	0.48
1:A:52:SER:CB	1:A:132:VAL:HG22	2.28	0.48
1:B:122:LYS:HE3	1:B:163:GLU:OE1	2.14	0.48
1:D:111:ALA:O	1:D:115:LEU:HD23	2.13	0.48
1:C:73:SER:C	1:C:75:LEU:N	2.67	0.48
1:B:53:LEU:HD13	1:B:108:ALA:HB1	1.96	0.48
1:A:60:ARG:CA	1:A:60:ARG:HH11	2.27	0.48
1:D:91:LEU:HD11	1:D:117:LEU:HD12	1.95	0.48
1:A:2:LEU:HG	1:A:2:LEU:O	2.14	0.48
1:C:174:VAL:HG13	1:C:380:HIS:ND1	2.28	0.48
1:B:232:ILE:HD13	1:B:341:ILE:HD12	1.95	0.48
1:B:180:GLU:HG3	1:B:181:ASP:N	2.29	0.48
1:A:384:SER:O	1:A:385:LEU:CB	2.60	0.48
1:A:134:TRP:HB3	1:A:393:LEU:HD21	1.96	0.48
1:A:135:SER:OG	1:A:137:LEU:HB2	2.14	0.48
1:B:291:TYR:O	1:B:295:GLU:HG3	2.14	0.48
1:A:66:ARG:O	1:A:70:LEU:CD1	2.62	0.48
1:B:278:VAL:HG11	1:B:294:LEU:CD1	2.44	0.48
1:A:83:PRO:HG2	1:A:194:ARG:HB3	1.96	0.48
1:D:50:ASP:HA	1:D:61:ALA:HA	1.95	0.48
1:B:103:VAL:HG12	1:B:107:LEU:HD13	1.96	0.48
1:A:390:GLN:HA	1:A:393:LEU:HB2	1.96	0.48
1:D:138:PRO:HD2	1:D:143:LEU:HD23	1.96	0.48
1:D:101:CYS:O	1:D:102:ALA:C	2.51	0.48
1:B:151:VAL:CG1	1:B:377:VAL:HG21	2.43	0.48
1:D:192:GLY:O	1:D:195:MET:HB3	2.14	0.48
1:C:64:VAL:CG1	1:C:128:SER:HB3	2.43	0.48
1:D:158:LEU:HD21	1:D:184:LEU:HG	1.95	0.48
1:B:40:ARG:HB3	1:B:132:VAL:CG1	2.44	0.48
1:B:52:SER:HB3	1:B:132:VAL:CG2	2.44	0.48
1:D:374:ALA:HB1	1:D:375:PRO:CD	2.43	0.48
1:A:68:GLN:HG3	1:A:126:LEU:HB2	1.96	0.48
1:D:155:ALA:HA	1:D:185:ILE:HD12	1.96	0.47
1:D:47:GLY:C	1:D:64:VAL:HG13	2.35	0.47
1:B:343:LEU:HG	1:B:344:LEU:N	2.29	0.47
1:D:75:LEU:HB2	1:D:121:ARG:NE	2.30	0.47
1:C:302:GLN:HE21	1:C:302:GLN:HA	1.79	0.47
1:D:183:GLU:OE2	1:D:210:TRP:HZ2	1.97	0.47
1:C:119:ILE:HD13	1:C:157:LEU:HB2	1.95	0.47
1:C:7:LEU:HB2	1:C:380:HIS:O	2.13	0.47
1:C:386:ASP:C	1:C:388:ARG:H	2.17	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:234:LEU:HD12	1:C:341:ILE:HD12	1.95	0.47
1:D:385:LEU:C	1:D:387:SER:H	2.17	0.47
1:C:370:THR:OG1	1:C:371:SER:N	2.46	0.47
1:C:166:ASN:HB3	1:C:169:LYS:CE	2.44	0.47
1:C:83:PRO:HG3	1:C:198:GLY:O	2.14	0.47
1:D:52:SER:C	1:D:54:PRO:HD3	2.34	0.47
1:A:55:ASN:ND2	1:A:134:TRP:NE1	2.63	0.47
1:A:129:LEU:HD12	1:A:131:ILE:HD11	1.97	0.47
1:C:21:ALA:HB1	1:C:26:LYS:HB2	1.96	0.47
1:A:305:LEU:O	1:A:310:VAL:HG22	2.15	0.47
1:B:295:GLU:OE2	1:B:328:HIS:HD2	1.98	0.47
1:A:298:ILE:HD12	1:A:330:LYS:HG2	1.97	0.47
1:D:123:GLN:HG3	1:D:124:ARG:N	2.30	0.47
1:D:111:ALA:HB2	1:D:196:ILE:HD11	1.95	0.47
1:B:13:LYS:HB2	1:B:207:VAL:CG1	2.39	0.47
1:A:84:THR:CG2	1:A:86:GLU:H	2.20	0.47
1:D:70:LEU:HD22	1:D:94:VAL:HG11	1.94	0.47
1:C:36:ARG:HG2	1:C:36:ARG:HH11	1.79	0.47
1:B:68:GLN:C	1:B:70:LEU:H	2.17	0.47
1:B:89:GLU:O	1:B:92:LYS:HB2	2.15	0.47
1:C:343:LEU:HD12	1:C:344:LEU:N	2.29	0.47
1:A:268:ILE:O	1:A:271:ILE:HB	2.15	0.47
1:C:288:PRO:C	1:C:290:GLN:H	2.17	0.47
1:A:244:ARG:HG3	1:C:289:GLU:CB	2.45	0.47
1:D:113:LEU:O	1:D:117:LEU:HG	2.14	0.47
1:B:323:ARG:HD2	1:B:323:ARG:HA	1.72	0.47
1:A:260:ILE:HD12	1:A:260:ILE:N	2.30	0.47
1:B:144:GLY:HA2	2:B:455:HOH:O	2.14	0.47
1:A:21:ALA:CB	1:A:26:LYS:HB2	2.44	0.47
1:C:261:VAL:O	1:C:264:LEU:HB3	2.15	0.47
1:C:221:ILE:HG22	1:C:222:SER:N	2.30	0.47
1:B:3:SER:H	1:B:169:LYS:CD	2.28	0.47
1:A:13:LYS:O	1:A:13:LYS:HE2	2.15	0.47
1:C:121:ARG:HG3	1:C:122:LYS:N	2.29	0.47
1:A:164:ILE:HG23	1:A:181:ASP:CG	2.35	0.47
1:A:33:LEU:CD2	1:A:370:THR:HG21	2.41	0.46
1:D:22:VAL:O	1:D:24:HIS:N	2.48	0.46
1:C:103:VAL:HG13	1:C:104:THR:N	2.30	0.46
1:B:312:HIS:ND1	1:B:314:SER:OG	2.47	0.46
1:B:12:GLY:CA	1:B:137:LEU:HD11	2.43	0.46
1:C:182:LEU:O	1:C:185:ILE:N	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:VAL:CG1	1:A:82:THR:HG23	2.45	0.46
1:D:51:LEU:HD21	1:D:53:LEU:CD2	2.42	0.46
1:A:97:LEU:CD1	1:A:106:ARG:HG3	2.41	0.46
1:A:22:VAL:HG13	1:A:28:ALA:HB2	1.97	0.46
1:A:84:THR:CG2	1:A:86:GLU:HB3	2.45	0.46
1:D:64:VAL:HG23	1:D:65:ALA:N	2.30	0.46
1:A:63:ASP:O	1:A:66:ARG:N	2.48	0.46
1:A:19:GLU:OE1	1:A:332:THR:HA	2.14	0.46
1:A:315:LEU:HD13	1:A:331:LEU:HB3	1.97	0.46
1:D:269:ASP:O	1:D:273:LEU:HD13	2.14	0.46
1:D:160:VAL:CG1	1:D:161:CYS:N	2.78	0.46
1:D:74:PHE:CE1	1:D:75:LEU:HG	2.49	0.46
1:A:332:THR:HB	1:A:341:ILE:CD1	2.46	0.46
1:D:176:ARG:HG2	1:D:378:SER:HG	1.81	0.46
1:C:228:PRO:HG2	1:C:230:LEU:HD21	1.98	0.46
1:B:11:PRO:CD	1:B:376:GLY:HA2	2.45	0.46
1:C:190:PHE:O	1:C:193:GLU:HB2	2.15	0.46
1:D:292:LEU:O	1:D:295:GLU:HG2	2.15	0.46
1:D:295:GLU:HA	1:D:298:ILE:HD12	1.97	0.46
1:D:362:SER:C	1:D:364:GLY:H	2.17	0.46
1:C:320:GLN:HG3	2:D:427:HOH:O	2.16	0.46
1:A:64:VAL:HG23	1:A:65:ALA:N	2.31	0.46
1:A:166:ASN:OD1	1:A:168:LEU:HB2	2.16	0.46
1:A:174:VAL:HA	1:A:379:ILE:O	2.16	0.46
1:D:39:LEU:CD2	1:D:131:ILE:HG23	2.36	0.46
1:D:19:GLU:H	1:D:19:GLU:CD	2.19	0.46
1:D:120:CYS:O	1:D:123:GLN:HB3	2.16	0.46
1:B:164:ILE:HG12	1:B:165:PRO:HD2	1.98	0.46
1:D:158:LEU:HD21	1:D:184:LEU:CG	2.46	0.46
1:D:164:ILE:CD1	1:D:165:PRO:HD2	2.46	0.46
1:A:55:ASN:ND2	1:A:134:TRP:CD1	2.84	0.46
1:C:37:THR:OG1	1:C:135:SER:HB2	2.15	0.46
1:D:193:GLU:HG3	1:D:205:ASN:HD22	1.81	0.46
1:A:330:LYS:HG3	1:A:330:LYS:O	2.15	0.46
1:A:181:ASP:O	1:A:185:ILE:HG13	2.16	0.46
1:B:362:SER:C	1:B:364:GLY:N	2.67	0.46
1:D:349:GLU:O	1:D:353:VAL:HG12	2.16	0.46
1:C:26:LYS:HB3	1:C:269:ASP:HB2	1.97	0.46
1:B:277:ARG:HD3	2:B:443:HOH:O	2.16	0.46
1:C:42:GLN:HE21	1:C:44:HIS:CD2	2.34	0.45
1:C:6:LEU:HD12	1:C:379:ILE:CD1	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:PHE:CZ	1:A:385:LEU:HD21	2.51	0.45
1:D:41:LEU:HD23	1:D:41:LEU:O	2.16	0.45
1:B:175:ASN:O	1:B:379:ILE:HG22	2.16	0.45
1:B:65:ALA:O	1:B:68:GLN:HB3	2.16	0.45
1:A:261:VAL:O	1:A:262:ALA:C	2.54	0.45
1:C:7:LEU:C	1:C:379:ILE:HD12	2.35	0.45
1:C:318:LEU:C	1:C:318:LEU:HD23	2.36	0.45
1:A:33:LEU:HA	1:A:372:ILE:HD12	1.97	0.45
1:A:119:ILE:C	1:A:121:ARG:N	2.70	0.45
1:B:261:VAL:O	1:B:264:LEU:N	2.50	0.45
1:D:164:ILE:HD13	1:D:165:PRO:CG	2.46	0.45
1:B:51:LEU:HD11	1:B:112:PHE:CB	2.47	0.45
1:B:2:LEU:CA	1:B:169:LYS:HG3	2.42	0.45
1:D:226:ARG:O	1:D:227:SER:C	2.53	0.45
1:D:381:SER:CB	1:D:383:THR:HG22	2.46	0.45
1:D:387:SER:O	1:D:390:GLN:CB	2.65	0.45
1:D:312:HIS:CE1	1:D:314:SER:H	2.34	0.45
1:A:160:VAL:C	1:A:162:GLU:H	2.19	0.45
1:A:124:ARG:NH1	2:A:421:HOH:O	2.48	0.45
1:C:151:VAL:HG12	1:C:377:VAL:HG11	1.98	0.45
1:A:121:ARG:NH1	1:A:121:ARG:CG	2.80	0.45
1:D:385:LEU:HD13	1:D:387:SER:HB3	1.98	0.45
1:C:252:ASN:HA	1:C:255:LEU:HD22	1.99	0.45
1:A:64:VAL:HG11	1:A:128:SER:HB3	1.98	0.45
1:D:350:GLN:O	1:D:354:GLU:HB2	2.15	0.45
1:C:158:LEU:HD23	1:C:164:ILE:HD12	1.98	0.45
1:B:157:LEU:HA	1:B:160:VAL:HG12	1.99	0.45
1:D:158:LEU:HD21	1:D:184:LEU:CD2	2.45	0.45
1:D:27:VAL:HG22	1:D:217:HIS:CD2	2.51	0.45
1:A:377:VAL:HG13	1:A:377:VAL:O	2.15	0.45
1:B:202:GLY:HA2	1:B:205:ASN:HD21	1.81	0.45
1:C:381:SER:C	1:C:383:THR:H	2.20	0.45
1:A:214:LEU:HD12	1:A:223:SER:HA	1.99	0.45
1:C:167:PRO:HB2	1:C:379:ILE:CG2	2.46	0.45
1:C:47:GLY:O	1:C:48:LYS:CG	2.62	0.45
1:B:33:LEU:HD23	1:B:33:LEU:HA	1.77	0.45
1:C:352:GLU:O	1:C:355:ALA:N	2.50	0.45
1:C:31:VAL:HG21	1:C:372:ILE:HG12	1.98	0.45
1:D:18:GLY:O	1:D:19:GLU:C	2.55	0.45
1:D:225:LYS:HG3	1:D:226:ARG:N	2.32	0.45
1:C:257:PHE:HB3	1:C:260:ILE:HD12	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:160:VAL:C	1:B:162:GLU:N	2.70	0.45
1:C:385:LEU:CD2	1:C:390:GLN:HB2	2.40	0.45
1:A:196:ILE:HG13	1:A:197:HIS:CG	2.52	0.45
1:C:101:CYS:SG	1:C:106:ARG:HB2	2.57	0.45
1:A:17:HIS:ND1	1:A:301:ASN:ND2	2.61	0.45
1:C:160:VAL:O	1:C:160:VAL:HG12	2.16	0.45
1:B:167:PRO:HD3	1:B:177:TRP:NE1	2.32	0.45
1:B:63:ASP:C	1:B:65:ALA:N	2.70	0.45
1:D:41:LEU:HD22	1:D:156:ALA:HB1	1.99	0.45
1:B:388:ARG:HA	1:B:388:ARG:NE	2.32	0.45
1:B:42:GLN:OE1	1:B:44:HIS:HE1	1.99	0.45
1:C:254:LEU:HD12	1:C:254:LEU:O	2.17	0.45
1:B:306:ASN:HD22	1:B:311:GLY:HA3	1.81	0.45
1:C:268:ILE:HA	1:C:271:ILE:HD12	1.99	0.45
1:A:21:ALA:HB1	1:A:26:LYS:CG	2.46	0.44
1:B:327:LEU:HD21	1:B:348:LEU:HD11	1.99	0.44
1:A:280:GLY:O	1:A:282:MET:N	2.49	0.44
1:C:22:VAL:HA	1:C:26:LYS:O	2.17	0.44
1:B:289:GLU:O	1:B:292:LEU:HB3	2.16	0.44
1:A:169:LYS:HG2	1:A:169:LYS:O	2.17	0.44
1:D:5:VAL:HG13	1:D:42:GLN:HB3	1.98	0.44
1:B:158:LEU:HB3	1:B:164:ILE:CG2	2.47	0.44
1:B:49:VAL:HG11	1:B:116:TYR:CZ	2.52	0.44
1:C:350:GLN:O	1:C:353:VAL:HG13	2.17	0.44
1:B:383:THR:OG1	1:B:384:SER:N	2.50	0.44
1:D:385:LEU:HD12	1:D:385:LEU:O	2.17	0.44
1:A:190:PHE:HD1	1:A:205:ASN:HD21	1.66	0.44
1:C:10:ALA:O	1:C:36:ARG:HA	2.17	0.44
1:C:209:THR:HA	1:C:377:VAL:HG22	1.99	0.44
1:B:160:VAL:CG1	1:B:161:CYS:N	2.81	0.44
1:D:70:LEU:HD23	1:D:72:THR:CG2	2.48	0.44
1:C:13:LYS:HD3	1:C:13:LYS:C	2.37	0.44
1:B:319:CYS:O	1:B:323:ARG:HB2	2.18	0.44
1:B:243:THR:O	1:B:247:VAL:HG23	2.17	0.44
1:C:362:SER:HB3	2:C:408:HOH:O	2.17	0.44
1:D:177:TRP:HB3	1:D:181:ASP:HB2	1.98	0.44
1:A:55:ASN:ND2	1:A:134:TRP:HE1	2.15	0.44
1:C:292:LEU:O	1:C:293:VAL:C	2.55	0.44
1:A:199:ASN:CB	1:C:281:GLU:HG3	2.47	0.44
1:A:237:THR:HA	1:A:365:PHE:CD2	2.53	0.44
1:D:199:ASN:C	1:D:199:ASN:HD22	2.19	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:179:LYS:O	1:C:182:LEU:HB2	2.18	0.44
1:D:243:THR:N	1:D:244:ARG:NH2	2.65	0.44
1:A:82:THR:N	1:A:83:PRO:CD	2.81	0.44
1:D:97:LEU:CB	1:D:98:PRO:HD2	2.38	0.44
1:D:278:VAL:HG11	1:D:294:LEU:HD13	2.00	0.44
1:B:237:THR:C	1:B:239:VAL:H	2.20	0.44
1:B:7:LEU:CD1	1:B:382:ALA:HA	2.48	0.44
1:B:60:ARG:HH22	1:B:97:LEU:HD23	1.83	0.44
1:A:22:VAL:C	1:A:24:HIS:N	2.71	0.44
1:C:285:ALA:N	1:C:286:PRO:HD3	2.33	0.44
1:B:264:LEU:HD21	1:B:307:ALA:HB3	2.00	0.44
1:A:322:THR:HG23	1:A:327:LEU:CB	2.45	0.44
1:D:242:ASN:C	1:D:246:LEU:HD23	2.37	0.44
1:C:36:ARG:HG2	1:C:36:ARG:NH1	2.33	0.44
1:B:181:ASP:O	1:B:185:ILE:HG12	2.17	0.44
1:B:52:SER:C	1:B:54:PRO:HD3	2.37	0.44
1:A:215:ARG:N	1:A:222:SER:O	2.43	0.44
1:B:381:SER:O	1:B:382:ALA:HB2	2.18	0.44
1:B:164:ILE:HD12	1:B:177:TRP:NE1	2.33	0.44
1:A:197:HIS:O	1:A:199:ASN:N	2.51	0.44
1:B:92:LYS:HG2	1:B:110:LEU:HD21	2.00	0.44
1:B:285:ALA:O	1:B:286:PRO:O	2.36	0.44
1:C:35:LEU:HD12	1:C:35:LEU:HA	1.89	0.44
1:A:177:TRP:HB3	1:A:181:ASP:HB2	1.99	0.44
1:A:376:GLY:O	1:A:377:VAL:C	2.55	0.44
1:C:350:GLN:HA	1:C:353:VAL:HG13	2.01	0.43
1:B:390:GLN:O	1:B:394:ASP:CB	2.66	0.43
1:D:22:VAL:HG23	1:D:23:VAL:N	2.32	0.43
1:B:70:LEU:C	1:B:70:LEU:HD23	2.36	0.43
1:B:151:VAL:CG1	1:B:377:VAL:CG2	2.95	0.43
1:B:53:LEU:CD1	1:B:108:ALA:HB1	2.48	0.43
1:C:302:GLN:NE2	1:C:302:GLN:HA	2.32	0.43
1:A:160:VAL:O	1:A:162:GLU:N	2.51	0.43
1:C:165:PRO:HD2	1:C:181:ASP:OD1	2.19	0.43
1:C:48:LYS:N	1:C:128:SER:HB2	2.33	0.43
1:B:119:ILE:HD12	1:B:119:ILE:N	2.32	0.43
1:B:83:PRO:HG2	1:B:84:THR:H	1.82	0.43
1:B:38:PHE:O	1:B:133:VAL:HG13	2.17	0.43
1:A:22:VAL:C	1:A:24:HIS:H	2.21	0.43
1:B:121:ARG:C	1:B:123:GLN:H	2.21	0.43
1:A:358:GLN:HA	1:A:361:THR:OG1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:216:TYR:HE1	1:B:219:GLY:CA	2.31	0.43
1:B:41:LEU:HD23	1:B:41:LEU:C	2.38	0.43
1:C:7:LEU:CD1	1:C:382:ALA:HB2	2.47	0.43
1:B:371:SER:O	1:B:372:ILE:HD12	2.18	0.43
1:A:14:VAL:HG12	1:A:143:LEU:HD12	1.99	0.43
1:A:237:THR:C	1:A:239:VAL:N	2.72	0.43
1:A:158:LEU:CB	1:A:164:ILE:HD12	2.48	0.43
1:D:218:GLN:HB2	1:D:218:GLN:HE21	1.54	0.43
1:A:72:THR:HA	1:A:74:PHE:CE1	2.54	0.43
1:B:64:VAL:O	1:B:68:GLN:HB2	2.18	0.43
1:D:39:LEU:CD1	1:D:153:LEU:HD23	2.43	0.43
1:C:290:GLN:C	1:C:292:LEU:N	2.70	0.43
1:A:280:GLY:O	1:A:281:GLU:C	2.57	0.43
1:B:41:LEU:HD21	1:B:129:LEU:HD22	2.01	0.43
1:A:199:ASN:C	1:A:199:ASN:ND2	2.66	0.43
1:D:75:LEU:HD13	1:D:121:ARG:HE	1.83	0.43
1:D:15:ILE:HD12	1:D:333:GLY:HA2	2.01	0.43
1:B:124:ARG:HD3	2:B:451:HOH:O	2.18	0.43
1:C:70:LEU:N	1:C:70:LEU:HD22	2.33	0.43
1:A:262:ALA:HB3	1:A:263:PRO:CD	2.44	0.43
1:A:97:LEU:HA	1:A:98:PRO:HD2	1.88	0.43
1:A:199:ASN:ND2	1:A:199:ASN:O	2.52	0.43
1:D:69:SER:C	1:D:71:ASP:N	2.72	0.43
1:A:256:LYS:HZ1	1:B:292:LEU:HD12	1.84	0.43
1:D:304:HIS:O	1:D:307:ALA:HB3	2.19	0.43
1:B:379:ILE:HG23	1:B:379:ILE:O	2.19	0.43
1:D:164:ILE:HD13	1:D:165:PRO:HG2	2.01	0.43
1:D:35:LEU:HD12	1:D:136:GLU:HB3	2.00	0.43
1:B:278:VAL:HG21	1:B:293:VAL:HG11	2.00	0.43
1:B:3:SER:H	1:B:169:LYS:HD2	1.84	0.43
1:A:289:GLU:O	1:A:293:VAL:HG23	2.18	0.43
1:A:9:SER:HA	1:A:37:THR:O	2.19	0.43
1:A:186:ASN:OD1	1:A:210:TRP:CH2	2.72	0.43
1:C:157:LEU:C	1:C:159:THR:N	2.71	0.43
1:B:32:SER:OG	1:B:374:ALA:N	2.52	0.43
1:C:182:LEU:CD2	1:C:185:ILE:HD12	2.38	0.43
1:C:287:ALA:HB3	1:C:290:GLN:HE21	1.82	0.43
1:A:70:LEU:HD12	1:A:70:LEU:N	2.33	0.43
1:B:113:LEU:O	1:B:114:TYR:C	2.58	0.43
1:D:177:TRP:HB2	1:D:182:LEU:HD21	2.00	0.42
1:A:53:LEU:HD21	1:A:133:VAL:HB	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:64:VAL:CG2	1:D:65:ALA:N	2.82	0.42
1:A:99:ASP:HB2	1:A:100:ASP:H	1.55	0.42
1:C:22:VAL:O	1:C:23:VAL:C	2.57	0.42
1:C:248:ALA:O	1:C:251:ARG:HB3	2.20	0.42
1:B:351:PRO:O	1:B:354:GLU:N	2.52	0.42
1:C:252:ASN:O	1:C:255:LEU:CD2	2.67	0.42
1:D:160:VAL:O	1:D:162:GLU:HG3	2.19	0.42
1:C:17:HIS:ND1	1:C:301:ASN:ND2	2.67	0.42
1:C:147:ALA:HB1	1:C:205:ASN:CA	2.49	0.42
1:D:92:LYS:NZ	1:D:106:ARG:CZ	2.82	0.42
1:D:173:CYS:SG	1:D:384:SER:HB3	2.59	0.42
1:C:163:GLU:CA	1:C:163:GLU:OE2	2.67	0.42
1:C:166:ASN:HA	1:C:167:PRO:HD3	1.73	0.42
1:B:33:LEU:HD13	1:B:35:LEU:HD23	2.01	0.42
1:B:119:ILE:HD12	1:B:119:ILE:H	1.85	0.42
1:B:116:TYR:HA	1:B:157:LEU:HD13	2.01	0.42
1:C:40:ARG:HH12	1:C:390:GLN:CG	2.32	0.42
1:D:10:ALA:O	1:D:37:THR:N	2.43	0.42
1:D:8:VAL:O	1:D:38:PHE:HA	2.20	0.42
1:B:348:LEU:HD22	1:B:352:GLU:CD	2.40	0.42
1:D:22:VAL:C	1:D:24:HIS:N	2.72	0.42
1:B:84:THR:O	1:B:88:VAL:HG23	2.19	0.42
1:D:33:LEU:CD2	1:D:35:LEU:HD23	2.49	0.42
1:A:287:ALA:N	1:A:290:GLN:HE21	2.14	0.42
1:D:19:GLU:OE1	1:D:330:LYS:NZ	2.49	0.42
1:D:221:ILE:CG2	1:D:222:SER:N	2.82	0.42
1:C:98:PRO:HG2	1:C:101:CYS:HB3	2.02	0.42
1:D:385:LEU:C	1:D:387:SER:N	2.72	0.42
1:C:242:ASN:O	1:C:245:ALA:HB3	2.19	0.42
1:C:155:ALA:O	1:C:157:LEU:N	2.53	0.42
1:D:188:TRP:HA	1:D:188:TRP:CE3	2.54	0.42
1:B:54:PRO:C	1:B:57:GLY:H	2.22	0.42
1:C:141:ALA:CB	1:C:143:LEU:CD2	2.96	0.42
1:B:284:GLU:OE1	1:D:92:LYS:HE2	2.20	0.42
1:C:22:VAL:HG23	1:C:23:VAL:H	1.84	0.42
1:C:50:ASP:N	1:C:129:LEU:O	2.40	0.42
1:B:70:LEU:HB2	1:B:72:THR:HG22	2.01	0.42
1:C:66:ARG:HG3	1:C:70:LEU:HD21	2.01	0.42
1:B:207:VAL:CG2	1:B:214:LEU:HD22	2.50	0.42
1:A:13:LYS:HE2	1:A:13:LYS:C	2.40	0.42
1:D:174:VAL:HG12	1:D:175:ASN:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:119:ILE:CG2	1:B:158:LEU:HD12	2.50	0.42
1:D:177:TRP:HB2	1:D:182:LEU:CD2	2.49	0.42
1:D:60:ARG:NH2	1:D:60:ARG:HG3	2.35	0.42
1:C:213:ALA:C	1:C:214:LEU:HD12	2.39	0.42
1:A:287:ALA:O	1:A:290:GLN:HB2	2.20	0.42
1:A:268:ILE:HA	1:A:271:ILE:HD12	2.01	0.42
1:D:207:VAL:HA	1:D:214:LEU:HD11	2.02	0.42
1:B:166:ASN:OD1	1:B:168:LEU:O	2.38	0.42
1:C:44:HIS:O	1:C:46:ASN:N	2.53	0.42
1:D:179:LYS:HG2	1:D:180:GLU:N	2.34	0.42
1:C:58:ILE:HD13	1:C:105:GLU:HG3	2.01	0.42
1:C:315:LEU:O	1:C:318:LEU:HB3	2.20	0.42
1:A:84:THR:HG21	1:A:86:GLU:HB3	2.01	0.42
1:C:225:LYS:CB	1:C:225:LYS:NZ	2.80	0.42
1:D:231:GLN:HE22	1:D:371:SER:HB3	1.83	0.42
1:A:35:LEU:HA	1:A:35:LEU:HD12	1.85	0.42
1:D:273:LEU:N	1:D:273:LEU:CD1	2.83	0.42
1:B:60:ARG:HG3	1:B:60:ARG:HH21	1.85	0.42
1:C:13:LYS:HG2	1:C:14:VAL:N	2.35	0.42
1:B:108:ALA:O	1:B:149:TYR:OH	2.24	0.42
1:D:16:LEU:HG	1:D:17:HIS:CD2	2.55	0.42
1:B:358:GLN:HB2	1:B:358:GLN:HE21	1.65	0.42
1:C:49:VAL:O	1:C:61:ALA:HA	2.19	0.42
1:D:184:LEU:HG	1:D:188:TRP:HD1	1.85	0.41
1:D:9:SER:HB3	1:D:38:PHE:CD2	2.55	0.41
1:A:312:HIS:CE1	1:A:314:SER:HG	2.36	0.41
1:D:91:LEU:HD12	1:D:113:LEU:HB3	2.01	0.41
1:D:104:THR:HG23	2:D:441:HOH:O	2.18	0.41
1:C:91:LEU:O	1:C:91:LEU:HD12	2.20	0.41
1:A:151:VAL:O	1:A:154:ALA:HB3	2.20	0.41
1:C:157:LEU:O	1:C:159:THR:N	2.53	0.41
1:C:83:PRO:HD3	1:C:194:ARG:HG3	2.02	0.41
1:C:54:PRO:HD3	1:C:132:VAL:HG13	2.01	0.41
1:B:158:LEU:HD22	1:B:185:ILE:HD13	2.02	0.41
1:B:49:VAL:HG11	1:B:116:TYR:CE2	2.55	0.41
1:A:49:VAL:CG1	1:A:62:TRP:HB2	2.48	0.41
1:C:182:LEU:O	1:C:183:GLU:C	2.58	0.41
1:A:211:GLY:HA3	1:A:375:PRO:O	2.19	0.41
1:A:312:HIS:ND1	1:A:314:SER:OG	2.50	0.41
1:D:75:LEU:HB2	1:D:121:ARG:HD2	2.00	0.41
1:C:44:HIS:O	1:C:46:ASN:ND2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:46:ASN:OD1	1:B:48:LYS:HB2	2.20	0.41
1:D:41:LEU:CB	1:D:131:ILE:HG12	2.50	0.41
1:D:251:ARG:NH1	1:D:251:ARG:HG2	2.32	0.41
1:B:147:ALA:O	1:B:148:ALA:C	2.58	0.41
1:D:345:LYS:HA	1:D:346:PRO:HD3	1.87	0.41
1:A:318:LEU:C	1:A:318:LEU:HD23	2.40	0.41
1:C:83:PRO:HG3	1:C:198:GLY:CA	2.45	0.41
1:B:174:VAL:HB	1:B:175:ASN:H	1.60	0.41
1:D:165:PRO:HG2	1:D:181:ASP:OD1	2.19	0.41
1:B:264:LEU:C	1:B:266:THR:N	2.71	0.41
1:D:221:ILE:HG22	1:D:222:SER:H	1.86	0.41
1:C:201:SER:O	1:C:221:ILE:HD11	2.20	0.41
1:D:242:ASN:O	1:D:246:LEU:HD23	2.20	0.41
1:A:318:LEU:HD23	1:A:318:LEU:O	2.20	0.41
1:B:94:VAL:HG12	1:B:94:VAL:O	2.21	0.41
1:C:119:ILE:CD1	1:C:158:LEU:HD13	2.20	0.41
1:B:88:VAL:O	1:B:92:LYS:HG3	2.21	0.41
1:C:86:GLU:O	1:C:90:LYS:HG2	2.20	0.41
1:B:187:LYS:HD3	1:B:187:LYS:HA	1.79	0.41
1:A:239:VAL:HG21	1:A:314:SER:OG	2.20	0.41
1:A:192:GLY:HA2	1:A:195:MET:HB3	2.03	0.41
1:C:350:GLN:HE21	1:C:354:GLU:CG	2.26	0.41
1:B:261:VAL:O	1:B:262:ALA:C	2.57	0.41
1:A:255:LEU:O	1:A:258:PRO:HD3	2.21	0.41
1:C:190:PHE:CZ	1:C:194:ARG:NH1	2.88	0.41
1:C:34:ASN:CB	1:C:374:ALA:HB2	2.49	0.41
1:A:280:GLY:O	1:A:283:GLY:N	2.53	0.41
1:D:81:THR:CG2	1:D:82:THR:N	2.84	0.41
1:D:261:VAL:O	1:D:262:ALA:C	2.59	0.41
1:D:263:PRO:O	1:D:266:THR:HB	2.20	0.41
1:C:264:LEU:O	1:C:267:SER:N	2.51	0.41
1:A:9:SER:O	1:A:377:VAL:HA	2.20	0.41
1:B:177:TRP:CH2	1:B:379:ILE:HB	2.55	0.41
1:C:354:GLU:HA	1:C:354:GLU:OE2	2.20	0.41
1:D:22:VAL:C	1:D:24:HIS:H	2.22	0.41
1:D:117:LEU:O	1:D:121:ARG:HB2	2.21	0.41
1:C:254:LEU:HD13	1:C:261:VAL:HG12	2.01	0.41
1:B:16:LEU:HG	1:B:17:HIS:CD2	2.55	0.41
1:C:181:ASP:O	1:C:184:LEU:HB3	2.20	0.41
1:B:162:GLU:HG3	2:B:404:HOH:O	2.21	0.41
1:D:60:ARG:HE	1:D:97:LEU:HD23	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:287:ALA:O	1:D:290:GLN:HB2	2.20	0.41
1:D:287:ALA:HB3	1:D:290:GLN:NE2	2.34	0.41
1:A:237:THR:C	1:A:239:VAL:H	2.25	0.41
1:A:6:LEU:HB2	1:A:41:LEU:HB3	2.03	0.41
1:B:44:HIS:HD2	1:B:46:ASN:HD21	1.68	0.41
1:B:60:ARG:HG3	1:B:60:ARG:NH2	2.36	0.41
1:A:2:LEU:O	1:A:3:SER:HB2	2.21	0.41
1:D:264:LEU:HD21	1:D:307:ALA:HB3	2.03	0.41
1:A:394:ASP:O	1:A:395:GLY:O	2.39	0.41
1:A:348:LEU:N	1:A:348:LEU:HD12	2.36	0.41
1:B:109:VAL:O	1:B:111:ALA:N	2.54	0.41
1:A:280:GLY:C	1:A:282:MET:N	2.75	0.41
1:C:242:ASN:O	1:C:245:ALA:N	2.49	0.41
1:C:36:ARG:HG3	1:C:36:ARG:H	1.56	0.40
1:D:389:VAL:HG12	1:D:389:VAL:O	2.22	0.40
1:D:14:VAL:CG2	1:D:372:ILE:HD11	2.51	0.40
1:D:273:LEU:N	1:D:273:LEU:HD12	2.36	0.40
1:A:42:GLN:HA	1:A:43:PRO:HD3	1.85	0.40
1:B:67:LEU:HD13	1:B:116:TYR:HE2	1.86	0.40
1:B:52:SER:HB3	1:B:132:VAL:CB	2.51	0.40
1:C:340:GLY:O	1:C:341:ILE:HD12	2.20	0.40
1:D:137:LEU:HD22	1:D:143:LEU:HB3	2.02	0.40
1:A:215:ARG:NH1	1:A:276:GLU:CD	2.74	0.40
1:D:301:ASN:O	1:D:305:LEU:HG	2.21	0.40
1:C:349:GLU:HB2	1:C:352:GLU:HG3	2.04	0.40
1:C:107:LEU:HG	1:C:196:ILE:HB	2.03	0.40
1:C:6:LEU:CD1	1:C:379:ILE:HD13	2.46	0.40
1:D:39:LEU:C	1:D:39:LEU:HD23	2.41	0.40
1:D:63:ASP:OD2	1:D:65:ALA:HB3	2.22	0.40
1:A:241:ARG:HH12	1:A:338:GLY:HA3	1.87	0.40
1:A:278:VAL:O	1:A:282:MET:HB2	2.21	0.40
1:B:318:LEU:O	1:B:322:THR:HG23	2.20	0.40
1:D:385:LEU:HD22	1:D:391:GLN:CG	2.52	0.40
1:C:335:GLY:C	1:C:337:GLY:H	2.25	0.40
1:C:164:ILE:HD13	1:C:181:ASP:HB3	2.04	0.40
1:C:287:ALA:O	1:C:290:GLN:HB2	2.22	0.40
1:A:312:HIS:CE1	1:A:314:SER:OG	2.73	0.40
1:C:37:THR:HG23	1:C:135:SER:HB3	2.04	0.40
1:A:256:LYS:NZ	1:B:292:LEU:HD12	2.37	0.40
1:D:67:LEU:HB3	1:D:126:LEU:CD1	2.52	0.40
1:A:292:LEU:HD21	2:A:420:HOH:O	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	386/396 (98%)	327 (85%)	44 (11%)	15 (4%)	4	5
1	B	384/396 (97%)	304 (79%)	58 (15%)	22 (6%)	2	2
1	C	386/396 (98%)	292 (76%)	73 (19%)	21 (5%)	2	2
1	D	385/396 (97%)	310 (80%)	58 (15%)	17 (4%)	3	3
All	All	1541/1584 (97%)	1233 (80%)	233 (15%)	75 (5%)	3	3

All (75) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	GLU
1	A	95	ALA
1	A	99	ASP
1	A	169	LYS
1	A	284	GLU
1	A	382	ALA
1	B	72	THR
1	B	83	PRO
1	B	101	CYS
1	B	162	GLU
1	B	286	PRO
1	B	381	SER
1	B	386	ASP
1	C	19	GLU
1	C	36	ARG
1	C	45	SER
1	C	48	LYS
1	C	70	LEU
1	C	101	CYS
1	C	165	PRO

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Mol	Chain	Res	Type
1	D	19	GLU
1	D	169	LYS
1	D	170	ASP
1	D	179	LYS
1	A	161	CYS
1	A	171	GLY
1	A	198	GLY
1	A	283	GLY
1	B	65	ALA
1	B	70	LEU
1	B	281	GLU
1	B	351	PRO
1	B	377	VAL
1	B	382	ALA
1	C	72	THR
1	C	74	PHE
1	C	124	ARG
1	C	140	GLY
1	C	156	ALA
1	C	286	PRO
1	D	165	PRO
1	D	171	GLY
1	D	375	PRO
1	A	34	ASN
1	A	375	PRO
1	A	385	LEU
1	B	100	ASP
1	B	352	GLU
1	C	141	ALA
1	C	167	PRO
1	C	168	LEU
1	D	228	PRO
1	D	387	SER
1	D	390	GLN
1	B	161	CYS
1	B	175	ASN
1	B	375	PRO
1	C	4	GLU
1	C	179	LYS
1	D	74	PHE
1	D	172	ASP
1	D	347	GLY

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Mol	Chain	Res	Type
1	B	88	VAL
1	B	391	GLN
1	C	389	VAL
1	D	23	VAL
1	D	225	LYS
1	B	3	SER
1	C	202	GLY
1	D	103	VAL
1	A	47	GLY
1	A	228	PRO
1	D	374	ALA
1	C	139	PRO
1	B	174	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	321/326 (98%)	284 (88%)	37 (12%)	7	13
1	B	319/326 (98%)	289 (91%)	30 (9%)	11	20
1	C	321/326 (98%)	295 (92%)	26 (8%)	15	27
1	D	320/326 (98%)	298 (93%)	22 (7%)	19	35
All	All	1281/1304 (98%)	1166 (91%)	115 (9%)	12	22

All (115) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	LYS
1	A	33	LEU
1	A	35	LEU
1	A	51	LEU
1	A	55	ASN
1	A	60	ARG
1	A	63	ASP
1	A	99	ASP

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Mol	Chain	Res	Type
1	A	113	LEU
1	A	121	ARG
1	A	123	GLN
1	A	129	LEU
1	A	143	LEU
1	A	146	SER
1	A	170	ASP
1	A	172	ASP
1	A	175	ASN
1	A	176	ARG
1	A	199	ASN
1	A	214	LEU
1	A	241	ARG
1	A	244	ARG
1	A	273	LEU
1	A	290	GLN
1	A	292	LEU
1	A	294	LEU
1	A	296	GLU
1	A	314	SER
1	A	320	GLN
1	A	329	SER
1	A	332	THR
1	A	348	LEU
1	A	350	GLN
1	A	361	THR
1	A	375	PRO
1	A	388	ARG
1	A	391	GLN
1	B	13	LYS
1	B	22	VAL
1	B	33	LEU
1	B	35	LEU
1	B	44	HIS
1	B	70	LEU
1	B	72	THR
1	B	74	PHE
1	B	82	THR
1	B	104	THR
1	B	121	ARG
1	B	122	LYS
1	B	164	ILE

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Mol	Chain	Res	Type
1	B	168	LEU
1	B	170	ASP
1	B	172	ASP
1	B	178	THR
1	B	186	ASN
1	B	241	ARG
1	B	273	LEU
1	B	300	MET
1	B	302	GLN
1	B	314	SER
1	B	320	GLN
1	B	350	GLN
1	B	356	THR
1	B	358	GLN
1	B	383	THR
1	B	388	ARG
1	B	389	VAL
1	C	4	GLU
1	C	13	LYS
1	C	22	VAL
1	C	33	LEU
1	C	36	ARG
1	C	41	LEU
1	C	69	SER
1	C	107	LEU
1	C	115	LEU
1	C	129	LEU
1	C	158	LEU
1	C	170	ASP
1	C	174	VAL
1	C	175	ASN
1	C	186	ASN
1	C	215	ARG
1	C	242	ASN
1	C	255	LEU
1	C	277	ARG
1	C	304	HIS
1	C	341	ILE
1	C	353	VAL
1	C	358	GLN
1	C	372	ILE
1	C	377	VAL

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Mol	Chain	Res	Type
1	C	394	ASP
1	D	33	LEU
1	D	38	PHE
1	D	44	HIS
1	D	97	LEU
1	D	99	ASP
1	D	143	LEU
1	D	160	VAL
1	D	164	ILE
1	D	170	ASP
1	D	188	TRP
1	D	194	ARG
1	D	199	ASN
1	D	208	SER
1	D	218	GLN
1	D	241	ARG
1	D	244	ARG
1	D	320	GLN
1	D	348	LEU
1	D	361	THR
1	D	385	LEU
1	D	391	GLN
1	D	394	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	ASN
1	A	68	GLN
1	A	87	GLN
1	A	123	GLN
1	A	175	ASN
1	A	186	ASN
1	A	199	ASN
1	A	205	ASN
1	A	290	GLN
1	A	301	ASN
1	A	317	GLN
1	A	358	GLN
1	A	390	GLN
1	A	391	GLN
1	B	44	HIS

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Mol	Chain	Res	Type
1	B	55	ASN
1	B	123	GLN
1	B	186	ASN
1	B	205	ASN
1	B	252	ASN
1	B	290	GLN
1	B	301	ASN
1	B	302	GLN
1	B	303	HIS
1	B	306	ASN
1	B	317	GLN
1	B	328	HIS
1	B	350	GLN
1	B	358	GLN
1	B	390	GLN
1	C	42	GLN
1	C	175	ASN
1	C	186	ASN
1	C	191	GLN
1	C	205	ASN
1	C	236	ASN
1	C	242	ASN
1	C	290	GLN
1	C	301	ASN
1	C	302	GLN
1	C	306	ASN
1	C	320	GLN
1	C	350	GLN
1	C	358	GLN
1	C	391	GLN
1	D	42	GLN
1	D	44	HIS
1	D	55	ASN
1	D	186	ASN
1	D	199	ASN
1	D	205	ASN
1	D	218	GLN
1	D	231	GLN
1	D	290	GLN
1	D	301	ASN
1	D	302	GLN
1	D	306	ASN

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Mol	Chain	Res	Type
1	D	350	GLN
1	D	391	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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, 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	390/396 (98%)	-0.12	14 (3%) 46 51	10, 37, 71, 90	0
1	B	388/396 (97%)	-0.00	4 (1%) 84 86	9, 41, 74, 94	0
1	C	390/396 (98%)	0.48	24 (6%) 24 27	27, 56, 76, 86	0
1	D	389/396 (98%)	0.32	18 (4%) 36 41	27, 53, 77, 82	0
All	All	1557/1584 (98%)	0.17	60 (3%) 43 48	9, 49, 75, 94	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	81	THR	7.4
1	B	82	THR	7.1
1	A	82	THR	6.2
1	C	82	THR	5.6
1	B	83	PRO	4.5
1	D	69	SER	4.5
1	C	2	LEU	4.4
1	C	81	THR	4.1
1	D	98	PRO	4.0
1	A	394	ASP	4.0
1	A	169	LYS	4.0
1	C	80	VAL	3.8
1	A	385	LEU	3.8
1	D	2	LEU	3.8
1	D	48	LYS	3.7
1	C	67	LEU	3.6
1	D	389	VAL	3.6
1	D	285	ALA	3.5
1	A	285	ALA	3.4
1	A	389	VAL	3.3
1	C	58	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	73	SER	3.1
1	D	388	ARG	3.0
1	D	384	SER	2.9
1	D	351	PRO	2.9
1	D	57	GLY	2.9
1	C	49	VAL	2.8
1	D	97	LEU	2.8
1	A	383	THR	2.8
1	A	80	VAL	2.8
1	A	395	GLY	2.7
1	D	75	LEU	2.6
1	C	169	LYS	2.6
1	C	179	LYS	2.6
1	C	178	THR	2.5
1	C	3	SER	2.5
1	C	387	SER	2.5
1	C	101	CYS	2.4
1	C	160	VAL	2.4
1	C	50	ASP	2.4
1	C	133	VAL	2.3
1	A	81	THR	2.3
1	C	147	ALA	2.3
1	D	393	LEU	2.3
1	B	58	ILE	2.3
1	C	173	CYS	2.3
1	C	353	VAL	2.2
1	A	100	ASP	2.2
1	A	387	SER	2.1
1	D	188	TRP	2.1
1	A	391	GLN	2.1
1	C	208	SER	2.1
1	C	181	ASP	2.1
1	D	383	THR	2.1
1	C	376	GLY	2.1
1	C	184	LEU	2.1
1	D	15	ILE	2.0
1	D	283	GLY	2.0
1	A	388	ARG	2.0
1	C	122	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.