



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 01:51 am GMT

PDB ID : 1DO2
Title : TRIGONAL CRYSTAL FORM OF HEAT SHOCK LOCUS U (HSLU) FROM
ESCHERICHIA COLI
Authors : Bochtler, M.; Hartmann, C.; Song, H.K.; Bourenkov, G.P.; Bartunik, H.D.
Deposited on : 1999-12-18
Resolution : 4.00 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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

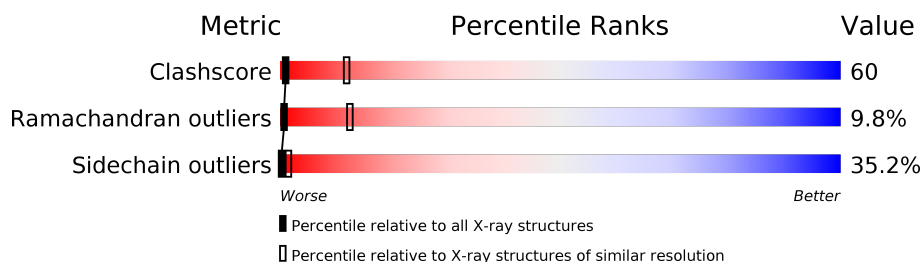
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	1187 (4.40-3.60)
Ramachandran outliers	110173	1139 (4.40-3.60)
Sidechain outliers	110143	1126 (4.40-3.60)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	442	
1	B	442	
1	C	442	
1	D	442	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ANP	A	900	-	-	X	-
2	ANP	C	905	-	-	X	-

2 Entry composition [i](#)

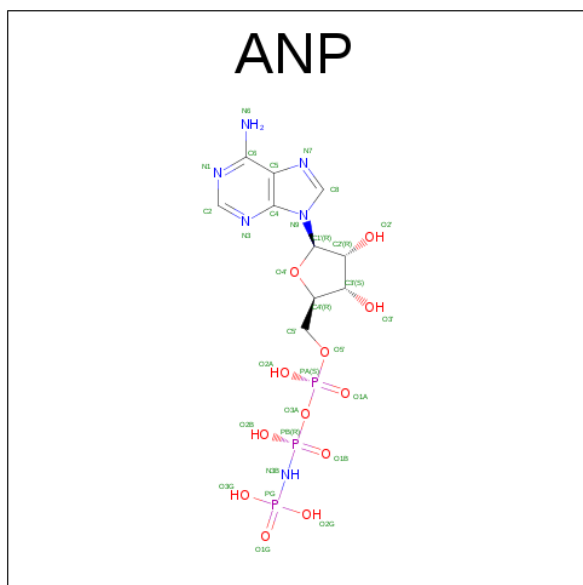
There are 2 unique types of molecules in this entry. The entry contains 12926 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PROTEIN (HEAT SHOCK LOCUS U).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	126	0	0
			3216	2008	574	624	10			
1	B	407	Total	C	N	O	S	492	0	0
			3216	2008	574	624	10			
1	C	407	Total	C	N	O	S	103	0	0
			3216	2008	574	624	10			
1	D	407	Total	C	N	O	S	484	0	0
			3216	2008	574	624	10			

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



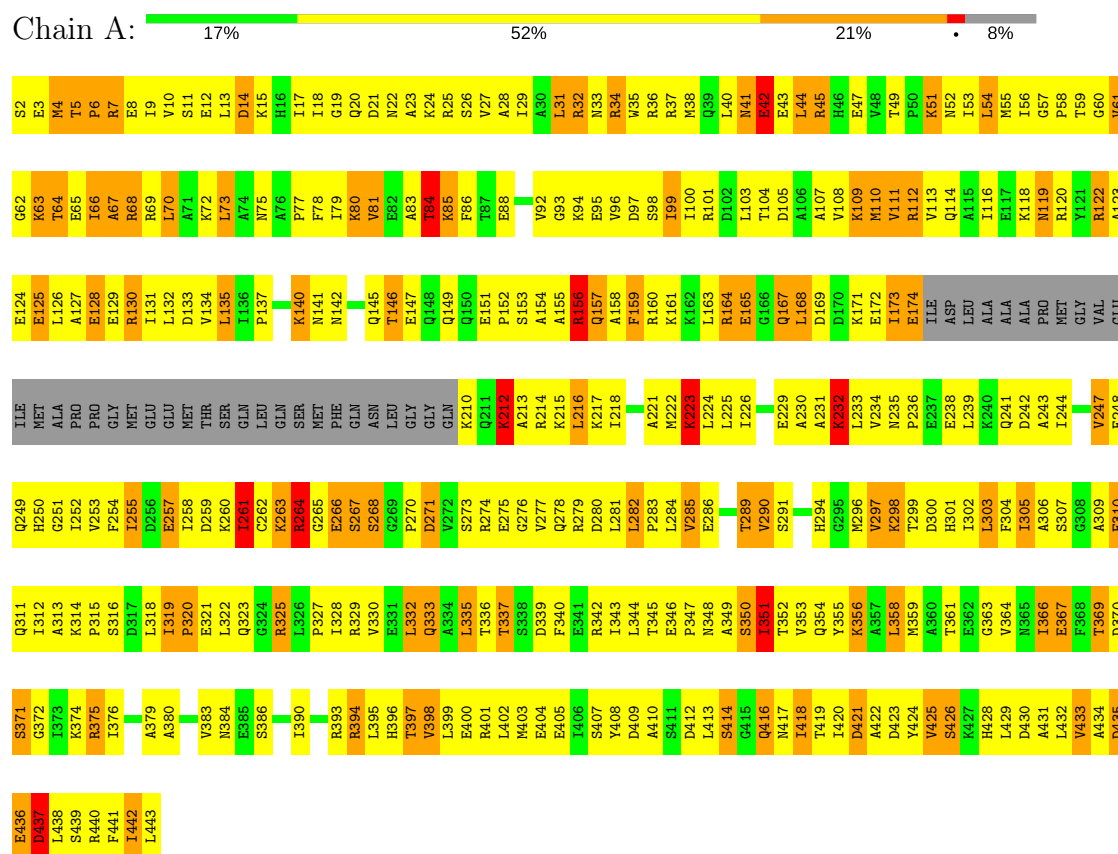
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	C	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

3 Residue-property plots

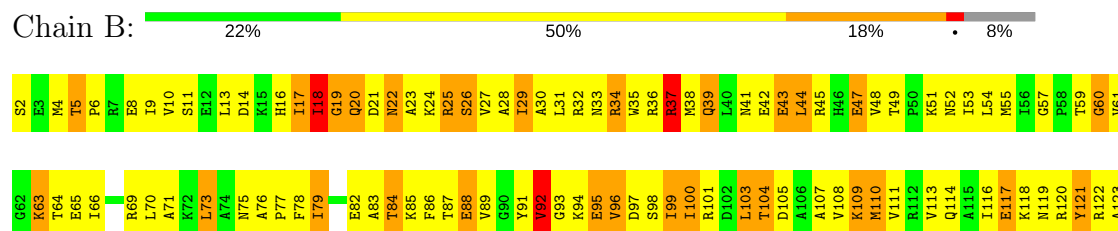
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

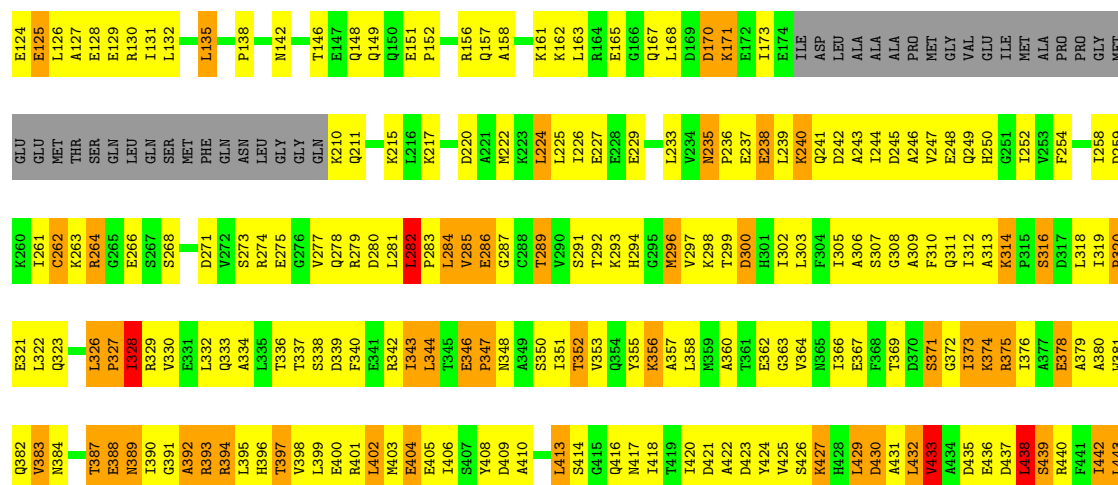
Note EDS was not executed.

• Molecule 1: PROTEIN (HEAT SHOCK LOCUS U)



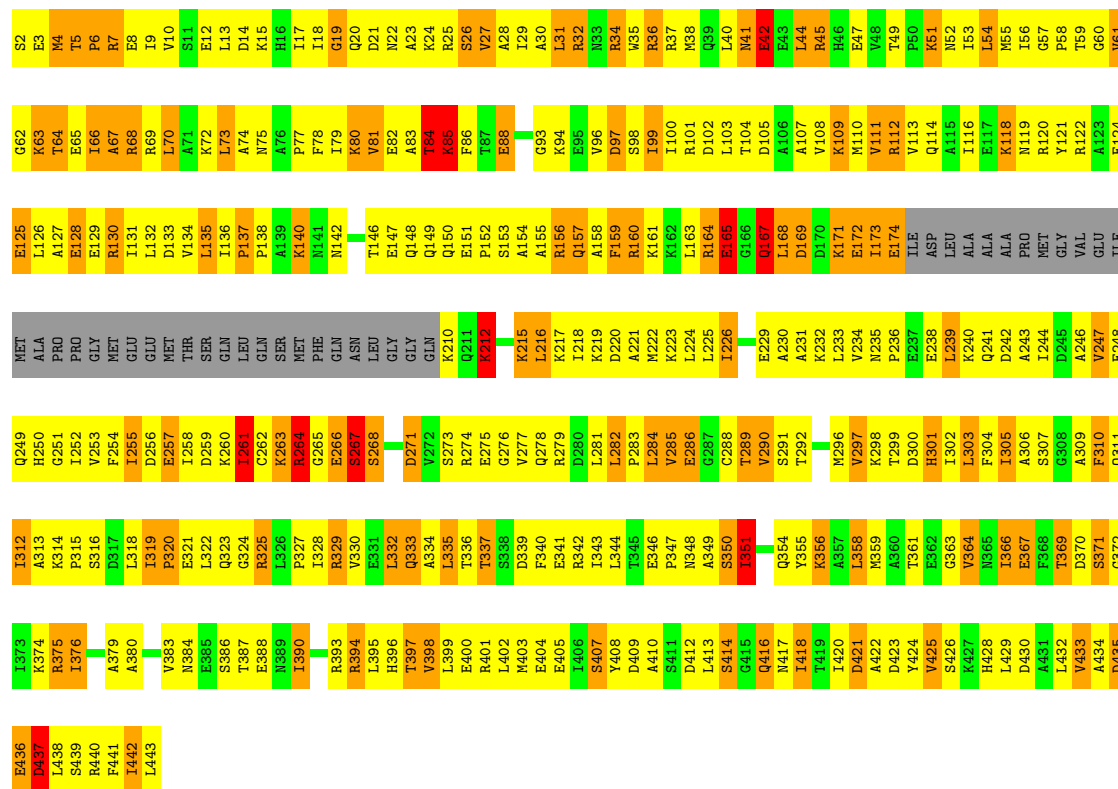
• Molecule 1: PROTEIN (HEAT SHOCK LOCUS U)





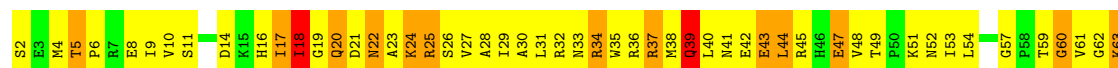
• Molecule 1: PROTEIN (HEAT SHOCK LOCUS U)

Chain C: 16% 50% 24% 8%



• Molecule 1: PROTEIN (HEAT SHOCK LOCUS U)

Chain D: 21% 53% 16% 8%



A379	A380	W381	Q382	V383	N384	T387	E388	N389	I390	G391	A392	R393	R394	L395	H396	T397	V398	L399	E400	R401	L402	M403	E404	E405	Y408	L413	S414	G415	Q416	N417	I418	T419	I420	D421	A422	D423	Y424	Y425	S426	K427	H428	L429	D430	A431	L432	V433	E436	D437	L438	S439	R440	F441	I442	L443								
L318	I319	F320	E321	L322	Q323	G324	R325	L326	P327	I328	R329	V330	E331	L332	Q333	A334	T335	V336	T337	S338	D339	F340	E341	R342	T343	L344	T345	E346	P347	N348	A349	S350	T351	T352	V353	Q354	Y355	K356	A357	L358	G359	A360	T361	E362	G363	V364	N365	L366	T369	D370	S371	G372	I373	K374	R375	L376	A377	E378				
E257	I258	K259	K260	I261	C262	K263	K264	G265	E266	S267	S268	D271	V272	S273	R274	E275	G276	V277	Q278	R279	D280	L281	L282	P283	L284	V285	E286	G287	C288	T289	V290	S291	T292	K293	H294	G295	M296	V297	K298	T299	D300	H301	I302	L303	F304	I305	A306	S307	G308	A309	F310	Q311	I312	G313	T314	V315	S316	D317				
MET	THR	SER	GLN	LEU	GLN	SER	MET	PHE	GLN	ASN	LEU	GLY	GLY	GLN	K210	Q211	K215	L216	K217	L218	K219	D220	A221	H222	K223	L224	L225	I226	E227	E228	E229	A230	A231	K232	L233	V234	N235	P236	E237	E238	L239	K240	Q241	D242	A243	I244	D245	A246	V247	E248	Q249	H250	G251	I252	V253	F254	L255	D256				
T64	E65	L66	R69	L70	A71	K72	L73	A74	N75	A76	P77	F78	I79	K80	V81	E82	A83	T84	K85	F86	T87	E88	R156	Q157	V89	G90	Y91	K161	K162	G93	K94	R164	E165	G166	Q167	S98	L168	I100	D101	D102	L103	T104	D105	A106	A107	V108	K109	M110	V111	MET	G112	V113	Q114	A115	I116	E117	R120	Y121	R122	A123	E124	E125
L126	A127	E128	E129	R130	L131	L132	D133	V134	L135	P138	N142	Q145	T146	E147	Q148	Q149	Q150	E151	R156	Q157	A158	K161	K162	L163	K164	E165	G166	Q167	S98	L168	I100	D101	D102	L103	T104	D105	A106	A107	V108	K109	M110	V111	MET	G112	V113	Q114	A115	I116	E117	R120	Y121	R122	A123	E124	E125							

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	201.78Å 201.78Å 171.63Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	15.00 – 4.00	Depositor
% Data completeness (in resolution range)	95.8 (15.00-4.00)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	10.50	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.229 , 0.285	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12926	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.30	0/3255	0.58	3/4385 (0.1%)
1	B	0.28	0/3255	0.50	0/4385
1	C	0.29	0/3255	0.51	0/4385
1	D	0.28	0/3255	0.52	0/4385
All	All	0.29	0/13020	0.53	3/17540 (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	A	156	ARG	CB-CG-CD	12.03	142.87	111.60
1	A	223	LYS	CB-CG-CD	8.81	134.51	111.60
1	A	232	LYS	N-CA-CB	5.85	121.13	110.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3216	0	3284	386	0
1	B	3216	0	3284	289	0
1	C	3216	0	3284	434	0
1	D	3216	0	3284	316	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	31	0	13	9	0
2	C	31	0	13	11	0
All	All	12926	0	13162	1411	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 60.

All (1411) 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:A:356:LYS:HA	1:A:366:ILE:HD11	1.38	1.01
1:C:54:LEU:HD13	1:C:56:ILE:HD11	1.39	1.01
1:A:366:ILE:HD13	1:A:366:ILE:H	1.28	0.98
1:A:54:LEU:HD13	1:A:56:ILE:HD11	1.43	0.97
1:A:282:LEU:HD21	1:A:321:GLU:HB3	1.46	0.97
1:C:426:SER:O	1:C:430:ASP:HB2	1.66	0.96
1:C:299:THR:HA	1:C:302:ILE:HD12	1.47	0.96
1:C:4:MET:HB3	1:C:8:GLU:HB3	1.46	0.96
1:C:366:ILE:HD13	1:C:366:ILE:H	1.30	0.95
1:D:429:LEU:HD22	1:D:429:LEU:H	1.32	0.94
1:C:153:SER:HA	1:C:156:ARG:HB3	1.50	0.94
1:A:4:MET:HB3	1:A:8:GLU:HB3	1.51	0.93
1:A:109:LYS:HG3	1:A:112:ARG:HH21	1.34	0.92
1:C:356:LYS:HA	1:C:366:ILE:HD11	1.50	0.91
1:D:123:ALA:HB1	1:D:226:ILE:HG23	1.52	0.90
1:C:131:ILE:O	1:C:134:VAL:HG12	1.70	0.90
1:A:27:VAL:HG22	1:A:70:LEU:HD13	1.53	0.88
1:A:153:SER:HA	1:A:156:ARG:HB3	1.55	0.87
1:A:18:ILE:H	2:A:900:ANP:HN61	1.23	0.87
1:C:59:THR:HA	2:C:905:ANP:O1G	1.73	0.87
1:C:258:ILE:HG13	1:C:306:ALA:HB1	1.56	0.86
1:C:439:SER:HA	1:C:443:LEU:HD13	1.56	0.85
1:B:235:ASN:HD22	1:B:238:GLU:HG2	1.41	0.84
1:B:83:ALA:HB1	1:B:261:ILE:HD11	1.59	0.84
1:B:356:LYS:HA	1:B:366:ILE:HD11	1.56	0.84
1:C:282:LEU:HD21	1:C:321:GLU:HB3	1.59	0.84
1:A:426:SER:O	1:A:430:ASP:HB2	1.76	0.84
1:D:59:THR:HG21	1:D:390:ILE:HA	1.59	0.84
1:B:429:LEU:HD22	1:B:429:LEU:H	1.43	0.83
1:C:18:ILE:H	2:C:905:ANP:HN61	1.26	0.83
1:D:319:ILE:HG23	1:D:322:LEU:HB3	1.58	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:442:ILE:HG12	1:C:443:LEU:HD12	1.61	0.83
1:D:271:ASP:HA	1:D:274:ARG:HB2	1.60	0.83
1:D:356:LYS:HA	1:D:366:ILE:HD11	1.57	0.83
1:B:319:ILE:HG23	1:B:322:LEU:HB3	1.60	0.82
1:A:42:GLU:HA	1:A:45:ARG:HB2	1.61	0.82
1:A:131:ILE:O	1:A:134:VAL:HG12	1.77	0.82
1:A:59:THR:HA	2:A:900:ANP:O1G	1.79	0.82
1:B:26:SER:HA	1:B:29:ILE:HD12	1.62	0.82
1:C:27:VAL:HG22	1:C:70:LEU:HD13	1.61	0.82
1:A:24:LYS:O	1:A:27:VAL:HG12	1.79	0.82
1:C:369:THR:OG1	1:C:421:ASP:HA	1.80	0.82
1:C:319:ILE:HG12	1:C:320:PRO:HD2	1.60	0.82
1:C:42:GLU:HA	1:C:45:ARG:HB2	1.60	0.82
1:A:113:VAL:HA	1:A:116:ILE:HD12	1.62	0.81
1:A:344:LEU:HA	1:A:351:ILE:HD11	1.62	0.80
1:D:235:ASN:HD22	1:D:238:GLU:HG2	1.47	0.80
1:D:282:LEU:HD21	1:D:321:GLU:HB3	1.63	0.80
1:A:226:ILE:O	1:A:230:ALA:HB2	1.80	0.80
1:A:68:ARG:HB3	1:A:68:ARG:HH11	1.45	0.80
1:B:299:THR:HA	1:B:302:ILE:HG13	1.64	0.79
1:B:432:LEU:HD12	1:B:432:LEU:H	1.46	0.79
1:A:299:THR:HA	1:A:302:ILE:HD12	1.65	0.79
1:B:271:ASP:HA	1:B:274:ARG:HB2	1.62	0.79
1:C:113:VAL:HA	1:C:116:ILE:HD12	1.65	0.79
1:D:96:VAL:HG11	1:D:280:ASP:HB3	1.65	0.79
1:C:79:ILE:HG22	1:C:103:LEU:HD13	1.62	0.79
1:A:319:ILE:HG12	1:A:320:PRO:HD2	1.64	0.79
1:B:123:ALA:HB1	1:B:226:ILE:HG23	1.64	0.79
1:C:109:LYS:HG3	1:C:112:ARG:HH21	1.48	0.78
1:D:364:VAL:HG22	1:D:414:SER:HA	1.65	0.78
1:D:299:THR:HA	1:D:302:ILE:HG13	1.66	0.78
1:D:41:ASN:ND2	1:D:43:GLU:HB3	1.98	0.78
1:A:439:SER:HA	1:A:443:LEU:HD13	1.63	0.78
1:C:100:ILE:HD12	1:C:100:ILE:H	1.46	0.78
1:B:364:VAL:HG22	1:B:414:SER:HA	1.64	0.77
1:C:96:VAL:HG12	1:C:284:LEU:HD11	1.65	0.77
1:C:24:LYS:O	1:C:27:VAL:HG12	1.84	0.77
1:C:318:LEU:HD11	1:C:322:LEU:HD23	1.67	0.77
1:B:41:ASN:ND2	1:B:43:GLU:HB3	2.00	0.77
1:C:66:ILE:HD12	1:C:66:ILE:H	1.49	0.77
1:D:432:LEU:H	1:D:432:LEU:HD12	1.50	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:390:ILE:O	1:C:393:ARG:HG3	1.84	0.76
1:B:6:PRO:HA	1:B:9:ILE:HD12	1.67	0.76
1:C:26:SER:HA	1:C:29:ILE:HD12	1.67	0.76
1:C:111:VAL:HG11	1:C:243:ALA:HB2	1.68	0.75
1:C:319:ILE:HD11	1:C:321:GLU:HB2	1.66	0.75
1:A:66:ILE:HD12	1:A:66:ILE:H	1.52	0.75
1:A:390:ILE:HD11	1:A:394:ARG:NE	2.02	0.75
1:D:17:ILE:HG23	1:D:18:ILE:N	2.01	0.75
1:D:355:TYR:OH	1:D:403:MET:HB3	1.86	0.75
1:D:26:SER:HA	1:D:29:ILE:HD12	1.69	0.75
1:B:17:ILE:HG23	1:B:18:ILE:N	1.99	0.74
1:A:100:ILE:H	1:A:100:ILE:HD12	1.52	0.74
1:B:327:PRO:O	1:B:329:ARG:HG2	1.88	0.74
1:A:79:ILE:HG22	1:A:103:LEU:HD13	1.69	0.74
1:B:59:THR:HG21	1:B:390:ILE:HA	1.68	0.74
1:B:61:VAL:O	1:B:61:VAL:HG13	1.87	0.74
1:B:318:LEU:HD21	1:B:322:LEU:HD23	1.69	0.74
1:B:336:THR:HA	1:B:381:TRP:CZ3	2.22	0.74
1:A:442:ILE:HG12	1:A:443:LEU:HD12	1.69	0.73
1:B:263:LYS:HG3	1:B:264:ARG:N	2.02	0.73
1:C:383:VAL:HB	1:C:394:ARG:HH11	1.52	0.73
1:A:390:ILE:HD11	1:A:394:ARG:HE	1.52	0.73
1:B:91:TYR:HB3	1:B:95:GLU:HB2	1.71	0.73
1:D:426:SER:O	1:D:430:ASP:HB2	1.89	0.73
1:D:83:ALA:HB1	1:D:261:ILE:HD11	1.69	0.73
1:A:361:THR:HG21	1:B:36:ARG:HA	1.70	0.72
1:D:61:VAL:O	1:D:61:VAL:HG13	1.88	0.72
1:D:261:ILE:HG22	1:D:278:GLN:HE21	1.55	0.72
1:A:369:THR:OG1	1:A:421:ASP:HA	1.90	0.71
1:C:390:ILE:HD11	1:C:394:ARG:HE	1.55	0.71
1:B:426:SER:O	1:B:430:ASP:HB2	1.89	0.71
1:A:390:ILE:O	1:A:393:ARG:HG3	1.89	0.71
1:B:384:ASN:HD21	1:B:391:GLY:H	1.38	0.71
1:D:397:THR:HG21	1:D:443:LEU:HA	1.72	0.71
1:B:336:THR:HA	1:B:381:TRP:HZ3	1.54	0.71
1:C:226:ILE:O	1:C:230:ALA:HB2	1.90	0.71
1:B:282:LEU:HD21	1:B:321:GLU:HB3	1.73	0.70
1:C:223:LYS:O	1:C:226:ILE:HG22	1.90	0.70
1:C:438:LEU:O	1:C:442:ILE:HD13	1.91	0.70
1:A:429:LEU:HD23	1:A:429:LEU:N	2.07	0.70
1:C:234:VAL:HG23	1:C:236:PRO:HD3	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:289:THR:HG23	1:C:298:LYS:HG2	1.73	0.70
1:D:6:PRO:HA	1:D:9:ILE:HD12	1.74	0.70
1:A:132:LEU:HA	1:A:135:LEU:HD23	1.74	0.70
1:C:235:ASN:HB3	1:C:238:GLU:HG2	1.73	0.70
1:C:61:VAL:HA	1:C:335:LEU:HD11	1.74	0.70
1:B:387:THR:OG1	1:B:388:GLU:N	2.25	0.69
1:A:319:ILE:HD11	1:A:321:GLU:HB2	1.73	0.69
1:C:100:ILE:HD13	1:C:290:VAL:HG21	1.74	0.69
1:C:413:LEU:O	1:C:416:GLN:HB2	1.93	0.69
1:B:397:THR:HG21	1:B:443:LEU:HA	1.75	0.69
1:C:112:ARG:HB3	1:C:239:LEU:HD11	1.75	0.69
1:A:383:VAL:HB	1:A:394:ARG:HH11	1.58	0.69
1:D:109:LYS:O	1:D:113:VAL:HG13	1.92	0.69
1:D:23:ALA:HA	1:D:330:VAL:HG21	1.74	0.69
1:D:43:GLU:O	1:D:47:GLU:HB2	1.92	0.69
1:D:423:ASP:O	1:D:427:LYS:HB2	1.91	0.69
1:A:278:GLN:HB3	1:A:319:ILE:HG21	1.75	0.69
1:C:70:LEU:HA	1:C:73:LEU:HD22	1.75	0.69
1:D:245:ASP:O	1:D:249:GLN:HB2	1.93	0.69
1:D:24:LYS:O	1:D:27:VAL:HG22	1.92	0.69
1:A:100:ILE:HD13	1:A:290:VAL:HG21	1.75	0.68
1:A:291:SER:HA	1:A:296:MET:SD	2.33	0.68
1:B:122:ARG:CZ	1:B:126:LEU:HD11	2.24	0.68
1:D:387:THR:OG1	1:D:388:GLU:N	2.23	0.68
1:A:222:MET:O	1:A:226:ILE:HB	1.92	0.68
1:C:277:VAL:HG12	1:C:281:LEU:HD11	1.74	0.68
1:C:86:PHE:HD1	1:C:93:GLY:HA2	1.57	0.68
1:D:117:GLU:HA	1:D:120:ARG:NE	2.08	0.68
1:A:65:GLU:OE2	1:A:69:ARG:HD3	1.93	0.68
1:B:384:ASN:ND2	1:B:391:GLY:H	1.90	0.68
1:A:86:PHE:HD1	1:A:93:GLY:HA2	1.57	0.68
1:C:31:LEU:HD23	1:C:70:LEU:HD11	1.74	0.68
1:A:318:LEU:HD11	1:A:322:LEU:HD23	1.76	0.68
1:B:100:ILE:HG21	1:B:297:VAL:HG21	1.76	0.68
1:C:303:LEU:HD12	1:C:305:ILE:HG12	1.76	0.68
1:A:413:LEU:O	1:A:416:GLN:HB2	1.94	0.67
1:A:234:VAL:HG23	1:A:236:PRO:HD3	1.75	0.67
1:C:216:LEU:HD11	1:C:221:ALA:HB2	1.76	0.67
1:A:258:ILE:HG13	1:A:306:ALA:HB1	1.76	0.67
1:C:125:GLU:OE1	1:C:126:LEU:HG	1.95	0.67
1:C:264:ARG:HB3	1:C:264:ARG:HH11	1.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:318:LEU:HD23	1:D:319:ILE:N	2.10	0.67
1:D:336:THR:HA	1:D:381:TRP:CZ3	2.29	0.67
1:C:59:THR:HG23	2:C:905:ANP:O3G	1.93	0.67
1:A:422:ALA:O	1:A:425:VAL:HG23	1.95	0.67
1:B:245:ASP:C	1:B:247:VAL:H	1.98	0.67
1:A:96:VAL:HG12	1:A:284:LEU:HD11	1.77	0.67
1:A:70:LEU:HA	1:A:73:LEU:HD22	1.77	0.67
1:D:394:ARG:O	1:D:398:VAL:HG13	1.95	0.67
1:D:129:GLU:HA	1:D:132:LEU:HB2	1.76	0.67
1:D:282:LEU:O	1:D:286:GLU:N	2.27	0.67
1:A:397:THR:HG21	1:A:443:LEU:HA	1.75	0.67
1:A:59:THR:HG23	2:A:900:ANP:O3G	1.94	0.67
1:C:132:LEU:HD12	1:C:133:ASP:N	2.09	0.67
1:C:278:GLN:HB3	1:C:319:ILE:HG21	1.77	0.67
1:C:63:LYS:HB2	2:C:905:ANP:O1B	1.95	0.67
1:D:327:PRO:O	1:D:329:ARG:HG2	1.94	0.67
1:D:127:ALA:O	1:D:131:ILE:HG12	1.95	0.67
1:B:23:ALA:HB2	1:B:332:LEU:HD11	1.75	0.66
1:B:261:ILE:HG22	1:B:278:GLN:HE21	1.58	0.66
1:C:68:ARG:HH11	1:C:68:ARG:HB3	1.60	0.66
1:B:127:ALA:HA	1:B:225:LEU:HB3	1.77	0.66
1:B:129:GLU:HA	1:B:132:LEU:HB2	1.77	0.66
1:D:5:THR:O	1:D:9:ILE:HG13	1.96	0.66
1:A:223:LYS:O	1:A:226:ILE:HG22	1.94	0.66
1:B:278:GLN:OE1	1:B:319:ILE:HG22	1.95	0.66
1:D:245:ASP:C	1:D:247:VAL:H	1.99	0.66
1:A:372:GLY:O	1:A:376:ILE:HD12	1.96	0.66
1:A:435:ASP:OD2	1:A:438:LEU:HD23	1.96	0.66
1:B:281:LEU:O	1:B:284:LEU:HG	1.95	0.66
1:C:366:ILE:HD13	1:C:366:ILE:N	2.09	0.66
1:C:390:ILE:HD11	1:C:394:ARG:NE	2.10	0.66
1:A:130:ARG:HA	1:A:133:ASP:HB2	1.78	0.66
1:C:132:LEU:HA	1:C:135:LEU:HD23	1.76	0.65
1:C:248:GLU:HG3	1:C:297:VAL:HG12	1.78	0.65
1:C:65:GLU:O	1:C:68:ARG:HG2	1.96	0.65
1:D:430:ASP:O	1:D:433:VAL:HG23	1.96	0.65
1:B:281:LEU:HD23	1:B:284:LEU:HD11	1.78	0.65
1:A:105:ASP:O	1:A:108:VAL:HB	1.96	0.65
1:A:132:LEU:HD12	1:A:133:ASP:N	2.11	0.65
1:A:57:GLY:O	1:A:309:ALA:HB2	1.97	0.65
1:B:430:ASP:O	1:B:433:VAL:HG23	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:284:LEU:HA	1:D:299:THR:OG1	1.97	0.65
1:A:31:LEU:HD23	1:A:70:LEU:HD11	1.76	0.65
1:D:281:LEU:O	1:D:284:LEU:HG	1.97	0.65
1:A:344:LEU:HA	1:A:351:ILE:CD1	2.27	0.65
1:B:24:LYS:O	1:B:27:VAL:HG22	1.96	0.65
1:B:383:VAL:HB	1:B:394:ARG:HH11	1.60	0.65
1:A:128:GLU:HA	1:A:131:ILE:HD12	1.79	0.65
1:C:22:ASN:HA	1:C:25:ARG:HG3	1.79	0.65
1:D:318:LEU:HD21	1:D:322:LEU:HD23	1.78	0.65
1:A:327:PRO:HG2	1:A:328:ILE:HD12	1.78	0.64
1:C:128:GLU:HA	1:C:131:ILE:CD1	2.27	0.64
1:C:319:ILE:CD1	1:C:321:GLU:HB2	2.27	0.64
1:C:103:LEU:HD23	1:C:247:VAL:HG12	1.79	0.64
1:C:397:THR:HG21	1:C:443:LEU:HA	1.78	0.64
1:B:4:MET:HB3	1:B:8:GLU:HB3	1.80	0.64
1:D:110:MET:O	1:D:113:VAL:HG22	1.98	0.64
1:D:336:THR:HG22	1:D:339:ASP:CG	2.18	0.64
1:D:70:LEU:HD23	1:D:71:ALA:N	2.13	0.64
1:D:336:THR:HA	1:D:381:TRP:HZ3	1.61	0.64
1:A:153:SER:CA	1:A:156:ARG:HB3	2.25	0.64
1:C:337:THR:O	1:C:340:PHE:HB2	1.97	0.64
1:D:278:GLN:HA	1:D:281:LEU:HD12	1.80	0.64
1:A:66:ILE:CD1	1:A:66:ILE:H	2.11	0.63
1:D:278:GLN:O	1:D:281:LEU:HB2	1.98	0.63
1:A:61:VAL:HA	1:A:335:LEU:HD11	1.78	0.63
1:B:310:PHE:HB3	1:B:313:ALA:O	1.98	0.63
1:D:235:ASN:O	1:D:239:LEU:HG	1.97	0.63
1:A:277:VAL:HG12	1:A:281:LEU:HD11	1.81	0.63
1:B:83:ALA:HB1	1:B:261:ILE:CD1	2.28	0.63
1:B:395:LEU:HA	1:B:398:VAL:HG22	1.78	0.63
1:C:128:GLU:HA	1:C:131:ILE:HG13	1.80	0.63
1:C:277:VAL:HG12	1:C:281:LEU:CD1	2.29	0.63
1:D:395:LEU:O	1:D:398:VAL:HG22	1.98	0.63
1:A:173:ILE:O	1:A:212:LYS:HB3	1.97	0.63
1:B:254:PHE:HD2	1:B:305:ILE:HB	1.62	0.63
1:A:22:ASN:HA	1:A:25:ARG:HG3	1.80	0.63
1:A:96:VAL:HG11	1:A:281:LEU:HG	1.79	0.63
1:B:245:ASP:O	1:B:249:GLN:HB2	1.98	0.63
1:B:318:LEU:HD23	1:B:319:ILE:N	2.13	0.63
1:B:23:ALA:O	1:B:27:VAL:HG13	1.99	0.63
1:C:222:MET:O	1:C:226:ILE:HB	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:LYS:NZ	1:A:367:GLU:HA	2.13	0.63
1:B:423:ASP:O	1:B:427:LYS:HB2	1.98	0.63
1:D:21:ASP:HA	1:D:24:LYS:HG3	1.80	0.63
1:A:125:GLU:OE1	1:A:126:LEU:HG	1.99	0.62
1:A:24:LYS:O	1:A:28:ALA:N	2.31	0.62
1:C:128:GLU:HA	1:C:131:ILE:CG1	2.29	0.62
1:C:23:ALA:HB2	1:C:332:LEU:HD11	1.80	0.62
1:A:99:ILE:HG22	1:A:100:ILE:N	2.15	0.62
1:B:121:TYR:O	1:B:125:GLU:HB3	1.99	0.62
1:C:439:SER:HA	1:C:443:LEU:CD1	2.29	0.62
1:D:278:GLN:OE1	1:D:319:ILE:HG22	1.99	0.62
1:D:41:ASN:HD21	1:D:43:GLU:HB3	1.63	0.62
1:B:60:GLY:HA2	1:B:63:LYS:CG	2.30	0.62
1:C:20:GLN:HB3	1:C:332:LEU:HD12	1.81	0.62
1:A:13:LEU:C	1:A:15:LYS:H	2.03	0.62
1:C:35:TRP:CZ3	1:C:36:ARG:HG3	2.33	0.62
1:D:254:PHE:HD2	1:D:305:ILE:HB	1.64	0.62
1:D:383:VAL:HB	1:D:394:ARG:HH11	1.65	0.62
1:D:375:ARG:HA	1:D:378:GLU:HB2	1.82	0.62
1:A:63:LYS:HB2	2:A:900:ANP:O1B	2.00	0.62
1:B:289:THR:HA	1:B:297:VAL:O	2.00	0.62
1:C:363:GLY:O	1:C:414:SER:HA	2.00	0.62
1:C:438:LEU:HB3	1:C:442:ILE:HD11	1.81	0.62
1:D:257:GLU:O	1:D:260:LYS:HB2	2.00	0.62
1:D:83:ALA:HB1	1:D:261:ILE:CD1	2.30	0.62
1:A:129:GLU:O	1:A:132:LEU:HG	2.00	0.62
1:A:265:GLY:O	1:A:266:GLU:HB2	2.00	0.61
1:A:303:LEU:HD12	1:A:305:ILE:HG12	1.81	0.61
1:A:310:PHE:N	1:A:310:PHE:HD2	1.98	0.61
1:B:282:LEU:O	1:B:286:GLU:N	2.33	0.61
1:A:358:LEU:HD11	1:B:33:ASN:HD22	1.65	0.61
1:B:394:ARG:O	1:B:398:VAL:HG13	2.00	0.61
1:C:128:GLU:HA	1:C:131:ILE:HD12	1.80	0.61
1:B:340:PHE:O	1:B:343:ILE:HG13	2.00	0.61
1:C:312:ILE:HG13	1:C:313:ALA:H	1.65	0.61
1:A:366:ILE:N	1:A:366:ILE:HD13	2.07	0.61
1:C:23:ALA:HA	1:C:330:VAL:HG21	1.83	0.61
1:C:57:GLY:O	1:C:309:ALA:HB2	2.00	0.61
1:D:310:PHE:HB3	1:D:313:ALA:O	2.00	0.61
1:C:105:ASP:O	1:C:108:VAL:HB	2.01	0.61
1:C:97:ASP:HB2	1:C:290:VAL:HG11	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:271:ASP:HA	1:D:274:ARG:CB	2.29	0.61
1:B:355:TYR:OH	1:B:403:MET:HB3	2.00	0.61
1:A:122:ARG:HB3	1:A:126:LEU:HD12	1.81	0.61
1:A:23:ALA:HA	1:A:330:VAL:HG21	1.83	0.61
1:A:282:LEU:O	1:A:285:VAL:HG23	2.00	0.61
1:B:96:VAL:HG11	1:B:280:ASP:HB3	1.82	0.61
1:C:253:VAL:O	1:C:305:ILE:HG13	2.00	0.61
1:C:255:ILE:O	1:C:306:ALA:HA	2.01	0.61
1:C:265:GLY:O	1:C:266:GLU:HB2	2.00	0.61
1:D:91:TYR:HB3	1:D:95:GLU:HB2	1.82	0.61
1:A:264:ARG:HH11	1:A:264:ARG:HB3	1.65	0.61
1:A:65:GLU:O	1:A:68:ARG:HG2	2.01	0.61
1:A:312:ILE:HG13	1:A:313:ALA:H	1.66	0.61
1:B:319:ILE:HD12	1:B:320:PRO:HD2	1.83	0.61
1:C:86:PHE:HA	1:C:93:GLY:HA2	1.83	0.61
1:B:235:ASN:O	1:B:239:LEU:HG	2.01	0.61
1:B:284:LEU:HA	1:B:299:THR:OG1	2.01	0.61
1:C:66:ILE:CD1	1:C:66:ILE:H	2.13	0.60
1:A:258:ILE:HA	1:A:261:ILE:HD11	1.82	0.60
1:B:278:GLN:O	1:B:281:LEU:HB2	2.00	0.60
1:C:12:GLU:HG2	1:C:73:LEU:HD12	1.83	0.60
1:D:128:GLU:O	1:D:132:LEU:HB2	2.00	0.60
1:D:263:LYS:HG3	1:D:264:ARG:N	2.16	0.60
1:A:418:ILE:N	1:A:418:ILE:HD13	2.16	0.60
1:A:438:LEU:O	1:A:442:ILE:HD13	2.01	0.60
1:B:438:LEU:CD2	1:B:442:ILE:HD11	2.31	0.60
1:C:281:LEU:O	1:C:284:LEU:HG	2.02	0.60
1:A:5:THR:HB	1:A:6:PRO:HD2	1.84	0.60
1:B:122:ARG:HG3	1:B:233:LEU:HD21	1.81	0.60
1:B:436:GLU:O	1:B:438:LEU:N	2.34	0.60
1:D:27:VAL:HB	1:D:70:LEU:HD13	1.84	0.60
1:A:5:THR:N	1:A:8:GLU:HB2	2.16	0.60
1:C:212:LYS:HE2	1:C:225:LEU:HD13	1.84	0.60
1:C:77:PRO:O	1:C:103:LEU:HD11	2.02	0.60
1:D:44:LEU:HA	1:D:47:GLU:CB	2.31	0.60
1:A:319:ILE:CD1	1:A:321:GLU:HB2	2.32	0.60
1:C:65:GLU:OE2	1:C:69:ARG:HD3	2.02	0.60
1:C:64:THR:HG22	1:C:68:ARG:HD3	1.83	0.60
1:A:339:ASP:O	1:A:343:ILE:HG13	2.01	0.60
1:D:100:ILE:HD11	1:D:284:LEU:HB3	1.84	0.60
1:D:223:LYS:HA	1:D:226:ILE:HD12	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:235:ASN:ND2	1:D:238:GLU:HG2	2.15	0.60
1:C:100:ILE:HG12	1:C:299:THR:CG2	2.31	0.60
1:C:13:LEU:C	1:C:15:LYS:H	2.04	0.60
1:C:376:ILE:HG13	1:C:425:VAL:HG11	1.83	0.60
1:D:117:GLU:HA	1:D:120:ARG:HG3	1.84	0.60
1:A:275:GLU:O	1:A:278:GLN:HB2	2.02	0.59
1:A:310:PHE:N	1:A:310:PHE:CD2	2.69	0.59
1:B:278:GLN:HA	1:B:281:LEU:HD12	1.83	0.59
1:D:340:PHE:O	1:D:343:ILE:HG13	2.02	0.59
1:A:64:THR:O	1:A:67:ALA:HB3	2.02	0.59
1:B:87:THR:O	1:B:88:GLU:HB2	2.01	0.59
1:C:129:GLU:O	1:C:132:LEU:HG	2.02	0.59
1:C:111:VAL:HG13	1:C:112:ARG:H	1.67	0.59
1:C:344:LEU:HA	1:C:351:ILE:HD11	1.82	0.59
1:D:285:VAL:C	1:D:287:GLY:H	2.05	0.59
1:B:43:GLU:O	1:B:47:GLU:HB2	2.03	0.59
1:B:83:ALA:O	1:B:86:PHE:HD2	1.84	0.59
1:C:340:PHE:O	1:C:344:LEU:HD13	2.01	0.59
1:D:23:ALA:O	1:D:27:VAL:HG13	2.02	0.59
1:B:240:LYS:HG2	1:B:294:HIS:HB3	1.85	0.59
1:C:173:ILE:O	1:C:212:LYS:HB3	2.03	0.59
1:D:4:MET:HB3	1:D:8:GLU:HB3	1.85	0.59
1:D:339:ASP:O	1:D:343:ILE:HG12	2.03	0.59
1:A:108:VAL:HG21	1:A:294:HIS:CE1	2.38	0.59
1:A:153:SER:HA	1:A:157:GLN:H	1.68	0.59
1:B:397:THR:CG2	1:B:443:LEU:HA	2.33	0.59
1:A:77:PRO:O	1:A:103:LEU:HD11	2.02	0.59
1:D:320:PRO:HA	1:D:323:GLN:HB3	1.84	0.59
1:A:212:LYS:HE2	1:A:225:LEU:HD13	1.85	0.58
1:A:47:GLU:O	1:A:47:GLU:HG3	2.03	0.58
1:A:64:THR:HG22	1:A:68:ARG:HD3	1.83	0.58
1:C:151:GLU:N	1:C:152:PRO:HD2	2.19	0.58
1:C:366:ILE:H	1:C:366:ILE:CD1	2.10	0.58
1:B:235:ASN:ND2	1:B:238:GLU:HG2	2.13	0.58
1:B:91:TYR:HB3	1:B:95:GLU:CB	2.33	0.58
1:D:384:ASN:HD21	1:D:391:GLY:H	1.51	0.58
1:D:5:THR:HG23	1:D:8:GLU:CD	2.22	0.58
1:D:244:ILE:O	1:D:248:GLU:HG2	2.03	0.58
1:D:252:ILE:N	1:D:252:ILE:HD12	2.18	0.58
1:A:5:THR:HA	1:A:32:ARG:NH1	2.18	0.58
1:B:293:LYS:HE2	1:B:294:HIS:NE2	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:116:ILE:O	1:D:120:ARG:HG3	2.03	0.58
1:A:109:LYS:HA	1:A:112:ARG:NH2	2.19	0.58
1:A:366:ILE:CD1	1:A:366:ILE:H	2.08	0.58
1:A:438:LEU:O	1:A:441:PHE:N	2.35	0.58
1:A:44:LEU:H	1:A:44:LEU:HD12	1.68	0.58
1:D:51:LYS:HB2	1:D:328:ILE:HD11	1.84	0.58
1:A:244:ILE:HA	1:A:247:VAL:HG23	1.86	0.58
1:B:128:GLU:O	1:B:132:LEU:HB2	2.03	0.58
1:A:62:GLY:C	1:A:66:ILE:HD13	2.24	0.58
1:B:110:MET:O	1:B:113:VAL:HG22	2.04	0.58
1:B:21:ASP:HA	1:B:24:LYS:HG3	1.86	0.58
1:C:234:VAL:HG23	1:C:235:ASN:H	1.69	0.58
1:C:248:GLU:HG2	1:C:298:LYS:H	1.69	0.58
1:C:383:VAL:HB	1:C:394:ARG:NH1	2.18	0.58
1:C:5:THR:HB	1:C:6:PRO:HD2	1.85	0.58
1:A:4:MET:H	1:A:4:MET:HE3	1.68	0.58
1:C:339:ASP:O	1:C:343:ILE:HG13	2.04	0.58
1:D:31:LEU:O	1:D:34:ARG:HB2	2.04	0.58
1:D:442:ILE:O	1:D:443:LEU:HG	2.04	0.58
1:C:319:ILE:HD13	1:C:322:LEU:H	1.69	0.57
1:D:127:ALA:HA	1:D:225:LEU:HB3	1.86	0.57
1:D:281:LEU:HD23	1:D:284:LEU:HD11	1.86	0.57
1:D:70:LEU:O	1:D:73:LEU:HG	2.04	0.57
1:A:315:PRO:O	1:A:318:LEU:HB3	2.03	0.57
1:B:339:ASP:O	1:B:343:ILE:HG12	2.05	0.57
1:C:279:ARG:O	1:C:283:PRO:HD2	2.04	0.57
1:C:394:ARG:O	1:C:398:VAL:HG23	2.04	0.57
1:C:422:ALA:O	1:C:425:VAL:HG23	2.05	0.57
1:C:435:ASP:OD2	1:C:438:LEU:HD23	2.04	0.57
1:C:64:THR:O	1:C:67:ALA:HB3	2.04	0.57
1:A:65:GLU:O	1:A:66:ILE:C	2.42	0.57
1:C:258:ILE:HG13	1:C:306:ALA:CB	2.30	0.57
1:A:356:LYS:CA	1:A:366:ILE:HD11	2.23	0.57
1:B:224:LEU:HA	1:B:227:GLU:OE2	2.04	0.57
1:D:442:ILE:C	1:D:443:LEU:HG	2.23	0.57
1:A:350:SER:OG	1:A:351:ILE:HD12	2.05	0.57
1:A:438:LEU:HB3	1:A:442:ILE:HD11	1.86	0.57
1:A:323:GLN:HG3	1:A:329:ARG:NH2	2.19	0.57
1:A:337:THR:O	1:A:340:PHE:HB2	2.04	0.57
1:C:432:LEU:HD23	1:C:443:LEU:HD11	1.86	0.57
1:A:439:SER:HA	1:A:443:LEU:CD1	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:ILE:HD12	1:A:66:ILE:N	2.18	0.57
1:B:252:ILE:N	1:B:252:ILE:HD12	2.20	0.57
1:C:418:ILE:N	1:C:418:ILE:HD13	2.19	0.57
1:C:402:LEU:CD1	1:C:425:VAL:HA	2.35	0.57
1:C:96:VAL:O	1:C:99:ILE:HD13	2.05	0.57
1:B:5:THR:HG23	1:B:8:GLU:CD	2.25	0.57
1:C:429:LEU:HD23	1:C:429:LEU:N	2.19	0.57
1:C:47:GLU:O	1:C:47:GLU:HG3	2.05	0.57
1:C:442:ILE:HD13	1:C:442:ILE:H	1.70	0.56
1:B:20:GLN:O	1:B:23:ALA:HB3	2.05	0.56
1:C:12:GLU:O	1:C:12:GLU:HG3	2.04	0.56
1:C:320:PRO:HA	1:C:323:GLN:HB3	1.87	0.56
1:A:212:LYS:O	1:A:213:ALA:HB3	2.04	0.56
1:D:60:GLY:HA2	1:D:63:LYS:CG	2.35	0.56
1:B:336:THR:HG22	1:B:339:ASP:CG	2.25	0.56
1:C:66:ILE:N	1:C:66:ILE:HD12	2.19	0.56
1:D:84:THR:O	1:D:86:PHE:N	2.39	0.56
1:C:53:ILE:HG22	1:C:54:LEU:N	2.20	0.56
1:C:23:ALA:CB	1:C:332:LEU:HD11	2.36	0.56
1:C:403:MET:O	1:C:407:SER:HB2	2.06	0.56
1:B:125:GLU:HG3	1:B:126:LEU:N	2.18	0.56
1:C:109:LYS:HA	1:C:112:ARG:NH2	2.21	0.56
1:C:351:ILE:HA	1:C:354:GLN:HE21	1.70	0.56
1:C:355:TYR:OH	1:C:403:MET:HB2	2.06	0.56
1:D:384:ASN:ND2	1:D:391:GLY:H	2.04	0.56
1:D:84:THR:C	1:D:86:PHE:H	2.09	0.56
1:A:12:GLU:HG3	1:A:12:GLU:O	2.06	0.56
1:A:69:ARG:HD2	1:A:69:ARG:N	2.20	0.56
1:B:442:ILE:C	1:B:443:LEU:HG	2.25	0.56
1:B:27:VAL:HB	1:B:70:LEU:HD13	1.87	0.56
1:C:122:ARG:HA	1:C:125:GLU:CG	2.36	0.56
1:C:282:LEU:O	1:C:285:VAL:HG23	2.05	0.56
1:C:101:ARG:HA	1:C:292:THR:HG22	1.88	0.56
1:A:173:ILE:HG22	1:A:174:GLU:H	1.71	0.56
1:A:356:LYS:HA	1:A:366:ILE:CD1	2.25	0.56
1:A:277:VAL:HG12	1:A:281:LEU:CD1	2.35	0.56
1:A:62:GLY:O	1:A:63:LYS:C	2.44	0.56
1:B:245:ASP:O	1:B:247:VAL:N	2.36	0.56
1:B:41:ASN:HD21	1:B:43:GLU:HB3	1.71	0.56
1:C:229:GLU:O	1:C:232:LYS:HE2	2.06	0.56
1:C:344:LEU:HA	1:C:351:ILE:CD1	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:371:SER:HB2	1:C:422:ALA:HB2	1.87	0.56
1:D:41:ASN:O	1:D:45:ARG:HB2	2.05	0.56
1:A:21:ASP:O	1:A:24:LYS:N	2.39	0.56
1:A:367:GLU:HB3	1:A:419:THR:HG22	1.88	0.56
1:B:70:LEU:O	1:B:73:LEU:HG	2.06	0.56
1:C:262:CYS:O	1:C:263:LYS:HG3	2.06	0.56
1:D:389:ASN:C	1:D:390:ILE:HG13	2.25	0.56
1:D:53:ILE:HG12	1:D:328:ILE:HB	1.88	0.56
1:A:151:GLU:N	1:A:152:PRO:HD2	2.21	0.55
1:B:271:ASP:HA	1:B:274:ARG:CB	2.36	0.55
1:C:174:GLU:HA	1:C:212:LYS:HB3	1.88	0.55
1:C:278:GLN:OE1	1:C:319:ILE:HG22	2.05	0.55
1:B:395:LEU:O	1:B:398:VAL:HG22	2.06	0.55
1:B:432:LEU:CD1	1:B:432:LEU:H	2.17	0.55
1:B:41:ASN:O	1:B:45:ARG:HB2	2.06	0.55
1:B:70:LEU:HD23	1:B:71:ALA:N	2.21	0.55
1:C:109:LYS:HG3	1:C:112:ARG:NH2	2.19	0.55
1:C:319:ILE:HD11	1:C:321:GLU:OE2	2.07	0.55
1:A:394:ARG:O	1:A:398:VAL:HG23	2.06	0.55
1:D:59:THR:O	1:D:61:VAL:N	2.40	0.55
1:A:6:PRO:HD3	1:A:32:ARG:HD3	1.87	0.55
1:C:323:GLN:HG3	1:C:329:ARG:NH2	2.22	0.55
1:D:52:ASN:C	1:D:328:ILE:HD12	2.27	0.55
1:A:432:LEU:HD23	1:A:443:LEU:HD11	1.88	0.55
1:A:86:PHE:HA	1:A:93:GLY:HA2	1.89	0.55
1:C:275:GLU:O	1:C:278:GLN:HB2	2.06	0.55
1:C:438:LEU:HD22	1:C:438:LEU:H	1.70	0.55
1:A:356:LYS:HZ2	1:A:367:GLU:HA	1.70	0.55
1:B:10:VAL:HG12	1:B:14:ASP:OD1	2.07	0.55
1:B:98:SER:O	1:B:99:ILE:C	2.44	0.55
1:C:163:LEU:C	1:C:165:GLU:H	2.09	0.55
1:C:399:LEU:O	1:C:403:MET:HG2	2.07	0.55
1:C:319:ILE:HG23	1:C:322:LEU:CB	2.37	0.55
1:D:402:LEU:HB2	1:D:429:LEU:HD21	1.89	0.55
1:A:351:ILE:HA	1:A:354:GLN:HE21	1.72	0.54
1:C:136:ILE:HD12	1:C:156:ARG:HA	1.88	0.54
1:C:315:PRO:O	1:C:318:LEU:HB3	2.07	0.54
1:A:254:PHE:CD2	1:A:305:ILE:HB	2.42	0.54
1:C:99:ILE:HG22	1:C:100:ILE:N	2.21	0.54
1:C:18:ILE:HD13	1:C:343:ILE:HG12	1.88	0.54
1:A:145:GLN:OE1	1:A:145:GLN:HA	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:318:LEU:HD21	1:B:322:LEU:CD2	2.37	0.54
1:B:375:ARG:HA	1:B:378:GLU:HB2	1.89	0.54
1:B:57:GLY:C	1:B:309:ALA:HB2	2.27	0.54
1:A:132:LEU:HA	1:A:135:LEU:HB2	1.89	0.54
1:C:261:ILE:HG22	1:C:274:ARG:HB3	1.89	0.54
1:D:229:GLU:HA	1:D:232:LYS:HD2	1.89	0.54
1:D:57:GLY:C	1:D:309:ALA:HB2	2.28	0.54
1:A:55:MET:HE3	1:A:254:PHE:HE2	1.72	0.54
1:C:60:GLY:H	2:C:905:ANP:PG	2.31	0.54
1:A:127:ALA:HB2	1:A:226:ILE:HA	1.90	0.54
1:B:31:LEU:O	1:B:34:ARG:HB2	2.07	0.54
1:C:114:GLN:O	1:C:118:LYS:HB2	2.07	0.54
1:C:402:LEU:HD13	1:C:425:VAL:HA	1.88	0.54
1:A:100:ILE:HD11	1:A:284:LEU:HD22	1.90	0.54
1:B:59:THR:O	1:B:61:VAL:N	2.41	0.54
1:C:229:GLU:HB3	1:C:232:LYS:NZ	2.23	0.54
1:C:322:LEU:O	1:C:325:ARG:N	2.41	0.54
1:C:45:ARG:C	1:C:47:GLU:H	2.11	0.54
1:D:224:LEU:HA	1:D:227:GLU:OE2	2.08	0.54
1:C:397:THR:O	1:C:398:VAL:C	2.45	0.54
1:A:358:LEU:HD11	1:B:33:ASN:ND2	2.22	0.54
1:B:104:THR:O	1:B:107:ALA:HB3	2.07	0.54
1:C:26:SER:CA	1:C:29:ILE:HD12	2.38	0.54
1:C:69:ARG:N	1:C:69:ARG:HD2	2.22	0.54
1:A:278:GLN:OE1	1:A:319:ILE:HG22	2.08	0.54
1:A:84:THR:C	1:A:86:PHE:H	2.11	0.54
1:C:288:CYS:O	1:C:298:LYS:HD3	2.07	0.54
1:C:64:THR:C	1:C:68:ARG:HD3	2.28	0.54
1:A:109:LYS:O	1:A:112:ARG:HB3	2.07	0.53
1:B:127:ALA:O	1:B:131:ILE:HG12	2.08	0.53
1:D:236:PRO:O	1:D:240:LYS:HB2	2.08	0.53
1:A:399:LEU:O	1:A:402:LEU:HB3	2.09	0.53
1:C:291:SER:HA	1:C:296:MET:SD	2.49	0.53
1:C:358:LEU:HD11	1:D:33:ASN:HD22	1.73	0.53
1:A:230:ALA:C	1:A:232:LYS:H	2.12	0.53
1:A:367:GLU:O	1:A:420:ILE:N	2.41	0.53
1:B:275:GLU:O	1:B:278:GLN:HB2	2.08	0.53
1:C:310:PHE:N	1:C:310:PHE:HD2	2.06	0.53
1:D:289:THR:HA	1:D:297:VAL:O	2.07	0.53
1:D:340:PHE:HA	1:D:343:ILE:HD11	1.90	0.53
1:A:155:ALA:O	1:A:158:ALA:HB3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:ILE:HG22	1:A:54:LEU:N	2.23	0.53
1:A:20:GLN:HB3	1:A:332:LEU:HD12	1.91	0.53
1:A:397:THR:O	1:A:398:VAL:C	2.46	0.53
1:B:17:ILE:C	1:B:18:ILE:HD13	2.29	0.53
1:C:254:PHE:CD2	1:C:305:ILE:HB	2.44	0.53
1:A:100:ILE:HG12	1:A:299:THR:CG2	2.38	0.53
1:A:55:MET:O	1:A:307:SER:HA	2.09	0.53
1:B:109:LYS:O	1:B:113:VAL:HG13	2.08	0.53
1:B:51:LYS:HB2	1:B:328:ILE:HD11	1.91	0.53
1:C:112:ARG:HG2	1:C:112:ARG:HH11	1.74	0.53
1:D:104:THR:O	1:D:107:ALA:HB3	2.09	0.53
1:A:322:LEU:O	1:A:325:ARG:N	2.41	0.53
1:B:100:ILE:CG2	1:B:297:VAL:HG21	2.39	0.53
1:B:84:THR:C	1:B:86:PHE:H	2.12	0.53
1:D:235:ASN:H	1:D:235:ASN:HD22	1.57	0.53
1:D:52:ASN:O	1:D:327:PRO:HD2	2.08	0.53
1:A:234:VAL:HG23	1:A:235:ASN:H	1.73	0.53
1:A:383:VAL:HB	1:A:394:ARG:NH1	2.23	0.53
1:A:432:LEU:O	1:A:434:ALA:N	2.42	0.53
1:A:5:THR:HG23	1:A:8:GLU:CD	2.30	0.53
1:B:375:ARG:HA	1:B:375:ARG:HE	1.74	0.53
1:C:140:LYS:H	1:C:140:LYS:HD3	1.72	0.53
1:C:65:GLU:O	1:C:66:ILE:C	2.47	0.53
1:A:163:LEU:C	1:A:165:GLU:H	2.11	0.53
1:A:325:ARG:O	1:A:327:PRO:HD3	2.08	0.53
1:A:109:LYS:HE2	1:B:289:THR:HB	1.91	0.53
1:D:243:ALA:O	1:D:247:VAL:HG23	2.09	0.53
1:D:355:TYR:CZ	1:D:403:MET:HB3	2.43	0.53
1:D:397:THR:CG2	1:D:443:LEU:HA	2.38	0.53
1:B:299:THR:HA	1:B:302:ILE:CG1	2.35	0.52
1:C:234:VAL:HG23	1:C:235:ASN:N	2.24	0.52
1:C:310:PHE:CD2	1:C:310:PHE:N	2.76	0.52
1:C:44:LEU:HD12	1:C:44:LEU:H	1.73	0.52
1:D:356:LYS:CA	1:D:366:ILE:HD11	2.36	0.52
1:D:83:ALA:O	1:D:86:PHE:HD2	1.91	0.52
1:A:279:ARG:O	1:A:283:PRO:HD2	2.10	0.52
1:A:18:ILE:N	2:A:900:ANP:HN61	2.01	0.52
1:A:248:GLU:HG3	1:A:297:VAL:HG12	1.90	0.52
1:B:100:ILE:HD11	1:B:284:LEU:HB3	1.91	0.52
1:B:84:THR:O	1:B:86:PHE:N	2.43	0.52
1:C:9:ILE:HG23	1:C:73:LEU:HD11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:248:GLU:HA	1:D:302:ILE:HD11	1.91	0.52
1:A:23:ALA:HB2	1:A:332:LEU:HD11	1.90	0.52
1:C:319:ILE:HG12	1:C:320:PRO:CD	2.37	0.52
1:C:65:GLU:HA	1:C:68:ARG:CG	2.40	0.52
1:D:240:LYS:CG	1:D:294:HIS:HB3	2.40	0.52
1:D:78:PHE:CE1	1:D:254:PHE:HB2	2.45	0.52
1:A:112:ARG:HG3	1:A:112:ARG:HH11	1.75	0.52
1:A:371:SER:HB2	1:A:422:ALA:HB2	1.91	0.52
1:B:340:PHE:HA	1:B:343:ILE:HG13	1.92	0.52
1:D:44:LEU:HA	1:D:47:GLU:HB2	1.90	0.52
1:A:320:PRO:HA	1:A:323:GLN:HB3	1.92	0.52
1:D:123:ALA:O	1:D:127:ALA:HB2	2.10	0.52
1:D:17:ILE:C	1:D:18:ILE:HD13	2.29	0.52
1:A:216:LEU:HD11	1:A:221:ALA:HB2	1.91	0.52
1:B:367:GLU:HG2	1:B:417:ASN:HD21	1.75	0.52
1:C:432:LEU:O	1:C:434:ALA:N	2.43	0.52
1:C:84:THR:C	1:C:86:PHE:H	2.13	0.52
1:D:22:ASN:H	1:D:22:ASN:ND2	2.06	0.52
1:D:235:ASN:N	1:D:235:ASN:ND2	2.57	0.52
1:D:271:ASP:CA	1:D:274:ARG:HB2	2.37	0.52
1:D:375:ARG:HA	1:D:375:ARG:HE	1.75	0.52
1:B:340:PHE:HA	1:B:343:ILE:HD11	1.91	0.52
1:C:6:PRO:HD3	1:C:32:ARG:HD3	1.90	0.52
1:A:9:ILE:HG23	1:A:73:LEU:HD11	1.92	0.52
1:B:402:LEU:HB2	1:B:429:LEU:HD21	1.92	0.52
1:C:231:ALA:O	1:C:234:VAL:HG22	2.10	0.52
1:C:107:ALA:HB1	1:C:247:VAL:HG22	1.91	0.52
1:D:319:ILE:HD12	1:D:320:PRO:HD2	1.91	0.52
1:A:128:GLU:O	1:A:131:ILE:HB	2.10	0.52
1:C:239:LEU:HD23	1:C:240:LYS:N	2.25	0.52
1:C:327:PRO:HG2	1:C:328:ILE:HD12	1.92	0.52
1:C:418:ILE:H	1:C:418:ILE:HD13	1.75	0.52
1:A:68:ARG:NH1	1:A:68:ARG:HB3	2.19	0.51
1:C:135:LEU:O	1:C:137:PRO:HD3	2.09	0.51
1:C:127:ALA:HB2	1:C:226:ILE:HA	1.92	0.51
1:D:59:THR:CG2	1:D:390:ILE:HA	2.37	0.51
1:A:12:GLU:HG2	1:A:73:LEU:HD12	1.92	0.51
1:B:344:LEU:HD21	1:B:376:ILE:CG2	2.40	0.51
1:C:442:ILE:HG12	1:C:443:LEU:CD1	2.38	0.51
1:A:45:ARG:C	1:A:47:GLU:H	2.13	0.51
1:A:80:LYS:HA	1:A:254:PHE:HB3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:5:THR:HA	1:C:32:ARG:NH1	2.24	0.51
1:C:5:THR:N	1:C:8:GLU:HB2	2.24	0.51
1:D:35:TRP:CE3	1:D:36:ARG:HG2	2.45	0.51
1:D:432:LEU:H	1:D:432:LEU:CD1	2.20	0.51
1:A:104:THR:O	1:A:107:ALA:HB3	2.09	0.51
1:B:5:THR:O	1:B:9:ILE:HG13	2.10	0.51
1:C:55:MET:O	1:C:307:SER:HA	2.10	0.51
1:D:87:THR:O	1:D:88:GLU:HB2	2.10	0.51
1:B:281:LEU:O	1:B:282:LEU:C	2.49	0.51
1:B:389:ASN:C	1:B:390:ILE:HG13	2.29	0.51
1:C:107:ALA:HB2	1:C:247:VAL:HG13	1.93	0.51
1:C:21:ASP:O	1:C:24:LYS:N	2.44	0.51
1:D:25:ARG:O	1:D:28:ALA:HB3	2.10	0.51
1:A:127:ALA:O	1:A:225:LEU:HD23	2.11	0.51
1:A:103:LEU:HD23	1:A:247:VAL:HG12	1.92	0.51
1:A:395:LEU:O	1:A:396:HIS:C	2.48	0.51
1:C:130:ARG:HB2	1:C:225:LEU:HD21	1.92	0.51
1:C:258:ILE:HA	1:C:261:ILE:HD11	1.92	0.51
1:C:282:LEU:O	1:C:286:GLU:HB2	2.11	0.51
1:C:100:ILE:HG12	1:C:299:THR:HG22	1.92	0.51
1:C:319:ILE:HG23	1:C:322:LEU:HB2	1.93	0.51
1:D:351:ILE:CD1	1:D:399:LEU:HD13	2.40	0.51
1:D:44:LEU:HA	1:D:47:GLU:HB3	1.92	0.51
1:A:340:PHE:O	1:A:343:ILE:HB	2.11	0.51
1:D:281:LEU:O	1:D:282:LEU:C	2.49	0.51
1:D:86:PHE:CE1	1:D:96:VAL:HA	2.46	0.51
1:A:128:GLU:HA	1:A:131:ILE:CD1	2.40	0.51
1:A:64:THR:C	1:A:68:ARG:HD3	2.30	0.51
1:B:100:ILE:O	1:B:101:ARG:C	2.49	0.51
1:A:252:ILE:HG23	1:A:303:LEU:HB3	1.92	0.51
1:A:442:ILE:HD13	1:A:442:ILE:H	1.76	0.51
1:A:140:LYS:HD3	1:A:140:LYS:H	1.76	0.51
1:A:248:GLU:HG2	1:A:298:LYS:H	1.76	0.51
1:B:126:LEU:HB2	1:B:229:GLU:HG3	1.93	0.51
1:B:55:MET:O	1:B:307:SER:HA	2.11	0.51
1:C:135:LEU:HB3	1:C:159:PHE:CD1	2.46	0.51
1:C:244:ILE:HA	1:C:247:VAL:HG23	1.92	0.51
1:C:421:ASP:OD1	1:C:423:ASP:HB2	2.11	0.51
1:C:438:LEU:O	1:C:441:PHE:N	2.39	0.51
1:D:371:SER:O	1:D:422:ALA:HB2	2.11	0.51
1:B:61:VAL:O	1:B:61:VAL:CG1	2.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:420:ILE:HD12	1:B:420:ILE:N	2.26	0.50
1:C:53:ILE:HG12	1:C:328:ILE:HB	1.93	0.50
1:D:285:VAL:O	1:D:287:GLY:N	2.44	0.50
1:D:354:GLN:O	1:D:357:ALA:HB3	2.11	0.50
1:A:86:PHE:CD1	1:A:93:GLY:HA2	2.43	0.50
1:C:104:THR:HA	1:C:247:VAL:HG11	1.93	0.50
1:C:310:PHE:HB3	1:C:313:ALA:O	2.11	0.50
1:C:18:ILE:N	2:C:905:ANP:N6	2.48	0.50
1:D:105:ASP:O	1:D:108:VAL:HG12	2.11	0.50
1:A:131:ILE:HD11	1:A:222:MET:HA	1.92	0.50
1:B:429:LEU:O	1:B:431:ALA:N	2.45	0.50
1:C:31:LEU:O	1:C:34:ARG:HB2	2.11	0.50
1:C:344:LEU:HD11	1:C:395:LEU:HD13	1.94	0.50
1:C:64:THR:HG22	1:C:68:ARG:CD	2.41	0.50
1:A:13:LEU:C	1:A:15:LYS:N	2.65	0.50
1:B:105:ASP:O	1:B:108:VAL:HG12	2.12	0.50
1:B:374:LYS:O	1:B:378:GLU:HB2	2.11	0.50
1:B:383:VAL:HB	1:B:394:ARG:NH1	2.24	0.50
1:C:127:ALA:O	1:C:131:ILE:HG13	2.11	0.50
1:C:254:PHE:HD2	1:C:305:ILE:HB	1.77	0.50
1:D:235:ASN:ND2	1:D:235:ASN:H	2.08	0.50
1:B:98:SER:O	1:B:101:ARG:N	2.45	0.50
1:C:299:THR:HA	1:C:302:ILE:CD1	2.31	0.50
1:D:125:GLU:O	1:D:128:GLU:HG2	2.11	0.50
1:D:356:LYS:HA	1:D:366:ILE:CD1	2.37	0.50
1:D:395:LEU:HA	1:D:398:VAL:HG22	1.92	0.50
1:A:429:LEU:O	1:A:430:ASP:C	2.50	0.50
1:A:64:THR:HG22	1:A:68:ARG:CD	2.42	0.50
1:A:96:VAL:O	1:A:99:ILE:HD13	2.12	0.50
1:B:285:VAL:O	1:B:287:GLY:N	2.45	0.50
1:C:24:LYS:O	1:C:28:ALA:N	2.41	0.50
1:C:346:GLU:N	1:C:347:PRO:HD2	2.26	0.50
1:D:27:VAL:HB	1:D:70:LEU:CD1	2.42	0.50
1:A:24:LYS:HA	1:A:27:VAL:HG12	1.93	0.50
1:A:5:THR:CB	1:A:6:PRO:HD2	2.41	0.50
1:B:240:LYS:HE2	1:B:294:HIS:HD2	1.77	0.50
1:B:35:TRP:CE3	1:B:36:ARG:HG2	2.47	0.50
1:C:174:GLU:HA	1:C:212:LYS:CB	2.41	0.50
1:C:25:ARG:O	1:C:28:ALA:HB3	2.12	0.50
1:C:372:GLY:O	1:C:376:ILE:HD12	2.12	0.50
1:D:237:GLU:C	1:D:239:LEU:H	2.13	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:255:ILE:HG21	1:D:258:ILE:HD11	1.94	0.50
1:B:340:PHE:HA	1:B:343:ILE:CG1	2.42	0.50
1:B:405:GLU:O	1:B:408:TYR:N	2.45	0.50
1:C:396:HIS:H	1:C:396:HIS:CD2	2.28	0.50
1:C:155:ALA:O	1:C:158:ALA:HB3	2.12	0.49
1:C:320:PRO:O	1:C:321:GLU:C	2.49	0.49
1:D:245:ASP:O	1:D:247:VAL:N	2.44	0.49
1:B:23:ALA:HA	1:B:330:VAL:HG21	1.94	0.49
1:B:439:SER:HA	1:B:443:LEU:HD12	1.94	0.49
1:C:31:LEU:HD23	1:C:70:LEU:CD1	2.42	0.49
1:D:350:SER:CB	1:D:353:VAL:HG23	2.42	0.49
1:A:21:ASP:HA	1:A:24:LYS:HD2	1.93	0.49
1:C:420:ILE:HG23	1:C:424:TYR:CD1	2.47	0.49
1:C:62:GLY:O	1:C:63:LYS:C	2.51	0.49
1:C:79:ILE:HG22	1:C:103:LEU:CD1	2.38	0.49
1:B:53:ILE:O	1:B:305:ILE:HA	2.12	0.49
1:C:298:LYS:C	1:C:300:ASP:H	2.14	0.49
1:C:86:PHE:CD1	1:C:93:GLY:HA2	2.42	0.49
1:D:111:VAL:HG21	1:D:243:ALA:HA	1.93	0.49
1:D:275:GLU:O	1:D:278:GLN:HB2	2.11	0.49
1:A:271:ASP:C	1:A:273:SER:H	2.16	0.49
1:A:346:GLU:N	1:A:347:PRO:HD2	2.25	0.49
1:B:113:VAL:HG23	1:B:114:GLN:HG3	1.93	0.49
1:B:243:ALA:O	1:B:247:VAL:HG23	2.11	0.49
1:C:225:LEU:HG	1:C:229:GLU:HG3	1.95	0.49
1:C:244:ILE:O	1:C:248:GLU:HB2	2.12	0.49
1:C:347:PRO:HG2	1:C:350:SER:HB2	1.95	0.49
1:D:366:ILE:HB	1:D:420:ILE:HD11	1.95	0.49
1:B:245:ASP:C	1:B:247:VAL:N	2.65	0.49
1:B:421:ASP:OD2	1:B:423:ASP:HB2	2.13	0.49
1:C:102:ASP:O	1:C:105:ASP:HB2	2.11	0.49
1:C:420:ILE:HG23	1:C:424:TYR:HD1	1.77	0.49
1:D:344:LEU:HD21	1:D:376:ILE:CG2	2.41	0.49
1:A:25:ARG:O	1:A:28:ALA:HB3	2.13	0.49
1:A:438:LEU:H	1:A:438:LEU:HD22	1.77	0.49
1:B:238:GLU:O	1:B:242:ASP:HB2	2.13	0.49
1:B:285:VAL:C	1:B:287:GLY:H	2.16	0.49
1:B:28:ALA:O	1:B:29:ILE:C	2.51	0.49
1:D:340:PHE:HA	1:D:343:ILE:CG1	2.43	0.49
1:D:428:HIS:HB2	1:D:429:LEU:HD22	1.95	0.49
1:D:98:SER:O	1:D:99:ILE:C	2.50	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:310:PHE:HB3	1:A:313:ALA:O	2.13	0.49
1:B:54:LEU:HB2	1:B:326:LEU:HG	1.95	0.49
1:C:27:VAL:HG13	1:C:70:LEU:HD13	1.94	0.49
1:D:318:LEU:HD22	1:D:323:GLN:CA	2.42	0.49
1:D:421:ASP:OD2	1:D:423:ASP:HB2	2.12	0.49
1:A:124:GLU:O	1:A:127:ALA:HB3	2.13	0.49
1:A:26:SER:HA	1:A:29:ILE:HD12	1.94	0.49
1:B:438:LEU:HD22	1:B:442:ILE:HD11	1.94	0.49
1:B:86:PHE:HB2	1:B:277:VAL:HG13	1.93	0.49
1:C:413:LEU:O	1:C:414:SER:C	2.51	0.49
1:C:62:GLY:O	1:C:64:THR:N	2.46	0.49
1:C:74:ALA:O	1:C:75:ASN:HB3	2.13	0.49
1:C:96:VAL:HG11	1:C:281:LEU:HG	1.94	0.49
1:A:153:SER:HA	1:A:156:ARG:CB	2.38	0.49
1:A:413:LEU:O	1:A:414:SER:C	2.51	0.49
1:B:111:VAL:HG11	1:B:243:ALA:HB2	1.95	0.49
1:C:107:ALA:CB	1:C:247:VAL:HG22	2.43	0.49
1:C:108:VAL:O	1:C:111:VAL:HG12	2.13	0.49
1:C:252:ILE:HG23	1:C:303:LEU:HB3	1.94	0.49
1:D:20:GLN:O	1:D:23:ALA:HB3	2.12	0.49
1:A:235:ASN:OD1	1:A:238:GLU:HB3	2.13	0.48
1:A:83:ALA:O	1:A:85:LYS:N	2.46	0.48
1:D:405:GLU:O	1:D:408:TYR:N	2.46	0.48
1:D:438:LEU:CD2	1:D:442:ILE:HD11	2.43	0.48
1:A:75:ASN:HD21	1:A:114:GLN:HE22	1.59	0.48
1:A:21:ASP:O	1:A:22:ASN:C	2.52	0.48
1:A:355:TYR:OH	1:A:403:MET:HB2	2.13	0.48
1:B:438:LEU:HD21	1:B:442:ILE:HD11	1.95	0.48
1:C:103:LEU:CD2	1:C:247:VAL:HG12	2.43	0.48
1:C:65:GLU:HA	1:C:68:ARG:HG2	1.96	0.48
1:A:18:ILE:HD13	1:A:343:ILE:HG12	1.94	0.48
1:B:17:ILE:CG2	1:B:18:ILE:N	2.70	0.48
1:C:271:ASP:C	1:C:273:SER:H	2.16	0.48
1:A:319:ILE:HG12	1:A:320:PRO:CD	2.40	0.48
1:B:25:ARG:O	1:B:28:ALA:HB3	2.13	0.48
1:C:5:THR:CB	1:C:6:PRO:HD2	2.42	0.48
1:A:316:SER:HA	1:A:323:GLN:HE22	1.79	0.48
1:A:52:ASN:O	1:A:327:PRO:HD2	2.13	0.48
1:B:319:ILE:HD12	1:B:320:PRO:CD	2.43	0.48
1:C:240:LYS:C	1:C:242:ASP:H	2.16	0.48
1:D:240:LYS:HE2	1:D:294:HIS:HD2	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:288:CYS:O	1:D:299:THR:N	2.41	0.48
1:D:432:LEU:N	1:D:432:LEU:HD12	2.25	0.48
1:A:21:ASP:HA	1:A:24:LYS:HG3	1.96	0.48
1:B:44:LEU:HA	1:B:47:GLU:CB	2.43	0.48
1:C:259:ASP:HB3	1:C:310:PHE:CE2	2.49	0.48
1:C:80:LYS:HG3	1:C:81:VAL:N	2.27	0.48
1:D:54:LEU:HD23	1:D:329:ARG:HD3	1.95	0.48
1:A:327:PRO:HG2	1:A:328:ILE:CD1	2.43	0.48
1:A:367:GLU:CB	1:A:419:THR:HG22	2.44	0.48
1:A:384:ASN:HD22	1:A:394:ARG:NH1	2.11	0.48
1:A:92:VAL:O	1:A:95:GLU:HB2	2.13	0.48
1:C:64:THR:O	1:C:68:ARG:HD3	2.14	0.48
1:D:285:VAL:C	1:D:287:GLY:N	2.65	0.48
1:A:437:ASP:O	1:A:440:ARG:N	2.47	0.48
1:A:69:ARG:O	1:A:73:LEU:HB3	2.14	0.48
1:A:6:PRO:HA	1:A:9:ILE:HD12	1.95	0.48
1:B:44:LEU:O	1:B:45:ARG:C	2.52	0.48
1:D:23:ALA:HB2	1:D:332:LEU:HD11	1.96	0.48
1:C:239:LEU:O	1:C:242:ASP:HB2	2.12	0.48
1:C:278:GLN:HG2	1:C:322:LEU:CD2	2.43	0.48
1:C:320:PRO:O	1:C:323:GLN:N	2.47	0.48
1:C:361:THR:C	1:C:363:GLY:H	2.17	0.48
1:C:32:ARG:HG2	1:C:36:ARG:NE	2.29	0.48
1:C:69:ARG:O	1:C:73:LEU:HB3	2.14	0.48
1:D:229:GLU:OE1	1:D:232:LYS:HD2	2.14	0.48
1:A:10:VAL:O	1:A:13:LEU:N	2.42	0.48
1:A:282:LEU:HA	1:A:285:VAL:HG23	1.96	0.48
1:B:429:LEU:O	1:B:430:ASP:C	2.52	0.48
1:C:13:LEU:C	1:C:15:LYS:N	2.67	0.48
1:C:325:ARG:HD3	1:C:325:ARG:HA	1.55	0.48
1:D:398:VAL:HG23	1:D:399:LEU:N	2.29	0.48
1:C:384:ASN:ND2	1:C:394:ARG:HG2	2.29	0.47
1:D:383:VAL:HB	1:D:394:ARG:NH1	2.29	0.47
1:D:62:GLY:O	1:D:65:GLU:N	2.47	0.47
1:A:244:ILE:O	1:A:248:GLU:HB2	2.14	0.47
1:A:363:GLY:O	1:A:414:SER:HA	2.15	0.47
1:A:27:VAL:CG2	1:A:70:LEU:HD13	2.34	0.47
1:A:98:SER:O	1:A:101:ARG:HB3	2.14	0.47
1:B:379:ALA:O	1:B:380:ALA:C	2.52	0.47
1:C:131:ILE:HD11	1:C:222:MET:HA	1.96	0.47
1:C:13:LEU:HD23	1:C:24:LYS:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:372:GLY:O	1:B:375:ARG:N	2.47	0.47
1:C:169:ASP:H	1:C:218:ILE:HG22	1.79	0.47
1:C:241:GLN:HA	1:C:244:ILE:HD11	1.97	0.47
1:D:100:ILE:HG21	1:D:297:VAL:HG21	1.97	0.47
1:C:390:ILE:HG22	1:D:320:PRO:HB3	1.97	0.47
1:D:374:LYS:O	1:D:378:GLU:HB2	2.15	0.47
1:A:254:PHE:HD2	1:A:305:ILE:HB	1.78	0.47
1:B:54:LEU:HG	1:B:54:LEU:O	2.14	0.47
1:A:111:VAL:HG13	1:A:112:ARG:N	2.28	0.47
1:A:396:HIS:H	1:A:396:HIS:CD2	2.31	0.47
1:C:289:THR:HA	1:C:297:VAL:O	2.15	0.47
1:D:288:CYS:O	1:D:298:LYS:HA	2.14	0.47
1:A:7:ARG:HA	1:A:10:VAL:HB	1.97	0.47
1:C:127:ALA:O	1:C:225:LEU:HD23	2.15	0.47
1:C:151:GLU:H	1:C:152:PRO:HD2	1.78	0.47
1:C:77:PRO:HD2	1:C:250:HIS:O	2.14	0.47
1:C:18:ILE:N	2:C:905:ANP:HN61	2.02	0.47
1:A:214:ARG:CZ	1:B:233:LEU:HG	2.45	0.47
1:A:168:LEU:N	1:A:218:ILE:CG2	2.78	0.47
1:A:402:LEU:CD1	1:A:425:VAL:HA	2.45	0.47
1:B:27:VAL:HG23	1:B:28:ALA:N	2.29	0.47
1:D:107:ALA:O	1:D:110:MET:N	2.47	0.47
1:D:356:LYS:HD3	1:D:366:ILE:O	2.15	0.47
1:C:10:VAL:O	1:C:13:LEU:N	2.47	0.47
1:C:124:GLU:O	1:C:127:ALA:HB3	2.14	0.47
1:D:113:VAL:HG23	1:D:114:GLN:HG3	1.97	0.47
1:D:131:ILE:HD11	1:D:222:MET:SD	2.55	0.47
1:A:320:PRO:O	1:A:321:GLU:C	2.52	0.47
1:A:319:ILE:HD13	1:A:322:LEU:H	1.80	0.47
1:B:105:ASP:C	1:B:107:ALA:N	2.68	0.47
1:B:17:ILE:HG23	1:B:18:ILE:H	1.77	0.47
1:C:173:ILE:HG22	1:C:174:GLU:H	1.79	0.47
1:C:20:GLN:HB3	1:C:332:LEU:CD1	2.45	0.47
1:D:244:ILE:HD11	1:D:296:MET:O	2.15	0.47
1:D:21:ASP:CA	1:D:24:LYS:HG3	2.45	0.47
1:A:316:SER:HA	1:A:323:GLN:OE1	2.14	0.47
1:A:35:TRP:CZ3	1:A:36:ARG:HG3	2.50	0.47
1:B:307:SER:OG	1:B:308:GLY:N	2.47	0.47
1:B:438:LEU:C	1:B:438:LEU:HD13	2.35	0.47
1:B:52:ASN:C	1:B:328:ILE:HD12	2.35	0.47
1:C:52:ASN:O	1:C:328:ILE:HD12	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:429:LEU:O	1:D:430:ASP:C	2.52	0.47
1:B:23:ALA:HB2	1:B:332:LEU:CD1	2.42	0.46
1:C:21:ASP:O	1:C:22:ASN:C	2.53	0.46
1:C:316:SER:HA	1:C:323:GLN:OE1	2.15	0.46
1:D:237:GLU:C	1:D:239:LEU:N	2.69	0.46
1:D:298:LYS:HB3	1:D:300:ASP:OD2	2.15	0.46
1:D:365:ASN:O	1:D:418:ILE:HG12	2.15	0.46
1:A:18:ILE:HD12	1:A:18:ILE:N	2.29	0.46
1:A:277:VAL:O	1:A:278:GLN:C	2.53	0.46
1:A:436:GLU:O	1:A:437:ASP:C	2.53	0.46
1:C:399:LEU:HD23	1:C:400:GLU:N	2.30	0.46
1:C:64:THR:HG22	1:C:68:ARG:NE	2.30	0.46
1:A:132:LEU:O	1:A:135:LEU:HB2	2.15	0.46
1:A:275:GLU:O	1:A:276:GLY:C	2.54	0.46
1:B:237:GLU:N	1:B:237:GLU:CD	2.68	0.46
1:B:27:VAL:HG23	1:B:70:LEU:HD12	1.97	0.46
1:C:436:GLU:O	1:C:437:ASP:C	2.52	0.46
1:C:65:GLU:C	1:C:69:ARG:HG2	2.35	0.46
1:D:224:LEU:C	1:D:226:ILE:H	2.18	0.46
1:B:244:ILE:CG2	1:B:245:ASP:N	2.78	0.46
1:B:387:THR:C	1:B:388:GLU:HG2	2.35	0.46
1:B:406:ILE:HD11	1:B:424:TYR:OH	2.15	0.46
1:C:111:VAL:HG13	1:C:112:ARG:N	2.29	0.46
1:C:112:ARG:HD2	1:C:113:VAL:N	2.31	0.46
1:D:254:PHE:CZ	1:D:307:SER:HB2	2.51	0.46
1:B:86:PHE:HE1	1:B:95:GLU:O	1.98	0.46
1:C:344:LEU:CD1	1:C:395:LEU:HD13	2.46	0.46
1:D:360:ALA:HA	1:D:364:VAL:O	2.15	0.46
1:D:391:GLY:O	1:D:392:ALA:C	2.53	0.46
1:A:376:ILE:HG13	1:A:425:VAL:HG11	1.97	0.46
1:B:371:SER:O	1:B:422:ALA:HB2	2.16	0.46
1:B:432:LEU:N	1:B:432:LEU:HD12	2.23	0.46
1:C:261:ILE:H	1:C:261:ILE:HG13	1.29	0.46
1:C:442:ILE:O	1:C:443:LEU:HG	2.15	0.46
1:C:82:GLU:O	1:C:85:LYS:HG2	2.15	0.46
1:A:140:LYS:HE3	1:A:140:LYS:HB2	1.69	0.46
1:A:23:ALA:CB	1:A:332:LEU:HD11	2.45	0.46
1:A:285:VAL:HB	1:A:325:ARG:HG3	1.97	0.46
1:D:100:ILE:O	1:D:101:ARG:C	2.54	0.46
1:D:236:PRO:HA	1:D:239:LEU:HD12	1.98	0.46
1:A:130:ARG:O	1:A:133:ASP:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:270:PRO:O	1:A:274:ARG:HG3	2.15	0.46
1:A:65:GLU:HA	1:A:68:ARG:CG	2.46	0.46
1:B:285:VAL:C	1:B:287:GLY:N	2.68	0.46
1:C:240:LYS:C	1:C:242:ASP:N	2.69	0.46
1:C:285:VAL:HB	1:C:325:ARG:HG3	1.96	0.46
1:C:319:ILE:HD13	1:C:321:GLU:N	2.29	0.46
1:C:432:LEU:HD12	1:C:432:LEU:N	2.31	0.46
1:D:116:ILE:HD11	1:D:230:ALA:HB1	1.97	0.46
1:D:439:SER:HA	1:D:443:LEU:CD1	2.46	0.46
1:A:375:ARG:O	1:A:376:ILE:C	2.53	0.46
1:B:328:ILE:HG13	1:B:328:ILE:H	1.36	0.46
1:C:319:ILE:CD1	1:C:322:LEU:H	2.28	0.46
1:C:376:ILE:O	1:C:379:ALA:HB3	2.16	0.46
1:D:340:PHE:HA	1:D:343:ILE:HG13	1.97	0.46
1:D:436:GLU:O	1:D:438:LEU:N	2.42	0.46
1:A:80:LYS:HG3	1:A:81:VAL:N	2.29	0.46
1:B:340:PHE:HA	1:B:343:ILE:CD1	2.46	0.46
1:B:344:LEU:HD21	1:B:376:ILE:HG22	1.98	0.46
1:D:438:LEU:HD22	1:D:442:ILE:HD11	1.98	0.46
1:A:22:ASN:O	1:A:25:ARG:HB2	2.16	0.45
1:A:62:GLY:O	1:A:64:THR:N	2.49	0.45
1:B:125:GLU:O	1:B:128:GLU:HG2	2.16	0.45
1:B:362:GLU:OE1	1:B:410:ALA:HB3	2.16	0.45
1:B:65:GLU:O	1:B:66:ILE:C	2.54	0.45
1:C:98:SER:O	1:C:101:ARG:HB3	2.16	0.45
1:D:235:ASN:HB2	1:D:238:GLU:HB3	1.98	0.45
1:A:145:GLN:C	1:A:146:THR:HG23	2.36	0.45
1:A:347:PRO:HG2	1:A:350:SER:HB2	1.97	0.45
1:C:135:LEU:HB3	1:C:159:PHE:HD1	1.80	0.45
1:C:335:LEU:HD21	2:C:905:ANP:N1	2.31	0.45
1:D:17:ILE:HG13	1:D:18:ILE:H	1.80	0.45
1:D:44:LEU:O	1:D:47:GLU:N	2.45	0.45
1:A:261:ILE:HG22	1:A:274:ARG:HB3	1.98	0.45
1:A:350:SER:O	1:A:351:ILE:C	2.54	0.45
1:A:402:LEU:HD13	1:A:425:VAL:HA	1.97	0.45
1:B:105:ASP:C	1:B:107:ALA:H	2.20	0.45
1:C:172:GLU:HB3	1:C:215:LYS:HA	1.97	0.45
1:C:438:LEU:H	1:C:438:LEU:CD2	2.29	0.45
1:D:366:ILE:HB	1:D:420:ILE:CD1	2.46	0.45
1:D:33:ASN:HA	1:D:36:ARG:HG3	1.99	0.45
1:D:63:LYS:HB3	1:D:332:LEU:CD2	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:399:LEU:HD23	1:A:400:GLU:N	2.31	0.45
1:B:340:PHE:O	1:B:344:LEU:HB2	2.16	0.45
1:C:366:ILE:N	1:C:366:ILE:CD1	2.74	0.45
1:C:429:LEU:O	1:C:430:ASP:C	2.54	0.45
1:D:128:GLU:HB3	1:D:222:MET:SD	2.56	0.45
1:D:293:LYS:HE2	1:D:294:HIS:NE2	2.31	0.45
1:D:439:SER:HA	1:D:443:LEU:HD12	1.97	0.45
1:B:396:HIS:O	1:B:400:GLU:HB2	2.16	0.45
1:B:369:THR:HG23	1:B:420:ILE:O	2.17	0.45
1:C:102:ASP:O	1:C:105:ASP:N	2.49	0.45
1:C:128:GLU:O	1:C:131:ILE:HB	2.16	0.45
1:C:136:ILE:O	1:C:138:PRO:HD3	2.16	0.45
1:C:255:ILE:CG2	1:C:258:ILE:HD11	2.46	0.45
1:C:405:GLU:O	1:C:408:TYR:N	2.47	0.45
1:C:366:ILE:HG22	1:C:418:ILE:HD11	1.98	0.45
1:D:44:LEU:O	1:D:45:ARG:C	2.55	0.45
1:A:156:ARG:O	1:A:159:PHE:N	2.50	0.45
1:A:325:ARG:HA	1:A:325:ARG:HD3	1.55	0.45
1:A:402:LEU:HB2	1:A:429:LEU:HD21	1.99	0.45
1:B:44:LEU:HA	1:B:47:GLU:HB2	1.98	0.45
1:C:264:ARG:NH1	1:C:264:ARG:HB3	2.29	0.45
1:D:126:LEU:HB2	1:D:229:GLU:HG3	1.99	0.45
1:D:10:VAL:HG12	1:D:14:ASP:OD1	2.17	0.45
1:D:340:PHE:O	1:D:344:LEU:HB2	2.17	0.45
1:D:54:LEU:HA	1:D:306:ALA:HB3	1.99	0.45
1:C:153:SER:CA	1:C:156:ARG:HB3	2.34	0.45
1:C:4:MET:H	1:C:4:MET:HE3	1.82	0.45
1:C:97:ASP:HB2	1:C:290:VAL:CG1	2.46	0.45
1:A:34:ARG:NH2	1:A:250:HIS:HA	2.32	0.45
1:B:27:VAL:HA	1:B:53:ILE:CD1	2.47	0.45
1:C:153:SER:O	1:C:154:ALA:C	2.55	0.45
1:C:34:ARG:HH22	1:C:251:GLY:H	1.65	0.45
1:C:257:GLU:HG2	1:C:260:LYS:CG	2.47	0.45
1:C:350:SER:OG	1:C:351:ILE:HD12	2.17	0.45
1:C:375:ARG:O	1:C:376:ILE:C	2.54	0.45
1:C:44:LEU:HA	1:C:47:GLU:HB3	1.99	0.45
1:C:52:ASN:HB3	1:C:304:PHE:O	2.16	0.45
1:C:7:ARG:HG2	1:C:8:GLU:N	2.32	0.45
1:A:100:ILE:HG12	1:A:299:THR:HG22	1.99	0.45
1:A:234:VAL:HG23	1:A:235:ASN:N	2.32	0.45
1:A:44:LEU:N	1:A:44:LEU:HD12	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:318:LEU:HD21	1:B:322:LEU:CG	2.47	0.45
1:B:442:ILE:O	1:B:443:LEU:HG	2.17	0.45
1:C:122:ARG:HB3	1:C:126:LEU:HD12	1.98	0.45
1:C:34:ARG:NH2	1:C:251:GLY:H	2.15	0.45
1:C:83:ALA:O	1:C:84:THR:C	2.54	0.45
1:D:350:SER:O	1:D:353:VAL:HB	2.16	0.45
1:D:54:LEU:O	1:D:54:LEU:HG	2.16	0.45
1:D:79:ILE:HG12	1:D:81:VAL:HG23	1.99	0.45
1:A:277:VAL:O	1:A:280:ASP:N	2.50	0.45
1:C:101:ARG:HA	1:C:292:THR:CG2	2.47	0.45
1:C:18:ILE:HD12	1:C:18:ILE:N	2.31	0.45
1:C:259:ASP:HB3	1:C:310:PHE:CD2	2.52	0.45
1:C:335:LEU:HD11	2:C:905:ANP:H2	1.99	0.45
1:C:84:THR:O	1:C:86:PHE:N	2.47	0.45
1:D:100:ILE:HG12	1:D:299:THR:CG2	2.47	0.45
1:D:344:LEU:HD21	1:D:376:ILE:HG22	1.99	0.45
1:D:47:GLU:OE1	1:D:47:GLU:O	2.34	0.45
1:A:298:LYS:C	1:A:300:ASP:H	2.19	0.44
1:A:31:LEU:HD23	1:A:70:LEU:CD1	2.45	0.44
1:A:429:LEU:O	1:A:432:LEU:N	2.50	0.44
1:A:54:LEU:O	1:A:56:ILE:HD12	2.17	0.44
1:B:117:GLU:HA	1:B:120:ARG:NE	2.31	0.44
1:B:22:ASN:ND2	1:B:22:ASN:H	2.15	0.44
1:B:248:GLU:HA	1:B:302:ILE:HD11	1.99	0.44
1:C:61:VAL:HG12	1:C:335:LEU:HG	2.00	0.44
1:C:78:PHE:CG	1:C:79:ILE:N	2.84	0.44
1:C:442:ILE:HG22	1:D:329:ARG:CB	2.47	0.44
1:D:84:THR:C	1:D:86:PHE:N	2.70	0.44
1:A:174:GLU:HA	1:A:212:LYS:HB3	1.99	0.44
1:A:32:ARG:HG2	1:A:36:ARG:NE	2.33	0.44
1:B:29:ILE:O	1:B:32:ARG:N	2.49	0.44
1:D:105:ASP:C	1:D:107:ALA:N	2.70	0.44
1:D:318:LEU:HD22	1:D:323:GLN:N	2.33	0.44
1:D:357:ALA:O	1:D:360:ALA:HB3	2.18	0.44
1:D:421:ASP:OD1	1:D:424:TYR:HB2	2.18	0.44
1:D:92:VAL:HB	1:D:93:GLY:H	1.53	0.44
1:A:109:LYS:HA	1:A:112:ARG:HH21	1.82	0.44
1:A:257:GLU:HG2	1:A:260:LYS:CG	2.47	0.44
1:A:31:LEU:O	1:A:34:ARG:HB2	2.18	0.44
1:A:408:TYR:O	1:A:410:ALA:N	2.50	0.44
1:B:233:LEU:N	1:B:233:LEU:HD12	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:259:ASP:O	1:B:262:CYS:HB2	2.17	0.44
1:B:244:ILE:HD11	1:B:296:MET:O	2.17	0.44
1:B:53:ILE:HG12	1:B:328:ILE:HB	1.99	0.44
1:C:319:ILE:HG23	1:C:322:LEU:HB3	1.99	0.44
1:D:282:LEU:CB	1:D:283:PRO:HD3	2.47	0.44
1:A:78:PHE:CG	1:A:79:ILE:N	2.85	0.44
1:A:60:GLY:H	2:A:900:ANP:PG	2.40	0.44
1:B:235:ASN:H	1:B:235:ASN:ND2	2.15	0.44
1:B:252:ILE:HA	1:B:303:LEU:O	2.17	0.44
1:B:356:LYS:CA	1:B:366:ILE:HD11	2.37	0.44
1:B:391:GLY:O	1:B:392:ALA:C	2.56	0.44
1:C:275:GLU:O	1:C:276:GLY:C	2.54	0.44
1:C:395:LEU:O	1:C:396:HIS:C	2.55	0.44
1:D:284:LEU:H	1:D:284:LEU:HG	1.53	0.44
1:D:360:ALA:O	1:D:363:GLY:N	2.48	0.44
1:D:95:GLU:O	1:D:98:SER:OG	2.32	0.44
1:A:316:SER:HA	1:A:323:GLN:NE2	2.33	0.44
1:B:360:ALA:O	1:B:363:GLY:N	2.48	0.44
1:B:375:ARG:NH1	1:B:426:SER:HB3	2.33	0.44
1:D:274:ARG:O	1:D:277:VAL:N	2.50	0.44
1:D:27:VAL:HA	1:D:53:ILE:CD1	2.48	0.44
1:A:120:ARG:HA	1:A:123:ALA:CB	2.48	0.44
1:A:231:ALA:O	1:A:234:VAL:HG22	2.18	0.44
1:B:44:LEU:O	1:B:47:GLU:N	2.49	0.44
1:C:318:LEU:HG	1:C:319:ILE:N	2.32	0.44
1:C:367:GLU:O	1:C:420:ILE:N	2.45	0.44
1:A:119:ASN:HA	1:A:119:ASN:HD22	1.52	0.44
1:A:21:ASP:HA	1:A:24:LYS:CG	2.48	0.44
1:A:34:ARG:NH2	1:A:251:GLY:H	2.15	0.44
1:B:298:LYS:HB3	1:B:300:ASP:OD2	2.18	0.44
1:C:125:GLU:HG3	1:C:126:LEU:H	1.82	0.44
1:C:372:GLY:O	1:C:375:ARG:HB2	2.17	0.44
1:D:128:GLU:O	1:D:132:LEU:N	2.50	0.44
1:D:284:LEU:O	1:D:299:THR:HB	2.18	0.44
1:D:379:ALA:O	1:D:380:ALA:C	2.56	0.44
1:D:421:ASP:O	1:D:425:VAL:HG23	2.18	0.44
1:A:361:THR:C	1:A:363:GLY:H	2.20	0.44
1:A:432:LEU:C	1:A:434:ALA:N	2.71	0.44
1:B:351:ILE:CD1	1:B:399:LEU:HD13	2.48	0.44
1:C:387:THR:HA	1:C:440:ARG:NH2	2.32	0.44
1:D:362:GLU:C	1:D:364:VAL:H	2.21	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:375:ARG:HG3	1:D:422:ALA:HA	2.00	0.44
1:D:78:PHE:CZ	1:D:254:PHE:HB2	2.53	0.44
1:A:350:SER:HB3	1:A:353:VAL:HG23	2.00	0.44
1:B:355:TYR:CZ	1:B:403:MET:HB3	2.53	0.44
1:B:84:THR:C	1:B:86:PHE:N	2.72	0.44
1:C:21:ASP:HA	1:C:24:LYS:HD2	1.99	0.44
1:C:220:ASP:O	1:C:223:LYS:N	2.50	0.44
1:C:65:GLU:O	1:C:69:ARG:HG2	2.17	0.44
1:D:125:GLU:HG3	1:D:126:LEU:N	2.32	0.44
1:D:340:PHE:HA	1:D:343:ILE:CD1	2.48	0.44
1:B:432:LEU:O	1:B:433:VAL:C	2.56	0.43
1:C:399:LEU:O	1:C:402:LEU:HB3	2.18	0.43
1:C:54:LEU:HD23	1:C:306:ALA:C	2.39	0.43
1:C:86:PHE:HA	1:C:93:GLY:CA	2.44	0.43
1:D:100:ILE:N	1:D:100:ILE:HD12	2.33	0.43
1:D:246:ALA:HA	1:D:250:HIS:ND1	2.32	0.43
1:A:11:SER:HA	1:A:14:ASP:OD1	2.18	0.43
1:A:61:VAL:HG11	1:A:333:GLN:O	2.19	0.43
1:A:348:ASN:O	1:A:349:ALA:HB3	2.19	0.43
1:A:68:ARG:O	1:A:69:ARG:C	2.57	0.43
1:B:116:ILE:O	1:B:120:ARG:HG3	2.17	0.43
1:B:123:ALA:O	1:B:127:ALA:HB2	2.18	0.43
1:B:356:LYS:HA	1:B:366:ILE:CD1	2.36	0.43
1:B:375:ARG:HG3	1:B:422:ALA:HA	1.99	0.43
1:B:69:ARG:HG3	1:B:73:LEU:HD23	1.99	0.43
1:A:130:ARG:CA	1:A:133:ASP:HB2	2.46	0.43
1:B:282:LEU:O	1:B:283:PRO:C	2.56	0.43
1:B:379:ALA:O	1:B:383:VAL:HG23	2.17	0.43
1:C:168:LEU:N	1:C:218:ILE:CG2	2.81	0.43
1:C:278:GLN:HG2	1:C:322:LEU:HD22	2.00	0.43
1:A:399:LEU:O	1:A:402:LEU:N	2.51	0.43
1:A:18:ILE:N	2:A:900:ANP:N6	2.47	0.43
1:B:318:LEU:HD22	1:B:323:GLN:CA	2.48	0.43
1:B:92:VAL:HB	1:B:93:GLY:H	1.54	0.43
1:D:117:GLU:HA	1:D:120:ARG:CZ	2.48	0.43
1:D:343:ILE:O	1:D:347:PRO:HG2	2.19	0.43
1:A:253:VAL:O	1:A:305:ILE:HG13	2.19	0.43
1:A:83:ALA:O	1:A:84:THR:C	2.56	0.43
1:C:437:ASP:O	1:C:440:ARG:N	2.51	0.43
1:C:6:PRO:HA	1:C:9:ILE:HD12	1.99	0.43
1:D:251:GLY:HA3	1:D:302:ILE:HG23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:398:VAL:CG2	1:D:399:LEU:N	2.81	0.43
1:A:223:LYS:HA	1:A:226:ILE:HB	2.01	0.43
1:A:342:ARG:O	1:A:347:PRO:HD2	2.18	0.43
1:B:236:PRO:O	1:B:240:LYS:HB2	2.18	0.43
1:B:383:VAL:O	1:B:387:THR:HG23	2.18	0.43
1:C:369:THR:HB	1:C:372:GLY:H	1.84	0.43
1:C:432:LEU:O	1:C:433:VAL:C	2.56	0.43
1:D:22:ASN:N	1:D:22:ASN:ND2	2.67	0.43
1:D:240:LYS:HG2	1:D:294:HIS:HB3	2.00	0.43
1:D:387:THR:C	1:D:388:GLU:HG2	2.35	0.43
1:A:152:PRO:C	1:A:154:ALA:N	2.72	0.43
1:A:255:ILE:HD13	1:A:255:ILE:N	2.34	0.43
1:B:247:VAL:C	1:B:249:GLN:H	2.22	0.43
1:C:322:LEU:C	1:C:324:GLY:N	2.72	0.43
1:D:86:PHE:HB2	1:D:277:VAL:HG13	2.00	0.43
1:D:53:ILE:O	1:D:305:ILE:HA	2.18	0.43
1:D:310:PHE:N	1:D:310:PHE:CD2	2.87	0.43
1:D:319:ILE:HG23	1:D:319:ILE:O	2.19	0.43
1:D:350:SER:HB3	1:D:353:VAL:HG23	1.99	0.43
1:D:62:GLY:O	1:D:63:LYS:C	2.56	0.43
1:A:379:ALA:O	1:A:380:ALA:C	2.56	0.43
1:A:366:ILE:HA	1:A:418:ILE:O	2.19	0.43
1:A:64:THR:HG22	1:A:68:ARG:NE	2.33	0.43
1:B:31:LEU:O	1:B:31:LEU:HD22	2.18	0.43
1:B:398:VAL:HG23	1:B:399:LEU:N	2.33	0.43
1:C:384:ASN:HD22	1:C:394:ARG:NH1	2.17	0.43
1:D:252:ILE:HA	1:D:303:LEU:O	2.19	0.43
1:A:258:ILE:HD13	1:A:261:ILE:HD11	2.00	0.43
1:A:372:GLY:O	1:A:375:ARG:HB2	2.19	0.43
1:A:405:GLU:O	1:A:408:TYR:N	2.51	0.43
1:A:409:ASP:O	1:A:413:LEU:HD23	2.18	0.43
1:B:117:GLU:HA	1:B:120:ARG:HG3	1.99	0.43
1:B:282:LEU:CB	1:B:283:PRO:HD3	2.49	0.43
1:B:357:ALA:O	1:B:360:ALA:HB3	2.19	0.43
1:B:391:GLY:O	1:B:393:ARG:N	2.52	0.43
1:C:216:LEU:HD11	1:C:221:ALA:CB	2.45	0.43
1:C:255:ILE:HD13	1:C:255:ILE:N	2.33	0.43
1:C:342:ARG:O	1:C:347:PRO:HD2	2.19	0.43
1:C:77:PRO:CD	1:C:246:ALA:HB1	2.49	0.43
1:D:307:SER:OG	1:D:308:GLY:N	2.52	0.43
1:D:310:PHE:CD1	1:D:314:LYS:HA	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:76:ALA:CB	1:D:252:ILE:HD11	2.49	0.43
1:A:351:ILE:HD12	1:A:352:THR:H	1.84	0.43
1:A:440:ARG:HB3	1:B:316:SER:CB	2.49	0.43
1:A:5:THR:HG23	1:A:8:GLU:OE2	2.19	0.43
1:B:103:LEU:HD21	1:B:247:VAL:HG13	2.01	0.43
1:B:274:ARG:O	1:B:277:VAL:N	2.51	0.43
1:B:54:LEU:HD13	1:B:306:ALA:HB3	2.00	0.43
1:B:351:ILE:HG13	1:B:352:THR:N	2.32	0.43
1:C:104:THR:O	1:C:107:ALA:HB3	2.19	0.43
1:C:169:ASP:H	1:C:218:ILE:CG2	2.32	0.43
1:C:171:LYS:O	1:C:172:GLU:HB3	2.19	0.43
1:C:168:LEU:N	1:C:218:ILE:HG22	2.33	0.43
1:C:277:VAL:C	1:C:281:LEU:HD12	2.39	0.43
1:C:379:ALA:O	1:C:380:ALA:C	2.57	0.43
1:C:366:ILE:HA	1:C:418:ILE:O	2.19	0.43
1:C:439:SER:O	1:C:443:LEU:HB2	2.18	0.43
1:C:12:GLU:CG	1:C:73:LEU:HD12	2.47	0.43
1:D:224:LEU:C	1:D:226:ILE:N	2.72	0.43
1:D:123:ALA:CB	1:D:226:ILE:HG23	2.36	0.43
1:D:111:VAL:HG21	1:D:243:ALA:CA	2.49	0.43
1:D:351:ILE:HG13	1:D:352:THR:N	2.34	0.43
1:A:168:LEU:N	1:A:218:ILE:HG22	2.34	0.42
1:A:53:ILE:HG12	1:A:328:ILE:HB	2.00	0.42
1:B:129:GLU:HA	1:B:132:LEU:CB	2.45	0.42
1:B:236:PRO:HA	1:B:239:LEU:HD12	2.00	0.42
1:B:384:ASN:HD21	1:B:391:GLY:N	2.10	0.42
1:C:235:ASN:OD1	1:C:238:GLU:HB3	2.18	0.42
1:C:62:GLY:C	1:C:66:ILE:HD13	2.39	0.42
1:D:103:LEU:HD23	1:D:104:THR:N	2.34	0.42
1:D:69:ARG:O	1:D:73:LEU:HD23	2.19	0.42
1:A:107:ALA:HB1	1:A:247:VAL:HG22	2.01	0.42
1:A:259:ASP:HB3	1:A:310:PHE:CE2	2.54	0.42
1:A:52:ASN:O	1:A:328:ILE:HD12	2.18	0.42
1:A:361:THR:HG21	1:B:36:ARG:CA	2.45	0.42
1:B:100:ILE:HD12	1:B:100:ILE:N	2.33	0.42
1:B:13:LEU:CD1	1:B:73:LEU:HD21	2.49	0.42
1:B:381:TRP:C	1:B:381:TRP:CD1	2.92	0.42
1:B:405:GLU:O	1:B:406:ILE:C	2.57	0.42
1:B:439:SER:HA	1:B:443:LEU:CD1	2.49	0.42
1:A:131:ILE:CG2	1:A:218:ILE:HD11	2.50	0.42
1:A:319:ILE:HG23	1:A:322:LEU:CB	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:420:ILE:HG23	1:A:424:TYR:HD1	1.83	0.42
1:A:65:GLU:HA	1:A:68:ARG:HG2	2.01	0.42
1:A:5:THR:O	1:A:8:GLU:HB2	2.19	0.42
1:B:263:LYS:HG3	1:B:264:ARG:H	1.79	0.42
1:B:404:GLU:HB3	1:B:405:GLU:H	1.69	0.42
1:B:78:PHE:CG	1:B:79:ILE:N	2.86	0.42
1:C:216:LEU:HD11	1:C:221:ALA:CA	2.49	0.42
1:C:27:VAL:CG2	1:C:70:LEU:HD13	2.39	0.42
1:D:271:ASP:C	1:D:273:SER:N	2.71	0.42
1:D:320:PRO:CA	1:D:323:GLN:HB3	2.49	0.42
1:D:340:PHE:O	1:D:341:GLU:C	2.57	0.42
1:D:381:TRP:CD1	1:D:382:GLN:N	2.87	0.42
1:A:135:LEU:HD13	1:A:135:LEU:HA	1.88	0.42
1:A:230:ALA:C	1:A:232:LYS:N	2.72	0.42
1:A:319:ILE:HG23	1:A:322:LEU:HB2	2.01	0.42
1:A:44:LEU:HA	1:A:47:GLU:HB3	2.02	0.42
1:B:59:THR:C	1:B:61:VAL:N	2.73	0.42
1:C:34:ARG:NH2	1:C:250:HIS:HA	2.34	0.42
1:C:340:PHE:O	1:C:341:GLU:C	2.57	0.42
1:C:68:ARG:NH1	1:C:68:ARG:HB3	2.31	0.42
1:A:424:TYR:CZ	1:A:428:HIS:NE2	2.87	0.42
1:A:432:LEU:HD12	1:A:432:LEU:N	2.35	0.42
1:A:54:LEU:HD23	1:A:306:ALA:C	2.39	0.42
1:B:27:VAL:CG2	1:B:28:ALA:N	2.81	0.42
1:C:112:ARG:HG2	1:C:112:ARG:NH1	2.32	0.42
1:C:167:GLN:HB2	1:C:218:ILE:CG2	2.49	0.42
1:C:267:SER:O	1:C:268:SER:C	2.57	0.42
1:C:350:SER:O	1:C:351:ILE:C	2.58	0.42
1:C:358:LEU:HD11	1:D:33:ASN:ND2	2.33	0.42
1:C:380:ALA:HB2	1:C:398:VAL:HG21	2.01	0.42
1:A:110:MET:O	1:A:111:VAL:C	2.58	0.42
1:A:282:LEU:O	1:A:286:GLU:HB2	2.20	0.42
1:A:351:ILE:H	1:A:351:ILE:HG13	1.57	0.42
1:A:42:GLU:O	1:A:43:GLU:C	2.57	0.42
1:B:235:ASN:N	1:B:235:ASN:ND2	2.66	0.42
1:C:256:ASP:OD1	1:C:257:GLU:N	2.53	0.42
1:C:104:THR:HG21	1:C:297:VAL:HG21	2.01	0.42
1:C:298:LYS:C	1:C:300:ASP:N	2.73	0.42
1:C:333:GLN:H	1:C:333:GLN:CD	2.23	0.42
1:D:117:GLU:O	1:D:120:ARG:HB2	2.20	0.42
1:D:129:GLU:HA	1:D:132:LEU:CB	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:325:ARG:O	1:D:327:PRO:HD3	2.20	0.42
1:A:167:GLN:HB2	1:A:168:LEU:H	1.46	0.42
1:A:212:LYS:O	1:A:213:ALA:CB	2.66	0.42
1:A:262:CYS:O	1:A:263:LYS:HG3	2.20	0.42
1:A:442:ILE:O	1:A:443:LEU:HG	2.19	0.42
1:A:64:THR:O	1:A:68:ARG:HD3	2.20	0.42
1:C:322:LEU:HD12	1:C:322:LEU:HA	1.89	0.42
1:D:253:VAL:HG21	1:D:304:PHE:CE2	2.55	0.42
1:D:330:VAL:O	1:D:330:VAL:HG13	2.19	0.42
1:A:366:ILE:N	1:A:366:ILE:CD1	2.73	0.42
1:C:100:ILE:O	1:C:104:THR:HG23	2.20	0.42
1:C:277:VAL:O	1:C:278:GLN:C	2.57	0.42
1:C:340:PHE:O	1:C:343:ILE:N	2.53	0.42
1:C:344:LEU:HD11	1:C:395:LEU:CD1	2.49	0.42
1:D:302:ILE:HG22	1:D:303:LEU:N	2.34	0.42
1:D:31:LEU:HD22	1:D:31:LEU:O	2.20	0.42
1:A:120:ARG:HA	1:A:123:ALA:HB3	2.02	0.42
1:A:241:GLN:HA	1:A:244:ILE:HD11	2.00	0.42
1:A:437:ASP:O	1:A:438:LEU:C	2.58	0.42
1:B:103:LEU:HD21	1:B:247:VAL:CG1	2.50	0.42
1:B:29:ILE:O	1:B:30:ALA:C	2.59	0.42
1:C:135:LEU:C	1:C:137:PRO:HD3	2.40	0.42
1:C:350:SER:O	1:C:354:GLN:HG3	2.20	0.42
1:D:131:ILE:HD11	1:D:222:MET:HG2	2.02	0.42
1:D:238:GLU:O	1:D:242:ASP:HB2	2.20	0.42
1:D:245:ASP:C	1:D:247:VAL:N	2.67	0.42
1:A:17:ILE:HG23	2:A:900:ANP:N6	2.35	0.42
1:B:284:LEU:H	1:B:284:LEU:HG	1.61	0.42
1:B:37:ARG:NH2	1:B:45:ARG:O	2.52	0.42
1:C:375:ARG:HA	1:C:375:ARG:HD3	1.94	0.42
1:C:379:ALA:O	1:C:383:VAL:HG23	2.20	0.42
1:D:124:GLU:HA	1:D:127:ALA:HB3	2.02	0.42
1:D:439:SER:C	1:D:441:PHE:H	2.23	0.42
1:D:442:ILE:HD13	1:D:442:ILE:N	2.35	0.42
1:A:340:PHE:O	1:A:344:LEU:HD13	2.19	0.41
1:C:130:ARG:HA	1:C:133:ASP:HB2	2.01	0.41
1:C:172:GLU:O	1:C:172:GLU:HG3	2.19	0.41
1:C:325:ARG:C	1:C:327:PRO:HD3	2.41	0.41
1:D:292:THR:CG2	1:D:297:VAL:HG22	2.49	0.41
1:D:429:LEU:O	1:D:431:ALA:N	2.53	0.41
1:D:69:ARG:HG3	1:D:73:LEU:CD2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:THR:HA	1:A:297:VAL:O	2.19	0.41
1:A:344:LEU:HD11	1:A:395:LEU:HD22	2.02	0.41
1:B:27:VAL:HB	1:B:70:LEU:CD1	2.50	0.41
1:B:302:ILE:HG22	1:B:303:LEU:N	2.34	0.41
1:B:86:PHE:CE1	1:B:96:VAL:HA	2.55	0.41
1:C:163:LEU:C	1:C:165:GLU:N	2.74	0.41
1:C:167:GLN:HB2	1:C:218:ILE:HG23	2.02	0.41
1:C:282:LEU:HA	1:C:285:VAL:HG23	2.03	0.41
1:C:29:ILE:O	1:C:32:ARG:N	2.53	0.41
1:D:122:ARG:HD3	1:D:233:LEU:HD21	2.02	0.41
1:D:76:ALA:HB1	1:D:252:ILE:HD11	2.02	0.41
1:D:271:ASP:HA	1:D:274:ARG:CG	2.49	0.41
1:D:318:LEU:HD21	1:D:322:LEU:CD2	2.47	0.41
1:D:369:THR:HG23	1:D:420:ILE:O	2.20	0.41
1:A:258:ILE:HG13	1:A:306:ALA:CB	2.48	0.41
1:A:322:LEU:HD12	1:A:322:LEU:HA	1.84	0.41
1:A:340:PHE:O	1:A:343:ILE:N	2.53	0.41
1:A:431:ALA:O	1:A:434:ALA:HB3	2.20	0.41
1:C:98:SER:O	1:C:101:ARG:N	2.52	0.41
1:C:108:VAL:HG12	1:C:109:LYS:N	2.34	0.41
1:C:17:ILE:HA	2:C:905:ANP:HN61	1.84	0.41
1:C:257:GLU:O	1:C:258:ILE:C	2.56	0.41
1:C:442:ILE:HD13	1:C:442:ILE:N	2.35	0.41
1:D:134:VAL:HG23	1:D:134:VAL:O	2.20	0.41
1:D:255:ILE:N	1:D:255:ILE:HD13	2.34	0.41
1:D:320:PRO:O	1:D:321:GLU:C	2.57	0.41
1:D:54:LEU:HD23	1:D:329:ARG:CD	2.50	0.41
1:A:108:VAL:HG12	1:A:109:LYS:N	2.36	0.41
1:A:21:ASP:O	1:A:24:LYS:HB2	2.21	0.41
1:A:259:ASP:HB3	1:A:310:PHE:CD2	2.54	0.41
1:A:333:GLN:N	1:A:333:GLN:CD	2.74	0.41
1:A:33:ASN:HA	1:A:36:ARG:HD3	2.02	0.41
1:A:432:LEU:O	1:A:433:VAL:C	2.59	0.41
1:A:436:GLU:O	1:A:438:LEU:N	2.53	0.41
1:A:63:LYS:O	1:A:66:ILE:HB	2.19	0.41
1:A:70:LEU:O	1:A:73:LEU:HD23	2.21	0.41
1:A:109:LYS:NZ	1:B:298:LYS:HG2	2.35	0.41
1:B:395:LEU:O	1:B:396:HIS:C	2.58	0.41
1:B:76:ALA:HB1	1:B:77:PRO:HD2	2.01	0.41
1:C:278:GLN:HA	1:C:281:LEU:HD12	2.00	0.41
1:C:344:LEU:HD11	1:C:395:LEU:HD22	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:375:ARG:HB2	1:C:425:VAL:HG21	2.03	0.41
1:C:83:ALA:O	1:C:85:LYS:N	2.53	0.41
1:D:247:VAL:C	1:D:249:GLN:H	2.22	0.41
1:D:27:VAL:HG23	1:D:70:LEU:HD12	2.01	0.41
1:A:255:ILE:O	1:A:306:ALA:HA	2.21	0.41
1:A:442:ILE:HA	1:B:329:ARG:HG3	2.02	0.41
1:A:63:LYS:O	1:A:64:THR:C	2.58	0.41
1:B:107:ALA:O	1:B:110:MET:N	2.53	0.41
1:B:19:GLY:O	1:B:24:LYS:HE2	2.20	0.41
1:B:372:GLY:O	1:B:373:ILE:C	2.57	0.41
1:C:109:LYS:HA	1:C:112:ARG:CZ	2.50	0.41
1:C:348:ASN:O	1:C:349:ALA:HB3	2.21	0.41
1:D:336:THR:HG22	1:D:339:ASP:OD2	2.19	0.41
1:A:153:SER:O	1:A:154:ALA:C	2.58	0.41
1:A:127:ALA:CB	1:A:226:ILE:HA	2.50	0.41
1:A:111:VAL:HG11	1:A:243:ALA:HB2	2.03	0.41
1:A:84:THR:O	1:A:86:PHE:N	2.51	0.41
1:B:409:ASP:O	1:B:413:LEU:HD11	2.20	0.41
1:C:108:VAL:O	1:C:109:LYS:C	2.59	0.41
1:C:140:LYS:HD3	1:C:140:LYS:N	2.35	0.41
1:C:156:ARG:O	1:C:159:PHE:N	2.54	0.41
1:D:105:ASP:C	1:D:107:ALA:H	2.23	0.41
1:D:337:THR:O	1:D:341:GLU:HG3	2.20	0.41
1:D:399:LEU:O	1:D:402:LEU:HD23	2.21	0.41
1:B:394:ARG:HA	1:B:394:ARG:HD3	1.76	0.41
1:B:432:LEU:O	1:B:435:ASP:N	2.53	0.41
1:C:301:HIS:O	1:C:302:ILE:HG13	2.21	0.41
1:C:424:TYR:CZ	1:C:428:HIS:NE2	2.89	0.41
1:D:271:ASP:C	1:D:274:ARG:H	2.23	0.41
1:D:65:GLU:O	1:D:66:ILE:C	2.56	0.41
1:A:156:ARG:O	1:A:157:GLN:C	2.59	0.41
1:A:384:ASN:ND2	1:A:394:ARG:NH1	2.68	0.41
1:A:64:THR:HB	2:A:900:ANP:O1A	2.20	0.41
1:B:282:LEU:CB	1:B:283:PRO:CD	2.99	0.41
1:B:310:PHE:CD1	1:B:314:LYS:HA	2.56	0.41
1:C:156:ARG:O	1:C:157:GLN:C	2.58	0.41
1:C:278:GLN:O	1:C:281:LEU:HB2	2.21	0.41
1:C:29:ILE:O	1:C:30:ALA:C	2.59	0.41
1:C:61:VAL:HG11	1:C:334:ALA:HA	2.03	0.41
1:C:410:ALA:O	1:C:413:LEU:N	2.54	0.41
1:C:55:MET:HE3	1:C:254:PHE:HE2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:18:ILE:N	1:D:18:ILE:HD13	2.36	0.41
1:B:127:ALA:CA	1:B:225:LEU:HB3	2.49	0.41
1:B:336:THR:HG23	1:B:338:SER:HB3	2.03	0.41
1:C:344:LEU:N	1:C:344:LEU:HD12	2.36	0.41
1:C:429:LEU:O	1:C:432:LEU:N	2.54	0.41
1:D:261:ILE:HG22	1:D:261:ILE:O	2.21	0.41
1:D:345:THR:C	1:D:347:PRO:HD2	2.40	0.41
1:A:255:ILE:HD11	1:A:304:PHE:HB3	2.03	0.41
1:A:56:ILE:HD12	1:A:56:ILE:N	2.36	0.41
1:B:54:LEU:HD23	1:B:329:ARG:HD3	2.03	0.41
1:C:157:GLN:HA	1:C:160:ARG:HB3	2.02	0.41
1:D:107:ALA:O	1:D:110:MET:HB2	2.20	0.41
1:D:240:LYS:HE2	1:D:294:HIS:CD2	2.55	0.41
1:C:22:ASN:O	1:C:25:ARG:HB2	2.21	0.41
1:C:355:TYR:CZ	1:C:403:MET:HB2	2.56	0.41
1:C:430:ASP:O	1:C:433:VAL:HG22	2.21	0.41
1:C:7:ARG:HA	1:C:10:VAL:HB	2.03	0.41
1:A:55:MET:HE3	1:A:305:ILE:HG21	2.02	0.40
1:B:271:ASP:CA	1:B:274:ARG:HB2	2.41	0.40
1:B:362:GLU:C	1:B:364:VAL:H	2.24	0.40
1:C:151:GLU:N	1:C:152:PRO:CD	2.84	0.40
1:C:387:THR:OG1	1:C:388:GLU:N	2.50	0.40
1:C:405:GLU:O	1:C:409:ASP:N	2.52	0.40
1:D:100:ILE:CG2	1:D:297:VAL:HG21	2.51	0.40
1:A:109:LYS:O	1:A:110:MET:C	2.60	0.40
1:A:278:GLN:HG2	1:A:322:LEU:CD2	2.52	0.40
1:A:320:PRO:O	1:A:323:GLN:N	2.53	0.40
1:A:438:LEU:O	1:A:441:PHE:HB2	2.21	0.40
1:B:318:LEU:HD22	1:B:323:GLN:N	2.36	0.40
1:B:6:PRO:HD3	1:B:32:ARG:HD3	2.04	0.40
1:C:136:ILE:O	1:C:136:ILE:HG22	2.22	0.40
1:C:252:ILE:HG22	1:C:253:VAL:N	2.36	0.40
1:D:271:ASP:HA	1:D:274:ARG:HG3	2.03	0.40
1:D:29:ILE:O	1:D:30:ALA:C	2.58	0.40
1:C:442:ILE:HA	1:D:329:ARG:HG3	2.03	0.40
1:D:32:ARG:O	1:D:35:TRP:N	2.53	0.40
1:D:39:GLN:O	1:D:40:LEU:HD23	2.20	0.40
1:A:398:VAL:HG12	1:A:429:LEU:CD1	2.52	0.40
1:A:86:PHE:HA	1:A:93:GLY:CA	2.50	0.40
1:B:21:ASP:O	1:B:22:ASN:C	2.58	0.40
1:C:279:ARG:O	1:C:282:LEU:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:64:THR:HB	2:C:905:ANP:O1A	2.21	0.40
1:D:51:LYS:CB	1:D:328:ILE:HD11	2.50	0.40
1:D:41:ASN:C	1:D:45:ARG:HB2	2.41	0.40
1:A:17:ILE:HD11	1:A:69:ARG:CG	2.52	0.40
1:A:252:ILE:HG23	1:A:303:LEU:O	2.21	0.40
1:A:257:GLU:O	1:A:258:ILE:C	2.58	0.40
1:B:263:LYS:CG	1:B:264:ARG:N	2.77	0.40
1:B:320:PRO:O	1:B:321:GLU:C	2.59	0.40
1:B:98:SER:OG	1:B:99:ILE:N	2.55	0.40
1:C:19:GLY:O	1:C:24:LYS:HE3	2.21	0.40
1:C:80:LYS:HA	1:C:254:PHE:HB3	2.03	0.40
1:C:375:ARG:CB	1:C:425:VAL:HG21	2.52	0.40
1:C:438:LEU:N	1:C:438:LEU:HD22	2.37	0.40
1:D:328:ILE:HG13	1:D:328:ILE:H	1.35	0.40
1:D:86:PHE:HE1	1:D:95:GLU:O	2.04	0.40
1:A:153:SER:O	1:A:157:GLN:HB2	2.22	0.40
1:A:424:TYR:O	1:A:428:HIS:CD2	2.74	0.40
1:A:98:SER:O	1:A:99:ILE:C	2.59	0.40
1:B:103:LEU:HD23	1:B:104:THR:N	2.37	0.40
1:B:119:ASN:OD1	1:B:233:LEU:HD23	2.20	0.40
1:B:346:GLU:O	1:B:347:PRO:C	2.59	0.40
1:B:399:LEU:O	1:B:402:LEU:HD23	2.22	0.40
1:B:439:SER:O	1:B:443:LEU:HD12	2.20	0.40
1:B:96:VAL:CG1	1:B:97:ASP:N	2.85	0.40
1:D:282:LEU:CB	1:D:283:PRO:CD	2.99	0.40
1:D:33:ASN:O	1:D:34:ARG:C	2.60	0.40
1:D:439:SER:O	1:D:443:LEU:HD12	2.21	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	403/442 (91%)	262 (65%)	102 (25%)	39 (10%)	1	13
1	B	403/442 (91%)	251 (62%)	111 (28%)	41 (10%)	1	11
1	C	403/442 (91%)	258 (64%)	104 (26%)	41 (10%)	1	11
1	D	403/442 (91%)	251 (62%)	115 (28%)	37 (9%)	1	14
All	All	1612/1768 (91%)	1022 (63%)	432 (27%)	158 (10%)	1	12

All (158) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	45	ARG
1	A	63	LYS
1	A	110	MET
1	A	268	SER
1	A	398	VAL
1	A	436	GLU
1	A	437	ASP
1	B	17	ILE
1	B	99	ILE
1	B	135	LEU
1	B	171	LYS
1	B	262	CYS
1	B	392	ALA
1	B	404	GLU
1	B	430	ASP
1	B	437	ASP
1	C	45	ARG
1	C	63	LYS
1	C	110	MET
1	C	111	VAL
1	C	172	GLU
1	C	212	LYS
1	C	268	SER
1	C	398	VAL
1	C	436	GLU
1	C	437	ASP
1	D	17	ILE
1	D	135	LEU
1	D	171	LYS
1	D	262	CYS
1	D	327	PRO
1	D	392	ALA
1	D	404	GLU

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Mol	Chain	Res	Type
1	D	430	ASP
1	A	41	ASN
1	A	67	ALA
1	A	84	THR
1	A	99	ILE
1	A	165	GLU
1	A	212	LYS
1	A	264	ARG
1	A	397	THR
1	A	404	GLU
1	A	414	SER
1	A	433	VAL
1	B	18	ILE
1	B	39	GLN
1	B	60	GLY
1	B	85	LYS
1	B	89	VAL
1	B	138	PRO
1	B	246	ALA
1	B	327	PRO
1	B	328	ILE
1	B	334	ALA
1	B	353	VAL
1	B	416	GLN
1	B	425	VAL
1	B	438	LEU
1	C	19	GLY
1	C	42	GLU
1	C	99	ILE
1	C	165	GLU
1	C	264	ARG
1	C	267	SER
1	C	414	SER
1	C	433	VAL
1	D	18	ILE
1	D	19	GLY
1	D	39	GLN
1	D	60	GLY
1	D	75	ASN
1	D	85	LYS
1	D	89	VAL
1	D	99	ILE

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Mol	Chain	Res	Type
1	D	138	PRO
1	D	151	GLU
1	D	246	ALA
1	D	286	GLU
1	D	334	ALA
1	D	353	VAL
1	D	425	VAL
1	D	438	LEU
1	A	42	GLU
1	A	58	PRO
1	A	141	ASN
1	A	156	ARG
1	A	386	SER
1	B	37	ARG
1	B	151	GLU
1	B	158	ALA
1	B	286	GLU
1	C	40	LEU
1	C	41	ASN
1	C	58	PRO
1	C	84	THR
1	C	85	LYS
1	C	88	GLU
1	C	386	SER
1	C	404	GLU
1	D	150	GLN
1	D	169	ASP
1	D	264	ARG
1	D	416	GLN
1	D	437	ASP
1	A	6	PRO
1	A	85	LYS
1	A	88	GLU
1	A	164	ARG
1	A	261	ILE
1	A	267	SER
1	B	75	ASN
1	B	347	PRO
1	B	432	LEU
1	C	67	ALA
1	C	261	ILE
1	C	397	THR

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Mol	Chain	Res	Type
1	D	37	ARG
1	D	240	LYS
1	A	40	LEU
1	A	51	LYS
1	A	64	THR
1	B	170	ASP
1	C	6	PRO
1	C	51	LYS
1	C	164	ARG
1	D	158	ALA
1	A	19	GLY
1	A	426	SER
1	B	29	ILE
1	B	79	ILE
1	B	285	VAL
1	C	64	THR
1	C	137	PRO
1	C	167	GLN
1	D	328	ILE
1	D	408	TYR
1	A	137	PRO
1	B	92	VAL
1	B	433	VAL
1	C	351	ILE
1	C	376	ILE
1	D	92	VAL
1	D	347	PRO
1	B	19	GLY
1	B	100	ILE
1	B	152	PRO
1	B	320	PRO
1	C	320	PRO
1	D	282	LEU
1	C	66	ILE
1	A	111	VAL
1	A	320	PRO
1	A	351	ILE
1	B	282	LEU
1	C	364	VAL
1	C	390	ILE
1	A	66	ILE

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	349/376 (93%)	226 (65%)	123 (35%)	0	1
1	B	349/376 (93%)	227 (65%)	122 (35%)	0	2
1	C	349/376 (93%)	220 (63%)	129 (37%)	0	1
1	D	349/376 (93%)	231 (66%)	118 (34%)	0	2
All	All	1396/1504 (93%)	904 (65%)	492 (35%)	0	1

All (492) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	3	GLU
1	A	4	MET
1	A	5	THR
1	A	7	ARG
1	A	14	ASP
1	A	31	LEU
1	A	32	ARG
1	A	34	ARG
1	A	37	ARG
1	A	38	MET
1	A	41	ASN
1	A	42	GLU
1	A	44	LEU
1	A	49	THR
1	A	51	LYS
1	A	54	LEU
1	A	61	VAL
1	A	68	ARG
1	A	70	LEU
1	A	72	LYS
1	A	73	LEU
1	A	80	LYS
1	A	81	VAL

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Mol	Chain	Res	Type
1	A	84	THR
1	A	94	LYS
1	A	97	ASP
1	A	109	LYS
1	A	112	ARG
1	A	118	LYS
1	A	119	ASN
1	A	122	ARG
1	A	125	GLU
1	A	128	GLU
1	A	130	ARG
1	A	135	LEU
1	A	140	LYS
1	A	142	ASN
1	A	146	THR
1	A	147	GLU
1	A	149	GLN
1	A	156	ARG
1	A	157	GLN
1	A	159	PHE
1	A	160	ARG
1	A	161	LYS
1	A	164	ARG
1	A	167	GLN
1	A	168	LEU
1	A	169	ASP
1	A	171	LYS
1	A	172	GLU
1	A	173	ILE
1	A	174	GLU
1	A	210	LYS
1	A	212	LYS
1	A	215	LYS
1	A	216	LEU
1	A	217	LYS
1	A	223	LYS
1	A	224	LEU
1	A	229	GLU
1	A	232	LYS
1	A	233	LEU
1	A	239	LEU
1	A	242	ASP

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Mol	Chain	Res	Type
1	A	247	VAL
1	A	249	GLN
1	A	255	ILE
1	A	257	GLU
1	A	261	ILE
1	A	263	LYS
1	A	264	ARG
1	A	266	GLU
1	A	267	SER
1	A	268	SER
1	A	271	ASP
1	A	282	LEU
1	A	285	VAL
1	A	289	THR
1	A	290	VAL
1	A	297	VAL
1	A	298	LYS
1	A	301	HIS
1	A	303	LEU
1	A	305	ILE
1	A	310	PHE
1	A	311	GLN
1	A	314	LYS
1	A	319	ILE
1	A	325	ARG
1	A	332	LEU
1	A	333	GLN
1	A	335	LEU
1	A	336	THR
1	A	337	THR
1	A	345	THR
1	A	350	SER
1	A	351	ILE
1	A	356	LYS
1	A	358	LEU
1	A	359	MET
1	A	364	VAL
1	A	366	ILE
1	A	367	GLU
1	A	369	THR
1	A	370	ASP
1	A	371	SER

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Mol	Chain	Res	Type
1	A	374	LYS
1	A	375	ARG
1	A	394	ARG
1	A	401	ARG
1	A	407	SER
1	A	412	ASP
1	A	416	GLN
1	A	417	ASN
1	A	418	ILE
1	A	421	ASP
1	A	423	ASP
1	A	425	VAL
1	A	435	ASP
1	A	437	ASP
1	A	442	ILE
1	B	2	SER
1	B	5	THR
1	B	11	SER
1	B	16	HIS
1	B	18	ILE
1	B	20	GLN
1	B	22	ASN
1	B	25	ARG
1	B	26	SER
1	B	34	ARG
1	B	37	ARG
1	B	38	MET
1	B	39	GLN
1	B	42	GLU
1	B	43	GLU
1	B	44	LEU
1	B	47	GLU
1	B	48	VAL
1	B	49	THR
1	B	63	LYS
1	B	64	THR
1	B	73	LEU
1	B	82	GLU
1	B	84	THR
1	B	88	GLU
1	B	92	VAL
1	B	94	LYS

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Mol	Chain	Res	Type
1	B	95	GLU
1	B	96	VAL
1	B	103	LEU
1	B	104	THR
1	B	109	LYS
1	B	110	MET
1	B	117	GLU
1	B	118	LYS
1	B	121	TYR
1	B	124	GLU
1	B	125	GLU
1	B	130	ARG
1	B	135	LEU
1	B	142	ASN
1	B	146	THR
1	B	148	GLN
1	B	149	GLN
1	B	156	ARG
1	B	157	GLN
1	B	161	LYS
1	B	162	LYS
1	B	163	LEU
1	B	165	GLU
1	B	167	GLN
1	B	168	LEU
1	B	170	ASP
1	B	171	LYS
1	B	173	ILE
1	B	210	LYS
1	B	211	GLN
1	B	215	LYS
1	B	217	LYS
1	B	220	ASP
1	B	222	MET
1	B	224	LEU
1	B	235	ASN
1	B	238	GLU
1	B	240	LYS
1	B	241	GLN
1	B	250	HIS
1	B	258	ILE
1	B	264	ARG

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Mol	Chain	Res	Type
1	B	266	GLU
1	B	268	SER
1	B	273	SER
1	B	279	ARG
1	B	282	LEU
1	B	284	LEU
1	B	289	THR
1	B	291	SER
1	B	292	THR
1	B	296	MET
1	B	300	ASP
1	B	311	GLN
1	B	312	ILE
1	B	314	LYS
1	B	316	SER
1	B	326	LEU
1	B	328	ILE
1	B	333	GLN
1	B	337	THR
1	B	342	ARG
1	B	343	ILE
1	B	344	LEU
1	B	346	GLU
1	B	348	ASN
1	B	350	SER
1	B	352	THR
1	B	356	LYS
1	B	358	LEU
1	B	371	SER
1	B	373	ILE
1	B	374	LYS
1	B	375	ARG
1	B	378	GLU
1	B	382	GLN
1	B	383	VAL
1	B	387	THR
1	B	388	GLU
1	B	389	ASN
1	B	393	ARG
1	B	394	ARG
1	B	397	THR
1	B	401	ARG

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Mol	Chain	Res	Type
1	B	402	LEU
1	B	413	LEU
1	B	418	ILE
1	B	427	LYS
1	B	429	LEU
1	B	433	VAL
1	B	438	LEU
1	B	439	SER
1	B	440	ARG
1	B	442	ILE
1	B	443	LEU
1	C	2	SER
1	C	3	GLU
1	C	4	MET
1	C	5	THR
1	C	7	ARG
1	C	14	ASP
1	C	26	SER
1	C	27	VAL
1	C	31	LEU
1	C	32	ARG
1	C	34	ARG
1	C	36	ARG
1	C	37	ARG
1	C	38	MET
1	C	41	ASN
1	C	42	GLU
1	C	44	LEU
1	C	49	THR
1	C	51	LYS
1	C	54	LEU
1	C	61	VAL
1	C	68	ARG
1	C	70	LEU
1	C	72	LYS
1	C	73	LEU
1	C	80	LYS
1	C	81	VAL
1	C	84	THR
1	C	85	LYS
1	C	88	GLU
1	C	94	LYS

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Mol	Chain	Res	Type
1	C	97	ASP
1	C	109	LYS
1	C	112	ARG
1	C	118	LYS
1	C	119	ASN
1	C	120	ARG
1	C	121	TYR
1	C	125	GLU
1	C	128	GLU
1	C	130	ARG
1	C	135	LEU
1	C	140	LYS
1	C	142	ASN
1	C	146	THR
1	C	147	GLU
1	C	148	GLN
1	C	149	GLN
1	C	150	GLN
1	C	156	ARG
1	C	157	GLN
1	C	159	PHE
1	C	160	ARG
1	C	161	LYS
1	C	164	ARG
1	C	165	GLU
1	C	167	GLN
1	C	168	LEU
1	C	169	ASP
1	C	171	LYS
1	C	173	ILE
1	C	174	GLU
1	C	210	LYS
1	C	212	LYS
1	C	215	LYS
1	C	216	LEU
1	C	217	LYS
1	C	219	LYS
1	C	224	LEU
1	C	226	ILE
1	C	233	LEU
1	C	239	LEU
1	C	247	VAL

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Mol	Chain	Res	Type
1	C	249	GLN
1	C	255	ILE
1	C	257	GLU
1	C	261	ILE
1	C	263	LYS
1	C	264	ARG
1	C	266	GLU
1	C	267	SER
1	C	271	ASP
1	C	282	LEU
1	C	284	LEU
1	C	285	VAL
1	C	286	GLU
1	C	289	THR
1	C	290	VAL
1	C	297	VAL
1	C	301	HIS
1	C	303	LEU
1	C	305	ILE
1	C	310	PHE
1	C	311	GLN
1	C	312	ILE
1	C	314	LYS
1	C	319	ILE
1	C	325	ARG
1	C	329	ARG
1	C	332	LEU
1	C	333	GLN
1	C	335	LEU
1	C	336	THR
1	C	337	THR
1	C	350	SER
1	C	351	ILE
1	C	356	LYS
1	C	358	LEU
1	C	359	MET
1	C	364	VAL
1	C	366	ILE
1	C	367	GLU
1	C	369	THR
1	C	370	ASP
1	C	371	SER

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Mol	Chain	Res	Type
1	C	374	LYS
1	C	375	ARG
1	C	394	ARG
1	C	401	ARG
1	C	407	SER
1	C	412	ASP
1	C	416	GLN
1	C	417	ASN
1	C	418	ILE
1	C	421	ASP
1	C	425	VAL
1	C	435	ASP
1	C	437	ASP
1	C	442	ILE
1	D	2	SER
1	D	5	THR
1	D	11	SER
1	D	16	HIS
1	D	18	ILE
1	D	20	GLN
1	D	22	ASN
1	D	24	LYS
1	D	25	ARG
1	D	34	ARG
1	D	37	ARG
1	D	38	MET
1	D	39	GLN
1	D	42	GLU
1	D	43	GLU
1	D	44	LEU
1	D	47	GLU
1	D	48	VAL
1	D	49	THR
1	D	63	LYS
1	D	64	THR
1	D	73	LEU
1	D	82	GLU
1	D	84	THR
1	D	88	GLU
1	D	92	VAL
1	D	96	VAL
1	D	103	LEU

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Mol	Chain	Res	Type
1	D	104	THR
1	D	109	LYS
1	D	110	MET
1	D	121	TYR
1	D	122	ARG
1	D	124	GLU
1	D	125	GLU
1	D	130	ARG
1	D	135	LEU
1	D	142	ASN
1	D	145	GLN
1	D	146	THR
1	D	147	GLU
1	D	148	GLN
1	D	149	GLN
1	D	156	ARG
1	D	157	GLN
1	D	161	LYS
1	D	162	LYS
1	D	163	LEU
1	D	165	GLU
1	D	167	GLN
1	D	168	LEU
1	D	169	ASP
1	D	170	ASP
1	D	171	LYS
1	D	210	LYS
1	D	211	GLN
1	D	215	LYS
1	D	217	LYS
1	D	219	LYS
1	D	220	ASP
1	D	224	LEU
1	D	225	LEU
1	D	235	ASN
1	D	238	GLU
1	D	240	LYS
1	D	260	LYS
1	D	264	ARG
1	D	266	GLU
1	D	268	SER
1	D	271	ASP

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Mol	Chain	Res	Type
1	D	279	ARG
1	D	282	LEU
1	D	284	LEU
1	D	289	THR
1	D	291	SER
1	D	296	MET
1	D	300	ASP
1	D	311	GLN
1	D	312	ILE
1	D	314	LYS
1	D	316	SER
1	D	326	LEU
1	D	328	ILE
1	D	333	GLN
1	D	337	THR
1	D	342	ARG
1	D	343	ILE
1	D	344	LEU
1	D	346	GLU
1	D	348	ASN
1	D	350	SER
1	D	352	THR
1	D	356	LYS
1	D	358	LEU
1	D	369	THR
1	D	371	SER
1	D	373	ILE
1	D	375	ARG
1	D	378	GLU
1	D	382	GLN
1	D	383	VAL
1	D	387	THR
1	D	388	GLU
1	D	393	ARG
1	D	394	ARG
1	D	397	THR
1	D	401	ARG
1	D	402	LEU
1	D	413	LEU
1	D	418	ILE
1	D	427	LYS
1	D	429	LEU

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Mol	Chain	Res	Type
1	D	433	VAL
1	D	438	LEU
1	D	439	SER
1	D	440	ARG
1	D	442	ILE
1	D	443	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	GLN
1	A	75	ASN
1	A	119	ASN
1	A	149	GLN
1	A	249	GLN
1	A	294	HIS
1	A	323	GLN
1	A	348	ASN
1	A	354	GLN
1	A	384	ASN
1	A	396	HIS
1	A	417	ASN
1	B	16	HIS
1	B	22	ASN
1	B	33	ASN
1	B	235	ASN
1	B	323	GLN
1	B	382	GLN
1	B	384	ASN
1	B	417	ASN
1	C	39	GLN
1	C	75	ASN
1	C	119	ASN
1	C	149	GLN
1	C	294	HIS
1	C	384	ASN
1	C	396	HIS
1	C	417	ASN
1	D	16	HIS
1	D	22	ASN
1	D	33	ASN
1	D	41	ASN

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Mol	Chain	Res	Type
1	D	46	HIS
1	D	235	ASN
1	D	323	GLN
1	D	382	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](#)

2 ligands are modelled in this entry.

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	ANP	A	900	-	29,33,33	1.34	4 (13%)	28,52,52	1.54	2 (7%)
2	ANP	C	905	-	29,33,33	1.31	4 (13%)	28,52,52	1.53	2 (7%)

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	ANP	A	900	-	-	0/13/38/38	0/3/3/3
2	ANP	C	905	-	-	0/13/38/38	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	900	ANP	PG-O2G	-2.53	1.49	1.56
2	C	905	ANP	PG-O2G	-2.52	1.49	1.56
2	A	900	ANP	PB-O2B	-2.30	1.50	1.56
2	C	905	ANP	PB-O2B	-2.29	1.50	1.56
2	A	900	ANP	PB-O1B	2.75	1.49	1.46
2	C	905	ANP	PB-O1B	3.32	1.49	1.46
2	C	905	ANP	PG-O1G	3.65	1.50	1.46
2	A	900	ANP	PG-O1G	3.96	1.50	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	900	ANP	O1G-PG-N3B	-4.17	105.55	111.79
2	C	905	ANP	O1G-PG-N3B	-4.13	105.61	111.79
2	C	905	ANP	O2B-PB-O1B	4.94	120.14	109.87
2	A	900	ANP	O2B-PB-O1B	4.94	120.14	109.87

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	900	ANP	9	0
2	C	905	ANP	11	0

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.